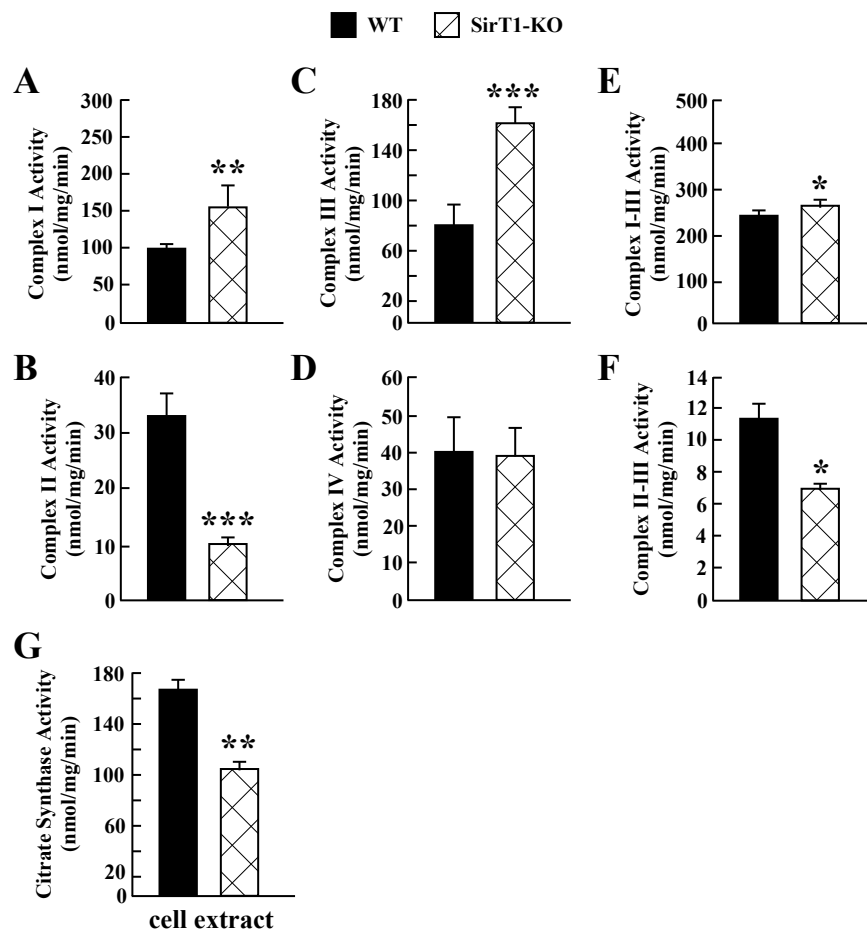


Negative Regulation of STAT3-mediated Cellular Respiration by SirT1

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Supplemental Figure 1. Effect of SirT1 deletion on mitochondrial enzyme activities in MEF cells. Enzymatic activities of complex I (A), complex II (B), complex III (C), complex IV (D), complexes I+III (E), and complexes II+III (F) were measured in solubilized mitochondria from WT (filled bars) and SirT1-KO MEFs (hatched bars) as described in Fig. 4. Values are expressed in nmoles of substrate (donor or acceptor) consumed by min per min protein. Activities were NOT normalized with respect to mitochondrial citrate synthase activity. (G) Citrate synthase activity was measured in total cell lysates from WT and SirT1-null MEFs. The data represents the average \pm SD of 3 independent experiments. *, ** and ***, $P < 0.05$, 0.01 , and 0.001 vs. WT groups.

