**Supplemantary Table 5: Manually curated description of all the differentially expressed genes (DEGs) for all the group comarisons (DEX vs. CTR and DEX-CLEN vs. CTR)**

| DEGs (DEX vs. CTR), FDR 0-5% | | | | | |
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| **Glucocorticoid/DEX related genes** | | | | | |
| **Gene** | **ENTREZ ID** | **Gene Full Name** | **FC *** | **NCBI** | **Gene Card** |
| **CYP1A1** | 282870 | **cytochrome P450, subfamily I** (aromatic compound-inducible), polypeptide 1 | -10.41 | http://www.ncbi.nlm.nih.gov/gene/?term=282870 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=CYP1A1&search=282870 |
| **FKBP5** | 535704 | FK506 binding protein 5 | -8.65 | he protein encoded by this gene is a member of the immunophilin protein family, which play a role in immunoregulation and basic cellular processes involving protein folding and trafficking. This encoded protein is a cis-trans prolyl isomerase that binds to the immunosuppressants FK506 and rapamycin. It is thought to mediate calcineurin inhibition. It also interacts functionally with mature hetero-oligomeric progesterone receptor complexes along with the 90 kDa heat shock protein and P23 protein. | FKBP5 (FK506 binding protein 5) is a protein-coding gene. Diseases associated with FKBP5 include major depressive disorder, and **glucocorticoid resistance**, and among its related super-pathways are Development Endothelin-1/EDNRA signaling and Integrated Cancer pathway. GO annotations related to this gene include FK506 binding and heat shock protein binding |
| **LYVE1** | 404179 | lymphatic vessel endothelial hyaluronan receptor 1 | -5.74 | http://www.ncbi.nlm.nih.gov/gene/?term=404179 | LYVE1 (lymphatic vessel endothelial hyaluronan receptor 1) is a protein-coding gene. Diseases associated with LYVE1 include androgen insensitivity syndrome, partial, and complete androgen insensitivity syndrome, and among its related super-pathways are Metabolism of carbohydrates and Hyaluronan metabolism. GO annotations related to this gene include hyaluronic acid binding and receptor activity |

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| **CCL24** | 617258 | chemokine (C-C motif) ligand 24 | -5.14 | This gene belongs to the subfamily of small cytokine CC genes. Cytokines are a family of secreted proteins involved in immunoregulatory and inflammatory processes. The CC cytokines are proteins characterized by two adjacent cysteines. The cytokine encoded by this gene displays chemotactic activity on resting T lymphocytes, a minimal activity on neutrophils, and is negative on monocytes and activated T lymphocytes. The protein is also a strong suppressor of colony formation by a multipotential hematopoietic progenitor cell line | CCL24 (chemokine (C-C motif) ligand 24) is a protein-coding gene. Diseases associated with CCL24 include papillary conjunctivitis, and giant papillary conjunctivitis, and among its related super-pathways are MIF Mediated **Glucocorticoid Regulation** and Chemokine signaling pathway. GO annotations related to this gene include chemokine activity |
| **RASD1** | 507449 | RAS, dexamethasone-induced 1 | -4.75 | This gene may play a role in dexamethasone-induced alterations in cell morphology, growth and cell extracellular matrix interactions. Epigenetic inactivation of this gene is closely correlated with resistance to dexamethasone in multiple myeloma cells. Alternatively spliced transcript variants encoding different isoforms have been found for this gene | http://www.genecards.org/cgi-bin/carddisp.pl?gene=RASD1&search=507449 |
| **MYOC** | 281342 | myocilin, trabecular meshwork inducible **glucocorticoid response** | -4.44 | MYOC encodes the protein myocilin, which is believed to have a role in cytoskeletal function. MYOC is expressed in many occular tissues, including the trabecular meshwork, and was revealed to be the trabecular meshwork glucocorticoid-inducible response protein (TIGR) | MYOC (myocilin, trabecular meshwork inducible **glucocorticoid response**) is a protein-coding gene. Diseases associated with MYOC include open-angle glaucoma, and ocular hypertension |
| **PFKFB4** | 534928 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 | -4.37 | http://www.ncbi.nlm.nih.gov/gene/?term=534928 | PFKFB4 (6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4) is a protein-coding gene. Diseases associated with PFKFB4 include hypoxia, and pancreatic cancer, and among its related super-pathways are Gluconeogenesis and p38 Signaling |
| **MEDAG** | 510187 | mesenteric estrogen-dependent adipogenesis | -3.28 | http://www.ncbi.nlm.nih.gov/gene/?term=510187 | Involved in processes that promote adipocyte differentiation, lipid accumulation, and glucose uptake in mature adipocytes |
| **SULT1A1** | 282485 | Sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1 | -2.54 | ulfotransferase enzymes catalyze the sulfate conjugation of many hormones, neurotransmitters, drugs, and xenobiotic compounds. This gene encodes one of two phenol sulfotransferases with thermostable enzyme activity | Diseases associated with SULT1A1 include batten disease, and familial prostate cancer, and among its related super-pathways are Tamoxifen Pathway, Pharmacokinetics and Phase II conjugation |

