The JAK–STAT Pathway Is Critical in Ventilator-Induced Diaphragm Dysfunction

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Supplementary Figure S1. Inhibition of JAK prevents the MV-induced reduction in gene expression of a core subunit of the mitochondrial respiratory chain (complex I), NDUFS3. Total RNAs were extracted from control (n=17), MV (n=11) and MV+R548 (Jak inhibitor, n=9) treated rat diaphragm muscle samples. Quantitative PCR was performed. Please note, NDUFS3 is suppressed by MV, but this suppression is reversed by the treatment of JAK inhibitor, R548.
Supplementary Figure S2. H2O2-induced protein oxidation and ubiquitination are reduced by JAK or STAT inhibitors. A) C2C12 myotubes were treated with H2O2 (400 μM, 24 h) in the presence or absence of pan-JAK inhibitor (JAK I, 0.2, 0.5 μM) and STAT inhibitor (Stattic, 0.2, 0.5 μM), respectively. Protein oxidation was examined by antibodies against DNP and nitrotyrosine. Fold changes shown by bars in bar charts represent change in oxidized protein amounts with increasing doses of inhibitors. B) H2O2-induced protein ubiquitination is reduced by JAK or Stat inhibitor. Fold changes shown by bars in bar charts represent change in oxidized protein amounts with increasing doses of inhibitors.
Supplementary Figure S3. Oxidative stress induced by H$_2$O$_2$ increases the expression of cytokines. Quantitative PCR was performed on H$_2$O$_2$ (400 mM)-treated C2C12 cells (6 h). Total RNA was extracted for RT-PCR. After normalized to actin expression levels, the gene expression levels are shown as fold changes (n=3, *p<0.05).

Supplementary Table S1. Potency of JAK inhibitors.

R545 (Rigel pharmaceuticals, Inc)

R545 is a JAK1/3 inhibitor with selectivity over JAK2 mediated signaling in cell-based assays. Compound potency (EC50 values) and selectivity (ratio between JAK2 and JAK1/3 assays) were assessed in the following cell-based assays: Interleukin-2 (IL2) mediated primary human T-cell proliferation (JAK1 and JAK3 signaling); Human primary cultured erythroid progenitor cell (CHEP) differentiation and survival assay (JAK2 signaling). Granulocyte-macrophage colony-stimulating factor (GM-CSF) stimulation of JAK2-dependent STAT5 phosphorylation in blood granulocytes.

| Signaling Kinase(s) | Cell-based assay | R545 EC50 (nM) | Ratio |
|---------------------|------------------|----------------|-------|
| JAK1, JAK3          | Primary T-cell: IL-2 proliferation | 0.03          | 37    |
| JAK2                | CHEPs: Erythropoietin Survival  | 1.111         |       |
| JAK1, JAK3          | Whole Blood lymphocytes: IL-2 induced pSTAT5 | 0.887         | 56    |
| JAK2                | Whole Blood granulocytes: GM-CSF induced pSTAT5 | >50           |       |

R548 (Rigel pharmaceuticals, Inc)

R548 is a JAK1/3 inhibitor with selectivity over JAK2-mediated signaling in cell based assays. Cell based assays were utilized to assess compound potency and selectivity. Interleukin-2 (IL2) drives primary human T-cell proliferation through JAK1 and JAK3. Erythropoietin (EPO) signaling through JAK2 us required for human primary cultured Erythroid progenitor cell (CHEP) differentiation and survival. IL-2 stimulates phosphorylation of STAT5 by JAK1 and JAK3 in blood lymphocytes. Granulocyte-macrophage colony-stimulating factor (GM-CSF) stimulates JAK2-dependent STAT5 phosphorylation in blood granulocytes.

| Signaling Kinase(s) | Cell-based assay | R507 EC50 (nM) | Ratio |
|---------------------|------------------|----------------|-------|
| JAK1, JAK3          | Primary T-cell: IL-2 proliferation | 0.021         | 23    |
| JAK2                | CHEPs: Erythropoietin Survival  | 0.49          |       |
| JAK1, JAK3          | Whole Blood lymphocytes: IL-2 induced pSTAT5 | 0.417         | 78    |
| JAK2                | Whole Blood granulocytes: GM-CSF induced pSTAT5 | 32.7          |       |

Jak I (Jak inhibitor I, EMD Millipore)