Supplemental Table 1. Microarray cDNA analysis of STAT family members in wild-type and SirT1-KO MEFS

| (avg int) | KI (fdr) | KU-W (fold chanç) | (mean)(SA (p) | KU-WU SYMBOL | (selector) | t (zratio) | KU ACCESSID | ARRAY_AI | AVG_Sign | AVG_Sign | AVG_Sign | AVG_Sign | AVG_Sign | AVG_Sign | AVG_Sign | AVG_Sign | AVG_Sign | CHROMO: | CYTOBAN | DEFINITIC | ENTREZ_I | GI | ID | ILMN_GE | OBSOLET | ONTOLOC | ONTOLOC | ONTOLOC | p(A)(SAMF | PROBE_C |
|-----------|----------|-------------------|---------------|--------------|------------|------------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|---------|---------|-----------|----------|----------|---------|---------|-----------|-------------|--------------|--------------|-----------|---------|
| -0.43575 | 9.85E-07 | 1.75298 | 0.241191 | 2.23E-07 | Stat1 | 0 | 1.033758 | NM_00926 | 240725 | 393.1018 | 376.5621 | 293.5254 | 303.0482 | 234.2979 | 189.5606 | 263.3484 | 186.9552 | 1 | 1qC1.1 | Mus musci | 20846 | 1.14E+08 | 240725 | STAT1 | | nucleus [g] | transcriptic | transcriptic | 0.000814 | + |
| -0.45316 | 0.01132 | -1.30037 | 0.120122 | 0.004922 | Stat6 | 0 | -0.65174 | NM_00926 | 3940161 | 279.451 | 248.8082 | 161.0938 | 207.145 | 369.8577 | 298.7921 | 334.7062 | 313.2094 | 10 | 10qD3 | Mus musci | 20852 | 1.28E+08 | 3940161 | STAT6 | | nucleus [g] | transcriptic | transcriptic | 0.031697 | + |
| -0.88551 | 1.21E-14 | 2.056802 | -0.28518 | 1.33E-15 | Stat5a | 0 | 1.311917 | NM_01148 | 4050619 | 243.3084 | 247.0932 | 164.4687 | 188.6333 | 123.469 | 93.03703 | 108.8393 | 117.6862 | 11 | 11qD | Mus musci | 20850 | 31981473 | 4050619 | STAT5A | STAT5; AA | nucleus [g] | signal tran: | positive re | 0.000117 | + |
| 0.185302 | 0 | 3.361813 | 0.815042 | 0 | Stat3 | 2 | 2.347927 | NM_21366 | 5310360 | 1225.926 | 1285.446 | 858.7106 | 982.2584 | 419.1821 | 301.969 | 371.9635 | 316.9784 | 11 | 11qD | Mus musci | 20848 | 76253927 | 5310360 | STAT3 | | nucleus [g] | transcriptic | eye photor | 4.55E-06 | - |
| -1.05902 | 0 | -1.17052 | -0.50301 | 0 | Stat2 | 0 | -0.43115 | NM_01996 | 6220594 | 110.5266 | 111.5686 | 95.62407 | 99.53232 | 154.0784 | 112.3134 | 147.6234 | 131.9094 | 10 | 10qD3 | Mus musci | 20847 | 9910571 | 6220594 | STAT2 | AW49648C | nucleus [g] | transcriptic | transcriptic | 0.009674 | + |
| -0.92678 | 0 | 2.028285 | -0.32808 | 0 | Stat3 | 0 | 1.29738 | NM_01148 | 6580553 | 219.7799 | 211.1154 | 157.0139 | 184.6821 | 104.0507 | 96.26723 | 118.3502 | 109.9755 | 11 | 11qD | Mus musci | 20848 | 76253924 | 6580553 | STAT3 | | nucleus [g] | transcriptic | eye photor | 0.000156 | - |
| 0.477273 | 0 | 4.084325 | 1.14989 | 0 | Stat3 | 2 | 2.730749 | NM_21366 | 6660176 | 2213.184 | 1847.356 | 1247.661 | 1541.955 | 515.2315 | 369.1342 | 567.7358 | 399.0903 | 11 | 11qD | Mus musci | 20848 | 76253927 | 6660176 | STAT3 | | nucleus [g] | transcriptic | eye photor | 3.75E-05 | - |
