

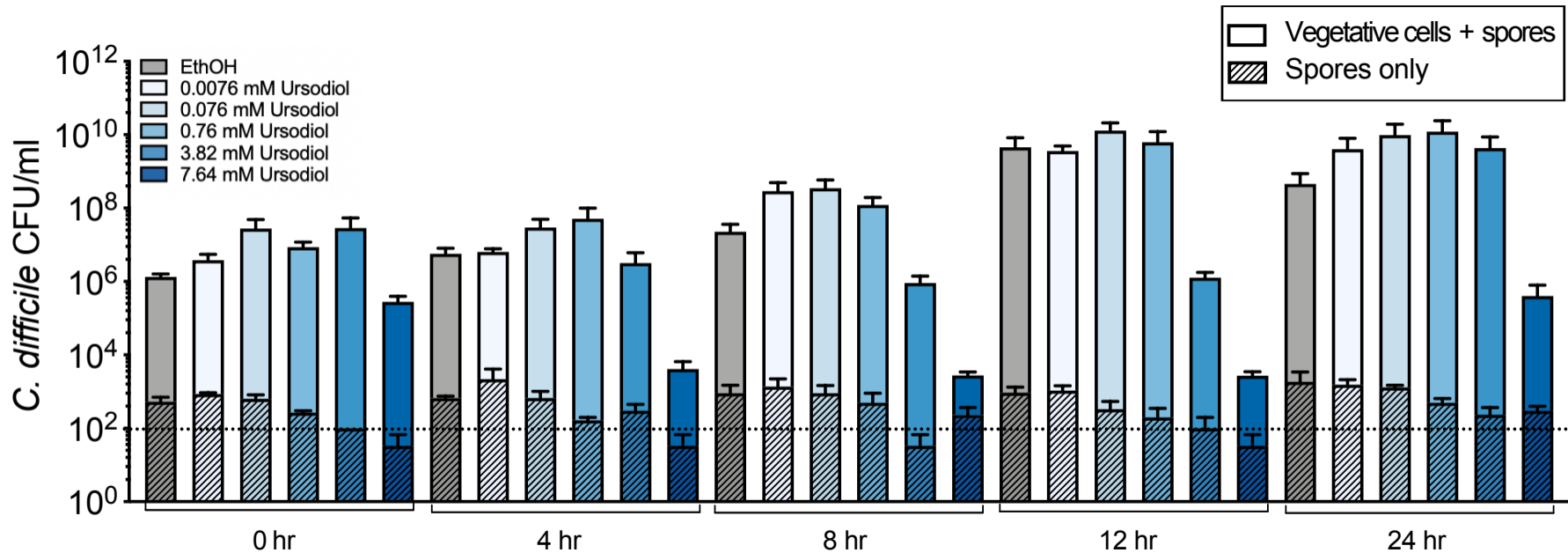
Supplemental Figure 1: Effect of ursodiol on viability and spore formation of *C. difficile*. Culture aliquots (100 μ L) of *C. difficile* R20291, grown in BHI media, were taken over a 24 hr period and enumerated on TBHI plates to obtain total CFU/ml of total vegetative cells and spores (solid bars) and spores only (hashed bars). The positive controls (EthOH, gray bars) represent *C. difficile* grown in BHI media with ethanol and the treatments groups (blue bars) represents *C. difficile* grown in BHI media with varying concentrations of ursodiol from lowest to highest concentration (left to right). The limit of detection for this assay is 10^2 CFU/ml. The data presented represents triplicate experiments. Significance was determined by Welch's t-test using log transformed CFU/ml.

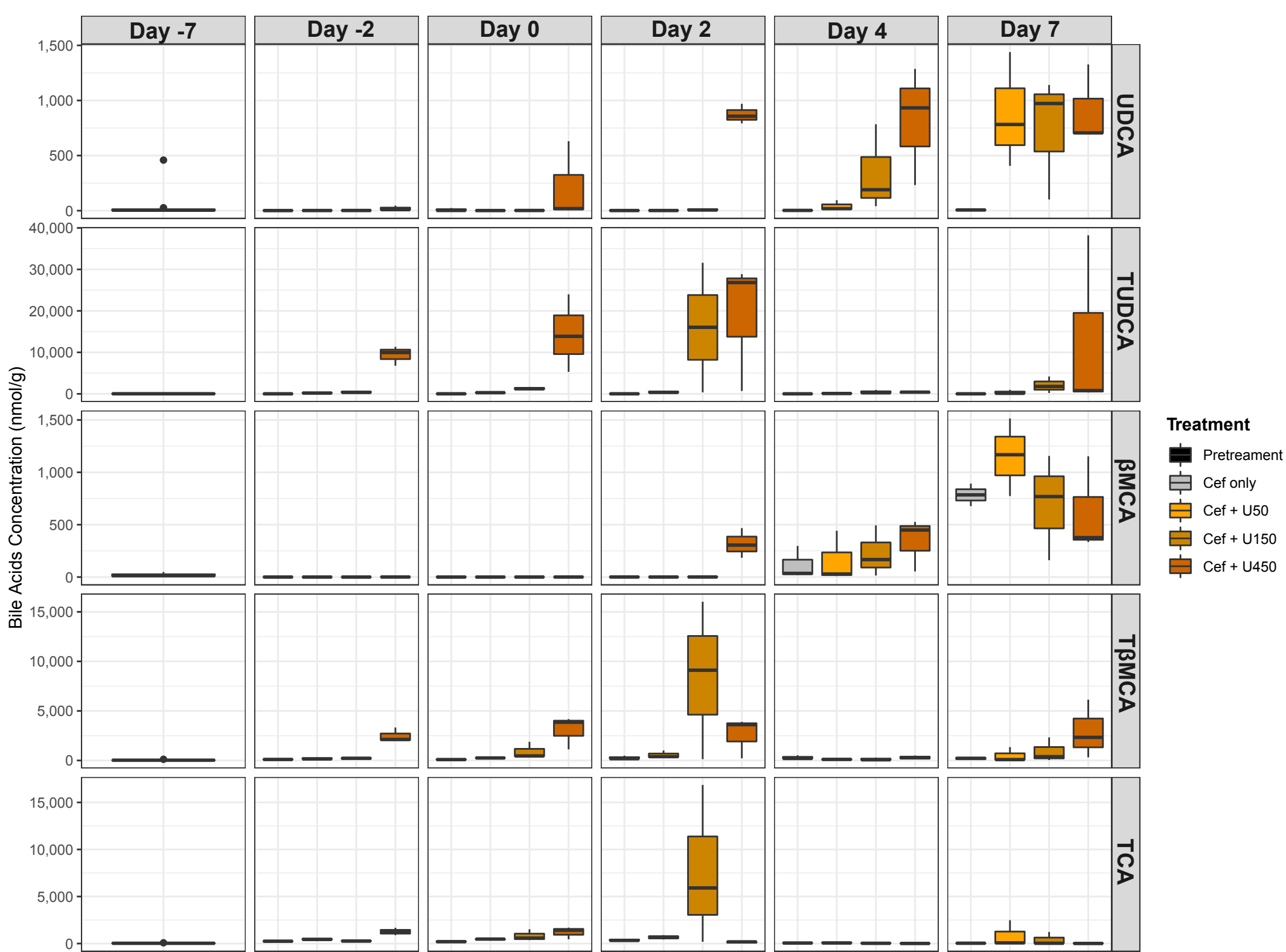
Supplemental Figure 2: Ursodiol treatment alters the bile acid metabolome. Box and whisker plots of bile acids that were significantly altered over the course of ursodiol treatment compared to mice that only received cefoperazone (based on a Two-way ANOVA with Tukey's multiple comparisons post hoc test). An n=3 mice/treatment group were then selected for bile acid metabolomic analysis.

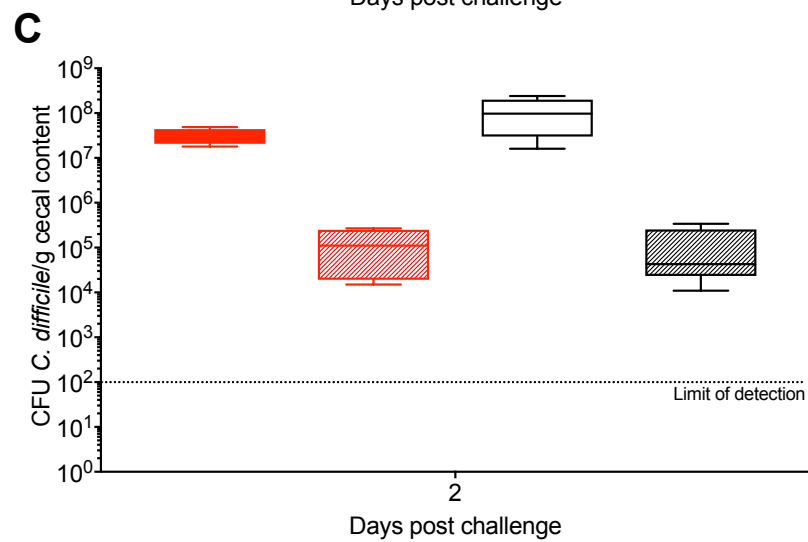
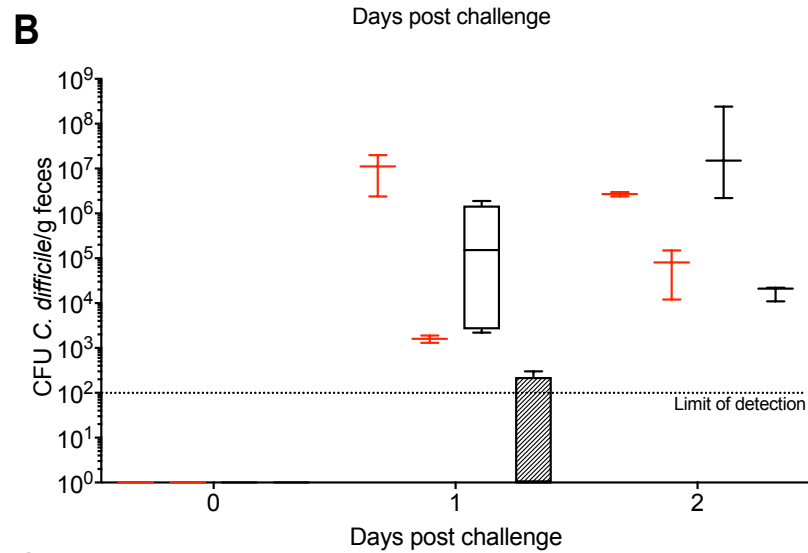
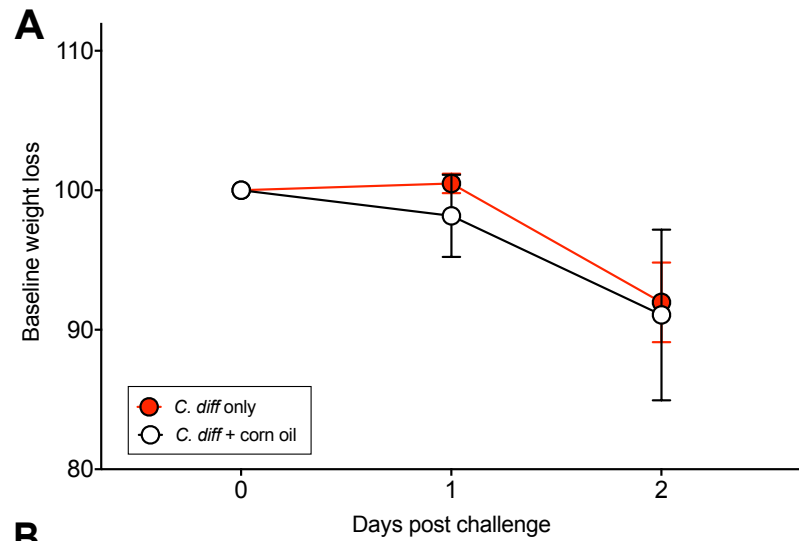
Supplemental Figure 3: No effect with corn oil vehicle alone on CDI in mice. (A) Baseline weight loss of cefoperazone treated mice challenged with *C. difficile* pretreated with (white, *C. diff* + corn oil) and without corn oil vehicle (red, *C. diff* only) (n=8 mice/treatment group). **(B)** *C. difficile* bacterial load in feces and **(C)** cecal content over the first 2 days post challenge. Solid boxes represent total vegetative cells and spores and hashed boxes represent spores only. Significance was determined by a two-way ANOVA test.

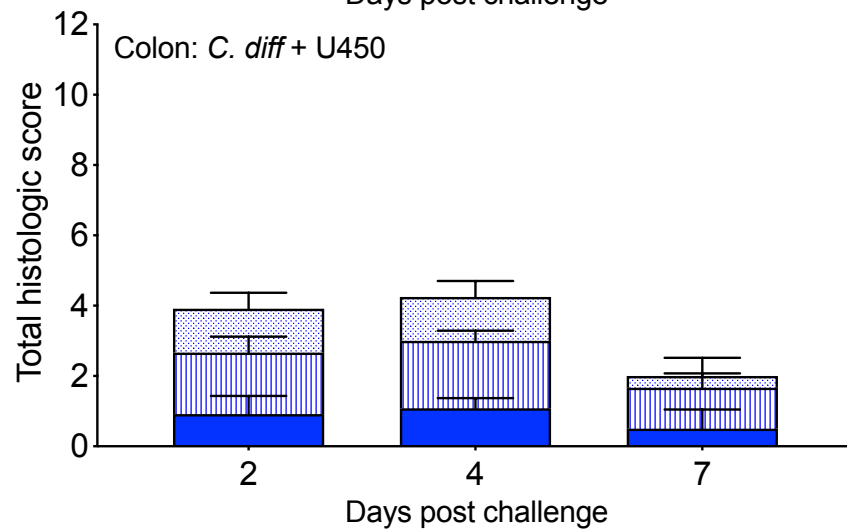
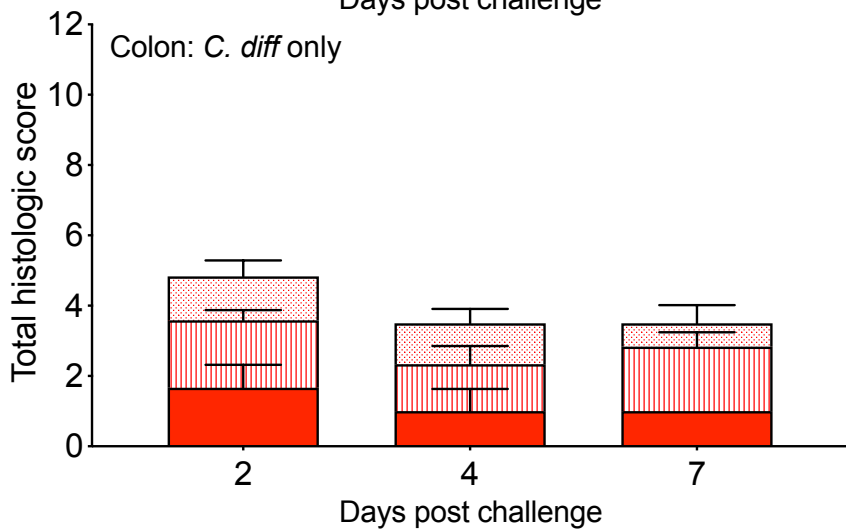
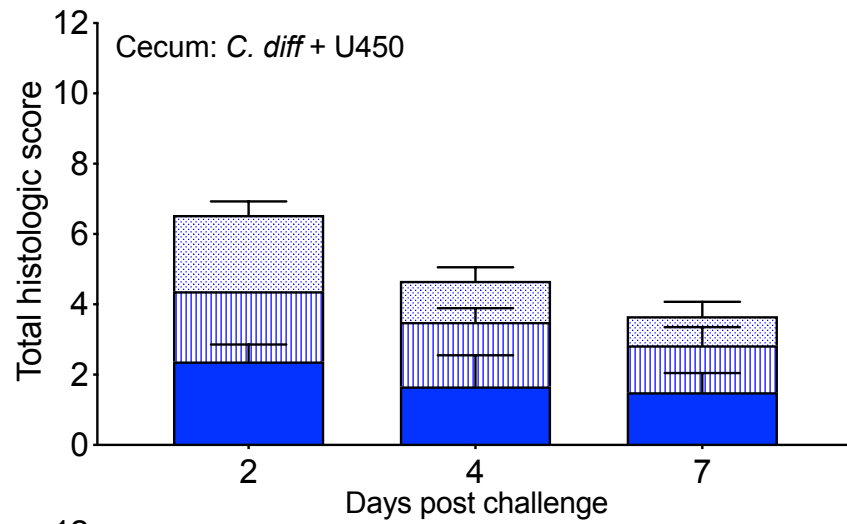
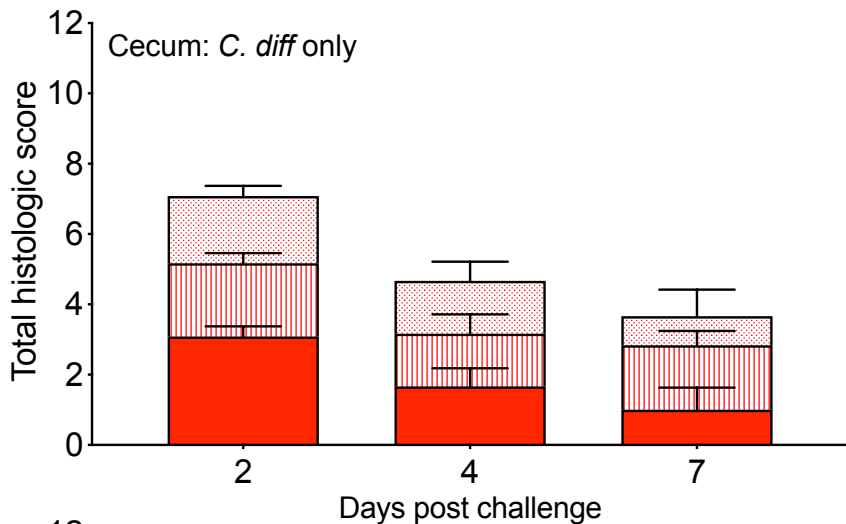
Supplemental Figure 4: Total histologic scores were not significantly different with ursodiol pretreatment. Histopathologic scoring of murine cecum and colon throughout CDI. Total histologic scores were calculated by adding all three scores from parameters assessed: epithelial damage, inflammation, and edema. Significance was determined by a two-way ANOVA with Sidak's multiple comparisons *post hoc* test. Error bars represent the standard deviations from the mean.