Jak I is a potent, reversible, cell-permeable, and ATP-competitive Jak inhibitor, with inhibitory activity against JAK1 (IC50 = 15 nM for murine JAK1), JAK2 (IC50 = 1 nM), JAK3 (Ki = 5 nM), and Tyk2 (IC50 = 1 nM). Inhibits other kinases at much higher concentrations.
**Supplementary Table S2.** Primers used in quantitative PCR.

| Forward Primer          | Reverse Primer          |
|------------------------|-------------------------|
| hu IL6-forward         | ACTCACCTCTTCAGAAGGATGG  |
| hu IL6-reverse         | CCATCTTTGGAAGGTTAGTTG   |
| hu IL24-forward        | CACACAGGCGGTTTCTGCTAT   |
| hu IL24-reverse        | TCCAACTGGTTGAGATCCTC    |
| hu IL20RB-forward      | GGCCACTGTGACCCTACAAC    |
| hu IL20RB-reverse      | TCTTTGGTACCTCCATCCA     |
| hu IL20RA-forward      | ACAAAATGTTCCAAATGGGCT   |
| hu IL20RA-reverse      | TGGGACACGGTCTGTTGAT     |
| hu IL6R-forward        | CCCCTCAGCAATGGTTTGT     |
| hu IL6R-reverse        | TCCGGGACTGCTACCTGG      |
| hu SOCS3-forward       | CCTGCGGCTCAAGACCTTC     |
| hu SOCS3-reverse       | GTCACTGCACCTCCAGTAAA    |
| hu COX5B-forward       | ATGCGCTTCAGTTACTTCGC    |
| hu COX5B-reverse       | CCGTTGAGGGCCAGTACATT    |
| hu Bim-forward         | CACATGAGCACAATTTCCCTC   |
| hu Bim-reverse         | AAGCACAACACTTGAGTAA     |
| mo IL6Ra-forward       | GCCACCGTTACCTGATTTG     |
| mo IL6Ra-reverse       | TCCTGGTGACTCTCCTCTG     |
| hu UCP2-forward        | GACCTATGACCTCAATCGC     |
| hu UCP2-reverse        | ATAGGGCGAACACTACACCG    |
| mo IL6-forward         | CTGCAAGAGACTTCCATCCAG   |
| mo IL6-reverse         | AGTGTTAGACAGGCTGTTG     |
| mo IL24-forward        | GAGCCTGCCCACCTTTTTGT    |
| mo IL24-reverse        | TGTTGGAAGAGGGGCCCAGT    |
| mo IL20RB-forward      | CGGATGCGAGTGCTGTTTACC   |
| mo IL20RB-reverse      | GGGTCTCACAATGAGATGC     |
| mo IL20RA-forward      | TGTCTCGTCTGGAATCCACC    |
| mo IL20RA-reverse      | CCTTTGGTACTCCCGCATTTAG  |
| mo VEGF-forward        | GGAGATCCTCCAGAGGACCTT   |
| mo VEGF-reverse        | GGCGATTAGCCAGAATAGAA    |
| mo VEGF-forward        | GGAGCGAGAAGTGCTGAGAC    |
| mo VEGF-reverse        | CTGCTCTCGTCTGTTG        |
### Supplementary Table S3. Altered signaling pathway in mechanically ventilated human diaphragm.

| Pathway | Gene | Accession No. | P-value | Exp 1. MV vs Con | Exp 2. MV vs Con | Exp 3. MV vs Con | Exp 4. MV vs Con |
|---------|------|---------------|---------|-----------------|-----------------|-----------------|-----------------|
| **Wnt signaling pathway** | CD41 | NM_001562 | 0.00739 | ![Green] | ![Green] | ![Green] | ![Green] |
| | CD42 | NM_001579 | 0.00779 | ![Green] | ![Green] | ![Green] | ![Green] |
| | HCAT | NM_014284 | 0.00809 | ![Green] | ![Green] | ![Green] | ![Green] |
| | ITG5 | NM_001779 | 0.00943 | ![Green] | ![Green] | ![Green] | ![Green] |
| | MRK5 | NM_001467 | 0.01164 | ![Green] | ![Green] | ![Green] | ![Green] |
| | PDK1 | NM_001370 | 0.00853 | ![Green] | ![Green] | ![Green] | ![Green] |
| | RAC2 | NM_002872 | 0.00853 | ![Green] | ![Green] | ![Green] | ![Green] |
| | SHC3 | NM_016486 | 0.00853 | ![Green] | ![Green] | ![Green] | ![Green] |

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Supplementary Table S3. Continued.