| -0.91643 | 0.00803 | 1.256681 | -0.29529 | 0.003364 | Stat5a | 0 | 0.349435 | NM_01148 | 7650575 | 150.2919 | 137.4299 | 145.7191 | 149.489 | 164.3138 | 121.6045 | 143.1401 | 124.0753 | 11 | 11qD | Mus musci | 20850 | 31981473 | 7650575 | STAT5A | STAT5; AA | nucleus [g] | signal tran: | positive re | 0.021837 | + |

| PROBE_C | PROBE_IL | PROBE_S | PROBE_S | PROBE_T | PROTEIN | REFSEQ_SEARCH_selector(A) | SOURCE | SOURCE | SPECIES | SYNONYM | TARGETIC | TRANSCR | UNIGENE | zscore_KC | zscore_KC | zscore_KC | zscore_KC | zscore_W1 | zscore_W1 | zscore_W1 | zscore_W1 | UT3 | |
|----------|----------|---------|---------|---------|---------|---------------------------|----------|----------|---------|---------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|----------|
| 52217485 | ILMN_265 | ACCCCGA | 3944 | S | | NP_03330 | NM_00928 | ILMN_194 | 2 | RefSeq | NM_00928 | Mus musci | AA408197 | STAT1 | ILMN_254 | 0.520581 | 0.530295 | 0.353845 | 0.351747 | -0.02549 | -0.00823 | 0.114347 | -0.12474 |
| 12709792 | ILMN_289 | GCTCTTA | 3687 | S | | NP_03331 | NM_00928 | ILMN_209 | 2 | RefSeq | NM_00928 | Mus musci | | STAT6 | ILMN_209 | 0.238949 | 0.202543 | -0.16551 | 0.04841 | 0.334107 | 0.354825 | 0.310126 | 0.30351 |
| 10074604 | ILMN_297 | GTGCTAG | 3396 | S | | NP_03561 | NM_01148 | ILMN_216 | 2 | RefSeq | NM_01148 | Mus musci | STAT5; AA | STAT5A | ILMN_216 | 0.124645 | 0.197072 | -0.14756 | -0.02623 | -0.53008 | -0.57608 | -0.60713 | -0.50888 |
| 10074966 | ILMN_258 | CGGGGT | 2901 | S | | NP_99882 | NM_21365 | ILMN_208 | 2 | RefSeq | NM_21365 | Mus musci | AW10995 | STAT3 | ILMN_243 | 1.459282 | 1.501354 | 1.283059 | 1.2893 | 0.432714 | 0.363263 | 0.396303 | 0.313438 |
| 12772948 | ILMN_285 | ACTTGTG | 3973 | S | | NP_06434 | NM_01996 | ILMN_215 | 2 | RefSeq | NM_01996 | Mus musci | AW49648 | STAT2 | ILMN_215 | -0.52659 | -0.4318 | -0.61698 | -0.53593 | -0.35563 | -0.42584 | -0.35826 | -0.41419 |
| 10074903 | ILMN_309 | CCCTGCC | 3477 | A | | NP_03561 | NM_01148 | ILMN_208 | 2 | RefSeq | NM_01148 | Mus musci | AW10995 | STAT3 | ILMN_208 | 0.040708 | 0.072615 | -0.18771 | -0.0431 | -0.66486 | -0.54885 | -0.53872 | -0.56512 |
| 10074955 | ILMN_269 | CCTTGCT | 3006 | S | | NP_99882 | NM_21365 | ILMN_208 | 2 | RefSeq | NM_21365 | Mus musci | AW10995 | STAT3 | ILMN_243 | 1.946825 | 1.788176 | 1.606449 | 1.648828 | 0.595221 | 0.523502 | 0.741572 | 0.504618 |
| 10074614 | ILMN_297 | GGGTCTC | 3497 | S | | NP_03561 | NM_01148 | ILMN_216 | 2 | RefSeq | NM_01148 | Mus musci | STAT5; AA | STAT5A | ILMN_216 | -0.27295 | -0.26691 | -0.25233 | -0.21165 | -0.30497 | -0.36243 | -0.38344 | -0.465 |

Supplemental Table 2. Phospho/non-Phospho Ratio change in untreated Sirt1-KO vs WT MEF cells

| Protein Name | Ratio | 95% CI | Protein Name | Ratio | 95% CI |
|--|-------|--------------|--|-------|-------------|
| Histone H3.1 (Phospho-Ser10) | 23.24 | [9.47-37.00] | Tau (Phospho-Ser404) | 0.80 | [0.60-1.01] |
| LCK (Phospho-Tyr192) | 10.97 | [8.70-13.24] | Fos (Phospho-Thr232) | 0.80 | [0.64-0.97] |