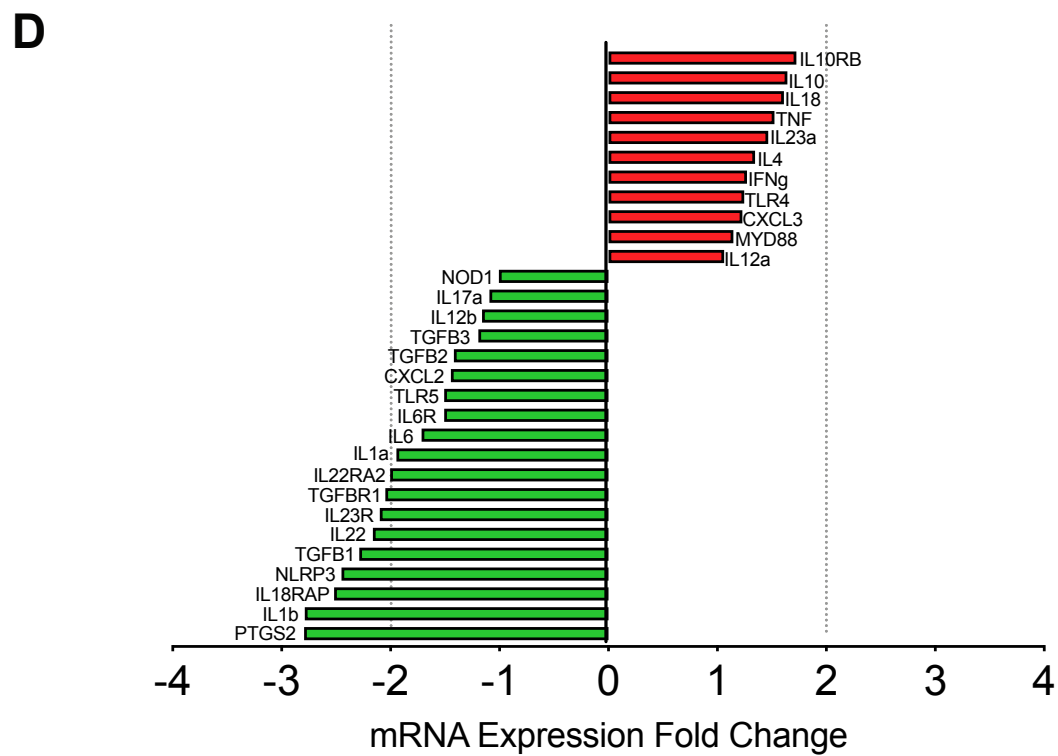
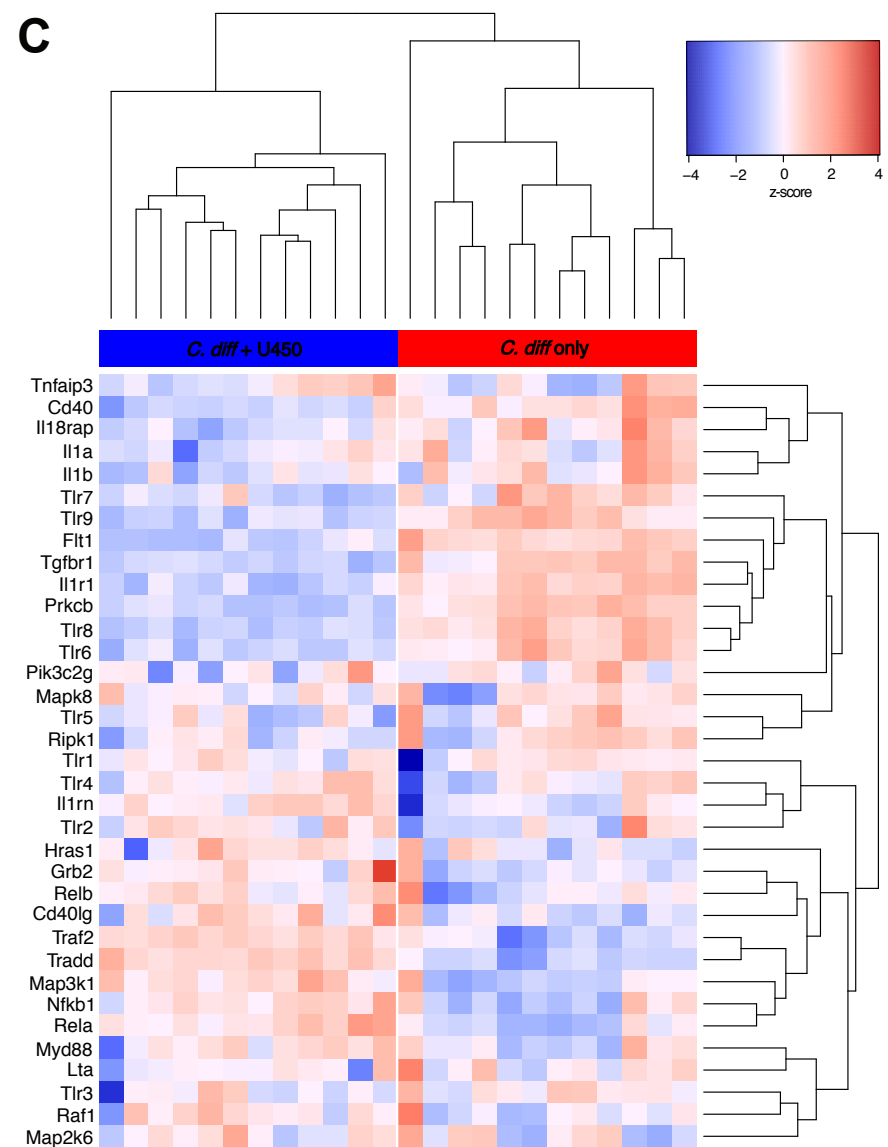
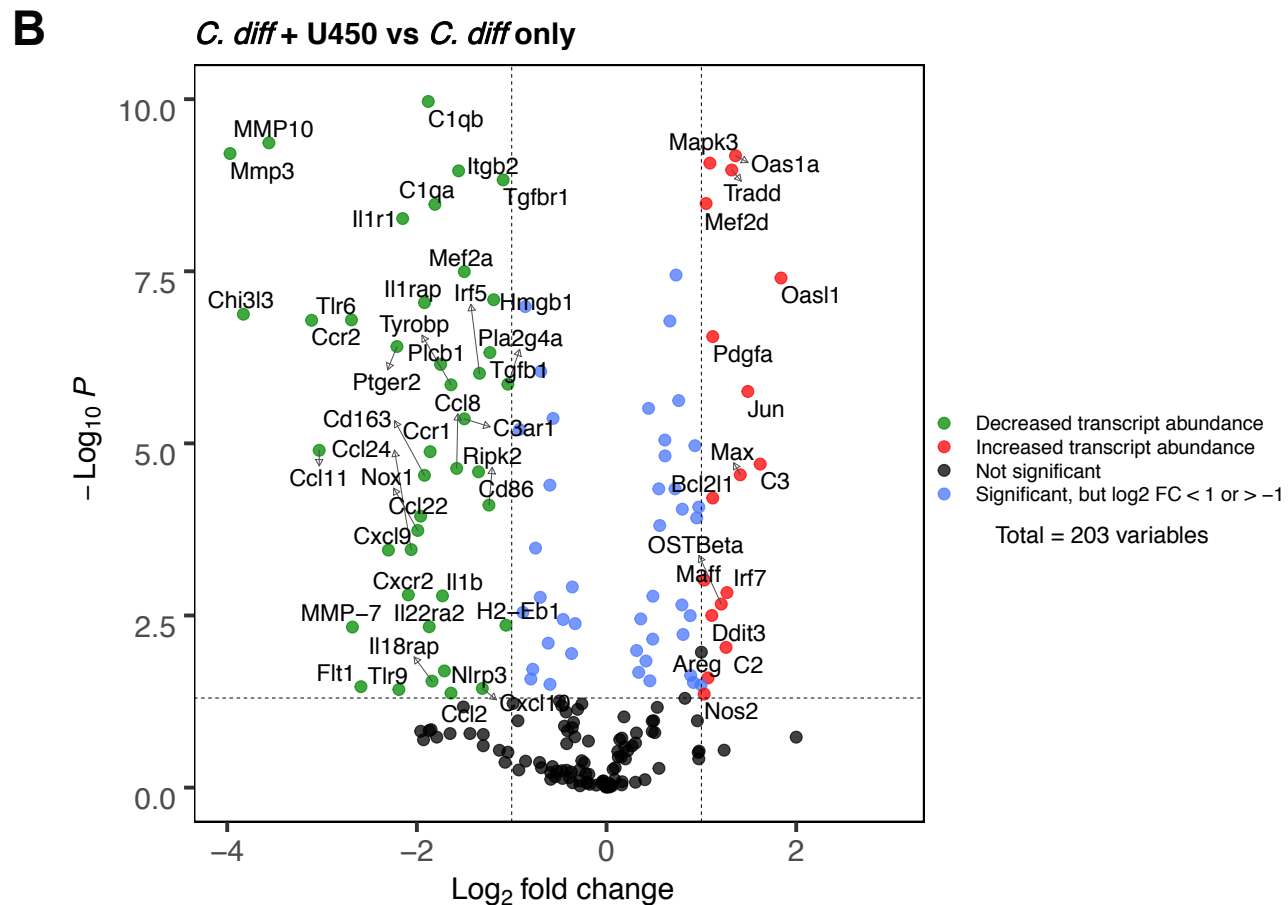
Supplemental Figure 5: Ursodiol alters the host inflammatory transcriptome of the colon early during CDI. (A) Venn diagram depicting the mRNA expression fold change comparing the ursodiol pretreated to untreated mice in colonic tissue at day 2 post challenge with *C. difficile*, from two independent experiments performed with a total of n=12 mice/treatment group. Of the 261 genes evaluated, a total of 139 colonic genes had significant gene expression fold changes (increased expression, red; decreased expression, green). **(B)** Volcano plots highlighting genes whose transcript levels changed by greater than 1-fold and met the significant threshold $p \leq 0.05$. Genes highlighted in red had increased transcript levels, while those highlighted in green had decreased levels. Blue points represent genes whose results were significant but did not meet the specify fold change. Black points represent genes whose results failed to meet the significance threshold. **(C)** Colonic inflammatory transcriptome heatmap of calculated z-scores for log₂ transformed count data of mRNA expression levels (y-axis) comparing ursodiol pretreated (blue) to untreated mice (red). Dendrograms represent unsupervised clustering. **(D)** mRNA expression fold differences in increased expression (red) and decreased expression (green) of genes involved with NF- κ B signaling in colonic tissue comparing ursodiol pretreated to untreated mice.











Supplemental Table 1: Nanostrings nCounter Mouse Inflammation V2 Panel Gene List

Continue Table S1: Nanostring nCounter SC Mouse Inflammation V2 Panel Gene List

Gene	Accession	Gene Name	Function	Sequence	Category
Ccl2	NM_011333.3	A1323594, HC11, JE, MCAF, MCP-1, MCP1, SMC-CF, Sycp2, Sgk1	Extracellular Region, Cytoplasm, Cell Soma, Extracellular Space, Negative Regulation Of Angiogenesis, Response To Heat, Inflammatory Response, Immune Response, Angiogenesis, Positive Regulation Of T Cell Activation, Regulation Of Cell Shape, Cellular Homeostasis, Anti Apoptosis, Transforming Growth Factor Beta Receptor Signaling Pathway, Cytokine And Ch...	TCTTCAGCACCTTTGATGTGAAGTTGACCCGTAATCTGAAGACTATGACATCCACTTCTTCCAAACCCCTCAA	chemokine (C-C motif) ligand 2
Ccl20	NM_016960.1	CK64, LARC, MIP-3A, MIP-3(a), MIP3A, ST38, Sycp20, exodus-1	Extracellular Region, Extracellular Space, Inflammatory Response, Immune Response, Chemokine Activity, Cytokine Activity	GCAGCAAGCAACTAGCACTGGCTCTGTACTACAGACGCGCTCTCTCCAGAGATTTGGTGGTTCAACAAGA	chemokine (C-C motif) ligand 20
Ccl22	NM_009137.2	ABCD-1, DCBCK, MDC, Sycp22	Extracellular Region, Extracellular Space, Inflammatory Response, Immune Response, Chemokine Activity, Cytokine Activity	CCAGATTAACAATCCACCCCTCTTCAACACATGCTAGGGTCTTTACTTCTCTGCCCAACACCTTGACTCTGGC	chemokine (C-C motif) ligand 22
Ccl24	NM_019577.4	CK6-6, MPFIF-2, Sycp24	Extracellular Region, Cytoplasm, Cytosol, Extracellular Space, Soluble Fraction, Cell Activation, Positive Regulation Of Transcription From Rna Polymerase II	CTGGATGCCAAGAAAAACAGCCTTCTAAAGGGGCCAAGGCAAGTGAAGAACCAAGTCTTCCAGACAGCCCGTG	chemokine (C-C motif) ligand 24
Ccl3	NM_011337.1	A1323804, G0S19-1, LD78alpha, MIP-1alpha, MIP1-(a), MIP1-alpha, Mip1a, Sycp3	Promoter, Response To Toxin, Calcium Mediated Signaling, Behavior, Calcium Ion Transport, Leukocyte Chemotaxis, Cell Cell Signaling, Inflammatory Response, Immune Response, Regulation Of Cell Shape...	TGTGTCACTCGTCAACATCATGAAGTCTCCACCAGCTCCCTGGCTGCTTCTCTGTACCCAGACCTGCAACCA	chemokine (C-C motif) ligand 3
Ccl4	NM_013652.1	AT744.1, Act-2, MIP-1B, Mip1b, Sycp4	Extracellular Region, Extracellular Space, Soluble Fraction, Response To Toxin, Leukocyte Chemotaxis, Inflammatory Response, Immune Response, Chemokine Activity, Cytokine Activity	TTCTCCAGCACTAAGGCTCTGACCCCTCCACTTCTGCTGTTCTCTTACACCTCCGGCAGCTTCAAGAAAGCTTTG	chemokine (C-C motif) ligand 4
Ccl7	NM_013654.2	MCP-3, Sycp7, fic, marc, mp3	Extracellular Region, Extracellular Space, Inflammatory Response, Immune Response, Regulation Of Cell Shape, Hepatin Binding, Chemokine Activity, Cytokine Activity	ACAGAAGGTCACCCAGTAGTCGCTGCTCCGGGAAGCTGTATCTCAAGCAAAAAGGGGATGAAGCTGTGTCT	chemokine (C-C motif) ligand 7
Ccr1	NM_009912.4	Cmkbr1, Mip-1a-R	External Side Of Plasma Membrane, Membrane, Integral To Membrane, Plasma Membrane, Signal Transduction, Calcium Ion Transport, Myeloid Cell Differentiation, Leukocyte Chemotaxis, Cell Cell Signaling, Inflammatory Response, Immune Response, Eicosanoid G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	CTTCTGATCAGACCATAGGTTCAACCAAGGAAGGCTGAAGAGAAATGAGGAGACAGATATATAGTCTCCAAGA	chemokine (C-C motif) receptor 1
Ccr2	NM_009915.2	Cc-ckr-2, Ccr2a, Ccr2b, Ckr2, Ckr2a, Ckr2b, Cmkbr2, mlsr	Membrane, Cytosol, Perinuclear Region Of Cytoplasm, Integral To Membrane, Integral To Plasma Membrane, Cell Soma, Dendrite, Plasma Membrane, Signal Transduction, Regulation Of Cell Migration, Hemopoiesis, Negative Regulation Of Angiogenesis, Inflammatory Response, Immune Response, Angiogenesis, Positive Regulation Of T Cell Activation, Cellular Homeostasis	ATGAACATACATAGACCTCAGGATTAACAGGACCTGTGGTTGTGTCTGTGGGCTATCCAAACATGGTGATTT	chemokine (C-C motif) receptor 2
Ccr3	NM_009914.4	CC-CXR3, CXR3, Cmkbr12, Cmkbr3	Membrane, Integral To Membrane, Endosome, Extracellular Space, Plasma Membrane, Signal Transduction, Positive Regulation Of Angiogenesis, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	CTATATTTTATTATCTGGGACACAGCCCTAGAATCTCAGAGAGTGTCTCTGTGATTGAAGTGTGCACTTATAGA	chemokine (C-C motif) receptor 3
Ccr4	NM_009916.2	CC-CXR4, CHEMR1, Cmkbr4, LESTR, Sdf1r	External Side Of Plasma Membrane, Membrane, Integral To Membrane, Cell Soma, Plasma Membrane, Signal Transduction, Inflammatory Response, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	GCTTGTAGAAGAAGCTCGTGGTCCAGAGAGGTTGAATGDCCTGTAATCTGACTCTCCGGGATAAGGCCAA	chemokine (C-C motif) receptor 4
Ccr7	NM_007719.2	CD197, Cdxr197, Cmkbr7, EBH1, Ebr1h	External Side Of Plasma Membrane, Membrane, Integral To Membrane, Plasma Membrane, Signal Transduction, Activation Of Jnk Activity, Positive Regulation Of T Cell Proliferation, Inflammatory Response, Immune Response, Actin Cytoskeleton Organization And Biogenesis, G Protein Coupled Receptor Protein Signaling Pathway, Cell Maturation, G Protein Coupled	CCAGATGGTTTGGTCTG	chemokine (C-C motif) receptor 7
Cd163	NM_053094.2	CD163v2, CD163v3	Extracellular Region, Membrane, Integral To Membrane, Plasma Membrane, Inflammatory Response, Receptor Mediated Endocytosis	TCAGCCGCACTTGTTGTGGAGCCTCTATTGGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	CD163 antigen
Cd4	NM_013488.2	L3T4, Ly-4	External Side Of Plasma Membrane, Cell Surface Membrane, Endoplasmic Reticulum Membrane, Integral To Membrane, Lipid Raft, Endoplasmic Reticulum Lumen, Plasma Membrane, Cell Surface Receptor Linked Signal Transduction Go 0007168, T Cell Differentiation, Regulation Of T Cell Activation, Cytokine Production, Immune Response, Positive Regulation Of T Cell	AAGAAGGTCTCCGACAAAAGTCCACCAAGACCTCAAGCTCAGCTGAAGGAGGAGAGAACCTCCACTCACCCCTAAGATA	CD4 antigen
Cd40	NM_011611.2	A1326936, Bp50, HG30, HGM1, IGM, IMD3, T-BAM, TRAP, Tnfrsf5, p50	External Side Of Plasma Membrane, Extracellular Region, Membrane, Integral To Membrane, Extracellular Space, Plasma Membrane, Signal Transduction, B Cell Differentiation, Inflammatory Response, Immune Response, Anti Apoptosis, Cytokine Activity	GCTGCCCCAACCCCGTACTCTGATTTGATCTCCCTGGCACTTCAAGTAAAGGAGGAGAACCAATCCAGAGGGTTG	CD40 antigen
Cd40lg	NM_011616.2	CD154, CD40-L, Cd40L, HGM1, IGM, IMD3, Ly-62, Ly62, T-BAM, TRAP, Tnfrsf5, gp39	External Side Of Plasma Membrane, Extracellular Region, Membrane, Integral To Membrane, Extracellular Space, Plasma Membrane, Signal Transduction, B Cell Differentiation, Inflammatory Response, Immune Response, Anti Apoptosis, Cytokine Activity	AGCAGTGGATCTGAGAAATCTACTCAAGCGCGAAATCCCAACAGTCTCCCTCCAGCTTGGAGCAGCAGTCTGTT	CD40 ligand
Cd55	NM_010016.2	Def, DaF-GPI, Def1, GPI-DAF	External Side Of Plasma Membrane, Cell Surface Membrane, Anchored To Membrane, Lipid Raft, Apical Plasma Membrane, Plasma Membrane, Innate Immune Response, Negative Regulation Of Catalytic Activity, Enzyme Inhibitor Activity	ACAGTTAAAGTTTACAGAACCCAGCATGACTCTTCAACAGAACACAGTACGCTCAACAAAGAACATCTACAGAC	CD55 antigen
Cd86	NM_019388.3	B7, B7-2, B7.2, B70, CLS1, Cd282, ETC-1, Ly-58, Ly58, MB7, MB7-2, TS1A-2	External Side Of Plasma Membrane, Membrane, Integral To Membrane, Plasma Membrane, Positive Regulation Of T Cell Proliferation, Defense Response To Virus, B Cell Activation, T Cell Activation, Receptor Binding, Receptor Activity	CAAAACATAAGCGTGAAGTGGTGAATTTTGGCAGGACGCAAGAAAGTGGTCTGTGACAGACATTTGGG	CD86 antigen
Cdc42	NM_008981.1	A1747189, AU018915	Golgi Membrane, Membrane, Cytoplasm, Cytoskeleton, Cell Projection, Apical Part Of Cell, Secretory Granule, Plasma Membrane, Nervous System Development, Regulation Of Protein Kinase Activity, Regulation Of Mitosis, Regulation Of Protein Metabolic Process, Actin Cytoskeleton Organization And Biogenesis, Cell Cell Adhesion, Endosome Transport, Establishmen	TGATGGTGGAGGCCATACACTCTTGAAGTCTTGTACTCGAGGCGAAGGAGATTAGCAGACTACGACCCGTA	cell division cycle 42
Cebpb	NM_008983.3	CIEPbeta, CRP2, IL-6DBP, LAP, LIP, NF-JL6, NF-M, NFkB	Cytoplasm, Nucleus, Nuclear Matrix, Nuclear Chromatin, Positive Regulation Of Transcription, DNA Dependent, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Negative Regulation Of Transcription Dna Dependent, Regulation Of Transcription Dna Dependent, Anti Apoptosis, Neuron Differentiation, Protein Homod	GGGGACCGGGGCGACGCACTGACAGGCGACCGGGTTGGGAGCTTATGCAATCCGGATCAACATGGCTGGAG	CCAAT/enhancer binding protein (CEBP), beta
Cfb	NM_008198.2	A195813, A1255840, B, Bf, Cf, Fb, Hf-Bf	Extracellular Region, Extracellular Space, Proteolysis, Cell Proliferation Go 0008283, Innate Immune Response, Serine Type Peptidase Activity, Peptidase Activity, Serine Type Endopeptidase Activity	GGTGGGCGCTGTGTGACTCGTGAACATCAATGCTTACCTTCCAAAAGGACATGAGCATCATGTTTAAAGT	complement factor B
Cfd	NM_013459.1	Adn, DF	Extracellular Region, Extracellular Space, Proteolysis, Notch Signaling Pathway, Innate Immune Response, Serine Type Peptidase Activity, Endopeptidase Activity, Peptidase Activity, Serine Type Endopeptidase Activity	AGTGTCAATCATGACCGGACCACTGCAACTCGCAGTACACAGTACAGCGGGTGTACCACTTAACATGATGTGTG	complement factor D (adpsin)
Cfl1	NM_007687.5	AA959946, Cof	Membrane, Cytoplasm, Nucleus, Cytoskeleton, Lamellipodium, Cell Projection, Leading Edge, Cortical Actin Cytoskeleton, Plasma Membrane, Actin Filament Organization, Cytokinesis, Protein Import Into Nucleus, Regulation Of Cell Morphogenesis, Cytoskeleton Organization And Biogenesis, Protein Amino Acid Phosphorylation, Actin Binding	TGCTGCCAACTTCAACCAATAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	cofilin 1, non-muscle
Creb1	NM_133828.2	2310001E10R1K, 352640Z2H1R1K, AV083133, Creb, Creb-1	Chromatin, Nucleus, Nuclear Chromatin, Mitochondrion, Transcription Factor Complex, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Axonogenesis, Regulation Of Transcription Dna Dependent, Transforming Growth Factor Beta Receptor Signaling Pathway, Protein Amino Acid Phosphorylation, Transcription Pro	CATGTCAACACAGGGTCCACTTCCAAAGTGAAGTCAAGCCAGGAAAGCAAGTCTGCTGCTGCCACCTTG	cAMP responsive element binding protein 1
Op	NM_007768.4	A1255847	Extracellular Space, Protein Polymerization, Protein Homodimerization Activity, Low Density Lipoprotein Binding	TTGTATTCCCAAGGATCAATGATCTTACTGTGTCTGTGGAAGCAGTGAAGAAGCCACTGAACACCTTACTGT	reactive protein, pentraxin-related
Csf1	NM_01113530.1	C87615, Csfm, MCSF, op	Extracellular Region, Membrane, Perinuclear Region Of Cytoplasm, Integral To Membrane, Receptor Complex, Extracellular Space, Plasma Membrane, Positive Regulation Of Cell Proliferation, Positive Regulation Of Cellular Protein Metabolic Process, Inflammatory Response, Cell Proliferation Go 0005283, Positive Regulation Of Cell Migration, Innate Immune R	TCCAGCTGTGGAGAAATCAAGAACTCTTAAAGAAACAAAGATCTCTTGAAGAGACTGAACATTTTACCAA	colony stimulating factor 1 (macrophage)