Nicotinate and nucleotide metabolism

Insulin signaling pathway

Complement and coagulation cascades

Toll-like receptor signaling pathway

Facial adhesion

Trypsinogen metabolism

Continued on next page
### Supplementary Table S3. Continued.

#### MEK/ERK signaling pathway

| Gene | Expression |
|------|------------|
| CACGR1B | NM_000735 |
| CASP1 | NM_033302 |
| CASP6 | NM_033356 |
| CD4 | NM_000569 |
| CDC42 | NM_044171 |
| DUSP1 | NM_044171 |
| DUSP10 | NM_007207 |
| FGFR1 | NM_002692 |
| FGFR2 | NM_002090 |
| FGFR3 | NM_002090 |
| FLNC | NM_001456 |
| FOS | NM_002522 |
| GADD45A | NM_016924 |
| GADD45B | NM_016873 |
| GADD45G | B171972 |
| MAK | NFKB1 | NM_004758 |
| MARK2 | NFKB2 | NM_004550 |
| MAX | NFKB1 | NM_014514 |
| MINK1 | NFKB1 | NM_003694 |
| MINK2 | NFKB1 | NM_130544 |
| MRAS | NM_012219 |
| MYC | A178811 |
| NTRK2 | NM_01007997 |
| PDK1 | NM_002096 |
| PDK2 | NM_002096 |
| RAC1 | NM_002572 |
| RAC2 | NM_002572 |
| RASSF1 | NM_055708 |
| TGFBR3 | NM_002935 |

#### SCF-receptor interaction

| Gene | Expression |
|------|------------|
| CD44 | U69401 |
| CD47 | NM_001377 |
| COL1A1 | NM_085629 |
| COL1A2 | NM_085679 |
| COL3A1 | AK021351 |
| COL5A1 | NM_000605 |
| COL5A1 | NM_001646 |
| FN1 | NM_022060 |
| FNG1 | NM_022060 |
| FSCN1 | NM_003523 |
| ITGAV | AK028265 |
| ITGB6 | NM_002214 |
| LAMB4 | NM_002200 |
| RELA | NM_050640 |
| SDC2 | NM_002996 |
| SDC4 | NM_002996 |
| THBS2 | NM_002347 |
| THBS4 | NM_002347 |

#### Regulation of actin cytoskeleton

| Gene | Expression |
|------|------------|
| ARHGEF4 | NM_013320 |
| ARHGEF7 | NM_145735 |
| BDNF | NM_006110 |
| CD4 | NM_005691 |
| CDC2 | NM_044472 |

#### Cell cycle

| Gene | Expression |
|------|------------|
| 0 | ATM | NM_000051 |
| 0 | CCNB1 | NM_033531 |
| 0 | CCNB2 | NM_035036 |
| 0 | CCNB2 | NM_001709 |
| 0 | CDC45L1 | NM_003504 |
| 0 | CDK4A1 | NM_074847 |
| 0 | CDK6B | NM_074847 |
| 0 | GADD45A | NM_010024 |
| 0 | GADD45B | NM_015875 |
| 0 | TGFBR3 | NM_002709 |

#### TGF-beta signaling pathway

| Gene | Expression |
|------|------------|
| 0 | CDK6B | NM_074847 |
| 0 | CNTF | NM_000055 |
| 0 | DCC | NM_000055 |
| 0 | FST | NM_013449 |
| 0 | ID2 | NM_021666 |
| 0 | ID4 | NM_015046 |
| 0 | IGF-1 | NM_021662 |
| 0 | MYC | NM_018011 |
| 0 | NEDD4 | NM_018055 |
| 0 | TGFB3 | NM_002359 |
| 0 | TGFB3 | NM_002347 |
| 0 | TGFB3 | NM_002348 |

#### Leukocyte transendothelial migration

| Gene | Expression |
|------|------------|
| 0 | CD24 | NM_044472 |
| 0 | CXCL12 | NM_019368 |
| 0 | CXCL14 | NM_044857 |
| 0 | CYBB | NM_006101 |
| 0 | ITGAM | NM_006832 |

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### Supplementary Table S3. Continued.