| Dab1 (Phospho-Tyr232) | 9.72 | [8.46-10.97] | MEF2A (Phospho-Ser408) | 0.80 | [0.67-0.93] |
| SAPK/JNK (Phospho-Tyr185) | 9.21 | [7.45-10.96] | c-Kit (Phospho-Tyr721) | 0.80 | [0.71-0.89] |
| LCK (Phospho-Ser59) | 8.14 | [6.70-9.57] | ATF4 (Phospho-Ser245) | 0.80 | [0.37-1.23] |
| DAB1 (Phospho-Tyr220) | 7.76 | [6.67-8.85] | Tau (Phospho-Ser396) | 0.80 | [0.66-0.93] |
| NFkB-p65 (Phospho-Ser529) | 6.54 | [5.39-7.68] | Mst1/Mst2 (Phospho-Thr183) | 0.80 | [0.37-1.22] |
| JAK1 (Phospho-Tyr1022) | 5.74 | [3.97-7.51] | PPAR-b (Phospho-Thr1457) | 0.79 | [0.54-1.04] |
| Tau (Phospho-Ser262) | 5.41 | [4.27-6.55] | AKT2 (Phospho-Ser474) | 0.79 | [0.65-0.94] |
| CDC2 (Phospho-Tyr15) | 5.25 | [3.14-7.37] | MAPKAPK-2 (Phospho-Thr222) | 0.79 | [0.32-1.25] |
| Elk1 (Phospho-Thr417) | 5.25 | [3.50-7.00] | eNOS (Phospho-Ser1177) | 0.78 | [0.50-1.07] |
| ASK1 (Phospho-Ser83) | 4.93 | [0.42-9.44] | TIE2 (Phospho-Tyr1108) | 0.78 | [0.51-1.04] |
| AKT1 (Phospho-Ser124) | 4.64 | [2.12-7.15] | Tyrosine Hydroxylase (TH) (Phospho-Ser8) | 0.77 | [0.54-1.00] |
| AURORA KINASE (Phospho-Thr288) | 4.27 | [2.45-6.08] | EGFR (Phospho-Tyr1110) | 0.76 | [0.48-1.04] |
| WEE1 (Phospho-Ser642) | 4.19 | [3.40-4.97] | FKHRL1/FOXO3A (Phospho-Ser253) | 0.75 | [0.48-1.02] |
| E2F1 (Phospho-Thr433) | 4.14 | [3.53-4.75] | PLCg2 (Phospho-Tyr1217) | 0.75 | [0.55-0.96] |
| CK1-A/A2 (Phospho-Tyr294) | 4.09 | [3.28-4.91] | Myc (Phospho-Thr358) | 0.75 | [0.35-1.15] |
| NFkB-p65 (Phospho-Ser468) | 4.03 | [3.04-5.03] | Stathmin 1 (Phospho-Ser37) | 0.75 | [0.35-1.16] |
| P38 MAPK (Phospho-Tyr182) | 4.01 | [1.66-6.35] | IKK-b (Phospho-Tyr199) | 0.74 | [0.49-1.00] |
| CDK7 (Phospho-Thr170) | 3.99 | [2.71-5.28] | p53 (Phospho-Thr81) | 0.74 | [0.58-0.90] |
| HDAC6 (Phospho-Ser22) | 3.87 | [3.31-4.44] | KIT (Phospho-Tyr703) | 0.74 | [0.54-0.94] |
| CD3Z (Phospho-Tyr142) | 3.80 | [2.46-5.14] | CaMKII (Phospho-Thr286) | 0.74 | [0.50-0.98] |
| NFkB-p65 (Phospho-Ser536) | 3.68 | [2.15-5.20] | RyR2 (Phospho-Ser2808) | 0.73 | [0.53-0.94] |
| Smad2/3 (Phospho-Thr8) | 3.67 | [3.09-4.24] | BCL-2 (Phospho-Ser70) | 0.73 | [0.64-0.83] |
| p44/42 MAP Kinase (Phospho-Tyr204) | 3.64 | [2.70-4.58] | Kv1.3/KCNA3 (Phospho-Tyr135) | 0.73 | [0.53-0.93] |
| GATA1 (Phospho-Ser310) | 3.62 | [3.35-3.88] | G3BP-1 (Phospho-Ser232) | 0.73 | [0.38-1.08] |
| Calmodulin (Phospho-Thr79/Ser81) | 3.61 | [2.89-4.34] | FAK (Phospho-Tyr861) | 0.73 | [0.49-0.97] |
| TYK2 (Phospho-Tyr1054) | 3.57 | [2.75-4.39] | Tau (Phospho-Thr205) | 0.73 | [0.23-1.22] |
| IkB-a (Phospho-Ser32/36) | 3.52 | [2.70-4.34] | eNOS (Phospho-Ser615) | 0.73 | [0.26-1.19] |
| SEK1/MKK4 (Phospho-Ser80) | 3.35 | [2.23-4.46] | MAPKAPK-2 (Phospho-Thr222) | 0.73 | [0.50-0.95] |
| NFkB-p105/p50 (Phospho-Ser932) | 3.28 | [1.27-5.30] | MITF (Phospho-Ser73) | 0.72 | [0.30-1.14] |
| FOXO1A/3A (Phospho-Ser322/325) | 3.28 | [2.79-3.78] | MAP3K1/MEKK1 (Phospho-Thr1381) | 0.72 | [0.14-1.29] |