Continue Table S1: Nanostring nCounter SC Mouse Inflammation V2 Panel Gene List

Gene	Accession	Symbol	Function	Sequence	Notes
Csf2	NM_009869.4	Csf2m, GM-CSF, Gm-CSF, MGI-HGM	Extracellular Region, Extracellular Space, Positive Regulation Of Cell Proliferation, Negative Regulation Of Apoptosis, Regulation Of Gene Expression, Immune Response, Regulation Of Cell Proliferation, Cytokine Activity, Growth Factor Activity	AAGTGTCTCTAACGAGTCTCTCCAGAAAGCTAACATGTGTGACAGCCCGCTGAAGATATGACAGCGGTCTACGGGGCAATTTCAACCAACTCAA	colony stimulating factor 2 (granulocyte-macrophage)
Csf3	NM_009971.1	Csf3, G-CSF, MGI-HG	Extracellular Region, Extracellular Space, Positive Regulation Of Cell Proliferation, Immune Response, Enzyme Binding, Cytokine Activity, Growth Factor Activity	TGTTCTCTCTCTAGACAGAGAGAAAGGCTCTGTGTCTCTCTGTGGAGCCGGAGGAGGATGGTAAATACCAAGTATTGATCTCTGCTGCTGC	colony stimulating factor 3 (granulocyte)
Cxcl1	NM_008176.1	Fsp, Gc1, KC, Mgsa, N51, Szyb1, gro	Extracellular Region, Extracellular Space, Inflammatory Response, Immune Response, Acute Inflammatory Response, Chemokine Activity, Cytokine Activity, Growth Factor Activity	TGCTAGTAAAGGGTGTGGCGAAAGAGTGCAGAGATAGATTTGATATTATTTGATATTAGGGTGAAGCATGTGTGGAGGCTGTGT	chemokine (C-X-C motif) ligand 1
Cxcl10	NM_021274.1	C7, CRG-2, INP10, IP-10, IP10, Ifi10, Szyb10, gp1-10, mob-1	External Side Of Plasma Membrane, Extracellular Region, Extracellular Space, Positive Regulation Of Cell Proliferation, Signal Transduction, Negative Regulation Of Angiogenesis, Defense Response To Virus, Inflammatory Response, Immune Response, Protein Secretion, Positive Regulation Of Cell Migration, Chemokine Activity, Cytokine Activity	AGGACGGTCCCTGCACTCATCATGATGACGGCCGAGTGAAGTGAAGGCGCATAGGAAAGCTGAATACTCCCTGCGACCTATCTCGCCACC	chemokine (C-X-C motif) ligand 10
Cxcl2	NM_009140.2	CINC-2a, GROb, Gm2, MIP-2, MIP-2a, Mgsa-b, Mip2, Szyb, Szyb2	Extracellular Region, Extracellular Space, Leukocyte Chemotaxis, Inflammatory Response, Immune Response, Chemokine Activity, Cytokine Activity	GGTGGGGTGGGGCAATAGATGCGATGCGTTCCTGATGGAAGGTGTGTCATGTCATCATTTTTTGTATGACACCGAGAGACTAAGACACG	chemokine (C-X-C motif) ligand 2
Cxcl3	NM_203320.2	Dcp1, Gm1960	Extracellular Region, Extracellular Space, Inflammatory Response, Immune Response, Chemokine Activity, Cytokine Activity	AGCTCGAAGATGTGAAGATTTGCTCAACCCCAAGGCCAGGCTTCAGATATCATCAAGAAAGACTGAAGAGGGCAAGCTCAGCTGACGG	chemokine (C-X-C motif) ligand 3
Cxcl5	NM_009141.2	AMCF-II, ENA-78, GCP-2, LIX, Szyb5, Szyb6	Extracellular Region, Extracellular Space, Cytokine Production, Inflammatory Response, Chemokine Activity	CCGAGTGAAGTAAAGAAAGGGCTGATCTCTCCACCAGGATTTCTTTATGAACTCCGCTGTTGATGAGAAAGGGAAACATTGTCCCTGAAG	chemokine (C-X-C motif) ligand 5
Cxcl9	NM_008509.2	BB139920, CMK, Mlg, MuMIG, Szyb9, cgp-10	External Side Of Plasma Membrane, Extracellular Region, Extracellular Space, Defense Response To Virus, Cytokine Activity	TAGAACTCAGCTGTCGATGAAGTCGGTGTCTTTCTCTGGGACATCTCTCTGGAGCAGTGTGGATGTGGAGAACCTAGTGATAAGGAATGG	chemokine (C-X-C motif) ligand 9
Cxcr1	NM_178241.4	Il8ra	Membrane, Integral To Membrane, Plasma Membrane, Signal Transduction, Cell Surface Receptor Linked Signal Transduction, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity	TCTCTTGAAGCCACTTGATTGAAGATCTGCGAACCGCAATGACATGACCGACCCCTGTATTACTAGATCCTGGGCTTTCTCATAGTTGT	chemokine (C-X-C motif) receptor 1
Cxcr2	NM_009093.3	CD128, CDw128, Cmkar2, Gpcr16, IL-8Rb, IL-8rb, IL8RA, Il8b, mL-8RH	Cell Surface, Membrane, Integral To Membrane, Plasma Membrane, G Protein Signaling Coupled To Ip3 Second Messenger, Phospholipase C Activating, Positive Regulation Of Cell Proliferation, Signal Transduction, Cell Surface Receptor Linked Signal Transduction, G Protein Coupled Receptor Activity	CCTTGGCTGTGGCTGCATCAAGTAAATGAGTGAAGTGTTCCTCAACCCGTGGAGAGATTTCTCATAGTGAAGAGGTACTCTCACAGGAG	chemokine (C-X-C motif) receptor 2
Cxcr4	NM_009911.3	CD184, Cmkar4, LESTR, PB-CRK, PBSF/SDF-1, Sdf1r	External Side Of Plasma Membrane, Cell Surface, Membrane, Cytoplasmic Vesicle, Integral To Membrane, Endosome, Cytoplasmic Membrane, Cytoplasmic Vesicle, Leading Edge, Growth Cone, Plasma Membrane, Nervous System Development, L Cell Proliferation, Signal Transduction, Regulation Of Cell Migration, Calcium Mediated Signaling Pathway, Brain Development, Organ Morphogenesis	GTTCATTCACGATATAATGGTGGTCTCGCTCCGCCGATCGTATCTCTCTGACTGCATCACTCTCTAAGCTGCACACTCAAGGGCC	chemokine (C-X-C motif) receptor 4
Cyslr1	NM_021478.4	BB147369, CyslT1R, Cysr1	Membrane, Integral To Membrane, Plasma Membrane, Signal Transduction, Positive Regulation Of Angiogenesis, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	TGAAGATTGGATCTGCTTCAGGAGAAAGAACACTAACTGAGTGGATGAACTGACGAGCTGAAAGCTACTCTGACACTACATAAGAACAGT	cysteinyl leukotriene receptor 1
Cyslr2	NM_001162412.1	2300001H05RK, CYSLR2, Chr2, Cyslr2	Membrane, Integral To Membrane, Plasma Membrane, Signal Transduction, Positive Regulation Of Angiogenesis, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	GGAGGGGGTCAACDATTGTATGTCATGATCACTCTCTCTCTCTCTCTGATCACTGACCTGGGACCCCTCCACTTGGTACATGGGATA	cysteinyl leukotriene receptor 2
Daxx	NM_007829.3		Cytoplasm, Nucleus, Cytosol, Cell Cortex, Pml Body, Neuron Projection, Transcription Dna Dependent, Negative Regulation Of Transcription Dna Dependent, Regulation Of Transcription, Dna Dependent, Angiogenesis, Receptor Signaling Pathway, Apoptosis, G Protein Homodimerization Activity, Protein N-Terminal Binding, Transcription Coactivator Activity, Transcription	CTTGGGAAAATGGAACCTGGCCATGACCGGCTGATGAGGTTCATCCAAATGATCAATGATGCAACACAGAACATGAGGGGGGAGAGAGAGA	Fas death domain-associated protein
Ddx3	NM_007837.3	CHOP-10, CHOP10, chop, gadd153	Cytoplasm, Nucleus, Positive Regulation Of Transcription, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Regulation Of Transcription, Dna Dependent, Sequence Specific Dna Binding, Transcription Factor Activity, Regul	CCTGACTGAAATGGGGCACCTATCTCTCCAGAAACGAAAGAGAGAGATCAAAACCTCACTACTCTTGGACCCCTGCTCAAGCTGTAC	DNA-damage inducible transcript 3
Elk1	NM_007822.4	Elk-1	Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Regulation Of Transcription, Dna Dependent, Sequence Specific Dna Binding, Transcription Factor Activity, Dna Binding	AGGGTCTCTCTTGGCTAACTACCACTGGGATACACTGCTGGCCATCAAGTCTCAAGATCTACTGCTTCTACTCTGGATTACCAAGTGTAC	ELK1, member of ETS oncogene family
Fasl	NM_010177.3	APT1L1, CD178, CD95L, CD95L, Fas-L, Faslg, Tnfrsf6, gld	External Side Of Plasma Membrane, Extracellular Region, Membrane, Cytoplasmic Vesicle, Perinuclear Region Of Cytoplasm, Integral To Membrane, Lipid Raft, Cytoplasmic Membrane Bound Vesicle, Extracellular Space, Lysosome, Plasma Membrane, Positive Regulation Of Cell Proliferation, Signal Transduction, Induction Of Apoptosis By Extracellular Signals, Nega	CATTTAACAGGAAACCCCACTCAAGTCCACTCCCTGTGAAGTGGAGAACACATATGGAACCCCTGTGATCTGTGAAGTGAATAAGAAAGGTGGCC	Fas ligand (TNF superfamily, member 6)
Fil1	NM_010228.3	A1323757, Fil-1, VEGFR-1, VEGFR1, sFR1	Golgi Apparatus, Membrane, Cytoplasm, Nucleus, Integral To Membrane, Integral To Plasma Membrane, Endosome, Plasma Membrane, Protein Amino Acid Autophosphorylation, Multicellular Organismal Development, Positive Regulation Of Map Kinase Activity, Angiogenesis, Embryonic Morphogenesis, Intracellular Receptor Mediated Signaling Pathway, Peptidyl Tyrosine	GAAAAGTCCGTGCTGGCTCCAAACCCACTCTCTATCCGCTGGGACGACAGACATCTCACTGACCCGCTGATGGCATCCCTGGCCGCAACATCA	FMS-like tyrosine kinase 1
Fos	NM_010234.2	D12Rfj1, c-fos, cFos	Nucleus, Membrane Fraction, Transcription Factor Complex, Positive Regulation Of Transcription, Dna Dependent, Nervous System Development, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Regulation Of Transcription, Dna Dependent, Cellular Response To Extracellular Stimulus, Transforming Growth Factor Beta Receptor Signaling Path	AGCTGGTGCATACAGAGGAGAAACACGCTTCCCTCGAAGTTCGCGTACAGGAGACCTCACTGCTGTCGTGAAACACACAGGCTGTGGCC	FBJ osteosarcoma oncogene
Fxyd2	NM_052823.2	Atp1g1	Membrane, Microsome, Integral To Membrane, Basolateral Plasma Membrane, Transport, Sodium Ion Transport, Potassium Ion Transport, Ion Transport, Regulation Of Cell Proliferation, Regulation Of Cell Growth, Ion Channel Activity	CTTGTGTGGTGGCTCTCACTCACTTCAGAAAGGTCGCGTGTGGGGGGGTGAAGAACATGAGCAGGTCATGTAAGATGACTGTGACAGAGAGCC	FXyD domain-containing ion transport regulator 2
Gnaq	NM_008139.5	1110005L02Rik, 6230401102Rik, AA408290, AW060788, Dsk1, Dsk10, Galphaq, Gq, Gq1	Cytoplasm, Membrane Fraction, Protein Complex, Plasma Membrane, G Protein Signaling Coupled To Ip3 Second Messenger, Phospholipase C Activating, Glutamate Signaling Pathway, Signal Transduction, Phospholipase C Activation, Skeletal Development, Behavior, Protein Stabilization, Regulation Of Action Potential, G Protein Signaling Adenylate Cyclase Activat	GAATGGGCGCTGAACCTAAGAAAGTGTGGACTATCAAAAGTACCCCTGAGTGTGCGTCAAGCATGTATTTATGACGATCATACTAGGAGGG	guanine nucleotide binding protein, alpha q polypeptide
Gnas	NM_010309.3	553040H020Rik, A830027G11Rik, C130027O20Rik, GP5A, GSP, Galphas, Gnas1, Gnasx, Gas, Nesp, Nesp1, Oesd-Sm1, Oesdsm1, P1, P2, P3, P4P1A, P4P1B, P4H	Extracellular Region, Intrinsic To Membrane, Membrane, Cytoplasm, Vesicle, Cytoplasmic Vesicle, Lipid Raft, Cell Projection, Ruffle, Endosome, Membrane Fraction, Plasma Membrane, Energy Reserve, Metabolic Process, Signal Transduction, Skeletal Development, Behavior, Sensory Perception Of Chemical Stimulus, G Protein Signaling Adenylate Cyclase Activ	CAGTTCAGATGGACATCACTTGAAGCTGATGAAGCTGGCCAACTTGACTCCCACTGAACTTCTATGAGCATGCCAAGGCTCTGGGGAGATGAGG	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus
Gnb1	NM_008142.3	AA409223, C77571, Gnb-1	G Protein Signaling Coupled To Ip3 Second Messenger, Phospholipase C Activating, Signal Transduction, Sensory Perception Of Taste, Cell Proliferation, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Binding, G-protein Activity, G-protein Binding	GGCATACCTCTCTGCGAATAATGTGGCGTGTGGTGGCTGGATAACATCTGCTCCATTAACACCTGAAAACCTGGTGAAGGAAATGCTGGTGTAGT	guanine nucleotide binding protein (G protein), beta 1
Gngt1	NM_010314.2	Glyt1, Gng1	Membrane, Plasma Membrane, Signal Transduction, Phototransduction, G Protein Coupled Receptor Protein Signaling Pathway, Protein Localization, Opase Activity	GAAAGAGATGACACTGGAGAGATGATGGTTCCAATGTTGTGAGAAAGTGAAGATATATTAAGAAAGAGCTGTGAGAAGACCTCTAGTGAAGGGG	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1
Gpr44	NM_009621.2	Ch2, Gpr45, Ptgdr2	Membrane, Integral To Membrane, Integral To Plasma Membrane, Plasma Membrane, G Protein Signaling Adenylate Cyclase Inhibiting Pathway, Signal Transduction, Calcium Mediated Signaling, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	GAAGCGCTCTGCTCACTTGGAGAGATGTCAGCTCCAAACACACAGCACTCTGACCTCCGCTCATCATGACCACTGGTGTGCTGTGGCACGGG	G protein-coupled receptor 44
Grb2	NM_008163.3	AA408164, Ash	Golgi Apparatus, Membrane, Cytoplasm, Nucleus, Endosome, Protein Complex, Plasma Membrane, Vesicle, Membrane, Positive Regulation Of Signal Transduction, Insulin Receptor Signaling Pathway, Regulation Of MapK Cascade, Ras Protein Signaling Transduction, Anatomical Structure Formation, Aging, Dna Damage Response, Signal Transduction, Protein Domain Specific B	AGGAGCTGTAAGAGACAGAGATGTTTCCCATCTGTAATGGCCGAGAGCTCGAAGCTCAGCTTTTACTTTGTGAGCTGCAACACTGCTTCACT	growth factor receptor bound protein 2
H2-Ea-ps	NM_010381.2	A1323765, E-alpha4, H2Ea, H2-Ea, H2Ealpa, Ia-3, Ia3	Transduction, Anatomical Structure Formation, Aging, Dna Damage Response, Signal Transduction, Protein Domain Specific B	ATCATGAAGGTTTAAAAAACCAATGTTGAGAACCCGCAAGGAGCGCTGTGAGATACCTGGAGGCAATGCCCTCAAGTAAAGTTCAGTGAAGAA	histocompatibility 2, class II antigen E alpha, pseudogene