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| **ICAM1** | 281839 | intercellular adhesion molecule 1 | -2.78 | This gene encodes a cell surface glycoprotein which is typically expressed on endothelial cells and cells of the immune system. It binds to integrins of type CD11a / CD18, or CD11b / CD18 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ICAM1&search=281839 |
| **Coagulation/Heparin related genes** | | | | | |
| **LIPG** | 509808 | Bos taurus endothelial lipase-like | -14.76 | The protein encoded by this gene has substantial phospholipase activity and may be involved in lipoprotein metabolism and vascular biology. This protein is designated a member of the TG lipase family by its sequence and characteristic lid region which provides substrate specificity for enzymes of the TG lipase family | LIPG (lipase, endothelial) is a protein-coding gene. Diseases associated with LIPG include endotheliitis, and cardiovascular disease risk factor ), and among its related super-pathways are Metabolism. GO annotations related to this gene include retinyl-palmitate esterase activity and **heparin binding** |
| **CRISPLD2** | 505329 | cysteine-rich secretory protein LCCL domain containing 2 | -7.07 | http://www.ncbi.nlm.nih.gov/gene/?term=505329 | CRISPLD2 (cysteine-rich secretory protein LCCL domain containing 2) is a protein-coding gene. Diseases associated with CRISPLD2 include cleft lip, and cleft palate. GO annotations related to this gene include **heparin binding** |
| **C1QC** | 509968 | complement component 1, q subcomponent, C chain | -3.66 | http://www.ncbi.nlm.nih.gov/gene/?term=509968 | Diseases associated with C1QC include chronic wasting disease, and glomerulonephritis, and among its related super-pathways are Complement and Coagulation Cascades and Immune response Lectin induced complement pathway |
| **C1QA** | 534961 | complement component 1, q subcomponent, A chain | -3.6 | http://www.ncbi.nlm.nih.gov/gene/?term=534961 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=C1QA&search=534961 |
| **FGL2** | 511711 | fibrinogen-like 2 | -3.16 | The protein encoded by this gene is a secreted protein that is similar to the beta- and gamma-chains of fibrinogen. The carboxyl-terminus of the encoded protein consists of the fibrinogen-related domains (FRED). The encoded protein forms a tetrameric complex which is stabilized by interchain disulfide bonds. This protein may play a role in physiologic functions at mucosal sites | Diseases associated with FGL2 include severe acute respiratory syndrome, and acute liver failure. GO annotations related to this gene include receptor binding |
| **CCDC80** | 515235 | coiled-coil domain containing 80 | -2.53 | http://www.ncbi.nlm.nih.gov/gene/?term=515235 | Diseases associated with CCDC80 include obesity, and pancreatic cancer. GO annotations related to this gene include **heparin binding and fibronectin binding** |

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| **HS3ST1** | 538691 | heparan sulfate (glucosamine) 3-O-sulfotransferase 1 | -2.53 | The enzyme encoded by this gene is a member of the heparan sulfate biosynthetic enzyme family. It possesses both **heparan sulfate** glucosaminyl 3-O-sulfotransferase activity, anticoagulant heparan sulfate conversion activity, and is a rate limiting enzyme for synthesis of anticoagulant heparan | Sulfotransferase that utilizes 3'-phospho-5'-adenylyl sulfate (PAPS) to catalyze the transfer of a sulfo group to position 3 of glucosamine residues in heparan. Catalyzes the rate limiting step in the biosynthesis of **heparan sulfate** (HSact). This modification is a crucial step in the biosynthesis of anticoagulant heparan sulfate as it completes the structure of the antithrombin pentasaccharide binding site |
| **C7** | 507339 | complement component 7 | -2.54 | C7 is a component of the complement system. It participates in the formation of Membrane Attack Complex (MAC). People with C7 deficiency are prone to bacterial infection | Diseases associated with C7 include c7 deficiency, and meningococcal infection, and among its related super-pathways are Immune response Lectin induced complement pathway and Complement Pathway |
| **Skeletal Muscle/Collagen/Lipid Metabolism related genes** | | | | | |
| **PTGES** | 282019 | Prostaglandin E synthase | **3.80** | Knockout studies in mice suggest that this gene may contribute to the pathogenesis of **collagen**-induced arthritis and mediate acute pain during inflammatory responses | Diseases associated with PTGES include pleurisy, and patent ductus arteriosus, and among its related super-pathways are Metabolic pathways and Arachidonic acid metabolism. GO annotations related to this gene include prostaglandin-E synthase activity and glutathione binding |
| **MMP2** | 282872 | Matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) | **2.58** | This gene encodes an enzyme which degrades type IV **collagen,** the major structural component of basement membranes. The enzyme plays a role in endometrial menstrual breakdown, regulation of vascularization and the inflammatory response | Dysregulatoin of MMPs has been implicated in many diseases including arthritis, chronic ulcers, encephalomyelitis and cancer. Tumour metastasis is a multistep process involving the dessemination of tumor cells from the primary tumor to secondarys at a distant organ or tissue |
| **OTHERS** | | | | | |
| **ABCA9** | 504278 | ATP-binding cassette, sub-family A (ABC1), member 9 | -3.49 | http://www.ncbi.nlm.nih.gov/gene/?term=504278 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ABCA9&search=504278 |
| **CD3E** | 281054 | CD3e molecule, epsilon (CD3-TCR complex) | -3.42 | http://www.ncbi.nlm.nih.gov/gene/?term=281054 | Diseases associated with CD3E include cd3epsilon deficiency, and hemometra, and among its related super-pathways are T cell receptor signaling pathway and Immune response IL-12-induced IFN-gamma production |
| **ANGPTL5** | 514285 | Angiopoietin-like 5 | -3.41 | http://www.ncbi.nlm.nih.gov/gene/?term=514285 | ANGPTL5 (angiopoietin-like 5) is a protein-coding gene. Diseases associated with ANGPTL5 include keratoconus. GO annotations related to this gene include receptor binding |