| MKK3 (Phospho-Ser189) | 3.10 | [2.49-3.71] | PTEN (Phospho-Ser370) | 0.72 | [0.25-1.19] |
| p27Kip1 (Phospho-Thr187) | 2.91 | [2.14-3.67] | MYPT1 (Phospho-Thr-853) | 0.72 | [0.35-1.08] |
| Hsp90 co-chaperone Cdc37 (Phospho-Ser13) | 2.89 | [1.85-3.94] | PLCg1 (Phospho-Tyr783) | 0.71 | [0.54-0.88] |
| IGF2R (Phospho-Ser2409) | 2.86 | [1.57-4.14] | SEK1/MKK4/JNKK1 (Phospho-Ser257) | 0.71 | [0.52-0.90] |
| IkB-a (Phospho-Tyr305) | 2.66 | [2.16-3.17] | FGFR1 (Phospho-Tyr766) | 0.71 | [0.48-0.94] |
| CREB (Phospho-Ser129) | 2.64 | [2.26-3.03] | CaMK2-b/g/d (Phospho-Thr287) | 0.71 | [0.30-1.11] |
| BCR (Phospho-Tyr177) | 2.57 | [1.65-3.48] | ACTIN Pan(a/b/g) (Phospho-Tyr55/53) | 0.70 | [0.44-0.97] |
| CDK2 (Phospho-Thr160) | 2.52 | [2.02-3.02] | SYN1-Synapsin1 (Phospho-Ser62) | 0.70 | [0.23-1.17] |
| ETK (Phospho-Tyr566) | 2.46 | [0.84-4.07] | PLCg1 (Phospho-Tyr1253) | 0.70 | [0.46-0.94] |
| P90RSK (Phospho-Ser380) | 2.44 | [2.09-2.79] | P70S6K (Phospho-Ser424) | 0.70 | [0.57-0.83] |
| Trk B (Phospho-Tyr705) | 2.43 | [1.14-3.71] | ATP1A1/Na+K+ ATPase1 (Phospho-Ser23) | 0.70 | [0.30-1.10] |
| Caspase 9 (Phospho-Ser144) | 2.40 | [2.07-2.74] | A-RAF (Phospho-Tyr301/302) | 0.70 | [0.33-1.07] |
| STAT1 (Phospho-Ser727) | 2.40 | [1.22-3.59] | Catalase (Phospho-Tyr385) | 0.70 | [0.47-0.92] |
| CDK1/CDC2 (Phospho-Thr14) | 2.40 | [0.70-4.09] | PKC z (Phospho-Thr560) | 0.69 | [0.03-1.35] |
| B-RAF (Phospho-Ser446) | 2.38 | [1.97-2.78] | PKC e (Phospho-Ser729) | 0.69 | [0.58-0.80] |
| p53 (Phospho-Ser315) | 2.33 | [1.85-2.80] | NFkB-p105/p50 (Phospho-Ser907) | 0.69 | [0.55-0.83] |
| Src (Phospho-Ser75) | 2.33 | [1.20-3.45] | VAV1 (Phospho-Tyr174) | 0.69 | [0.14-1.23] |

| | | | | | |
|---|------|-------------|--|------|-------------|
| SEK1/MKK4 (Phospho-Thr261) | 2.32 | [1.69-2.95] | PI3-kinase p85-a (Phospho-Tyr607) | 0.68 | [0.37-1.00] |
| p27Kip1 (Phospho-Ser10) | 2.31 | [1.65-2.97] | Rb (Phospho-Ser811) | 0.68 | [0.52-0.85] |
| Elk1 (Phospho-Ser389) | 2.31 | [1.69-2.92] | GSK3a/b (Phospho-Tyr216/279) | 0.68 | [0.26-1.10] |
| IL-4R/CD124 (Phospho-Tyr497) | 2.30 | [1.58-3.01] | MSK1 (Phospho-Ser376) | 0.68 | [0.31-1.05] |
| 4E-BP1 (Phospho-Thr70) | 2.29 | [1.43-3.15] | MSK1 (Phospho-Ser212) | 0.68 | [0.25-1.11] |
| Tyrosine Hydroxylase (Phospho-Ser19) | 2.29 | [1.63-2.95] | PLCg1 (Phospho-Tyr771) | 0.68 | [0.19-1.16] |
| JAK2 (Phospho-Tyr221) | 2.28 | [1.87-2.69] | MYPT1 (Phospho-Thr696) | 0.68 | [0.28-1.07] |
| STAT5A (Phospho-Ser780) | 2.27 | [1.23-3.30] | Chk2 (Phospho-Thr383) | 0.68 | [0.50-0.86] |
| Chk1 (Phospho-Ser301) | 2.26 | [1.35-3.18] | MEK1 (Phospho-Ser298) | 0.68 | [0.28-1.08] |
| c-Jun (Phospho-Ser63) | 2.25 | [1.67-2.84] | ALK (Phospho-Tyr1604) | 0.66 | [0.31-1.01] |
| Catenin b (Phospho-Ser33) | 2.25 | [2.01-2.50] | PLD1 (Phospho-Tyr561) | 0.66 | [0.45-0.87] |
| FKHR (Phospho-Ser319) | 2.22 | [1.72-2.72] | FLT3 (Phospho-Tyr969) | 0.66 | [0.39-0.92] |