Continue Table S1: Nanostring nCounter SC Mouse Inflammation V2 Panel Gene List

H2-Eb1	NM_010382.2	H2Eb, H2Eb, Ia-4, Ia4	External Side Of Plasma Membrane, Membrane, Integral To Membrane, Lysosomal Membrane, Protein Tetramerization, Immune Response	AAACATGTCTGCTGGCCCACTCCCTCCAGACACTGCTCTCCAGACCTGGCTCTCTGATTCCTCCCTGG GAGATGTGTCTGCTGATGGTGT CTACACACTGAATTTGGTGGCTACTCTCTTTGGTGAAGCCGGGGATTCATTTTCCATCAAGCAGGTTAAAGAT	histocompatibility 2, class II antigen E beta
Hc	NM_010406.1	C5, C5a, He	Extracellular Region, Extracellular Space, Soluble Fraction, Inflammatory Response, Positive Regulation Of Angiogenesis, Innate Immune Response	TCACCTGAGCAGGGCGTAGGA	hemolytic complement
Hdac4	NM_207225.1	4932408F19Rik, AID47265	Sarcomere, Cytoplasm, Nucleus, Cytosol, Histone Deacetylase Complex, Positive Regulation Of Transcription, Dna Dependent, Positive Regulation Of Cell Proliferation, Chromatin Remodeling, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Transcription Dna Dependent, Skeletal Development, Negative Regulation Of Transcription Dna Dependent	ACAGCGTGAAGTCTGGCAGCCCTCAGACGGTGGTATGCCTAGCCAAAGTGGTCCCGCATGGTGTACTGG TGTACTCGGGCTGATGCTGTG	histone deacetylase 4
Hif1a	NM_010431.2	AA959795, HIF1alpha, MOP1, hHLH78	Cytoplasm, Nucleus, Transcription Factor Complex, Nucleolus, Positive Regulation Of Transcription, Dna Dependent, Positive Regulation Of Cell Proliferation, Negative Regulation Of Apoptosis, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Signal Transduction, Transcription Dna Dependent, Negative Regulation Of Growth, Epithelial T	ACCATGATATGTTTAAAGCAGACGTCCACAGCAGCAGTACAGGATGCTGCCAAAAGAGGTGGATATGCTCGG GTTGAACTCAAGCACTGCTCAT	hypoxia inducible factor 1, alpha subunit
Hmg1	NM_010439.3	DEF, HMG-1, Hmg1, SBP-1, amphoterin, p30	Cell Surface, Extracellular Region, Cytoplasm, Nucleus, Extracellular Space, Condensed Chromosome, Neuron Projection, Nucleolus, Soluble Fraction, Chromosome, Positive Regulation Of Cell Proliferation, Nervous System Development, Neurite Development, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Positive Regulation Of Caspase Activity	GTGGACTTATAGGATCAAGCAATCGAACCTGTCTGTGGAAGCAGTGAAGAAAGTCTTATCTATCTTACAG AGGACTCTTCTTAAAGCCGAT	high mobility group box 1
Hmg2	NM_028252.3	C80539, HMG-2, Hmg2	Cytoplasm, Nucleus, Perinuclear Region Of Cytoplasm, Extracellular Space, Condensed Chromosome, Protein Complex, Nucleolus, Soluble Fraction, Chromosome, Positive Regulation Of Transcription, Dna Dependent, Nervous System Development, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Negative Regulation Of Transcription Dna Dependent	ATGTTGGGAACTGTGTAGATGTTGAAAGTATGATACAGGCTGGTGTGGGCGACATCATGCAATCCAG AGTGGAGGTAGAGAGGGCAG	high mobility group box 2
Hmg1	NM_028251.3	HMG-14, Hmg14	Chromatin, Cytoplasm, Nucleus, Establishment And Or Maintenance Of Chromatin Architecture, Chromatin Binding, Dna Binding	CCCTTGCCTCGCAACTGTGATCTGTGGTCTGAGGAGTCATTTCCTAACADTGTTGATATGCTGTGGAAG ATGGAAGTCTGAGTCTGTG	high mobility group nucleosomal binding domain 1
Hras1	NM_02824.2		Golgi Apparatus, Membrane, Microsome, Plasma Membrane, Soluble Fraction, Positive Regulation Of Cell Proliferation, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Signal Transduction, Ras Protein Signaling, Transcription, Negative Regulation Of Cell Proliferation, Cell Proliferation Go 0008283, Positive Regulation Of Epithelial Cell	CAATGTTCCAGTCCCTGTGTGTGTATCTGGGCTCCTGAGTATCATCTGGAGGCTGAGTCAACCTCGGAG CCTGTGGTCATGAACCTAAG	Harvey rat sarcoma virus oncogene
Hsh2d	NM_197844.1	ALX, Hsh2	Cytoplasm, Mitochondrion, Positive Regulation Of Signal Transduction, T Cell Activation, SH2 Adapter Activity	CCACCTTTGGCCCTGGGACTGATGAGACTTCTGTATCTGGGTATCTCATCTCTCTTAGTCCCATCTCTGT CCTCAGCCAGAGAACTGT	hematopoietic SH2 domain containing
Hspb1	NM_013560.2	27kDa, Hsp25	Cell Surface, Contractile Fiber, Cytoplasm, Insoluble Fraction, Proteasome Complex, Nucleus, Cytoskeleton, Plasma Membrane, Soluble Fraction, Negative Regulation Of Apoptosis, Response To Stress, Angiogenesis, Regulation Of I KappaB Kinase Nf KappaB Cascade, Ubiquitin Binding, Protein Kinase Binding	AGGGCACACTACCGTGGAGGCTCGTGGCCAAAGAGTCAAGCAGTCAAGGGAGATCAACCTCCGTTACTTCC GAGGCCCCGGCCCAATTTGGGG	heat shock protein 1
Hsp2	NM_024411.3	27kDa, 2810021G24Rik, HSP27, MKBP	Cytoplasm, Nucleus, Soluble Fraction, Response To Heat, Response To Stress	CTGTGTACTCCCTGGTGAATCCAAATCCACCACCCAGGGAGCAGCATCCCTGGGAGTGCATCGGTG CATGTTCAACAGTGTATGTTG	heat shock protein 2
It272a	NM_028903.1	2310061N23Rik, It27, Ig12, Ig12(b1)	Response To Virus, Aging	CTGGGGCAGCTGTTGGAGCTGCTCTGAGCTTGAAGAGTACACCTCTATACAGTCACTCAAGGCTGACAGCA ACCAGGAGATGAAGTTCACAA	interferon, alpha-inducible protein 27 like 2A
Irf4	NM_133871.2	A430056A10Rik, AW261460, MTPAP44, p44	Cytoplasm	CTGACAGATACCACTGTGATCCATGAACCAATCACATCAACCACTCCGAACTATACCATCAAGCCACTGCTGAGG ACCAATTCAGTGTGTGTTT	interferon-induced protein 44
Irf1	NM_008331.2	ISG56, Irf56, P56	Cytoplasm, Response To Virus	CAACTGAGCAGTCCGAAACA ACACAGATGAAGTCACTGAGAGCAACTCGGACAGCTAAATGCCATTTCAAGCACTGATAGAGAGA TGACTCTTGATGAGTTGAGG	interferon-induced protein with tetrapeptide repeats 1
Irf2	NM_008332.2	AV302338, Irf54, P54	Response To Virus	ATGAACTCAACAGCAGACTGTTCTGAAGCAGACTAGAGGAAAGCAAGAGAAAGTACGCTGGGAGA TGCTCTCACTGCTCTCAGTTGA	interferon-induced protein with tetrapeptide repeats 2
Irfb1	NM_010510.1	IFN-beta, IFNB, Irb	Extracellular Region, Extracellular Space, Response To Virus, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Defense Response, Defense Response To Virus, Defense Response To Bacterium, Humoral Immune Response, Caspase Activation, Hematopoietin Interferon Class200 Domain Cytokine Receptor Binding, Transcription Repressor Act	GATGAATCAACAGCAGACTGTTCTGAAGCAGACTAGAGGAAAGCAAGAGAAAGTACGCTGGGAGA TGCTCTCACTGCTCTCAGTTGA	interferon beta 1, fibroblast
Irfg	NM_008337.1	IFN-gamma, Irfg	Extracellular Region, Extracellular Space, Response To Virus, Positive Regulation Of Transcription, Dna Dependent, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Regulation Of Growth, Positive Regulation Of T Cell Proliferation, Defense Response To Virus, Immune Response, Unfolded Protein Response	CTAGCTCTGAGCAATGAAGCTCACACTGACTGCTTGTGCTGAGCTCTCTCATGCTGTCTTCTGGCTTACTG CCAGGCACTGCTTGAAG	interferon gamma
Irgp1	NM_021792.3	2900074L10Rik, AID46432, AW111922, Irgp1, Irgp, Irgp3	Golgi Apparatus, Membrane, Cytoplasm, Endoplasmic Reticulum, Endoplasmic Reticulum, Nucleus, Cytokine And Chemokine Mediated Signaling Pathway, Innate Immune Response, Hydrolase Activity Acting On Acid Anhydrides, Glp Binding, Nucleotide Binding, Identical Protein Binding, Gtpase Activity	GGCAAAAAGGGGATGCTTCCGAGTTAAAGAGTGGCCAGTGGTGAAGAATAGTCTCTCTCAAAGACCA GGATTTAATCCGCAAGCAACCACA	interferon inducible GTPase 1
Irf10	NM_010548.1	CSIF, Irf10, 6629401D04Rik, AID529744, CRF2-4, Ctrb4, D16H21556, D21S58b, Irf10R2, Irf102	Extracellular Region, Extracellular Space, Positive Regulation Of Transcription, Dna Dependent, Negative Regulation Of Apoptosis, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Inflammatory Response, Regulation Of Gene Expression, Positive Regulation Of Cytokine Secretion, Immune Response, Positive Regulation Of Transcription F	GGGCCCTTGTCTGTTGCTCTTCAATGTCTCTCATCCCTGAGTTCAGAGCTCTCAAGAGAGTGTGAAGAACCTCA CTTTACCTGGTCTCAGCCCAAAATGGAATGAGCTGAGAGCTGAGCACTGAAGAACTTATGACTCAT	interleukin 10
Irf10b	NM_008349.5		Receptor Activity	GGGCTTACAGATGCATACTG	interleukin 10 receptor, beta
Irf11	NM_008350.2	IL-11	Extracellular Region, Cytoplasm, Extracellular Space, Positive Regulation Of Cell Proliferation, Positive Regulation Of Mapkkin Cascade, Positive Regulation Of Peptidyl Tyrosine Phosphorylation, Cytokine Activity, Growth Factor Activity	GCGCTGGACATGGGATTTGACGCTCTGCTGTGTCAGCAAGGCTGAGTAGACTGATGCTCTCACTCCGG CATGTACAAAGCTGGGGCTG	interleukin 11
Irf12a	NM_008351.1	IL-12p35, Irf12a, L12a, p35	Extracellular Region, Cytoplasm, Extracellular Space, Positive Regulation Of Cell Proliferation, Immune Response, Positive Regulation Of Cell Adhesion, Cell Cycle Arrest Go 0007050, Cell Migration, Protein Heterodimerization Activity, Cytokine Activity, Growth Factor Activity	TCATGAAGACTCAACGGGCAACCAACAGCAGTGAAGACTGTTACCAGTGAAGTCAACCAAGAGGAGTGT GCTGCTGACTAGAGACTCT	interleukin 12a
Irf12b	NM_008352.1	IL-12b, IL-12p40, Irf12p40, p40	Extracellular Region, Membrane, Cytoplasm, Extracellular Space, Cell Surface Receptor Linked Signal Transduction Go 0007166, Positive Regulation Of T Cell Proliferation, Defense Response To Virus, Cytokine And Chemokine Mediated Signaling Pathway, Positive Regulation Of Cell Adhesion, Cell Cycle Arrest Go 0007050, Cell Migration, Hematopoietin Interf	TGTTAGAGAGACTCAACGAGTCAATGCAAGGGGGAAATGCTGGTCAAGCTCAGATGCTGATACAAAT TCTCTGTCAGCAAGTGGGCTG	interleukin 12b
Irf13	NM_008355.2	Irf13	Extracellular Region, Extracellular Space, Immune Response, Positive Regulation Of Protein Secretion, Hematopoietin Interferon Class200 Domain Cytokine Receptor Binding, Cytokine Activity	AGCTACAACAAAGCACTGTTGGCCAGCGCCCTCTAATGAGGAGAGACATCCCTGGCATCTCAGCTGTGACT GTTCTCTCTCACTCAGACT	interleukin 13
Irf15	NM_008357.1	AID53618, Irf15	Extracellular Region, Cytoplasm, Extracellular Space, Positive Regulation Of Cell Proliferation, Positive Regulation Of Immune Response, Positive Regulation Of T Cell Proliferation, Immune Response, Hematopoietin Interferon Class200 Domain Cytokine Receptor Binding, Cytokine Activity	GTTGTTGAGAGGCTGAGTTCCACTCAACGCTCAGAGAGGTCAGGAAGAATCCACTTGACATGGCCCTCTG GCTCTCAAAGCACTGCTCTCT	interleukin 15
Irf17a	NM_010552.3	Ctla-8, Ctla8, IL-17, IL-17A, Irf17	External Side Of Plasma Membrane, Extracellular Region, Extracellular Space, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Inflammatory Response, Cytokine Activity	ACCTCAAGTCTTAACTCCCTGGGCAAAAGTGAAGTCAAGAGCCCTCAGACTCACTCAACCGTCCAGCTCAC CTGACTCTCCACCGCAATGA	interleukin 17A
Irf18	NM_008360.1	Igf1, Irf18	Extracellular Region, Cytoplasm, Extracellular Space, Apical Plasma Membrane, Regulation Of Cell Adhesion, Inflammatory Response, Immune Response, Angiogenesis, Mapkkin Cascade Go 000165, Interferon Gamma Biosynthetic Process, Response To Hypoxia, Cytokine Activity	CCAGCATCAGGCAAAAGAGCGCCCTCAACCTCCAACTCACTCTCTGGCCAGGAACTGGCTGCATGTC AGAAGACTCTGGTCACTTC	interleukin 18
Irf18ap	NM_010553.2	AcPL, IL-18Rbeta, IL-18RacP, IL-18Rbeta, IL-18acPL	Intrinsic To Membrane, Membrane, Integral To Membrane, Signal Transduction, Cytokine And Chemokine Mediated Signaling Pathway, Innate Immune Response, Receptor Activity, Transmembrane Receptor Activity	CTTGAAGTGGTCCAGCGAGTCCAGGTTCTGAGCCAAATCGTTACCACATGCTGTGAGAACTCCAAAGGTT TATGTTCAAGGGCTCAAT	interleukin 18 receptor accessory protein
Irf1b	NM_008361.3	IL-1beta, Irf1b	Extracellular Region, Vesicle, Secretory Granule, Extracellular Space, Positive Regulation Of Transcription From Rna Polymerase Ii Promoter, Activation Of Mapk Activity, Activation Of Nf KappaB Transcription Factor, Positive Regulation Of I KappaB Kinase Nf KappaB Cascade, Positive Regulation Of T Cell Proliferation, Inflammatory Response, Response	GTTGATCAAGGGCAATAGGACGACTCTCTAGACAGAACTAGCTGTCAAGGTGGGGATGAAATGGTCA AGCCGCACTGAGGCTTTCAT	interleukin 1 beta