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| **AGTR1** | 281607 | Angiotensin II receptor, type 1 | -4.98 | Angiotensin II is a potent vasopressor hormone and a primary regulator of aldosterone secretion. It is an important effector controlling blood pressure and volume in the cardiovascular system. It acts through at least two types of receptors. | http://www.genecards.org/cgi-bin/carddisp.pl?gene=AGTR1&search=281607 |
| **ENPP1** | 615535 | Ectonucleotide pyrophosphatase/phosphodiesterase 1 | -2.97 | http://www.ncbi.nlm.nih.gov/gene/?term=615535 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ENPP1&search=615535 |
| **MGP** | 282660 | matrix Gla protein | -6.66 | The protein encoded by this gene is secreted and likely acts as an inhibitor of bone formation. The encoded protein is found in the organic matrix of bone and cartilage. Defects in this gene are a cause of Keutel syndrome (KS) | MGP (matrix Gla protein) is a protein-coding gene. Diseases associated with MGP include keutel syndrome, and acute apical periodontitis, and among its related super-pathways are Gamma-carboxylation, transport, and amino-terminal cleavage of proteins. GO annotations related to this gene include structural constituent of bone and calcium ion binding. |
| **CTSW** | 510967 | cathepsin W | -6.35 | http://www.ncbi.nlm.nih.gov/gene/?term=510967 | CTSW (cathepsin W) is a protein-coding gene. Diseases associated with CTSW include autoimmune atrophic gastritis, and atrophic gastritis. GO annotations related to this gene include cysteine-type peptidase activity |
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| **HPCAL1** | 513870 | Hippocalcin-like 1 | -2.48 | The protein encoded by this gene is a member of neuron-specific calcium-binding proteins family found in the retina and brain. May be involved in the calcium-dependent regulation of rhodopsin phosphorylation | Diseases associated with HPCAL1 include neuronitis, and hypertension. GO annotations related to this gene include calcium ion binding. |
| **EPS8** | 538419 | Epidermal growth factor receptor pathway substrate 8 | -2.19 | Acts as a direct regulator of actin dynamics by binding actin filaments and has both barbed-end actin filament capping and actin bundling activities depending on the context. | ignaling adapter that controls various cellular protrusions by regulating actin cytoskeleton dynamics and architecture |
| **RND3** | 540224 | Rho family GTPase 3 | -2.17 | http://www.ncbi.nlm.nih.gov/gene/?term=540224 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=RND3&search=RND3 |
| **GPCPD1** | 518469 | Glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae) | -2.38 | http://www.ncbi.nlm.nih.gov/gene/?term=518469 | May be involved in the negative regulation of **skeletal muscle differentiation**, independently of its glycerophosphocholine phosphodiesterase activity |
| **DDR2** | 533523 | Discoidin domain receptor tyrosine kinase 2 | -2.05 | http://www.ncbi.nlm.nih.gov/gene/?term=533523 | functions as cell surface receptor for **fibrillar collagen** and regulates cell differentiation, remodeling of the extracellular matrix, cell migration and cell proliferation. Required for normal bone development. Regulates osteoblast differentiation and chondrocyte maturation. Regulates remodeling of the extracellular matrix by up-regulation of the collagenases MMP1, **MMP2** and MMP13 |

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| **CCND3** | 540547 | Cyclin D3 | -2.17 | http://www.ncbi.nlm.nih.gov/gene/?term=540547 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=CCND3&search=540547 |
| **FZD4** | 445416 | Frizzled family receptor 4 | -2.37 | This protein may play a role as a positive regulator of the Wingless type MMTV integration site signaling pathway | May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues |
| **ITIH5** | 534787 | Inter-alpha-trypsin inhibitor heavy chain family, member 5 | -2.03 | http://www.ncbi.nlm.nih.gov/gene/?term=534787 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ITIH5&search=534787 |
| **SLAMF1** | 281489 | signaling lymphocytic activation molecule family member 1 | -4.93 | http://www.ncbi.nlm.nih.gov/gene/?term=281489 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=SLAMF1&search=281489 |
| **HPGD** | 512259 | hydroxyprostaglandin dehydrogenase 15-(NAD) | -4.88 | http://www.ncbi.nlm.nih.gov/gene/?term=512259 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=HPGD&search=512259 |
| **CD163** | 533844 | CD163 molecule | -4.8 | The protein encoded by this gene is a member of the scavenger receptor cysteine-rich (SRCR) superfamily, and is exclusively expressed in monocytes and macrophages. It functions as an acute phase-regulated receptor involved in the clearance and endocytosis of hemoglobin/haptoglobin complexes by macrophages, and may thereby protect tissues from free hemoglobin-mediated oxidative damage. This protein may also function as an innate immune sensor for bacteria and inducer of local inflammation. | http://www.genecards.org/cgi-bin/carddisp.pl?gene=CD163&search=533844 |
| **CPXM1** | 532219 | carboxypeptidase X (M14 family), member 1 | -4.71 | http://www.ncbi.nlm.nih.gov/gene/?term=532219 | CPXM1 (carboxypeptidase X (M14 family), member 1) is a protein-coding gene. Diseases associated with CPXM1 include lymphedema. GO annotations related to this gene include metallocarboxypeptidase activity and zinc ion binding |
| **CST7** | 617799 | cystatin F (leukocystatin) | -4.7 | http://www.ncbi.nlm.nih.gov/gene/?term=617799 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=CST7&search=617799 |
| **DKK1** | 504445 | dickkopf homolog 1 (Xenopus laevis) | -4.59 | http://www.ncbi.nlm.nih.gov/gene/?term=504445 | DKK1 (dickkopf WNT signaling pathway inhibitor 1) is a protein-coding gene. Diseases associated with DKK1 include myeloma, and multiple myeloma |
| **ABCA10** | 504909 | ATP-binding cassette, sub-family A (ABC1), member 10 | -4.54 | http://www.ncbi.nlm.nih.gov/gene/?term=504909 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ABCA10&search=504909 |
| **TRGC6** | 535300 | T-cell receptor gamma chain TRGC6 | -4.51 | http://www.ncbi.nlm.nih.gov/gene/?term=535300 | ///// |
| **ARRDC2** | 523285 | arrestin domain containing 2 | -4.4 | http://www.ncbi.nlm.nih.gov/gene/?term=523285 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ARRDC2&search=523285 |
| **EIF4B** | 505850 | eukaryotic translation initiation factor 4B | -4.34 | http://www.ncbi.nlm.nih.gov/gene/?term=505850 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=EIF4B&search=505850 |