#### Cell adhesion molecules (CAMs)

| Gene | Description |
|------|-------------|
| ITGB2 | Nil 0.0021 |
| NCF2 | Nil 0.00430 |
| NCF4 | Nil 0.00561 |
| PKRIR | Nil 0.18152 |
| PRKCB1 | Nil 0.20736 |
| RAC2 | Nil 0.05272 |
| RASGFr | Nil 0.05066 |
| RARV1 | Nil 0.05952 |
| VCA | Nil 0.05978 |
| VCL | Nil 0.01400 |
| VIL2 | Nil 0.05337 |

#### Glycan structures - biosynthesis 1

| Gene | Description |
|------|-------------|
| POE45B | Nil 0.30260 |
| POE4G0 | Nil 0.30260 |
| POELE2 | Nil 0.50262 |
| PRPS1L1 | Nil 0.17868 |

#### Cell Communication

| Gene | Description |
|------|-------------|
| COL11A1 | Nil 0.08652 |
| COL1A2 | Nil 0.09909 |
| COL1A3 | Nil 0.09131 |
| COL1D1 | Nil 0.05149 |
| COL1A1 | Nil 0.09909 |
| COL1A2 | Nil 0.05149 |
| COL4A1 | Nil 0.05149 |
| FN1 | Nil 0.21402 |
| GJA1 | Nil 0.20462 |
| GJA4 | Nil 0.15321 |
| KRT16 | Nil 0.20276 |
| KRT13 | Nil 0.20027 |
| KRT33A | Nil 0.04138 |
| LAMA4 | Nil 0.20239 |
| PREL1 | Nil 0.60922 |
| TNBS | Nil 0.15024 |
| TNFB | Nil 0.16910 |
| VIM | Nil 0.05330 |

#### Cytokine-cytokine receptor interaction

| Gene | Description |
|------|-------------|
| COL13 | Nil 0.05464 |
| COL17 | Nil 0.05067 |
| COL18 | Nil 0.02996 |
| COL18 | Nil 0.02996 |
| COL21 | Nil 0.02369 |
| COL22 | Nil 0.05064 |
| COL26 | Nil 0.07072 |
| COL5 | Nil 0.02966 |
| GCR1 | Nil 0.00195 |
| GCR2 | Nil 0.00195 |
| GCR5 | Nil 0.00557 |
| GCR7 | Nil 0.00153 |
| CSF1R | Nil 0.05211 |
| CSF3 | Nil 0.05735 |
| CXCL1 | Nil 0.02906 |
| CXCL1 | Nil 0.02906 |
| CXCL1 | Nil 0.02906 |
| CXCL1 | Nil 0.02906 |

#### Mitochondrial metabolism

| Gene | Description |
|------|-------------|
| AK5 | Nil 0.14658 |
| AMPD3 | Nil 0.06046 |
| ENPP1 | Nil 0.09306 |
| ENPP5 | Nil 0.05201 |
| GART | Nil 0.06810 |
| GDA | Nil 0.04970 |
| NTSE | Nil 0.05253 |
| POE1A | Nil 0.01000603 |
**Supplementary Table S3. Continued.**