Continue Table S1: Nanostring nCounter SC Mouse Inflammation V2 Panel Gene List

Il1r1	NM_001233382.1	CD121a, CD121b, IL-1R, IL-1R1	Cell Surface, Extracellular Region, Intrinsic To Membrane, Membrane, Integral To Membrane, Protein Complex, Plasma Membrane, Signal Transduction, Cytokine And Chemokine Mediated Signaling Pathway, Innate Immune Response, Receptor Activity, Transmembrane Receptor Activity	CTCTCGGATAAAGATAAATGTTGGTGAAGAAATGGCTGAGACACAGAGGGGATATATATGCGGTATGTCCATACCTCCGGGGGAGCA	interleukin 1 receptor, type 1
Il1rn	NM_031167.4	FK30041P17Rk, IL-1ra	Extracellular Region, Cytoplasm, Vesicle, Nucleus, Extracellular Space, Centrosome, Negative Regulation Of Apoptosis, Lipid Metabolic Process, Positive Regulation Of Jnk Activity, Receptor Activity	ACACTGAAATGTCACCTTTGTTAGTGAACATGACGCCAGCTAAGTCTGGAAACACAAAGGGGGCGGGA GATTTTCTTTATCTATGCTAGT	interleukin 1 receptor antagonist
Il2	NM_008366.3	Il-2	Extracellular Region, Extracellular Space, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Positive Regulation Of T Cell Proliferation, Immune Response, G Protein Coupled Receptor Protein Signaling Pathway, Positive Regulation Of Protein Amino Acid Phosphorylation, Carbohydrate Binding, Cytokine Activity, Growth Factor Activity	TTCCAGTCCGTAAGAAATGTCAGCTCGCGGATGCTGCTGAGTTCACCAAGAAAGCTTCAATGGA AGATGTCAGAAATTCATCAGC	interleukin 2
Il21	NM_021782.2		Extracellular Region, Extracellular Space, Positive Regulation Of T Cell Proliferation, Immune Response, Cell Maturation, Hematopoietin Interferon Class200 Domain, Cytokine Receptor Binding, Cytokine Activity	ATGGCCTGGGGATGGTTTGTACTAAGAAAAAGTGTCTGACCTCAGTGCCCTTAAACACAGCAGATCCCG GTGTACCCDCCATAGATAGACCA	interleukin 21
Il2ra2	NM_178258.5	CRF2-10, CRF2-e1, CRF2X, Il-22bp	Extracellular Region, Cytozol, Cytokine And Chemokine Mediated Signaling Pathway, Receptor Activity	TAGCATTCGCTTAGGTTCTCTCATCTACTCTTGAGGATGCAACAGAAATACACCACCTGTGTATCTCGAGG CCCCAGAGTCCGATTCAGC	interleukin 22 receptor, alpha 2
Il23a	NM_031252.1	IL-23, p19	Extracellular Region, Extracellular Space, Response To Virus, Positive Regulation Of Transcription From Rna Polymerase II Promoter, T Cell Proliferation, Positive Regulation Of T Cell Proliferation, Inflammatory Response, Immune Response, Innate Immune Response, Tissue Remodeling, Cytokine Activity	CAAGGACAAAGCCAGTCTGCTCCAAAGATCCGCCAGCTGTGGCTTTTATAGCACTGCTGACTGTGACAT CTTCAAAGGGAGGCTGCTCTA	interleukin 23, alpha subunit p19
Il23r	NM_144548.1	IL-23R	Membrane, Integral To Membrane, Integral To Plasma Membrane, Plasma Membrane, Jak Stat Cascade, Inflammatory Response, Cytokine And Chemokine Mediated Signaling Pathway, Innate Immune Response, Receptor Activity	AAGTATTTGGTGGTCCAGCTGCTCAATCCCTAGGATGGAAGCAACCACTCAACGCTCATGATGAT ATAGTGATACCTTGGCTCCA	interleukin 23 receptor
Il3	NM_010558.4	BPA, Cdmu, HCGF, p13, MCGF, PSF	Extracellular Region, Extracellular Space, Positive Regulation Of Cell Proliferation, Negative Regulation Of Apoptosis, Hemopoiesis, Regulation Of Gene Expression, Immune Response, Cytokine And Chemokine Mediated Signaling Pathway, Response To Hormone Stimulus, Positive Regulation Of Protein Amino Acid Phosphorylation, Regulation Of Apoptosis, Response	TGCGCTTATTGTCAGGAGATATAGGGAAGCTCCCAAGCTGAACCTCAAACTGATGATGAAGCCCTCTCG AGGAATAAGGCTTGGGAGAG	interleukin 3
Il4	NM_021283.1	BSF-1, Il-4	External Side Of Plasma Membrane, Extracellular Region, Extracellular Space, Positive Regulation Of Transcription, Positive Regulation Of Cell Proliferation, Negative Regulation Of Apoptosis, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Negative Regulation Of Transcription Dna Dependent, Regulation Of Phosphor	TGCTGAAGAAAGACTGATGTTCTGATGAGCTGACAGAGACTTTGGGGCTTTGGATGCCGTGATCATGGTA AGCTCCACATGAATGATCCA	interleukin 4
Il5	NM_010558.1	Il-5	Extracellular Region, Extracellular Space, Soluble Fraction, Positive Regulation Of Transcription, Positive Regulation Of Cell Proliferation, Immune Response, Positive Regulation Of Transcription Factor Activity, Cytokine And Chemokine Mediated Signaling Pathway, Positive Regulation Of Peptidyl Tyrosine Phosphorylation, Cytokine Activity	CAATGAGAGATGAGGCTCTGCTCCCTACTCAAAAATCCACCACTGATGATGGAAATCTTCAGGGGCTAGA CATACTAGAGATCAAACTGTC	interleukin 5
Il6	NM_031168.1	Il-6	External Side Of Plasma Membrane, Extracellular Region, Extracellular Space, Positive Regulation Of Transcription, Positive Regulation Of Transcription, Positive Regulation Of Cell Proliferation, Negative Regulation Of Apoptosis, Neurite Development, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Positive Regulation	CTCTCTCAAGAGACTCCATCCAGTTCCTTGGGACTGATCGTGGTGAACCAAGGCGCTTCCCTACTCCAAAT ATCCGAGAGAGACTCAGAG	interleukin 6
Il6ra	NM_010559.2	CD126, IL-6R, Il6r	Cell Surface, Extracellular Region, Membrane, Integral To Membrane, Extracellular Space, Apical Plasma Membrane, Positive Regulation Of Cell Proliferation, Cytokine And Chemokine Mediated Signaling Pathway, Positive Regulation Of Mapkk Homodimerization Activity, Receptor Activity	CACTCTCAAGAGACTCCATCCAGTTCCTTGGGACTGATCGTGGTGAACCAAGGCGCTTCCCTACTCCAAAT ATCCGAGAGAGACTCAGAG	interleukin 6 receptor, alpha
Il7	NM_008371.2	A630026I06Rk, Il-7, Ilb368	Extracellular Region, Extracellular Space, Negative Regulation Of Apoptosis, Regulation Of Gene Expression, Immune Response, Anti Apoptosis, Negative Regulation Of Catalytic Activity, Hematopoietin Interferon Class200 Domain, Cytokine Receptor Binding, Cytokine Activity, Growth Factor Activity	AAACATTCATGGTGAACCACTGGGGAGTGAAGCTCTCTTTAGACTGGAGACTGAGAGGGCTCACGGGTGAT GGATAGCTCTGAAACACAGA	interleukin 7
Il9	NM_008373.1	Il-9, P40	Extracellular Region, Extracellular Space, Soluble Fraction, Immune Response, Hematopoietin Interferon Class200 Domain, Cytokine Receptor Binding, Cytokine Activity, Growth Factor Activity	TCTGTTTGGCTTCAAGTCTGCTGGGCGCAGAGATGACGACCACTGGGGCTGACAGACCAATACCTTATT GAAATCTGAAGATGATCCAC	interleukin 9
Ilf1	NM_008390.1	AU020929, Ilf-1	Nucleus, Positive Regulation Of Transcription, Dna Dependent, Positive Regulation Of T Cell Proliferation, Kinase Nf Kappab Cascade, Positive Regulation Of Cytokine Secretion, Response To Bacterium, Regulation Of Transcription, Negative Regulation Of Transcription From Rna Polymerase II Promoter, Positive Regulation Of Transcription, Identical Pr	TGTTCCGAGTGGGGCCATCCACAGCGCCATACAAAGCAGGAAAGAAAGAGCCAGATCCCAAGCATGGAGGCG AAACCTCCGTTGGCCATGAATC	interleukin regulatory factor 1
Ilf3	NM_016849.3	C920001K05Rk, Ilf-3	Nucleus, Transcription Dna Dependent, Regulation Of Transcription, Dna Dependent, Transcription Factor Activity, Dna Binding	GCTGCTACCAAAAGAGTATTGCGGCGCATCATCTGCTGCTGACTGGCTGAGTGGTGTATTCTTCAACAGG CTGAGTCTCCCATCTGAGCT	interleukin regulatory factor 3
Ilf5	NM_012057.3	AW491843, Ilf5	Nucleus, Transcription Dna Dependent, Regulation Of Transcription, Dna Dependent, Transcription Factor Activity, Dna Binding	CTTTATGACCCAGGATCCAAATACCCAGGGTAGCCCACTTTAGAGTTCGCCCAATCTTCTAGCAAACTGCCCA AGGAGTGTGGGGGCTTCC	interleukin regulatory factor 5
Ilf7	NM_016850.2		Nucleus, Cytoplasm, Nuclear Chromatin, Transcription Factor Complex, Positive Regulation Of Transcription, Dna Dependent, Positive Regulation Of Cell Proliferation, Negative Regulation Of Apoptosis, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Negative Regulation Of Transcription, Dna Dependent, Negat	CGCTGTGCACTCCACAGCAGCGGTTTTATCTGCGCCAGCAATCAGGGATGATCCATGATCCCATAGGTT GTAGCCATGAGCGGAGGCTGG	interleukin regulatory factor 7
Ilfb2	NM_008404.4	2E6, A1528527, C618, LAD, LCAMB, Lfa1, MF17	Cell Surface, Membrane, Integral To Membrane, Lipid Raft, Membrane Fraction, Integrin Complex, Regulation Of Peptidyl Tyrosine Phosphorylation, Activation Of Nf Kappab Transcription Factor, Multicellular Organismal Development, Cell Cell Adhesion, Cell Matrix Adhesion, Positive Regulation Of Angiogenesis, Endothelial Cell Migration, Protein Complex Bin	GCTCGTTCCTTCCGCGATATATCAAGTCTGCGAGGTTTTGACGGAGTCTGCTCGAGCTGCCAATCTTCCGCG AGAGCCCTAAGAAATTCGCG	integrin beta 2
Jun	NM_010591.2	AP-1, Junc, c-jun	Nucleus, Cytoplasm, Nuclear Chromatin, Transcription Factor Complex, Positive Regulation Of Transcription, Dna Dependent, Positive Regulation Of Cell Proliferation, Negative Regulation Of Apoptosis, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Negative Regulation Of Transcription, Dna Dependent, Negat	CGCGACAGAAAGTGGACTTTTGGTAACTGACCAAGAACTGATGCACTTAACATTCAGTATTAA AGGGGGGGGGGGGTTACA	jun proto-oncogene
Kaap1	NM_016679.4	INRF2, mKIA0132	Cytoplasm, Endoplasmic Reticulum, Nucleus, Focal Adhesion, Centrosome, Transcription Dna Dependent, Regulation Of Transcription, Dna Dependent	TCTATTGCTGCTTGGCATGATCTGCTGACAGAGGCTCTGCTTCTGGGACACACAGTGTCTGTGCA GTTTCAGGGCATGAAAGCCA	kelch-like ECH-associated protein 1
Kng1	NM_023125.3	Kng	Extracellular Region, Microsome, Extracellular Space, Blood Coagulation, Inflammatory Response, Negative Regulation Of Cell Adhesion, Negative Regulation Of Map Kinase Activity, Positive Regulation Of Mapkk Cascade, Protease Inhibitor Activity, Receptor Binding	ACTTGATTTTACAGTGTCTCTTCAACCCATCCCTGACATGAGGGAATGGAGGCTCTCTAAAGCTGATGTT GCCACAGACGCTTATGATCT	kininogen 1
Link1	NM_010717.2		Golgi Apparatus, Cytoplasm, Nucleus, Perinuclear Region Of Cytoplasm, Focal Adhesion, Neuron Projection, Protein Amino Acid Phosphorylation, Phosphorylation, Nucleotide Binding, Zinc Ion Binding, Protein Kinase Activity, Kinase Activity, Protein Serine Threonine Kinase Activity, Protein Heterodimerization Activity, Transferrase Activity, Transferring Phos	CCACAAGTCTGCTGGCTGGAGAAAGGAGGAGTGGTGGGCCCATCTTGGCTGGCTGGACATGATCGATGAAA AGAATCAGCTGAAGACTTACGG	LIM-domain containing, protein kinase
Lta	NM_010735.1	LT, LT- β , LT- α , LT β , LT α , Lta, TNF- β , TNFSF1, Tnb, Tnf β , Ilb, Ilb382	Extracellular Region, Membrane, Extracellular Space, Positive Regulation Of Cell Proliferation, Inflammatory Response, Immune Response, Cell Proliferation, Go	AAAGCGGAAATGAAAGCCCTCAGTACAACTAGTCCACAGCAAGGTGTCTCACTCAGCAGAGCCCT ATCTAGAGAGAGATGGGAGAGA	lymphotoxin A
Ltb	NM_008518.2	A1662801, LTbeta, Tnf α , Tnf β , p33	Membrane, Integral To Membrane, Extracellular Space, Plasma Membrane, Immune Response, Cytokine Activity	ATCAGAGCGTGGTGGAGAGATCATTTGGCTCAGGACAGGCTCAGAAAGAGCTGATGACGAAACCCCTG GTGCACTTCCCTCCACCTCTAG	lymphotoxin B
Ltb4r1	NM_008519.2	BLT1, BLTR, Ltb4r, mBLTR	Membrane, Integral To Membrane, Plasma Membrane, Signal Transduction, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	AAACCCCTGCTTTTGGCTGCAACAGCTACATCTCTGAGAGCACTTCTCTGCTGGTGGATGCTCCCTGCTGTG TTGGCATTTGCTACTGCTCT	leukotriene B4 receptor 1
Ltb4r2	NM_020490.2	S830462007Rk, BLT2, LTB4-R2, LTB4-R2, LTB4-R2	Membrane, Integral To Membrane, Membrane Fraction, Plasma Membrane, Signal Transduction, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	GCACAGGGTGGGTGCTGGTGGCCGATGCTGCTGGCTTGGCTGCTGGCTGGCTTCCACACCGGCTAAT CTCTACAGGGGGTGGCCCGCT	leukotriene B4 receptor 2
Ly96	NM_016823.1	ESOP-1, MD2, MD2	Extracellular Region, Inflammatory Response, Innate Immune Response	GAGCTCTAAAGAGAGAGATGTGAATACCAATACCATCTCTTGGGAGGATACTTCTTAAGGGCCATTACA GATGTGTGCAAGACTTATCC	myophycine antigen 96