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| **NFKBIA** | 282291 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha | -4.26 | http://www.ncbi.nlm.nih.gov/gene/?term=282291 | Diseases associated with NFKBIA include ectodermal dysplasia, anhidrotic, with t-cell immunodeficiency, and autosomal dominant disease, and among its related super-pathways are DR3 Signaling and RANK Signaling in Osteoclasts |
| **NTRK2** | 505824 | neurotrophic tyrosine kinase, receptor, type 2 | -4.04 | http://www.ncbi.nlm.nih.gov/gene/?term=505824 | Diseases associated with NTRK2 include obesity hyperphagia and developmental delay, and mood disorder, and among its related super-pathways are Development Neurotrophin family signaling and Rac1 Pathway |
| **ARMC12** | 540812 | armadillo repeat containing 12 | -3.99 | http://www.ncbi.nlm.nih.gov/gene/?term=540812 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ARMC12&search=540812 |
| **PER1** | 516318 | period circadian clock 1 | -3.95 | This gene is a member of the Period family of genes and is expressed in a circadian pattern in the suprachiasmatic nucleus, the primary circadian pacemaker in the mammalian brain. Genes in this family encode components of the circadian rhythms of locomotor activity, metabolism, and behavior. Circadian expression in the suprachiasmatic nucleus continues in constant darkness, and a shift in the light/dark cycle evokes a proportional shift of gene expression in the suprachiasmatic nucleus. The specific function of this gene is not yet known | PER1 (period circadian clock 1) is a protein-coding gene. Diseases associated with PER1 include advanced sleep phase syndrome, and delayed sleep phase syndrome, and among its related super-pathways are Circadian Clock and Retrograde endocannabinoid signaling |
| **SLC11A1** | 282470 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 | -3.42 | http://www.ncbi.nlm.nih.gov/gene/?term=282470 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=SLC11A1&search=282470 |
| **PRF1** | 369025 | perforin 1 (pore forming protein) | -3.31 | http://www.ncbi.nlm.nih.gov/gene/?term=369025 | This protein is one of the main cytolytic proteins of cytolytic granules, and it is known to be a key effector molecule for T-cell- and natural killer-cell-mediated cytolysis. Defects in this gene cause familial hemophagocytic lymphohistiocytosis type 2 |
| **CD69** | 281058 | CD69 molecule | -3.31 | This gene encodes a member of the calcium dependent lectin superfamily of type II transmembrane receptors. Expression of the encoded protein is induced upon activation of T lymphocytes, and may play a role in proliferation. Furthermore, the protein may act to transmit signals in natural killer cells and platelets. | iseases associated with CD69 include intermediate uveitis, and coccidioidomycosis. GO annotations related to this gene include transmembrane signaling receptor activity and carbohydrate binding |
| **C1QTNF1** | 511774 | C1q and tumor necrosis factor related protein 1 | -3.17 | http://www.ncbi.nlm.nih.gov/gene/?term=511774 | C1QTNF1 (C1q and tumor necrosis factor related protein 1) is a protein-coding gene. Diseases associated with C1QTNF1 include macular degeneration, and age related macular degeneration |