| Survivin (Phospho-Thr117) | 2.22 | [1.18-3.26] | LYN (Phospho-Tyr507) | 0.66 | [0.27-1.04] |
| P70S6K (Phospho-Ser418) | 2.20 | [1.76-2.65] | p130Cas (Phospho-Tyr410) | 0.65 | [0.52-0.77] |
| AurB (Phospho-Thr232) | 2.20 | [1.17-3.24] | KIT (Phospho-Tyr936) | 0.65 | [0.53-0.77] |
| PKD1/PKC mu (Phospho-Ser205) | 2.17 | [1.30-3.03] | MEK1 (Phospho-Thr286) | 0.64 | [0.43-0.85] |
| Caspase-3 (Phospho-Ser150) | 2.16 | [1.23-3.09] | HDAC2 (Phospho-Ser394) | 0.64 | [0.32-0.96] |
| PKD1/PKC m (Phospho-Tyr463) | 2.14 | [1.40-2.88] | ATRIP (Phospho-Ser68/72) | 0.64 | [0.31-0.97] |
| JAK2 (Phospho-Tyr1007) | 2.12 | [1.61-2.64] | Smad1 (Phospho-Ser465) | 0.64 | [0.44-0.83] |
| IRS-1 (Phospho-Ser612) | 2.11 | [1.31-2.91] | ICAM-1 (Phospho-Tyr512) | 0.63 | [0.33-0.93] |
| VEGFR2 (Phospho-Tyr1059) | 2.10 | [0.96-3.24] | Ezrin (Phospho-Tyr478) | 0.63 | [0.46-0.80] |
| MKP-1 (Phospho-Ser359) | 2.08 | [1.71-2.46] | PKC pan activation sites (Phospho) | 0.63 | [0.25-1.00] |
| HSP27 (Phospho-Ser15) | 2.01 | [1.57-2.46] | BAD (Phospho-Ser112) | 0.63 | [0.52-0.74] |
| CASP9 (Phospho-Thr125) | 2.00 | [1.25-2.75] | CREB (Phospho-Ser142) | 0.62 | [0.53-0.72] |
| Tau (Phospho-Thr231) | 2.00 | [1.59-2.41] | MEK1 (Phospho-Thr291) | 0.62 | [0.32-0.92] |
| IRS-1 (Phospho-Ser636) | 1.99 | [1.22-2.77] | GAP43 (Phospho-Ser41) | 0.62 | [0.16-1.08] |
| Caspase 9 (Phospho-Tyr153) | 1.99 | [1.49-2.49] | HER2 (Phospho-Tyr1248) | 0.61 | [0.47-0.76] |
| HER3/ErbB3 (Phospho-Tyr1289) | 1.97 | [1.74-2.19] | EGFR (Phospho-Thr678) | 0.61 | [0.39-0.83] |
| Catenin b (CTNNB) (Phospho-Tyr489) | 1.96 | [1.63-2.29] | claudin 3 (Phospho-Tyr219) | 0.60 | [0.39-0.81] |
| HER4/ErbB4 (Phospho-Tyr1284) | 1.93 | [1.51-2.35] | BAD (Phospho-Ser155) | 0.60 | [0.54-0.66] |
| Breast tumor kinase (Phospho-Tyr447) | 1.93 | [1.34-2.51] | EPHB1/2 (Phospho-Tyr594/604) | 0.59 | [0.10-1.08] |
| Rac1/cdc42 (Phospho-Ser71) | 1.92 | [1.35-2.49] | PP2A-a (Phospho-Tyr307) | 0.58 | [0.24-0.92] |
| LAT (Phospho-Tyr191) | 1.88 | [1.40-2.36] | p21Cip1 (Phospho-Thr145) | 0.57 | [0.33-0.81] |
| Src (Phospho-Tyr418) | 1.87 | [0.67-3.07] | Cyclin B1 (phospho-Ser126) | 0.57 | [0.40-0.74] |
| ASK1 (Phospho-Ser966) | 1.86 | [1.54-2.17] | EGFR (Phospho-Tyr1197) | 0.57 | [0.43-0.70] |
| LKB1 (Phospho-Thr189) | 1.86 | [1.41-2.30] | BCL-2 (Phospho-Thr69) | 0.57 | [0.48-0.65] |
| Smad3 (Phospho-Ser213) | 1.85 | [0.38-3.31] | FAK (Phospho-Tyr397) | 0.56 | [0.20-0.93] |
| STAT2 (Phospho-Tyr690) | 1.84 | [1.32-2.35] | Myc (Phospho-Thr58) | 0.56 | [0.41-0.71] |
| AMPK1/AMPK2 (Phospho-Ser485/491) | 1.83 | [1.53-2.13] | CK1-A (Phospho-Thr321) | 0.54 | [0.47-0.61] |
| GATA1 (Phospho-Ser142) | 1.83 | [1.69-1.97] | PIP5K (Phospho-Ser307) | 0.53 | [0.27-0.79] |
| IkB-a (Phospho-Tyr42) | 1.82 | [1.29-2.35] | EGFR (Phospho-Thr693) | 0.53 | [0.40-0.66] |
| Estrogen Receptor-a (Phospho-Ser167) | 1.82 | [1.43-2.21] | MSK1 (Phospho-Ser360) | 0.52 | [0.32-0.72] |
| CREB (Phospho-Ser121) | 1.81 | [1.55-2.08] | CREB (Phospho-Thr100) | 0.51 | [0.36-0.66] |