Continue Table S1: Nanostring nCounter SC Mouse Inflammation V2 Panel Gene List

Maf	NM_010755.3		Nucleus,Transcription Dna Dependent,Regulation Of Transcription,Dependent,Sequence Specific Dna Binding,Transcription Factor Activity,Dna Binding	TGGGGAGGGCAACTTGGCTAAGTGGGGGGGGGGGAGCGGCTTAGGTTCTAAGTTCCCTGGGCTGAAAGCTGG GCTCAATGAAATGAGGCTGTG	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)
Mafg	XM_001002362.1	AA545192, C630022N07Rk	Nucleus,Regulation Of Cellular Ph,Transcription Dna Dependent,Regulation Of Transcription,Dependent,Regulation Of Cell Proliferation,Sequence Specific Dna Binding,Transcription Factor Activity,Dna Binding	AAGATGTCTCTGGGAAGGCTTTAGAAAGCTGAAATGAGGTTGAGCCGGAGGGGGGGCTGACTGAGGAGGGAC CTGTTTGGCTTTGTTCCCTGGCC	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)
Mafk	NM_010757.2	AW061068, NF-E2, Nfe2u	Nucleus,Nervous System Development,Transcription Dna Dependent,Regulation Of Transcription,Dependent,Sequence Specific Dna Binding,Transcription Factor Activity,Dna Binding	GGGTAGACACCATTGCTGCTCCCTTCTGGGCTGGCCGCTCTGCTCTTCAAGGCGCTCAACCTGCTTAG CTCTAGAGCCAGGCTCATGT	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)
Map2k1	NM_008927.3	MAPKK1, MEKK1, Mek1, Prkml1	Cdcp1 Apparatus,Cytoplasm,Nucleus,Cytosol,Cytoskeleton,Perinuclear Region Of Cytoplasm,Cell Cortex,Microtubule,Dendrite,Plasma Membrane,Soluble Fraction,Positive Regulation Of Cell Differentiation,Activation Of Mapk Activity,Response To Oxidative Stress,Keratinocyte Differentiation,Negative Regulation Of Cell Proliferation,Cell Proliferation	CTTTGTGCTGGGGCTATTGTCGTCTATCAAAACACTGCCAGCTGAACACAGTAAACCTAGTGAACCTGGTG GTGCTTCTTACTGATGTTGCA	mitogen-activated protein kinase kinase 1
Map2k4	NM_009157.4	JNKK1, MEK4, MKK4, PRKMK4, Sek1, Serk1	Cytoplasm,Nucleus,Cytosol,Activation Of Jnk Activity,Jnk Cascade,Response To Stress,MapkK Cascade Go 0000165,Protein Amino Acid Phosphorylation,Phosphorylation,Positive Regulation Of Protein Amino Acid Phosphorylation,Apoptosis Go,Nucleotide Binding,Protein Kinase Activity,Kinase Activity,Protein Serine Threonine Kinase Activity,Protein T	CTGCCAGACACCATGTCGAATAGACTGGTGTGTTCCATCATGTGTATCTCTGCTAGCTAGCTGTGCAT CCCTGTAATACCTGACTGATC	mitogen-activated protein kinase kinase 4
Map2k6	NM_011943.2	MEK6, MKK6, Prkm6, SAPKK3	Cytoplasm,Nucleus,Cytoskeleton,Transcription Dna Dependent,Activation Of Mapk Activity,Response To Stress,Regulation Of Transcription,Dependent,MapkK Cascade Go 0000165,Protein Amino Acid Phosphorylation,Phosphorylation,Apoptosis Go,Nucleotide Binding,Protein Kinase Activity,Kinase Activity,Protein Serine Threonine Kinase Activity,Prot	GGGCTTAAGTCCAAAGAGGGTTGAACAGCTGAGCCAGTCCACCOCGGCTGGGATTTAGACTCCAGG GCTGATGATCTATTGGAACACAG	mitogen-activated protein kinase kinase 6
Map3k1	NM_011945.2	MAPKKK1, MEKK1, Mekk	Cytoplasm,Cytoskeleton,Membrane Fraction,Protein Polyubiquitination,Protein Oligomerization,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Activation Of Jnk Activity,Regulation Of Cell Migration,Protein Amino Acid Autophosphorylation,Jnk Cascade,Positive Regulation Of Map Kinase Activity,Apoptotic Mitochondrial Change	CAGCAGATCCCTCCGCTTCAAAAGATTGGCCGAGCCATGATTCAGGTTGGTGAAGCACTGGTGGCTCTTA TTCTAGAAAACCTGAGCTAA	mitogen-activated protein kinase kinase kinase 1
Map3k5	NM_008580.4	7420452D20Rk, ASK, ASK1, MAPKKK5, MekK5	Cytoplasm,Endoplasmic Reticulum,Activation Of Mapk Activity,Jnk Cascade,Positive Regulation Of Caspase Activity,Response To Stress,MapkK Cascade Go 0000165,Protein Amino Acid Phosphorylation,Innate Immune Response,Phosphorylation,Apoptosis Go,Caspase Activation,Nucleotide Binding,Protein Homodimerization Activity,Protein Kinase Activity,K	CATCATCTCTACTGGGATTAATTCGATCTCACTCCACTCCCTGAAGAAATTTTGGCAGAGAATCTGTGTC ACGGGAACTACACTGATC	mitogen-activated protein kinase kinase kinase 5
Map3k7	NM_172688.2	B430101B05, C87327, Tak1	Membrane,Cytoplasm,Plasma Membrane,Soluble Fraction,Negative Regulation Of Apoptosis,Signal Transduction,Transcription Dna Dependent,Activation Of Mapk Activity,Jnk Cascade,Positive Regulation Of I Kappab Kinase Nf Kappab Cascade,Response To Stress,Angiogenesis,Regulation Of Transcription,Dependent,Transforming Growth Factor Beta Recept	CAATACTAAGTGTCCCACTGACTATTAAAGGTAGTGGTGGCACTGCTGTAAGAGCAAGTACTACTGA CTTTCGATGATCTATTGATGCTG	mitogen-activated protein kinase kinase kinase 7
Map3k9	NM_177395.2	E130314H24Rk, Mk1, Prke1	Transcription Dna Dependent,Protein Amino Acid Autophosphorylation,Response To Stress,Regulation Of Transcription,Dependent,Protein Amino Acid Phosphorylation,Phosphorylation,Apoptosis Go,Nucleotide Binding,Protein Kinase Activity,Kinase Activity,Protein Serine Threonine Kinase Activity,Protein Tyrosine Kinase Activity,Transferase Actv	AATGCCCTTAGGCAACAGTGCTTAGTGTGCTGATCTCACTGTAGCTGGAGGCTGGGAAACATTTCT TGATCTCTGTTTTTCAATGCG	mitogen-activated protein kinase kinase kinase 9
Mapk14	NM_011951.2	CSBP2, Cxk1, Cxlp1, Mx2, PRKM14, PRKM15, p38, p38-alpha, p38MAPK, p38a, p38alpha	Synapse,Pole,Cytoplasm,Cytosolic Part,Nucleus,Cytosol,Mitochondrion,Soluble Fraction,Glucose Metabolic Process,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Transcription Dna Dependent,Protein Amino Acid Autophosphorylation,Fatty Acid Oxidation,Response To Stress,Angiogenesis,Protein Kinase Cascade,Regulation Of Transcription,Dependent,MapkK Cascade Go 0000165,Protein Amino Acid Phosphorylation,Phosphorylation,Innate Immune Response,Phosphorylation,Apoptosis Go,Nucleotide Binding,Protein Kinase Activity,Protein Tyrosine Kinase Activity,Transferase Actv	GAAGACCTCTCACTGGAACTCCAAATACCTCAAGTCCCTCTTGTGAAGATCTCTGATGGTGAAGGGGT GCTGATGATCTATTGATGCTG	mitogen-activated protein kinase 14
Mapk3	NM_011952.2	Etk-1, Erk1, Erk2, Esk1, Mnk1, Map2k, Prkm3, p44, p44erk1, p44mapk	Nucleoplasm,Cytoplasm,Innate Immune Response,Positive Regulation Of Translation,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Signal Transduction,Transcription Dna Dependent,Response To Toxin,Organ Morphogenesis,Regulation Of Transcription Factor Activity,Protein Complex A	ACCTTAATTGCATCAATTAACATGAAGGCCGAACTACCTGAGCTGCTGCCCTGAAAACAAGGCTGGGCCA GCTTCTTCTTAATGCTGACTC	mitogen-activated protein kinase 3
Mapk8	NM_016700.3	A1849689, JNK, JNK1, Prkm8, SAPK1	Cytoplasm,Neurite Development,Signal Transduction,Response To Heat,Jnk Cascade,Inflammatory Response,Regulation Of Transcription,Dependent,Response To Uv,Positive Regulation Of Cell Migration,MapkK Cascade Go 0000165,Protein Amino Acid Phosphorylation,Phosphorylation	GAACAACGGCTAAATACGCTGGATAGTGTGAAGAACTGTTCCCGATGTGTTTTCCAGCTGACTCAGACAT AACCAACTAAGCCGCTGAG	mitogen-activated protein kinase 8
Mapkap2	NM_008551.1	AA960234, MAPKAP-K2, MK-2, MK2, Rps6kc1	Cytoplasm,Nucleus,Inflammatory Response,Response To Stress,Protein Amino Acid Phosphorylation,Phosphorylation,Response To Dna Damage Stimulus,Nucleotide Binding,Protein Kinase Activity,Kinase Activity,Protein Serine Threonine Kinase Activity,Transferase Activity,Transferring Phosphorus Containing Groups,Atp Binding	GTAGCCTGCTGCCCTTCTGCCACGATTAACCCACTTCTGAGTCTCTGAAATTTTGAACCTCTCAATGGG CTGTCACTCCACCGGTGAG	MAP kinase-activated protein kinase 2
Mapkap5	XM_990515.1	MK5, PRAK	Cytoplasm,Nucleus,Protein Amino Acid Autophosphorylation,Regulation Of Translation,Ras Protein Signal Transduction,Response To Stress,Protein Amino Acid Phosphorylation,Phosphorylation,Nucleotide Binding,Protein Kinase Activity,Kinase Activity,Protein Serine Threonine Kinase Activity,Transferase Activity,Transferring Phosphorus Containing	GGCTGAGGAGGCAACACTCTCCGACCCGCTAAGCTGACGAGGACGACGATCCGCGACGCTCCGCGCT CTTACGTCTTCAACCCAGCGCCAC	MAP kinase-activated protein kinase 5
Masp1	NM_008555.2	AW048060, CCP1I, Carf, Masp1/3	Extracellular Region,Extracellular Space,Proteolysis,Innate Immune Response,Serine Type Peptidase Activity,Protein Homodimerization Activity,Calcium Ion Binding,Peptidase Activity,Serine Type Endopeptidase Activity	COGGAGGAGGTTTGGAACTCAAGCTTTACTCATGCACTCACTGGAATCTCCTCTTGTGTAACGACTATGTG GAGGTAGAAAACAGAACGAC	mannan-binding lectin serine peptidase 1
Masp2	NM_010787.3	MASP-2, Msp19	Extracellular Region,Proteolysis,Innate Immune Response,Serine Type Peptidase Activity,Calcium Ion Binding,Peptidase Activity,Serine Type Endopeptidase Activity	TAACCTGGTCCAGCTAAAGTCACTTCCACTCCGACTCCCAAGTGAAGAGCGCTTCCAGCGTTGAGCGCTT TATGAGGCGAGGATGTGATG	mannan-binding lectin serine peptidase 2
Max	NM_008558.1	AA960152, A1875693, bHLH4, bHLH45, bHLH46, bHLH47, bHLH48	Complex Binding,Sequence Specific Dna Binding,Transcription Factor Activity,Protein Heterodimerization Activity,Dna Binding	CCGGCCCGCTCGACTGGCCGCTCCCTGGCCCTAGGAAATGAGCGATAAGTACATCGAGTGGAGGCGCA CGAAGAACAGGGAGGTTCACTCT	Max protein
Mb12	NM_010778.1	L-MBP, MBL, MBL-C, MBP-C	Extracellular Region,Extracellular Space,Collagen,Protein Oligomerization,Innate Immune Response,Sugar Binding,Receptor Binding	CCCTGAGAACTGGGTGCTCTCTCTCTGATGAAAAGTTGGAAGAAATTTTGTGAGCAGTGTAAAAGATGA GGCTTGACAGGATGAAGGCGCT	mannose-binding lectin (protein C) 2
Mef2a	XM_976032.1	A430079H05Rk	Nucleus,Nuclear Chromatin,Positive Regulation Of Transcription,Dependent,Nervous System Development,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Transcription Dna Dependent,Multicellular Organismal Development,Regulation Of Transcription From Rna Polymerase II Promoter,Regulation Of Transcription,Dependent,Neg	AAGTATCATCAATGGCTCTTACAGAACTGTGTATGCACTGTGCTCTCAACATTTTACAAAACAAGCAAC AAACAAGAAGCTGATGGAAG	myocyte enhancer factor 2A
Mef2b	NM_01045484.1	AH451606	Nucleus,Regulation Of Transcription,Dependent,Transcription Factor Activity	GACAGCTGGCCACGGTACGCTCCCAAGGTTCTCCAGGCTCCACAGATTCGCGAAGTCCAGGTTCCCTATCC ACCAGGAGGACGACGAGGCGCA	myocyte enhancer factor 2B
Mef2c_Mm	NM_025282.2		Nucleus,Positive Regulation Of Transcription,Dependent,Nervous System Development,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Transcription Dna Dependent,Multicellular Organismal Development,Regulation Of Transcription,Dependent,Transcription From Rna Polymerase II Promoter,Apoptosis Go,Protein Homodimerizat	ATAAATCGTAAGCCGATCTCCGCTTCTTATCCACCTGGCAGCAAGAACGATGCCATCGATGAATCAAAGGATA ATAACTCCAGTGGCTCAGT	myocyte enhancer factor 2C
Mef2d	NM_133665.3	C80750	Regulation Of Translation,Response To Stress,Protein Kinase Cascade,Protein Amino Acid Phosphorylation,Phosphorylation,Nucleotide Binding,Protein Kinase Activity,Kinase Activity,Protein Serine Threonine Kinase Activity,Transferase Activity,Transferring Phosphorus Containing Groups,Atp Binding	TCAGCTGTAAGAGGATGCGGCTGGATCTGGACATTAAGGATGTGCCATCCCTCCTTCAAGCTCCCTGAT GAAGATTTGCAACTCTCACCCG	myocyte enhancer factor 2D
Mnk1	NM_021461.4	2410048M24Rk, Mnk1	Proteinaceous Extracellular Matrix,Extracellular Region,Nucleus,Dendrite,Extracellular Space,Extracellular Matrix,Protein Complex,Regulation Of Cell Migration,Proteolysis,Zinc Ion Binding,Calcium Ion Binding,Metalloproteinase Activity,Protein Complex Binding,Peptidase Activity,Metalloendopeptidase Activity	AAGGCATTCGCTCCGCTGATCAAGCCAGAAACATCTGTGTAATCCAGAAAGGTTGCTCCGGTGAATTT GTGACTTTGACTTGGCCAGTGG	MAP kinase-interacting serine/threonine kinase 1
Mmp3	NM_010809.1	SLN-1, SLN1, STR-1, Stry1, Str1	Proteinaceous Extracellular Matrix,Extracellular Region,Extracellular Space,Extracellular Matrix,Protein Complex,Skeletal Development,Embryo Implantation,Proteolysis,Response To Oxidative Stress,Positive Regulation Of Angiogenesis,Tissue Remodeling,Response To Drug,Zinc Ion Binding,Metalloproteinase Activity,Protein Complex Binding,Peptidase	TCCTTGTGAAGAAAGTGGTCTTGTCAAGCTGTGCTATGGCAGACCAACAGGAGCTATGATGACCAACGCTCAAC GTCAAGTTGCAAGGATGTTCA	matrix metalloproteinase 3
Mmp9	NM_013599.2	AW743869, BMMMP9, C1g4b, MMP-9, pro-MMP-9	Proteinaceous Extracellular Matrix,Extracellular Region,Extracellular Space,Extracellular Matrix,Protein Complex,Skeletal Development,Embryo Implantation,Proteolysis,Response To Oxidative Stress,Positive Regulation Of Angiogenesis,Tissue Remodeling,Response To Drug,Zinc Ion Binding,Metalloproteinase Activity,Protein Complex Binding,Peptidase	CCTCTCAGAGTCTTGTAGTCCGAGACAACTCGCAATGTGGATGTTTTGTGCTATTGCTGATGACCCAGCGG CTCTGATTTCTCAAGGACGG	matrix metalloproteinase 9

Continue Table S1: Nanostring nCounter SC Mouse Inflammation V2 Panel Gene List

Mrc1	NM 008625.1	AWZ59686, CD206, MR	Cell Surface, Membrane, Integral To Membrane, Endosome, Plasma Membrane, Receptor Mediated Endocytosis, Sugar Binding, Receptor Activity, Transmembrane Receptor Activity	GTTCGGAAATTTGAGGGAATGGCTTGGTTGAACGCAATCTGTCTCTTTGCACTGGAAGGAGGGATCC	mannose receptor, C type 1
Mrc2	NM 013606.1	AIS28743, Mrc-2	Cytoplasm, Cytoplasm, Response To Virus, Innate Immune Response, Gtp Binding, Nucleotide Binding, G-protein Activity	GTTCCTCCCTGTGTCTCTCGATTGTGATTCAGGACGAGAAAGGGCTCCCTGGTATACACCCAGCGCT	myxovirus (influenza virus) resistance 2
Myc	NM 010849.4	AU016757, Myc2, Nard, Nrd, bHLHe39	Nucleoplasm, Axon, Cytoplasm, Nucleus, Spindle, Nuclear Body, Protein Complex, Nucleolus, Glucose Metabolic Process, Positive Regulation Of Transcription, DNA Dependent, Positive Regulation Of Cell Proliferation, Chromatin Remodeling, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Positive Regulation Of	CCCTCAAGGTGAACCTCACCAAGAGAACTAGACCTGACTAGACTCGTACAGCGCTTATTCATCGCGAGG	myelocytomatosis oncogene
Myd88	NM 010851.2		Cytoplasm, Cytoplasm, Protein Complex, Plasma Membrane, Response To Virus, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Signal Transduction, Cell Surface Receptor Linked Signal Transduction, Go 0007166, Activation Of NF KappaB Transcription Factor, Ikb, Cascade, Positive Regulation Of I KappaB Kinase NF KappaB I Cascade Inflammation	GCTCGAGGCTACGCTTCTTCCGCCAGGAGGTTGCATCTCTTATCTCCCTGCTTACCATAGAGGCA	myeloid differentiation primary response gene 88
Myo2	NM 010861.3	MLC2, MLC-2v, Mlc2v, Myhc	Myofibril, Cytoskeleton, Myosin Complex, Heart Development, Calcium Ion Binding	TGCTGCTAGGAGGAGTGCATGAAATGATCGAATGATGAAAGAGGCTCCAGGTCATTAATCT	myosin, light polypeptide 2, regulatory, cardiac, slow
Nfat3	NM 010901.2	C80703, DBErd281e, NFAT4, NFATx	Cytoplasm, Nucleus, Cytoplasm, Plasma Membrane, Nucleolus, Positive Regulation Of Transcription, DNA Dependent, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Regulation Of Transcription, DNA Dependent, Heart Development, Cellular Respiration, Transcription Factor Activity, Chromatin Binding, DNA Binding	GGGCTCACCATTGTCCCTGAGTTCTCCCTATCATCAACCCAGAGATACATCTGCGGTGAGGTCATTTATGTTG	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 3
Nfe2l2	NM 010902.3	A1194320, Nfe2	Chromatin, Cytoplasm, Nucleus, Centrosome, Plasma Membrane, Positive Regulation Of Transcription, DNA Dependent, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Unfolded Protein Response, Regulation Of Transcription, DNA Dependent, Protein Domain Specific Binding, Sequence Specific DNA Binding, Transcription	CCAGGAGCAATCAATGAAGCTCACTGCGATTGATCCGAGATACGAGGAGAGTAAAGAAATGCGCCGCC	nuclear factor, erythroid derived 2, like 2
Nfk1	NM 008689.2	NF-KB1, NF-kappaB, NF-kappaB1, p105, p50, p50/p105	Cytoplasm, Nucleus, Cytoplasm, Mitochondrion, Protein Complex, Positive Regulation Of Transcription, DNA Dependent, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Signal Transduction, Transcription Dna Dependent, Negative Regulation Of Transcription, DNA Dependent, Response To Oxidative Stress, Regulation Of Transcription, DNA Dependent	GTCTTACACTAGCCATCCACCTCCAGCTCAGCTGTGGAGGGATCTGCTGGAAGTCACATGGTTGATCTGTG	nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105
Nlr3	NM 145827.3	AGTAVPR1, AIMAVP, Cas1, FCAS, FCU, MWS, Mmig1, NALP3, Pypal1	Cytoplasm, Positive Regulation Of Caspase Activity, Defense Response To Virus, Inflammatory Response, Apoptosis, Go, Caspase Activation, Nucleotide Binding, Apb Binding	TTGTCAGGATCGCATGGTTGTGAGCTCCCAACTCTCTCCAGACGTACATGGAGAAATGCTTCGGGAGA	NLR family, pyrin domain containing 3
Nod1	NM 172729.2	C230079P11, Card4, F830007N14Rk, Nlr1	Membrane, Cytoplasm, Basolateral Plasma Membrane, Plasma Membrane, Interleukin 8 Biosynthetic Process, Defense Response, Activation Of NF KappaB Transcription Factor, Positive Regulation Of I KappaB Kinase NF KappaB Cascade, Defense Response To Bacterium, Regulation Of Apoptosis, Apoptosis, Go, Caspase Activation, Nucleotide Binding, Protein Homodimerization	TGGATCATCTCCGTGTCTCCAGCATCCAGAGGCTGTGAGGGCTCTCTCCAGTTCGGCGACTGCTGTGTG	nucleotide-binding oligomerization domain containing 1
Nod2	NM 145857.2	ACUG, BLAU, CD, Card15, F830032C23Rik, IBD1, Nlr2	Cell Surface, Cytoplasm, Vesicle, Cytoplasm, Plasma Membrane, Protein Oligomerization, Positive Regulation Of Cell Proliferation, Signal Transduction, Defense Response, Activation Of NF KappaB Transcription Factor, Positive Regulation Of I KappaB Kinase NF KappaB Cascade, Inflammatory Response, Activation Of Immune Response, Defense Response To Bacterium	CTGTGAAGAGGGGATATCTCTCGCAAGAGACTCAAGAAATCACTTGGAAATGTGAAGCTCCCAACA	nucleotide-binding oligomerization domain containing 2
Nos2	NM 010927.3	NOS-2, Nos-2, Nos2a, iNOS, iNOS	Cytoplasm, Nucleus, Cytoplasm, Peroxisome, Vesicle Membrane, Signal Transduction, Superoxide Metabolic Process, Regulation Of Phosphorylation, Inflammatory Response, Regulation Of Heart Contraction, Protein Kinase Cascade, Regulation Of Catalytic Activity, Defense Response To Bact	CCCCCTCCCTCCACCTACCAAGTAGTATTTACTTATGAGACTACTAACTCTCTCTCTCTCCCTCCCTCTCT	nitric oxide synthase 2, inducible
Nox1	NM 172203.1	GPB1-2, MOX1, NOH1, NOH1, NOX1a, NOX1alpha, Nox-1	Cell Junction, Membrane, Cytoplasm, Early Endosome, Integral To Membrane, Cell Projection, Endosome, Plasma Membrane, Positive Regulation Of Cell Proliferation, Signal Transduction, Superoxide Metabolic Process, Response To Stress, Angiogenesis, Transport, Cell Migration, Electron Carrier Activity, Oxidoreductase Activity	CTCCAACTGACAGATGATATGACAGTATTCAGAGTATGTCGGCCCTACTGAGAGTATGCCACTGATGCTTGGT	NADPH oxidase 1
Nrc3c1	NM 008173.3	GR, Gd-1, Gf1	Membrane, Cytoplasm, Nucleus, Cytoplasm, Protein Complex, Chromatin Remodeling, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Regulation Of Transcription, DNA Dependent, Anti Apoptosis, Regulation Of Cell Proliferation, Protein Homodimerization Activity, Hormone Binding, Protein Complex Binding, Transcription	ACAGGATTCAGAACTACCACTGGATGACCAAGTCCCTCTACAGTCTCATGATGTTCTTCACTGGATTGGCC	nuclear receptor subfamily 3, group C, member 1
Oas1a	NM 145211.2	L3	Regulation Of Transcription From Rna Polymerase II Promoter, Transcription Dna Dependent, Regulation Of Transcription, DNA Dependent, Anti Apoptosis, Regulation Of Cell Proliferation, Protein Homodimerization Activity, Hormone Binding, Protein Complex Binding, Transcription	TCTGATCAGGAGTGAGTTGATGTGTGCTGCCAGCTTGTGATGCTGGTCACTGTAATCACTCCAGCAAGCTGA	2'-5' oligoadenylate synthetase 1A
Oas2	NM 145227.2	Oasf11	Cytoplasm, Rna Catabolic Process, Zinc Ion Binding	CTGTGGAACTTAAAGAGGCGGTGCAACTCCAGGAGTGACTCTCTATGAAACACTCCATCCATTTCTGATGT	2'-5' oligoadenylate synthetase 2
Oasf1	NM 145209.2	7530414C13Rik, oasf9		ATGCTTTGAGTGGCTCAGCG	2'-5' oligoadenylate synthetase-like 1
Oasf1	NM 145209.2	7530414C13Rik, oasf9	Cell Surface, Extracellular Region, Membrane, Extracellular Space, Microvillus, Positive Regulation Of Cell Proliferation, Regulation Of Fc(gamma)R Tyrosine Phosphorylation, Multicellular Organismal Development, Organ Morphogenesis, Positive Regulation Of Map Kinase Activity, Angiogenesis, Actin Cytoskeleton Organization And Biogenesis, Positive Regulation	TGTGGTGGGTGACACTCTGCAACTATGATGTTGCTTCAATGAGGCTGGCTTGTCTCTCTCTCTCTCT	platelet derived growth factor, alpha
Pdgfra	NM 008808.3		Golgi Apparatus, Membrane, Nuclear Envelope, Plasma Membrane, Phosphoinositide Mediated Signaling, Phosphorylation, Nucleotide Binding, Phosphotransferase Activity	CTCACTTGAAGCAAGTCTGGCCGCTGTCTTAAAGAGTCACTGGTGTGTTTACTGAACCTTGAAGGACA	phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide
Pknox1	NM 011084.2	C80387, PK3K-C2-gamma	Golgi Apparatus, Cytoplasm, Endoplasmic Reticulum, Nucleus, Cytoplasmic Vesicle, Perinuclear Region Of Cytoplasm, Membrane Fraction, Lipid Catabolic Process, Positive Regulation Of Cell Proliferation, Response To Organic Substance, Regulation Of Cell Proliferation, Calcium Ion Binding, Phospholipase A2 Activity, Phospholipase Activity	TACCAAGGAGCAACCAAGCAAGTGGTCACTGGATGCTAATGGCTGGTGGAGGCTGGCTTATCAATACC	phospholipase A2, group IVA (cytosolic, calcium-dependent)
Pla2g4a	NM 008869.2	Pla2g4, cPLA2, cPLA2alpha	Cytoplasm, Nucleus, Cytoplasm, Membrane Fraction, Nuclear Chromatin, Nuclear Speck, Lipid Catabolic Process, Positive Regulation Of Transcription, DNA Dependent, Insulin Receptor Signaling Pathway, Glutamate Signaling Pathway, G2/M Transition Of Mitotic Cell Cycle, Signal Transduction, Negative Regulation Of Transcription Dna Dependent, Regulation Of G-Protein	CCAGGAGGCGCATCTCTTAAAACATCTAGTATGTTCTGACAGACGGAAGGCGTTGAACCTGACTAGAG	phospholipase C, beta 1
Pcb1	NM 010877.1	311004321Rik, A1132408, Pcb, mkIAA0581		GACTTCTAGGTGGAGTCAAGGA	phospholipase C, beta 1
Ppp1r12b	NM 001081307.1	18100370O3Rik, 9530009M10Rk, A1132431, Mypl2	Cytoplasm, Actin Cytoskeleton, Plasma Membrane	CACCGGACTTAACTCTGGCAAGTCAAGAGTCAAGAGTCTCTCAAGGAGTCAAGAAAGCTTGCATGAAA	protein phosphatase 1, regulatory (inhibitor) subunit 12B
Pkca	NM 011101.3	A1875142, Pkca	Membrane, Cytoplasm, Endoplasmic Reticulum, Nucleus, Cytoplasm, Peroxisome, Protein Complex, Plasma Membrane, Regulation Of Muscle Contraction, Protein Amino Acid Autophosphorylation, Regulation Of Peptidyl Tyrosine Phosphorylation, Angiogenesis, Negative Regulation Of Ca Membrane, Cytoplasm, Insoluble Fraction, Nucleus, Cytoplasm, Membrane Fraction, Centrosome, Plasma Membrane, Soluble Fraction, Transcription Dna Dependent, Regulation Of Growth, Calcium Ion Transport, Activation Of NF KappaB Transcription Factor, Positive Regulation Of I KappaB Kinase NF KappaB Cascade, Regulation Of Transcription From Rna Polymerase II P	TGGCTCAGCATGGTGGTGGTGGTGGTCAATGACAGAGACACACAGGTTGTAAACAGCCTTACTGTGACC	protein kinase C, alpha
Pkcb	NM 008852.2	A130082F03Rik, PKC-Beta, Pkcb, Pkcb1, Pkcb2	Membrane, Integral To Membrane, Plasma Membrane, Signal Transduction, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	TACGATTTAGCTGCCAAAGAGCCAGAGCACTGTGCTCCTACTCTGCTATTAGGCACTGACATCGAAGAG	protein kinase C, beta
Ptger1	NM 013841.2	42kDa, EP1, Ptgerp1	Membrane, Integral To Membrane, Plasma Membrane, Signal Transduction, G Protein Coupled Receptor Protein Signaling Pathway, G Protein Coupled Receptor Activity, Receptor Activity	TTGGCTGGCGGCTCTCTGGGCTAGTGTCACATGCGCTGCGGGGCTGGGCTGCTCCGCTCCGCTCGGAG	prostaglandin E receptor 1 (subtype EP1)
Ptger2	NM 008964.4	EP2, Ptgerp2	Membrane, Integral To Membrane, Plasma Membrane, Signal Transduction, G Protein Coupled Receptor Protein Signaling Pathway, Regulation Of Cell Proliferation, G Protein Coupled Receptor Activity, Receptor Activity	TGTAAAGGCTGGGATATAACAGATAACCTCCCTCGAAGAGCAGATGAACACAGCTTATGAGTATTGGGCG	prostaglandin E receptor 2 (subtype EP2)