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| **ALDH1A2** | 535075 | aldehyde dehydrogenase 1 family, member A2 | -3.14 | http://www.ncbi.nlm.nih.gov/gene/?term=535075 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ALDH1A2&search=535075 |
| **OAF** | 514557 | OAF homolog (Drosophila) | -3.09 | http://www.ncbi.nlm.nih.gov/gene/?term=514557 | Diseases associated with OAF include glottis carcinoma, and hypercalcemia |
| **LRAT** | 281285 | lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase) | -3.05 | http://www.ncbi.nlm.nih.gov/gene/?term=281285 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=LRAT&search=281285 |
| **FAM105A** | 534389 | family with sequence similarity 105, member A | -3.04 | http://www.ncbi.nlm.nih.gov/gene/?term=534389 | Diseases associated with FAM105A include amenorrhea |
| **E2F2** | 617024 | E2F transcription factor 2 | -3.02 | http://www.ncbi.nlm.nih.gov/gene/?term=617024 | Diseases associated with E2F2 include thymic epithelial tumor, and lynch syndrome, and among its related super-pathways are Cyclins and Cell Cycle Regulation and Cell cycle |
| **PLXDC1** | 536989 | plexin domain containing 1 | -2.99 | http://www.ncbi.nlm.nih.gov/gene/?term=536989 | Diseases associated with PLXDC1 include endotheliitis, and proliferative diabetic retinopathy. GO annotations related to this gene include protein binding |
| **TRD@** | 407199 | T-cell receptor delta chain | -2.94 | //// | //// |
| **PABPC5-like** | 511286 | polyadenylate-binding protein 5-like | -2.92 | http://www.ncbi.nlm.nih.gov/gene/?term=511286 | Diseases associated with PABPC5 include premature ovarian failure, and among its related super-pathways are Deadenylation-dependent mRNA decay |
| **SNAI2** | 520631 | snail homolog 2 (Drosophila) | -2.85 | http://www.ncbi.nlm.nih.gov/gene/?term=520631 | This protein is involved in epithelial-mesenchymal transitions and has antiapoptotic activity |
| **SORL1** | 533166 | sortilin-related receptor, L(DLR class) A repeats containing | -2.81 | http://www.ncbi.nlm.nih.gov/gene/?term=533166 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=SORL1&search=533166 |
| **C1QTNF9** | 523616 | C1q and tumor necrosis factor related protein 9 | -2.78 | http://www.ncbi.nlm.nih.gov/gene/?term=523616 | GO annotations related to this gene include hormone activity |
| **RECK** | 517232 | reversion-inducing-cysteine-rich protein with kazal motifs | -2.77 | http://www.ncbi.nlm.nih.gov/gene/?term=517232 | In normal cells, this membrane-anchored glycoprotein may serve as a negative regulator for matrix metalloproteinase-9, a key enzyme involved in tumor invasion and metastasis |
| **TDRD6** | 512705 | tudor domain containing 6 | -2.74 | http://www.ncbi.nlm.nih.gov/gene/?term=512705 | Involved in spermiogenesis, chromatoid body formation. Diseases associated with TDRD6 include autoimmune polyendocrine syndrome type 1, and autoimmune polyendocrine syndrome |
| **OLFML2B** | 513053 | olfactomedin-like 2B | -2.7 | http://www.ncbi.nlm.nih.gov/gene/?term=513053 | iseases associated with OLFML2B include atherosclerosis. GO annotations related to this gene include extracellular matrix binding |
| **PNP** | 493724 | purine nucleoside phosphorylase | -2.69 | http://www.ncbi.nlm.nih.gov/gene/?term=493724 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=PNP&search=493724 |
| **AOX1** | 338074 | aldehyde oxidase 1 | -2.69 | http://www.ncbi.nlm.nih.gov/gene/?term=529661 | |
| **TSKU** | 529661 | tsukushi small leucine rich proteoglycan homolog (Xenopus laevis) | -2.66 | http://www.ncbi.nlm.nih.gov/gene/?term=529661 | Diseases associated with TSKU include systemic scleroderma, and fibromyalgia |

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| **LOC509044** | 509044 | E2F transcription factor 6 pseudogene | -2.64 | http://www.ncbi.nlm.nih.gov/gene/?term=509044 | //// |
| **EHMT2** | 514062 | euchromatic histone-lysine N-methyltransferase 2 | -2.55 | The protein encoded by this gene is thought to be involved in intracellular protein-protein interaction. | Histone methyltransferases (HMTs) are a group of enyzmes that catalyze the transfer of methyl groups from S-adenosylmethionine (SAM) to histones and are closely related in biological activity to the DNA methyltransferases |
| **GPR116** | 532674 | G protein-coupled receptor 116 | -2.55 | http://www.ncbi.nlm.nih.gov/gene/?term=532674 | GO annotations related to this gene include G-protein coupled receptor activity |
| **FZD1** | 445417 | frizzled family receptor 1 | -2.54 | http://www.ncbi.nlm.nih.gov/gene/?term=445417 | GO annotations related to this gene include PDZ domain binding and G-protein coupled receptor activity |
| **KLF9** | 539139 | Kruppel-like factor 9 | -2.52 | The protein encoded by this gene is a transcription factor that binds to GC box elements located in the promoter. Binding of the encoded protein to a single GC box inhibits mRNA expression while binding to tandemly repeated GC box elements activates transcription | GO annotations related to this gene include DNA binding and sequence-specific DNA binding transcription factor activity |
| **NUMBL** | 510973 | numb homolog (Drosophila)-like | -2.48 | http://www.ncbi.nlm.nih.gov/gene/?term=510973 | GO annotations related to this gene include protein binding |
| **PCDHA13** | 523226 | protocadherin alpha 13 | -2.48 | This gene is a member of the protocadherin alpha gene cluster, one of three related gene clusters tandemly linked on chromosome five that demonstrate an unusual genomic organization similar to that of B-cell and T-cell receptor gene clusters | Diseases associated with PCDHA13 include neuronitis. GO annotations related to this gene include calcium ion binding |
| **GCNT1** | 281778 | glucosaminyl (N-acetyl) transferase 1, core 2 | -2.47 | This gene is a member of the beta-1,6-N-acetylglucosaminyltransferase gene family | Forms critical branches in O-glycans |
| **GLT8D2** | 523294 | glycosyltransferase 8 domain containing 2 | -2.46 | http://www.ncbi.nlm.nih.gov/gene/?term=523294 | GO annotations related to this gene include transferase activity, transferring glycosyl groups |
| **COL6A3** | 530657 | **collagen,** type VI, alpha 3 | -2.43 | This gene encodes the alpha-3 chain, one of the three alpha chains of type VI **collagen,** a beaded filament collagen found in most connective tissues | **Collagen** VI acts as a cell-binding protein |
| **GPC3** | 615239 | glypican 3 | -2.42 | Cell surface heparan sulfate proteoglycans are composed of a membrane-associated protein core substituted with a variable number of **heparan sulfate chains**. | GO annotations related to this gene include peptidyl-dipeptidase inhibitor activity and **heparan sulfate** proteoglycan binding |
| **CD244** | 513468 | CD244 molecule, natural killer cell receptor 2B4 | -2.36 | http://www.ncbi.nlm.nih.gov/gene/?term=513468 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=CD244&search=513468 |
| **STAT4** | 515988 | signal transducer and activator of transcription 4 | -2.35 | his protein is essential for mediating responses to IL12 in lymphocytes, and regulating the differentiation of T helper cells | Carries out a dual function: signal transduction and activation of transcription. Involved in IL12 signaling |