| Adipocytokine signaling pathway | 0.00004 FCGR1A | MW_000901 |
|-------------------------------|----------------|------------|
|                               | MSA2           | MW_001396 |
|                               | PIK3R1          | MW_110123 |
|                               | PLASKA         | MW_204340 |
|                               | PRKCB1         | MW_002738 |
|                               | PTGER5         | MW_000960 |
|                               | RAC2           | MW_002872 |
|                               | SYK             | MW_011771 |
|                               | VAV1           | MW_005428 |
|                               |                |            |
| Basal transcription factors   | 0.008141 GTF2RD1 | MW_000680 |
|                               | TAF13          | MW_000545 |
|                               | TAF9           | MW_000851 |
|                               | TAF5L          | MW_014409 |
|                               |                |            |
| VEGF signaling pathway        | 0.0000 COLDC2A | MW_004472 |
|                               | MAPKAPK22      | MW_004799 |
|                               | MAPKAPK2Q      | MW_004365 |
|                               | MKR1           | MW_012199 |
|                               | PIK3R1          | MW_110123 |
|                               | PLASKA         | MW_204340 |
|                               | PRKCB1         | MW_002738 |
|                               | RAC2           | MW_002872 |
|                               | VEGFA          | MW_010238 |
|                               |                |            |
| Glutathione metabolism        | 0.03461 GGT17  | MW_178626 |
|                               | GSHR           | MW_009537 |
|                               | GSTM5          | MW_009051 |
|                               | GGT1T          | MW_009533 |
|                               |                |            |
| Cysteine metabolism           | 0.00053 CAR8    | MW_001443 |
|                               | CHST8          | MW_021615 |
|                               | LYSX           | MW_002385 |
|                               | LOX-C          | MW_002361 |
|                               | IDS            | MW_000943 |
|                               |                |            |
| Type II diabetes mellitus     | 0.00241 ADPOQ  | MW_004797 |
|                               | KCNQ1          | MW_000325 |
|                               | PIK3R1         | MW_110123 |
|                               | SOC9           | MW_001235 |
|                               |                |            |
| Linoleic acid metabolism      | 0.00012 AKR1B10 | MW_002099 |
|                               | CYP3E1         | MW_000773 |
|                               | FA2S1          | MW_014003 |
|                               | FA2S2          | MW_004205 |
|                               | FA2S3          | MW_017377 |
|                               | PLASKA         | MW_204340 |
|                               |                |            |
| Tight junction                 | 0.0008 AMOTL1  | MW_130947 |
|                               | CCO2           | MW_004472 |
|                               | COX2           | MW_022970 |
|                               | CSDE           | MW_003851 |
|                               | HDN             | MW_179777 |
|                               | MII             | MW_012199 |
|                               |                |            |

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**Table S3. Continued.**

| Pathway                                                                 | Gene Symbol | Gene Name  | Category          | Score   |
|-------------------------------------------------------------------------|-------------|------------|-------------------|---------|
| **Glutamate metabolism**                                                | NADSYT1    | ALST1      | Glutamate         | 0.1418  |
|                                                                          | ALST2A     | ALST2      | Glutamate         | 0.1984  |
|                                                                          | MNAT2      | MNAT2      | Glutamate         | 0.2483  |
|                                                                          | GLUL       | GLUL       | Glutamate         | 0.3044  |
|                                                                          | GLUR2      | GLUR2      | Glutamate         | 0.3050  |
| **B cell receptor signaling pathway**                                   | NRAS       | NRAS       | B cell receptor   | 0.0004  |
|                                                                          | FCGR2B     | FCGR2B     | B cell receptor   | 0.00001 |
|                                                                          | SYK        | SYK        | B cell receptor   | 0.00017 |
|                                                                          | PLCB1      | PLCB1      | B cell receptor   | 0.00029 |
|                                                                          | NF2BB      | NF2BB      | B cell receptor   | 0.00031 |
|                                                                          | PKCD1      | PKCD1      | B cell receptor   | 0.00039 |
|                                                                          | RAC2       | RAC2       | B cell receptor   | 0.0004  |
| **Linoleic acid and palmitic degradation**                              | ACOX1      | ACOX1      | Linoleic acid     | 0.0021  |
|                                                                          | DHPR       | DHPR       | Linoleic acid     | 0.0025  |
|                                                                          | DHPS       | DHPS       | Linoleic acid     | 0.0029  |
|                                                                          | HUDP       | HUDP       | Linoleic acid     | 0.0031  |
| **T cell receptor signaling pathway**                                   | CD2B       | CD2B       | T cell receptor   | 0.0036  |
|                                                                          | CD3E       | CD3E       | T cell receptor   | 0.0047  |
|                                                                          | CD45       | CD45       | T cell receptor   | 0.0053  |
|                                                                          | HAVCR1     | HAVCR1     | T cell receptor   | 0.0057  |
|                                                                          | VAV1       | VAV1       | T cell receptor   | 0.0059  |
| **Propanoic metabolism**                                                | ACAA6      | ACAA6      | Propanoic         | 0.0053  |
|                                                                          | CK15       | CK15       | Propanoic         | 0.0106  |
|                                                                          | HADHA      | HADHA      | Propanoic         | 0.0107  |
|                                                                          | LCH1       | LCH1       | Propanoic         | 0.0128  |
|                                                                          | LCH2       | LCH2       | Propanoic         | 0.0176  |
| **Glycine, serine, and threonine metabolism**                           | AABP1      | AABP1      | Glycine, serine,  | 0.00513 |
|                                                                          | AKR1B10    | AKR1B10    | Glycine, serine,  | 0.0063  |
|                                                                          | ALAS2      | ALAS2      | Glycine, serine,  | 0.0067  |
|                                                                          | PFK2H4     | PFK2H4     | Glycine, serine,  | 0.0075  |
|                                                                          | PKP1       | PKP1       | Glycine, serine,  | 0.0077  |
|                                                                          | SOD2       | SOD2       | Glycine, serine,  | 0.0084  |
| **Toll-like receptor signaling**                                         | GIG1       | GIG1       | Toll-like         | 0.0054  |
|                                                                          | PDE4A      | PDE4A      | Toll-like         | 0.0109  |
|                                                                          | TAO2R10    | TAO2R10    | Toll-like         | 0.0122  |
| **Butyrate metabolism**                                                 | AADAC1     | AADAC1     | Butyrate          | 0.00241 |
|                                                                          | AKR1B10    | AKR1B10    | Butyrate          | 0.00289 |
|                                                                          | HADHA      | HADHA      | Butyrate          | 0.0032  |
|                                                                          | OXCT1      | OXCT1      | Butyrate          | 0.0037  |
| **Arachidonic acid metabolism**                                         | ACOX1      | ACOX1      | Arachidonic acid  | 0.00001 |
|                                                                          | DHPR       | DHPR       | Arachidonic acid  | 0.00031 |
|                                                                          | DHPS       | DHPS       | Arachidonic acid  | 0.00033 |
|                                                                          | HUDP       | HUDP       | Arachidonic acid  | 0.00039 |