| CaMK4 (Phospho-Thr196/200) | 1.80 | [1.53-2.07] | Tyrosine Hydroxylase (Phospho-Ser40) | 0.51 | [0.33-0.68] |
| PKC z (Phospho-Thr410) | 1.80 | [1.59-2.01] | 14-3-3 z/d (Phospho-Thr232) | 0.51 | [0.10-0.91] |
| JunD (Phospho-Ser255) | 1.79 | [0.74-2.84] | Myc (Phospho-Ser373) | 0.49 | [0.37-0.60] |
| IRS-1 (Phospho-Ser323) | 1.76 | [1.39-2.13] | BAD (Phospho-Ser136) | 0.45 | [0.34-0.55] |
| Chk2 (Phospho-Ser516) | 1.76 | [1.21-2.30] | Connexin 43 (Phospho-Ser367) | 0.44 | [0.36-0.51] |
| HDAC4 (Phospho-Ser632) | 1.75 | [1.22-2.27] | PI3-kinase p85-subunit a/g (Phospho-Tyr467/Tyr199) | 0.41 | [0.29-0.52] |
| ERK3 (Phospho-Ser189) | 1.74 | [0.92-2.58] | MSK1 (Phospho-Thr581) | 0.40 | [0.19-0.62] |
| RSK1/2/3/4 (Phospho-Ser221/227/218/232) | 1.74 | [0.91-2.57] | p63(Phospho-Ser455) | 0.40 | [0.14-0.66] |
| 4E-BP1 (Phospho-Thr36) | 1.73 | [1.35-2.12] | eNOS (Phospho-Thr495) | 0.39 | [0.07-0.71] |

| | | | | | |
|---------------------------------|------|-------------|-------------------------------|------|-------------|
| BTK (Phospho-Tyr222) | 1.73 | [1.23-2.23] | Pyk2 (Phospho-Tyr579) | 0.39 | [0.08-0.70] |
| SHP-2 (Phospho-Tyr580) | 1.72 | [0.87-2.57] | Stathmin 1(Phospho-Ser24) | 0.39 | [0.27-0.50] |
| FOXO1A (Phospho-Ser329) | 1.72 | [1.63-1.81] | BRCA1 (Phospho-Ser1524) | 0.38 | [0.31-0.46] |
| PAK1 (Phospho-Thr212) | 1.71 | [1.55-1.88] | CD19 (Phospho-Tyr531) | 0.38 | [0.29-0.47] |
| Zap-70 (Phospho-Tyr319) | 1.70 | [1.00-2.39] | GABA-RB (Phospho-Ser434) | 0.38 | [0.13-0.62] |
| Cyclin D3 (Phospho-Thr283) | 1.68 | [1.20-2.16] | XIAP (Phospho-Ser87) | 0.37 | [0.22-0.51] |
| MEK1 (Phospho-Ser217) | 1.68 | [1.18-2.17] | Integrin b-3 (Phospho-Tyr773) | 0.33 | [0.20-0.47] |
| IL3R (Phospho-Tyr593) | 1.66 | [0.88-2.44] | mTOR (Phospho-Ser2481) | 0.33 | [0.22-0.44] |
| CASP1 (Phospho-Ser376) | 1.64 | [0.90-2.39] | MEF2A (Phospho-Thr319) | 0.32 | [0.22-0.42] |
| 4E-BP1 (Phospho-Ser65) | 1.64 | [0.56-2.73] | NFkB-p65 (Phospho-Ser311) | 0.30 | [0.28-0.33] |
| LCK (Phospho-Tyr504) | 1.64 | [1.09-2.18] | CSFR (Phospho-Tyr561) | 0.28 | [0.22-0.35] |
| Ezrin (Phospho-Tyr353) | 1.64 | [1.16-2.12] | IRS-1 (Phospho-Ser307) | 0.25 | [0.18-0.32] |
| Chk2 (Phospho-Thr387) | 1.64 | [1.18-2.09] | DARPP-32 (Phospho-Thr75) | 0.25 | [0.22-0.27] |
| Smad3 (Phospho-Thr179) | 1.64 | [0.10-3.17] | PKD1/PKCm (Phospho-Ser910) | 0.24 | [0.20-0.29] |
| c-met (Phospho-Tyr1003) | 1.63 | [1.27-1.99] | LKB1 (Phospho-Ser428) | 0.23 | [0.16-0.30] |
| IRS-1 (Phospho-Ser794) | 1.63 | [1.09-2.17] | Raf1 (Phospho-Ser259) | 0.15 | [0.08-0.23] |
| eEF2K (Phospho-Ser366) | 1.62 | [1.26-1.99] | GAB1 (Phospho-Tyr659) | 0.15 | [0.08-0.21] |
| IL-2RA/CD25 (Phospho-Ser268) | 1.62 | [1.04-2.19] | BCL-XL (Phospho-Ser62) | 0.09 | [0.08-0.10] |
| AMPKb1 (Phospho-Ser182) | 1.62 | [0.94-2.30] | EEF2 (Phospho-Thr56) | 0.08 | [0.06-0.09] |
| VE-Cadherin (Phospho-Tyr731) | 1.61 | [0.79-2.43] | CrkL (Phospho-Tyr207) | 0.00 | [0.00-0.00] |