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| **DCN** | 280760 | decorin | -2.35 | This protein is a component of connective tissue, binds to type I collagen fibrils, and plays a role in matrix assembly | May affect the rate of fibrils formation |
| **DDIT4** | 529235 | DNA-damage-inducible transcript 4 | -2.35 | http://www.ncbi.nlm.nih.gov/gene/?term=529235 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=DDIT4&search=529235 |
| **B3GNT8** | 534859 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8 | -2.32 | http://www.ncbi.nlm.nih.gov/gene/?term=534859 | Post-translational protein modification and Mucin type O-Glycan biosynthesis. GO annotations related to this gene include protein N-acetylglucosaminyltransferase activity and galactosyltransferase activity |
| **MFAP2** | 281912 | microfibrillar-associated protein 2 | -2.32 | Major antigen of elastin-associated microfibrils and a candidate for involvement in the etiology of inherited connective tissue diseases | Component of the elastin-associated microfibrils |
| **LOC614109** | 614109 | sodium/bile acid cotransporter 7-like | -2.27 | http://www.ncbi.nlm.nih.gov/gene/?term=614109 | //// |
| **GSN** | 535077 | gelsolin | -2.26 | The protein encoded by this gene binds to the 'plus' ends of actin monomers and filaments to prevent monomer exchange. The encoded calcium-regulated protein functions in both assembly and disassembly of actin filaments. | Regulation of actin cytoskeleton and Apoptotic cleavage of cellular proteins. GO annotations related to this gene include actin binding and calcium ion binding |
| **COLEC12** | 504741 | collectin sub-family member 12 | -2.25 | This gene encodes a member of the C-lectin family, proteins that possess **collagen-like sequences** and carbohydrate recognition domains. It can bind to carbohydrate antigens on microorganisms, facilitating their recognition and removal. | Scavenger receptor that displays several functions associated with host defense. Promotes binding and phagocytosis of Gram positive, Gram-negative bacteria and yeast. Mediates the recognition, internalization and degradation of oxidatively modified low density lipoprotein (oxLDL) by vascular endothelial cells |
| **DMBT1** | 404104 | deleted in malignant brain tumors 1 | -2.24 | http://www.ncbi.nlm.nih.gov/gene/?term=404104 | Associates with the actin cytoskeleton and is involved in its remodeling during regulated exocytosis |
| **ANKRD44** | 526800 | ankyrin repeat domain 44 | -2.24 | http://www.ncbi.nlm.nih.gov/gene/?term=526800 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ANKRD44&search=526800 |
| **LOXL4** | 281904 | lysyl oxidase-like 4 | -2.22 | The prototypic member of the family is essential to the biogenesis of connective tissue, encoding an extracellular copper-dependent amine oxidase that catalyses the first step in the formation of crosslinks in **collagens and elastin** | May modulate the formation of a **collagenous extracellular matrix** |
| **SH2D3A** | 510173 | SH2 domain containing 3A | -2.21 | http://www.ncbi.nlm.nih.gov/gene/?term=510173 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=SH2D3A&search=510173 |
| **PIK3R1** | 282307 | phosphoinositide-3-kinase, regulatory subunit 1 (alpha) | -2.2 | http://www.ncbi.nlm.nih.gov/gene/?term=282307 | GO annotations related to this gene include protein phosphatase binding and 1-phosphatidylinositol binding |
| **ROBO1** | 536815 | roundabout, axon guidance receptor, homolog 1 (Drosophila) | -2.18 | http://www.ncbi.nlm.nih.gov/gene/?term=536815 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ROBO1&search=536815 |
| **GIMAP7** | 614871 | GTPase, IMAP family member 7 | -2.17 | http://www.ncbi.nlm.nih.gov/gene/?term=614871 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=GIMAP7&search=GIMAP7 |