**Note:** The scores in the table represent the significance of the gene expression changes in each pathway. The pathways are color-coded to indicate the direction of change (increased or decreased expression).
Supplementary Table S3. Continued.

| Metabolism | Significance | Expression | P-value |
|------------|--------------|------------|---------|
| SREBP1C    | 0.0120 E2F2  | NM_006284  | 0.00135 |
| SREBP1D    | 0.0058 E2F2  | NM_006286  | 0.00155 |
| SREBP1E    | 0.0048 E2F2  | NM_006287  | 0.00165 |
| SREBP1F    | 0.0039 E2F2  | NM_006288  | 0.00175 |
| SREBP1G    | 0.0029 E2F2  | NM_006289  | 0.00185 |
| SREBP1H    | 0.0019 E2F2  | NM_006290  | 0.00195 |
| SREBP1I    | 0.0010 E2F2  | NM_006291  | 0.00205 |
| SREBP1J    | 0.0001 E2F2  | NM_006292  | 0.00215 |

| Pathway | Description | Significance | Expression | P-value |
|---------|-------------|--------------|------------|---------|
| SREBP1C | SREBP1C     | 0.0120 E2F2  | NM_006284  | 0.00135 |
| SREBP1D | SREBP1D     | 0.0058 E2F2  | NM_006286  | 0.00155 |
| SREBP1E | SREBP1E     | 0.0048 E2F2  | NM_006287  | 0.00165 |
| SREBP1F | SREBP1F     | 0.0039 E2F2  | NM_006288  | 0.00175 |
| SREBP1G | SREBP1G     | 0.0029 E2F2  | NM_006289  | 0.00185 |
| SREBP1H | SREBP1H     | 0.0019 E2F2  | NM_006290  | 0.00195 |
| SREBP1I | SREBP1I     | 0.0010 E2F2  | NM_006291  | 0.00205 |
| SREBP1J | SREBP1J     | 0.0001 E2F2  | NM_006292  | 0.00215 |

| Pathway | Description | Significance | Expression | P-value |
|---------|-------------|--------------|------------|---------|
| SREBP1C | SREBP1C     | 0.0120 E2F2  | NM_006284  | 0.00135 |
| SREBP1D | SREBP1D     | 0.0058 E2F2  | NM_006286  | 0.00155 |
| SREBP1E | SREBP1E     | 0.0048 E2F2  | NM_006287  | 0.00165 |
| SREBP1F | SREBP1F     | 0.0039 E2F2  | NM_006288  | 0.00175 |
| SREBP1G | SREBP1G     | 0.0029 E2F2  | NM_006289  | 0.00185 |
| SREBP1H | SREBP1H     | 0.0019 E2F2  | NM_006290  | 0.00195 |
| SREBP1I | SREBP1I     | 0.0010 E2F2  | NM_006291  | 0.00205 |
| SREBP1J | SREBP1J     | 0.0001 E2F2  | NM_006292  | 0.00215 |