Continue Table S1: Nanostring nCounter SC Mouse Inflammation V2 Panel Gene List

Piger3	NM_011199.2	EP3, Pgersp3, Pgersp3	Plasma Membrane,G Protein Signaling Coupled To Iq3 Second Messenger,phospholipase C Activating,G Protein Signaling Coupled To Camp Nucleotide Second Messenger Receptor Activity	TCTAATAGCCATGAGCCAAACAGCAAAAAAGTCTACATGAGAGGCGAAGAGATTGTGCAAGGGTATTGTG CCAAGAGGTTACAGTACCAK	prostaglandin E receptor 3 (subtype EP3)
Piger4	NM_008965.1	EP4, Pgersp4	Membrane,Integral To Membrane,Plasma Membrane,Signal Transduction,Ink Cascade,Positive Regulation Of Cytokine Secretion,G Protein Signaling Coupled To Camp Nucleotide Second Messenger,G Protein Signaling Adenylate Cyclase Activating Pathway,G Protein Coupled Receptor Protein Signaling Pathway,G Protein Coupled Receptor Activity,Receptor Ac	GGTGGCCATCGTATGTTGCAAGTGGCGCAAGGAGCAGAAAGAGACCTTTTACACTGATGTGGGGCTGG GTCTCACTGACCTCTGGGCAAC	prostaglandin E receptor 4 (subtype EP4)
Pigr	NM_008966.3	A1957154, PGF, Ip	Membrane,Cytoplasm,Integral To Membrane,Plasma Membrane,Negative Regulation Of Apoptosis,Signal Transduction,G Protein Coupled Receptor Protein Signaling Pathway,G Protein Coupled Receptor Activity,Receptor Activity	TGGGCTTATTTCTGCTACGGAGGGTCTCTTAAAGCACTGTAACTTGGCCAGTGGCTGTGGATTAAGTC ATCAGCTTGCATCTGGGAAC	prostaglandin F receptor
Pigr	NM_008967.3	IP, PGI2	Membrane,Integral To Membrane,Plasma Membrane,Signal Transduction,G Protein Coupled Receptor Protein Signaling Pathway,G Protein Coupled Receptor Activity,Receptor Activity	GGTCTATGGCTCTCAAGAGGATTTCTCTCAAATAACCGAGGCTGGCAGGCTGCTGCGCCCTGGCTCTCC ATCATCTCTCTGCTAAATAT	prostaglandin I receptor (IP)
Pigs1	NM_008969.3	COX1, Cox-1, Cox-3, PGHS-1, PHS 1, Pghs1	Cytoplasmic Part,Golgi Apparatus,Membrane,Cytoplasm,Endoplasmic Reticulum,Nucleus,Microsome,Nuclear Envelope,Plasma Membrane,Fatty Acid Biosynthetic Process,Lipid Biosynthetic Process,Response To Oxidative Stress,Keratinocyte Differentiation,Regulation Of Blood Pressure,Regulation Of Cell Proliferation,Lipid Binding,Oxidoreductase Activity	TTTAGAGTTCTACCCGGGGTGGCTGGAGAGTGCACCGCAACCTCCATCTTGGAGAAGATATGATAGAGTGG GGGCTCCCTTTCCTCCAGGGCC	prostaglandin-endoperoxide synthase 1
Pigs2	NM_011198.3	COX2, Cox-2, PGHS-2, PHS-2, Pghs2, TIS10	Membrane,Cytoplasm,Endoplasmic Reticulum,Nucleus,Protein Complex,Neuron Projection,Positive Regulation Of Cell Proliferation,Negative Regulation Of Cell Cycle,Fatty Acid Biosynthetic Process,Lipid Biosynthetic Process,Inflammatory Response,Angiogenesis,Embryo Implantation,Response To Oxidative Stress,Keratinocyte Differentiation,Negative R	CCATCGATTTTTCAACAGCAGATCAATAGGAGGAGCTGGTTCACCGAGGACTGGGCCATGGAGTAAATC ACATTTATGGTAACTCTGGAC	prostaglandin-endoperoxide synthase 2
Pik2	NM_007982.2	FAK, FRNK, Fack, mKIAA4203, p125FAK	Membrane,Membrane,Cytoplasm,Lamellipodium,Nuclear Body,Basolateral Plasma Membrane,Focal Adhesion,Apical Plasma Membrane,Plasma Membrane,Nucleolus,Positive Regulation Of Cell Proliferation,Negative Regulation Of Apoptosis,Protein Amino Acid Autophosphorylation,Microtubule Cytoskeleton Org	GTGACATTTGCAAGAGAGTCTCAAGTGTCCCTGGCTCAAGTGATCATTTCTGGTAATGGCAATCGCGC CAGAAGAGGGATCATTTACT	PTK2 protein tyrosine kinase 2
Rac1	NM_009007.2	AL023026, D5Ems559e	Membrane,Membrane,Cytoplasm,Lamellipodium,Cytoplasmic Vesicle,Cell Projection,Cytoplasmic Membrane,Sound Vesicle,Membrane Fraction,Plasma Membrane,Actin Filament Organization,Axon Guidance,Regulation Of Cell Migration,Interleukin Junction Assembly And Maintenance,Actin Cytoskeleton Organization And Biog	GCCAAAATACCTCTGAACTAGTTGGGTGTGCTGAGAAACACCTAAGCACTAACTCTCTGGAAGCACTCTTGCT AAGAAGACCGCAGCTCTGGGA	RAS-related C3 botulinum substrate 1
Raf1	NM_029790.3	6430402F14Rik, AA90557, BB129353, Craf1, D83050J10Rik, Raf-1, c-Raf, v-Raf	Membrane,Cytoplasm,Insoluble Fraction,Nucleus,Cytoplasm,Mitochondrion,Plasma Membrane,Negative Regulation Of Apoptosis,Signal Transduction,Protein Kinase Cascade,Negative Regulation Of Cell Proliferation,MapkK Cascade Go 0000165,Cytoskeleton Organization And Biogenesis,Protein Amino Acid Phosphorylation,Phosphorylation,Apoptosis Go,Response	CCTCAGATGGCAAGCTCACGGATCTCTTAAGACAAGCACTACTCCGGTTTTCTGCCGAATAAGAAAGGA CTGTGGCTCAATCGCGGAATGG	vraf-leukemia viral oncogene 1
Rapgef2	NM_001099624.2	5830453M24Rik, CNRasGEF, Pdagef1, RA-GEF-1, mKIAA0313, nRapGEP	Membrane,Plasma Membrane,Signal Transduction,Regulation Of Catalytic Activity,Regulation Of Small GTPase Mediated Signal Transduction,Small GTPase Mediated Signal Transduction,Protein Kinase Binding,Guanyl Nucleotide Exchange Factor Activity	TTAATCAGTATGAGTGTGAGTGAGGAGCTGGGGTGGTGGAGGAGTCCAGCTGTGTACTGCTCTTCAAGA CAGCCTCCCTTTGGTGGATCC	Rap guanine nucleotide exchange factor (GEF) 2
Rela	NM_009045.4	p65	Cytoplasm,Nucleus,Cytoplasm,Transcription Factor Complex,Protein Complex,Positive Regulation Of Transcription,Dna Dependent,Positive Regulation Of Cell Proliferation,Negative Regulation Of Apoptosis,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Transcription Dna Dependent,Negative Regulation Of Transcription Dna Depend	GAGGCTGACTCTCCGACACCGCAGTATCCATGCTCCAGAACCTGGGATCCAGTGTGTGAAGAACGAGACCT GGAGCAAGCCATAGCCAGCA	v-rel reticulendotheliosis viral oncogene homolog A (avian)
Relb	NM_009046.2	shep	Cytoplasm,Nucleus,Cytoplasm,Cytoskeleton,Transcription Dna Dependent,Regulation Of Transcription,Dna Dependent,Transcription Factor Activity,Dna Binding	TTCCTTTGAGCCATTTTACAGAGTGTGAGTCGGAAGGAAAGGGGCTCTCGAGATGAGCCCTCTCAGCAGC AGATCTCGAGATGTTACATA	v-rel reticulendotheliosis viral (v-rel) oncogene related B
Reln1	NM_020500.3	RELNalpha, Xcp2	Extracellular Region,Hormone Activity	GAACTCAATGAGACCAAGATTCTCGTGGAGTAAGTCAAGGAACTCTGCCAATCCAGCTACTCATCTCCCTC CAGCTCAAGAGACTCTCTCT	resistin like alpha
Ripk1	NM_009056.3	D330015H01Rik, RIP, Rinp, Rip1	Membrane,Cytoplasm,Lipid Raft,Receptor Complex,Mitochondrion,Protein Complex,Plasma Membrane,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Signal Transduction,Protein Amino Acid Autophosphorylation,Activation Of Nf Kappab,Transcription Factor Protein Amino Acid Phosphorylation,Phosphorylation,Apoptosis Go,Nucleotide	GCTTTGGCCTTTGGTGGACTCTGGCACTATGGCACTTCTCTCTTTGGGCTACTCTGATCTAGCATAGGATA TTTGGAACTCTGGGCCCT	receptor (TNFRSF)interacting serine-threonine kinase 1
Ripk2	NM_138952.3	2210420D18Rik, CARD3, CARDIAC, CCK, D4Bwg0615e, RICK, RIP2	Cytoplasm,T Cell Proliferation,I Kappab Kinase Nf Kappab Cascade,Activation Of Nf Kappab,Transcription Factor,Positive Regulation Of I Kappab Kinase Nf Kappab Cascade,Protein Amino Acid Phosphorylation,Immun	CCAGGACATGACCTGACACCGAGTGGAGAAATTTGCCATTTGATTAACCTCATCGAGGCTCATGATCTCTAAT ACAGAGTGGATGGGCGCAAAAC	receptor (TNFRSF)interacting serine-threonine kinase 2
Rock2	NM_009072.2	B230113H15Rik, ROKalpha, rho-kinase, Rock-1, Rock2m, mKIAA0619	Membrane,Cytoplasm,Nucleus,Cytoskeleton,Centrosome,Plasma Membrane,Cytokinesis,Signal Transduction,Negative Regulation Of Angiogenesis,Actin Cytoskeleton Organization And Biogenesis,Protein Amino Acid Phosphorylation,Phosphorylation,Rho Protein Signal Transduction,Nucleotide Binding,Phospholipid Binding,Protein Kinase Activity,Kinase Activ	ATCACATTTGAGCTTCAACAGAGGTTCCAGCAGCAATAGCCAGAAATTTGGAGTGAATCCCTCAGCAGCGAT GCTGACTCATCTTTAAGAAAT	Rho-associated coiled-coil containing protein kinase 2
Rps6ka5	NM_153587.2	3110005L17Rik, 6330404E13Rik, A1854034, MSK1, MSPK1, RLPK	Cytoplasm,Nucleus,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Negative Regulation Of Transcription Dna Dependent,Activation Of Nf Kappab,Transcription Factor,Inflammatory Response,Response To Stress,Protein Kinase Cascade,Regulation Of Transcription,Dna Dependent,Protein Amino Acid Phosphorylation,Phosphorylation,Nu	TCCTCAGAGTGTGGCTGAGTGTGCTGGCTTAAAGATGTCTCGCTTCTCATTGGAATCGCTGGCTGAC GAAATTTTTCCGGGAAAGCCCT	ribosomal protein S6 kinase, polypeptide 5
Shc1	NM_011368.4	Shc, ShcA, p66, p66hac	Cytoplasm,Nucleus,Mitochondrion,Plasma Membrane,Insulin Receptor Signaling Pathway,Neurite Development,Regulation Of Growth,Activation Of Mapk Activity,Angiogenesis,Actin Cytoskeleton Organization And Biogenesis,Cell Cell Adhesion,Heart Development,MapkK Cascade Go 0000165,Neuron Differentiation,Protein Complex Binding,Insulin Like	AACAGCAAGTCTGAGGAGCTGGGTTCTCACTGGTGTGATCAAGGCTGTGTGGAGTCTACACCAATGG AGCCCTTGACTCAATACCGGA	src homology 2 domain-containing transforming protein C1
Smad7	NM_001042660.1	Madh7	Cytoplasm,Nucleus,Centrosome,Transcription Factor Complex,Protein Complex,Plasma Membrane,Nucleolus,Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway,Transcription Dna Dependent,Protein Stabilization,Regulation Of Transcription,Dna Dependent,Negative Regulation Of Transcription From Rna Polymerase II Promoter,Transf	CAGCCTGTAGAAGGCTGAACAGAACCAATGTTTTCATCCCTGTCTACTGCGGCTGTACCCCGCTCCATCTGTC GAGTGTCTTTTTGGCCATC	SMAD family member 7
Stat1	NM_009293.3	2010005J02Rik, AA408197	Axon,Cytoplasm,Nucleus,Dendrite,Nucleolus,Positive Regulation Of Transcription,Dna Dependent,Positive Regulation Of Cell Proliferation,Jak Stat Cascade,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Response To Nutrient,Transcription Dna Dependent,Negative Regulation Of Angiogenesis,Response To Bacterium,Cytokine And C	AGCCTGGGAAGCAACTAATGAGGGGCTCTCATTTGTCACGGAAGCACTCACTCTCTTCTTGAACCAAGTGT CCAGCCAGGCTGGTGTATGTA	signal transducer and activator of transcription 1
Stat2	NM_010963.1	1600010G07Rik, A1W96480	Cytoplasm,Nucleus,Plasma Membrane,Positive Regulation Of Transcription,Dna Dependent,Jak Stat Cascade,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Signal Transduction,Transcription Dna Dependent,Sexual	TCAGTGAACCTCTGAAAGGGGCACTTCTGTTGGTGGAGCACCAGGATGACGTAAGTCTGAAATCTACTCA GTGCGCCTACCAAGGAGT	signal transducer and activator of transcription 2
Stat3	NM_213650.2	1110034C02Rik, AW109958, Aprf	Reproduction,Protein Import Into Nucleus,Regulation Of Transcription,Dna Dependent,Intracellular Receptor Mediated Si	GGGGTCACTTCACTGGGTGGAAAGGACATCACTGGCAAGCCAGATCAGTCTGTAGAGCCATACCAAGCA GCAGCTGAACACATGCTATTG	signal transducer and activator of transcription 3
Tbx2r	NM_001277265.1	TP, TXA2-R	Membrane,Integral To Membrane,Plasma Membrane,Signal Transduction,Inflammatory Response,Second Messenger Mediated Signaling,Positive Regulation Of Angiogenesis,G Protein Coupled Receptor Protein Signaling Pathway,G Protein Coupled Receptor Activity,Receptor Activity	GCTCCTCTCTCTGCTGCTGCTGGGCTTCTTCCACGACTCTGGGGCTGCTAGTCAACGGGCCATCGTGG GTGGCAACACGCTGCTTGT	thromboxane A2 receptor
Tcf4	NM_013685.1	5730422P05Rik, ASP-42, E2-2, E2-2, ITF-2, ITF-2b, ITF2, ME2, MTF-2A, MTF-2B, SEF-2, SEF2, SEF2-1, TFE, Tcf-4, hLHb19	Nucleus,Transcription Factor Complex,Positive Regulation Of Transcription,Dna Dependent,Nervous System Development,Positive Regulation Of Transcription From Rna Polymerase II Promoter,Transcription Dna Dependent,Transcription Initiation,Protein Dna Complex Assembly,Multicellular Organismal Development,Regulation Of Transcription,Dna	AATTACCGGATTTGAATGGGGAAGCCGCGCTGCCCTGTAAACAAACCAAGCTCTGATGGCAAGGAAGT ATGACATTAGCCATCTTATGGG	transcription factor 4