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| **ANKRD13A** | 511883 | ankyrin repeat domain 13A | -2.17 | http://www.ncbi.nlm.nih.gov/gene/?term=511883 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=ANKRD13A&search=511883 |
| **PTPN13** | 282333 | protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) | -2.16 | PTP is a large intracellular protein. It has a catalytic PTP domain at its C-terminus and two major structural domains: a region with five PDZ domains and a FERM domain that binds to plasma membrane and cytoskeletal elements | Diseases associated with PTPN13 include tropical spastic paraparesis. GO annotations related to this gene include protein binding and protein tyrosine phosphatase activity. |
| **TRPM2** | 508029 | transient receptor potential cation channel, subfamily M, member 2 | -2.14 | The protein encoded by this gene is a calcium-permeable cation channel that is regulated by free intracellular ADP-ribose. | Nonselective, voltage-independent cation channel mediating sodium and calcium ion influx in response to oxidative stress |
| **TACC1** | 507012 | transforming, acidic coiled-coil containing protein 1 | -2.13 | http://www.ncbi.nlm.nih.gov/gene/?term=507012 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=TACC1&search=507012 |
| **MYO10** | 281935 | myosin X | -2.13 | This gene functions as an actin-based molecular motor and plays a role in integration of F-actin and microtubule cytoskeletons during meiosis | MYO10 binds to actin filaments and actin bundles and functions as plus end-directed motor.Stimulates the formation and elongation of filopodia. May play a role in neurite outgrowth and axon guidance. Plays a role in formation of the podosome belt in osteoclasts |
| **HMCN2** | 534512 | hemicentin 2 | -2.13 | http://www.ncbi.nlm.nih.gov/gene/?term=534512 | GO annotations related to this gene include calcium ion binding |
| **SERPING1** | 281035 | serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 | -2.13 | This gene encodes a highly glycosylated plasma protein involved in the regulation of the complement cascade | May play a potentially crucial role in regulating important physiological pathways including complement activation, blood coagulation, fibrinolysis and the generation of kinins. Very efficient inhibitor of FXIIa. Inhibits chymotrypsin and kallikrein |
| **LOC616702** | 616702 | polyhomeotic-like protein 2-like (pseudo gene) | -2.12 | //// | //// |
| **MS4A8B** | 415111 | membrane-spanning 4-domains, subfamily A, member 8B | -2.12 | http://www.ncbi.nlm.nih.gov/gene/?term=415111 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=MS4A8&search=415111 |
| **ZFHX4** | 539762 | zinc finger homeobox 4 | -2.12 | http://www.ncbi.nlm.nih.gov/gene/?term=539762 | May play a role in neural and **muscle differentiation** (By similarity). May be involved in transcriptional regulation |
| **COL5A2** | 538590 | **collagen,** type V, alpha 2 | -2.11 | ype V collagen is found in tissues containing type I collagen and appears to regulate the assembly of heterotypic fibers composed of both type I and type V collagen | Type V collagen is a member of group I collagen (fibrillar forming collagen). It is a minor connective tissue component of nearly ubiquitous distribution. Type V collagen binds to DNA, **heparan sulfate**, thrombospondin, heparin, and insulin. Type V collagen is a key determinant in the assembly of tissue-specific matrices |
| **CYFIP2** | 518833 | cytoplasmic FMR1 interacting protein 2 | -2.1 | http://www.ncbi.nlm.nih.gov/gene/?term=518833 | Regulation of actin cytoskeleton and Regulation of actin dynamics for phagocytic cup formation. GO annotations related to this gene include protein binding |
| **EGFR** | 407217 | epidermal growth factor receptor | -2.09 | http://www.ncbi.nlm.nih.gov/gene/?term=407217 | Known ligands include EGF, TGFA/TGF-alpha, amphiregulin, epigen/EPGN, BTC/betacellulin, epiregulin/EREG and HBEGF/**heparin-binding EGF** |

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| **PTPN9** | 505220 | protein tyrosine phosphatase, non-receptor type 9 | -2.09 | http://www.ncbi.nlm.nih.gov/gene/?term=505220 | Protein-tyrosine phosphatase that could participate in the transfer of hydrophobic ligands or in functions of the Golgi apparatus |
| **CORO7** | 527934 | coronin 7 | -2.09 | http://www.ncbi.nlm.nih.gov/gene/?term=527934 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=CORO7&search=527934 |
| **KRT26** | 539216 | keratin 26 | -2.08 | http://www.ncbi.nlm.nih.gov/gene/?term=539216 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=KRT26&search=539216 |
| **ZNF404** | 505067 | zinc finger protein 404 | -2.08 | http://www.ncbi.nlm.nih.gov/gene/?term=505067 | May be involved in transcriptional regulation |
| **BMP6** | 617566 | bone morphogenetic protein 6 | -2.07 | BMPs were originally identified by an ability of demineralized bone extract to induce endochondral osteogenesis in vivo in an extraskeletal site | Induces cartilage and bone formation |
| **PRDM8** | 507890 | PR domain containing 8 | -2.06 | http://www.ncbi.nlm.nih.gov/gene/?term=507890 | GO annotations related to this gene include chromatin binding and histone methyltransferase activity (H3-K9 specific) |
| **KLF6** | 505884 | Kruppel-like factor 6 | -2.04 | http://www.ncbi.nlm.nih.gov/gene/?term=505884 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=KLF6&search=505884 |
| **GABARAPL1** | 338472 | GABA(A) receptor-associated protein like 1 | -2.03 | http://www.ncbi.nlm.nih.gov/gene/?term=338472 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=GABARAPL1&search=338472 |
| **LGALS4** | 614804 | lectin, galactoside-binding, soluble, 4 | -2 | http://www.ncbi.nlm.nih.gov/gene/?term=614804 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=LGALS4&search=614804 |