| CaMK2 (Phospho-Thr305) | 1.59 | [0.88-2.29] | | | |
| NMDAR2B (Phospho-Tyr1472) | 1.58 | [0.90-2.25] | | | |
| BID (Phospho-Ser78) | 1.58 | [0.63-2.52] | | | |
| Raf1 (Phospho-Ser338) | 1.57 | [1.20-1.95] | | | |
| Catenin b (Phospho-Thr41/Ser45) | 1.57 | [1.38-1.77] | | | |
| HDAC5 (Phospho-Ser498) | 1.57 | [1.27-1.87] | | | |
| Filamin A (Phospho-Ser2152) | 1.57 | [0.98-2.16] | | | |
| HDAC3 (Phospho-Ser424) | 1.57 | [1.29-1.85] | | | |
| Gab2 (Phospho-Tyr643) | 1.56 | [1.15-1.98] | | | |
| Pyk2 (Phospho-Tyr580) | 1.55 | [0.88-2.22] | | | |
| Pim-1 (Phospho-Tyr309) | 1.54 | [0.68-2.40] | | | |
| Zap-70 (Phospho-Tyr493) | 1.54 | [0.77-2.30] | | | |
| CD45 (Phospho-Ser1007) | 1.54 | [0.93-2.14] | | | |
| MKP-1/2 (Phospho-Ser296) | 1.52 | [1.08-1.96] | | | |
| P95/NBS1 (Phospho-Ser343) | 1.52 | [0.87-2.16] | | | |
| Synuclein a (Phospho-Tyr125) | 1.51 | [1.16-1.87] | | | |
| Cyclin B1 (phospho-Ser147) | 1.51 | [0.98-2.03] | | | |

Supplemental Table 3. Induction of select target genes of NF- κ B in Sirt1-null MEFs

| Acc # | SYMBOL | mRNA | zratio KO/WT |
|----------------|--------|---|-----------------|
| NM_013599.2 | Mmp9 | matrix metalloproteinase 9 | 9.717 |
| NM_008176.3 | Cxcl1 | chemokine (C-X-C motif) ligand 1 | 4.889 |
| NM_011333.3 | Ccl2 | chemokine (C-C motif) ligand 2 | 4.168 |
| NM_013653.3 | Ccl5 | chemokine (C-C motif) ligand 5 | 4.017 |
| NM_011581.3 | Thbs2 | thrombospondin 2 | 3.988 |
| NM_001159396.1 | Irf1 | interferon regulatory factor 1 | 3.445 |
| NM_011905.3 | Tlr2 | toll-like receptor 2 | 3.364 |
| NM_010907.2 | Nfkbia | nuclear factor of kappa light polypeptide gene enhancer in B-cell | 3.346 |
| NM_007554.2 | Bmp4 | bone morphogenetic protein 4 | 3.181 |
| NM_011332.3 | Ccl17 | chemokine (C-C motif) ligand 17 | 3.052 |
| NM_008706.5 | Nqo1 | NAD(P)H dehydrogenase, quinone 1 | 2.850 |
| NM_009811.3 | Casp6 | caspase 6 | 2.756 |
| NM_001113529.1 | Csf1 | colony stimulating factor 1 (macrophage) | 2.541 |
| NM_011693.3 | Vcam1 | vascular cell adhesion molecule 1 | 2.512 |
| NM_011448.4 | Sox9 | SRY-box containing gene 9 | 2.496 |
| NM_008416.2 | Junb | Jun-B oncogene | 2.384 |
| NM_008091.3 | Gata3 | GATA binding protein 3 | 2.290 |
| NM_010442.2 | Hmox1 | heme oxygenase (decycling) 1 | 2.268 |
| NM_007987.2 | Fas | TNF receptor superfamily member 6 (Fas) | 2.200 |
| NM_008873.3 | Plau | plasminogen activator, urokinase | 2.040 |
| NM_019676.2 | Plcd1 | phospholipase C, delta 1 | 1.958 |
| NM_013671.3 | Sod2 | superoxide dismutase 2, mitochondrial | 1.881 |
| NM_010431.2 | Hif1a | hypoxia inducible factor 1, alpha subunit | 1.717 |
| NM_021274.1 | Cxcl10 | chemokine (C-X-C motif) ligand 10 | 1.691 |
| NM_009506.2 | Vegfc | vascular endothelial growth factor C | 1.557 |
| NM_008690.3 | Nfkbie | nuclear factor of kappa light polypeptide gene enhancer in B-cell | 1.458 |
| NM_009421.3 | Traf1 | TNF receptor-associated factor 1 | 1.359 |