Continue Table S1: Nanostring nCounter SC Mouse Inflammation V2 Panel Gene List

Tgfb1	NM_011577.1	TGF-beta1, TGFbeta1, Tgfb, Tgfb-1	Proteinaceous Extracellular Matrix, Cell Surface Axon, Extracellular Region, Cytoplasm, Nucleus, Cell Soma, Secretory Granule, Extracellular Space, Extracellular Matrix, Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway, Positive Regulation Of Transcription, DNA Dependent, Positive Regulation Of Cell Proliferation, Regulation Of D	GGAGTTGTACGGCAGTGGCGAACCAAGGAGCGGATACAGGGCTTGGATCCAGGCTCACTGCTCTGTGACAG CAAGATACAACTCCACGGTGG	transforming growth factor, beta 1
Tgfb2	NM_009367.1	BB105277, Tgf-beta2, Tgfb-2	Cell Surface, Axon, Extracellular Region, Basement Membrane, Cytoplasm, Cell Soma, Secretory Granule, Extracellular Space, Trans Golgi Network, Extracellular Matrix, Axon Guidance, Positive Regulation Of Cell Proliferation, Negative Regulation Of Apoptosis, Hemopoiesis, Skeletal Development, Epithelial To Mesenchymal Transition, Growth, Intercellular Junction	CCCAAAGCCAGAGTGGCCGAGCGGATGAAGTATCAATGCTTAAATCCAAAGACTTAACCTCCACCCAG CGCTACATGATGACAGAGGTTG	transforming growth factor, beta 2
Tgfb3	NM_009368.2	Tgfb-3	Cell Surface, Extracellular Region, Cytoplasm, Nucleus, Cell Soma, Secretory Granule, Extracellular Space, Extracellular Matrix, Positive Regulation Of Transcription, DNA Dependent, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Activation Of Mapk Activity, Organ Morphogenesis, Intercellular Junction Assembly And Maintenance, Post	TCATGTAATGATTTCTGGCCGACCACTAGCTATCTCAGCTGCTTAGAGTGTGGCTGACCAAGAGAGCTGAGA ATTGGTCTCTCATGTAATCC	transforming growth factor, beta 3
Tgfr1	NM_009370.2	ALK5, ALU17191, Alk-5, TbetaR4, TbetaRI	Cell Junction, Tight Junction, Membrane, Integral To Membrane, Receptor Complex, Basolateral Plasma Membrane, Apical Plasma Membrane, Protein Complex, Plasma Membrane Part, Plasma Membrane, Positive Regulation Of Transcription, DNA Dependent, Positive Regulation Of Cell Proliferation, Negative Regulation Of Apoptosis, Signal Transduction, Skeletal Develop	TCAGAAATGATGGCCAGCTGTCTCTAGTAGACAAATGAAGCTGAAGCTGAGCTGATCACTCTGCTACTACAGTA GTACTCCAGAAAGCTGGCTGAG	transforming growth factor, beta receptor I
Tr1	NM_030682.1		Intrinsic To Membrane, Membrane, Cytoplasmic Vesicle, Integral To Membrane, Plasma Membrane, Signal Transduction, Defense Response, Inflammatory Response, Immune Response, Innate Immune Response, Receptor Activity, Transmembrane Receptor Activity, Process, Heterodimerization Activity	TCAGCACTAGATGGTTTGGAACTGTCTACATCAAGTGTGCTTGAAGACAGGGGCTGCTTATTTCTACGTGC TTTGTCAAAGCTTGGAAAGA	tol-like receptor 1
Tlr2	NM_011905.2	Ly105	External Side Of Plasma Membrane, Cell Surface, Intrinsic To Membrane, Membrane, Cytoplasm, Cytoplasmic Vesicle, Integral To Membrane, Plasma Membrane, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Signal Transduction, Activation Of Nf-kappaB Transcription Factor, Inflammatory Response, Positive Regulation Of Cytokine Secretion	CGAGGGGTCACTGGCGAGGATGTGTCGCAATCATATTTCTGATGGTGAAGTTGACGGCAGCTCTCGCAGC CTAGAGTGGAAAGATGGTGTTC	tol-like receptor 2
Tlr3	NM_126166.2	AI957183	Cell Surface, Membrane, Cytoplasm, Endoplasmic Reticulum, Integral To Membrane, Endosome, Response To Virus, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Signal Transduction, Defense Response, Activation Of Nf-kappaB Transcription Factor, Positive Regulation Of Nf-kappaB Kinase Nf-kappaB Cascade, Defense Response To Virus, Infla	TTTCTGGGCTGAAGTGGACAACTCACCAGCTCGATTTCTTCAACAACCTCCATGATGTGGCAGCGGTTCC TTTCTCTATCCGACGGCTG	tol-like receptor 3
Tlr4	NM_021297.2	Lps, Ly87, Ran/MI, Ral2-6	External Side Of Plasma Membrane, Cell Surface, Membrane, Cytoplasm, Penetrator Region Of Cytoplasm, Integral To Membrane, Lipid Raft, Integral To Plasma Membrane, Plasma Membrane, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Signal Transduction, Activation Of Mapk Activity, Activation Of Nf-kappaB Transcription Factor, Post	AACGCCAATCTGACCTGAGGAGCAAACTCTGGGGCTCAAAACAGCTGTTGCAATTAATAATGCTACAGCT CACTGGGCGCTGCTGATGAC	tol-like receptor 4
Tlr5	NM_016928.2		Membrane, Integral To Membrane, Membrane Fraction, Signal Transduction, Inflammatory Response, Innate Immune Response, Receptor Activity	TCGGGAGCCAGATGCTGACCTGTCAGGAGGCTTCCAGAACCTCCCAACTTAGGATCTGGACTG GGCCAAAGCCAGATGGAAGTCT	tol-like receptor 5
Tlr6	NM_011604.3		Intrinsic To Membrane, Membrane, Cytoplasmic Vesicle, Integral To Membrane, Plasma Membrane, Signal Transduction, Positive Regulation Of Nf-kappaB Kinase Nf-kappaB Cascade, Inflammatory Response, Immune Response, Defense Response To Bacterium, Positive Regulation Of Jnk Activity, Innate Immune Response, Receptor Activity, Transmembrane Receptor Activity	ACCTGGATGCTCACACAATGGTGGAAATCTCTTCTGGCCCTTAGGGAGCTGAGGAGCTAGAAGCTCTCAT TCAATGACTTGTGTAAGTCC	tol-like receptor 6
Tlr7	NM_133211.3		Membrane, Cytoplasm, Endoplasmic Reticulum, Cytoplasmic Vesicle, Integral To Membrane, Endosome, Lysosome, Plasma Membrane, Signal Transduction, Defense Response To Virus, Inflammatory Response, Response To Chemical Stimulus, Innate Immune Response, Drug Binding, Double Stranded Rna Binding, Receptor Activity, Single Stranded Rna Binding	TCTGAGGAGCTGTCTGAGTGGCCGTAACAATCCAGGCTACCCATACTCTGGCAGCTGCAAAATGGCC TGACCACAGCAATCATGTGGC	tol-like receptor 7
Tlr8	NM_133212.2		Membrane, Integral To Membrane, Response To Virus, Signal Transduction, I-kappaB Kinase Nf-kappaB Cascade, Defense Response To Virus, Inflammatory Response, Innate Immune Response, Double Stranded Rna Binding, Receptor Activity, Dna Binding, Single Stranded Rna Binding	TCATAAAGCGAATTCAGAGACTCTCTGTGAGGAGTAAGGACACACTGGTGTGATGAGCAGATCGACC ATGGCAACTGCATGAAGTCC	tol-like receptor 8
Tlr9	NM_031178.2		Membrane, Cytoplasm, Endoplasmic Reticulum, Cytoplasmic Vesicle, Integral To Membrane, Endosome, Basolateral Plasma Membrane, Apical Plasma Membrane, Lysosome, Plasma Membrane, Response To Virus, Positive Regulation Of Transcription From Rna Polymerase II Promoter, Signal Transduction, Activation Of Nf-kappaB Transcription Factor, Positive Regulation Of	GGCCAAATTCAGTTTGTGACCACTGTCTGCTACAGAGCTTAGGCTGCCACACATGACATCATACCGTG TGCTCCACATCTCAACAGCA	tol-like receptor 9
Tnfr	NM_013693.1	DIF, TNF-alpha, TNFSF2, TNFalpha, Tnfa, Tnfa1a	External Side Of Plasma Membrane, Cell Surface, Extracellular Region, Membrane, Integral To Membrane, Lipid Raft, Integral To Plasma Membrane, Secretory Granule, Extracellular Space, Plasma Membrane, Response To Virus, Glucose Metabolic Process, Positive Regulation Of Transcription, DNA Dependent, Positive Regulation Of Cell Proliferation, Negative Regula	TTCTGAGTCTGCAAGGGAGAGTGGTCAAGTGGCTGTCTCAGAGTAGGCTGGATGAAGATCTCAGGCTCTCT ACTTGACACTTCCAGACTC	tumor necrosis factor
Tnfr3	NM_009397.2	A20, Tnfr3	Cytoplasm, Nucleus, Centrosome, Proteolysis, Anti Apoptosis, Response To Wounding, Apoptosis, Gs Kinase Binding, Zinc Ion Binding, Ligase Activity, Ubiquitin Binding, Cytokine Type Peptidase Activity, Peptidase Activity, Dna Binding, Ubiquitin Protein Ligase Activity	GGCTGAACAATCTTCTCAGGCTTGTATTTGAGCAATGGCGAAAGCTGTGAAGATAGGAGAGAACCCGAC AAGACATTTCAAACTCAAT	tumor necrosis factor, alpha-induced protein 3
Tnfrsf14	NM_019418.2	HVEM-L, HVEM-L, LIGHT, LTg, Ly113	Extracellular Region, Membrane, Integral To Membrane, Extracellular Space, Plasma Membrane, Immune Response, Receptor Binding, Cytokine Activity	CAGTAAAGAAAGTCAAGCTGGGGTATTTATGCTCTGATGCAAAACAGTAGATTTGGGCTTTCTGGTTTGGAGCTG GAGCCAGAAACCTCCAGAG	tumor necrosis factor (ligand) superfamily, member 14
Tollp	NM_023764.3	4930403G24Rk, 4931428G15Rk	Cytoplasm, Penetrator Region Of Cytoplasm, Nuclear Body, Signal Transduction, Inflammatory Response, Innate Immune Response, Phosphorylation, Kinase Binding	CTCAGCATCTGTGTACAGGCAAAATGGCAAGAAATGGCATGACTGTATGACCTACTGCTGCTGCTGCT CTGGCTATGCTTTTAAAGAA	tol interacting protein
Tradd	NM_001033161.2	9130005N23Rk, AA930854	Cytoplasm, Cytoskeleton, Lipid Raft, Receptor Complex, Protein Complex, Signal Transduction, Positive Regulation Of I-kappaB Kinase Nf-kappaB Cascade, Regulation Of Apoptosis, Apoptosis, Gs Kinase Binding, Identical Protein Binding, Molecular Adaptor Activity, Protein Complex Binding	AGTACTCTGCGAGTTGCAAGTCCCGGTTCTCTCCGACGAGGAGAAACCACTGCCGCCGCTCCAGACT TTTCTTGCCAGCGGAGCTGCT	TNFRSF1A-associated via death domain
Traf2	NM_009422.2	A1325259	Cytoplasm, Cell Cortex, Lipid Raft, Protein Complex, Signal Transduction, Cellular Protein Complex Assembly, Activation Of Nf-kappaB Transcription Factor, Regulation Of Jnk Cascade, Positive Regulation Of Transcription Factor Activity, Protein Catabolic Process, Anti Apoptosis, Plasma Membrane, Response To Virus, Positive Regulation Of Jnk Activity, Regulation O	CACAAGCTGTGCTGTCTGATGAAAGGCTGTATGAAAGGACTTCTATTGAGAGATGTTGGGCTTTCA GATAACGCTGCCCGAGAGAG	TNF receptor-associated factor 2
Trem2	NM_031254.2	TREM2, Trem2a, Trem2b, Trem2c	Extracellular Region, Membrane, Integral To Membrane, Plasma Membrane, Receptor Activity, Transmembrane Receptor Activity	GAATCAAGAGACTCTCCACDCACTCATTTCTCTCTGCTGGCTGGTCTCTGAGGAAGTTCTTGAGGCTC GACTCTCTGGCTGTGGCC	triggering receptor expressed on myeloid cells 2
Tslp	NM_021267.1		Extracellular Region, Extracellular Space, Cytokine Activity	CTGACTGTTAATGACAGCTCTGGAAGTGTCTTCCACCTCCCTGCACACACTACTCTAGGGCAACCAACTG TAGTAGAAGAGAAATGGAAG	thymic stromal lymphopoietin
Twist2	NM_007855.2	Dermo1, bHLHa39	Cytoplasm, Nucleus, Transcription Factor Complex, Negative Regulation Of Apoptosis, Transcription Dna Dependent, Negative Regulation Of Transcription Dna Dependent, Multicellular Organismal Development, Regulation Of Transcription From Rna Polymerase II Promoter, Negative Regulation Of Dna Binding, Regulation Of Transcription, DNA Dependent, Negative	GTGACTGTTGAGGAGCTGGAATCTTGGCCGATACCTCTGTTTAAAGTCTCCATGGCTGCTCAGCTAGCC GTGTTTCTATTCCTGCTCAG	twist basic helix-loop-helix transcription factor 2
Internal Reference Genes					
Ctct	NM_001003908.1	3110065L21Rk, CHC, R74732	Membrane, Spindle, Cytoplasmic Vesicle, Clathrin Coated Vesicle, Membrane Fraction, Membrane Coat, Mitochondrion, Intracellular Protein Transport, Vesicle Mediated Transport, Mitosis, Receptor Mediated Endocytosis, Peptide Binding, Structural Molecule Activity, Prote	GAGTCTACGCCAGGAAATTTGATGCTACTTAGGCTCCAGGATGCCAGATCAATACCGTACAGATGCA AAGCAAAATGTTGCTCTCA AGTTGTTCTCTGGACTTCAAGCAACCTCCACTCTCCACTTGGATGCGGGGCTGGACTTCTCAATGACA ACTTTTCAAGCTCATTTCTG	clathrin, heavy polypeptide (Hc)
Gsd3h	NM_001001303.1	Gsd3h	Endoplasmic Reticulum, Microsome, Lysosome, Soluble Fraction, Carbohydrate Metabolic Process, Sugar Binding, Cation Binding, Hydrolase Activity, Acting On Glycosyl Bonds, Hydrolase Activity, Hydrolyzing O-glycosyl Compounds	AATACGTGGTGGAGACTCATCTGAAATTTGGCCGACTCATGAGAACCCAGTCCAGTGAAGTATGGAAAC AAGAAGGGATCTTCACTGCA	glyceroldehyde-3-phosphate dehydrogenase
Gusb	NM_010368.1	g Gsd, Gur, asd, adipose storage deficiency, Gus+, Gus-, Gus+4, Gus+4, Gus	Cytoplasm, Cytosol Soluble Fraction, Carbohydrate Metabolic Process, Phosphorylation, Nucleotide Binding, Kinase Activity, Adp Binding, Atp Binding	CCGGATCTGCAAGCTCAAAGCGCACTGTCGCGCGTCTTCTCTCTCATCTCGGCGGTTGCACTTCC GGTGTGCCAAATGGTGCT	glucuronidase, beta
Pgk1	NM_008828.2	Pgk-1			phosphoglycerate kinase 1

Continue Table S1: Nanostring nCounter SC Mouse Inflammation V2 Panel Gene List

Tabb5	NM_011655.4	AA408537, AI596182, B130022C14Rik, Mbeta5	Cytoplasm, Cytoskeleton, Microtubule, Protein Complex, Microtubule Based Process, Protein Polymerization, Microtubule Based Movement, Gtp Binding, Nucleotide Binding, Protein Complex Binding, Structural Molecule Activity, Structural Constituent Of	ATTGGAAAGTGTCTCCCTGTATTGGTTCTCTCTCGGAGAGATGGGGTTGGGGTGGGCAAGTCTTGCTTTGGTCTCTGAACTCCCAATTCC	tubulin, beta 5 class I
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Supplemental Table 2: Nanostrings nCounter Mouse Custom Code Set Gene List

Table S2: Nanostring nCounter SC Mouse Custom Code Set Gene List

CODESET DETAILS									
Customer Identifier	Accession	Position	Target Sequence	Tm CP	Tm RP	Flags	HUGO Gene		
1 lbabp	NM_008375.2	163-262	ATCACAGAGGTCCAGCAGGACGGACAGGACTTCACTGGTCCCACTTACTCTGGGGCAACATTATGAGCAACAAGTCCACCATTGGCAAAGAAATGTG	83	82		Fabp6		
2 Fgf15	NM_008003.2	316-415	TCCGCTGGTCCCTATGTCTCAAAGTCTTCCGAAATCCGGAGCGACGCGCTCTGTGGACTGCCAGGAGGACCAAAACGAAACGAAATTTGGAAATTC	83	82		Fgf15		
3 TGR5	NM_174985.1	386-485	TCACCTGGGTACGCTCCCTGTTCTTGGCAGCCTGCCTGCTCTGGGCTGGAAACATTGGAGCCCTGATGCCAACTGCAGCTCCCAAGCTGTCTCCAGC	85	84		Gpbar1		
4 MMP10	NM_019471.2	1051-1150	CAGACTTAGATGCTGCCTATGAGGCTCACACACGGACAGTTCGATTTTAAAGGAAGTCACTTGGGCGAGTCCGAGGAAATGAAGTCCAAGCAGG	82	82		Mmp10		
5 MMP-2	NM_008610.2	2377-2476	AGTTAACCAAGCCCTTCTCCTCACCTGGTGAAGTTCAGATTTAAGAGGGTGGCTCTTTTGTGCCAAAGAAAGGTGCTGACTGTACCCCTCCCGGGTGGCTG	81	82		Mmp2		
6 MMP-7	NM_010810.4	351-450	CACCTACAGAATTGTATCCCTATACTTACAGACTTACCTGGATCGTAGTGGATCAAAATCGTGAAAAAGCTCTCAGAATGTGGAGTATGCAGATCCCACTG	78	82		Mmp7		
7 FXR	NM_009108.2	1176-1275	CAGTTTCTATAAAAGTGTGGGAACTCAAAATGACTCAGGAGGAGTACGCTCTGCTCACAGCGATCGTCATCCTCTCTCCAACAACAATACATCAAG	79	83		Nr1h4		
8 ASBT (Ibat)	NM_011388.2	661-760	CATTGTGCTCATAGCTGTGATTGGAGGAATCTGTACCAAGTGCCTGGATCATTGAACCCAAACTGTGGATTATAGGAACAATATCCCTATAGCTGGC	84	81		Slc10a2		
9 OSTalpha	NM_145932.3	1213-1312	CCTCCTACTCTTCTAAAATCAGGTCTCAAGTGATGAACTGCCACATGCTCATACTGGAGACCTTCTGATGACAGTGTGACACGAATGTACTATCGAA	83	85		Slc51a		
10 OSTBeta	NM_178933.2	196-295	ATGCAAGCATGTTCCCTCTGAGAAGGAGCATCTGGCAAAACAGAAATCGAAAAGCAGCCCAAGAACAAAGAAACAACAGAAAGCCTGCATCTTGATG	79	78		Slc51b		