***Note** : Genes/Cells markerd with YELLOW color are markers suggested by IPA*

** FC = Fold change*

| DEGs (DEX-CLEN vs. CTR), FDR 0-5% | | | | | |
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| | | | | Gene Summary | |
| **Gene** | **ENTREZ ID** | **Gene Full Name** | **FC** | **NCBI** | **Gene Card** |
| **PSPH** | 533630 | phosphoserine phosphatase | 2.19 | Deficiency of this protein is thought to be linked to Williams syndrome | Catalyzes the last step in the biosynthesis of serine from carbohydrates. The reaction mechanism proceeds via the formation of a phosphoryl-enzyme intermediates |
| **HSPA8** | 281831 | heat shock 70kDa protein 8 | 2.11 | May have a role in **glucocorticoid signaling** and lipd metablism | Acts as a repressor of transcriptional activation |
| **LRRN1** | 539619 | leucine rich repeat neuronal 1 | 3.86 | http://www.ncbi.nlm.nih.gov/gene/?term=539619 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=LRRN1&search=539619 |
| **STIP1** | 617109 | stress-induced-phosphoprotein 1 | 2.55 | http://www.ncbi.nlm.nih.gov/gene/?term=617109 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=STIP1&search=617109 |
| **ADAMTS20** | 536137 | ADAM metallopeptidase with thrombospondin type 1 motif, 20 | 2.72 | This protein may be involved in tissue remodeling | May play a role in tissue-remodeling process occurring in both normal and pathological conditions |
| **CDHR2** | 511921 | cadherin-related family member 2 | 2.00 | Encode for non-classical cadherins that function as calcium-dependent cell-cell adhesion molecules | Role in contact inhibition at the lateral surface of epithelial cells |
| **PAPPA** | 282647 | pregnancy-associated plasma protein A, pappalysin 1 | 2.71 | This gene encodes a secreted metalloproteinase which cleaves insulin-like growth factor binding proteins (IGFBPs). It is thought to be involved in local proliferative processes such as wound healing and bone remodeling. Low plasma level of this protein has been suggested as a biochemical marker for pregnancies with aneuploid fetuses. | http://www.genecards.org/cgi-bin/carddisp.pl?gene=PAPPA&search=282647 |
| **LHFPL3** | 520147 | lipoma HMGIC fusion partner-like 3 | 2.21 | http://www.ncbi.nlm.nih.gov/gene/?term=520147 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=LHFPL3&search=520147 |
| **MYRF** | 509704 | myelin regulatory factor | 2.16 | http://www.ncbi.nlm.nih.gov/gene/?term=509704 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=MYRF&search=509704 |
| **MRAP** | 505743 | melanocortin 2 receptor accessory protein | 2.09 | This gene encodes a melanocortin receptor-interacting protein. The encoded protein regulates trafficking and function of the melanocortin 2 receptor in the adrenal gland. The encoded protein can also modulate signaling of other melanocortin receptors | May be involved in the intracellular trafficking pathways in adipocyte cells |
| **KCNQ3** | 281884 | potassium voltage-gated channel, KQT-like subfamily, member 3 | 2.52 | http://www.ncbi.nlm.nih.gov/gene/?term=281884 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=KCNQ3&search=281884 |
| **TOX2** | 519845 | TOX high mobility group box family member 2 | 2.03 | http://www.ncbi.nlm.nih.gov/gene/?term=519845 | Putative transcriptional activator involved in the hypothalamo-pituitary-gonadal system |
| **HORMAD1** | 529615 | HORMA domain containing 1 | 2.44 | http://www.ncbi.nlm.nih.gov/gene/?term=529615 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=HORMAD1&search=529615 |

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| **AGRP** | 280987 | agouti related protein homolog (mouse) | 3.13 | This gene encodes an antagonist of the melanocortin-3 and melanocortin-4 receptor (associated with **glucocorticoid disorder**s). It appears to regulate hypothalamic control of feeding behavior via melanocortin receptor and/or intracellular calcium regulation, and thus plays a role in weight homeostasis. Delayed Puberty, obesity and fat disposition marker | Plays a role in weight homeostasis. Involved in the control of feeding behavior through the central melanocortin system. Acts as alpha melanocyte-stimulating hormone antagonist by inhibiting cAMP production mediated by stimulation of melanocortin receptors within the hypothalamus and adrenal gland |
| **DNAJC5G** | 616608 | DnaJ (Hsp40) homolog, subfamily C, member 5 gamma | 2.27 | http://www.ncbi.nlm.nih.gov/gene/?term=616608 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=DNAJC5G&search=616608 |
| **GRIA1** | 529618 | glutamate receptor, ionotropic, AMPA 1 | 2.32 | http://www.ncbi.nlm.nih.gov/gene/?term=529618 | http://www.genecards.org/cgi-bin/carddisp.pl?gene=GRIA1&search=529618 |
| **MYOF** | 513597 | myoferlin | -3.44 | he protein encoded by this gene is a type II membrane protein that is structurally similar to dysferlin. Mutations in dysferlin, a protein associated with the plasma membrane, can cause muscle weakness that affects both proximal and distal **muscles.** Also linked with formation of myoblast, size of the muscle and quantity of the myofibers | alcium/phospholipid-binding protein that plays a role in the plasmalemma repair mechanism of endothelial cells that permits rapid resealing of membranes disrupted by mechanical stress |
| **SLC50A1** | 520463 | solute carrier family 50 (sugar efflux transporter), member 1 | -7.28 | http://www.ncbi.nlm.nih.gov/gene/?term=520463 | Mediates sugar transport across membranes |
| **B3GNT8** | 534859 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8 | -4.10 | http://www.ncbi.nlm.nih.gov/gene/?term=534859 | Post-translational protein modification and Mucin type O-Glycan biosynthesis |
| **GPCPD1** | 518469 | glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae) | -2.92 | http://www.ncbi.nlm.nih.gov/gene/?term=518469 | May be involved in the negative regulation of **skeletal muscle differentiation**, independently of its glycerophosphocholine phosphodiesterase activity |
| **DSE** | 514028 | dermatan sulfate epimerase | -2.40 | http://www.ncbi.nlm.nih.gov/gene/?term=514028 | chondroitin sulfate biosynthesis and Metabolic pathways. Converts D-glucuronic acid to L-iduronic acid (IdoUA) residues |

***Note:*** *Genes/Cells markerd with YELLOW color are markers suggested by IPA*

** FC = Fold change*