**Table S1.** Proteins showing altered levels upon *Mjd* siRNA in undifferentiated C2C12 cells (Day 0). Cut-off (sketched line): proteins with fold changes ≥ 20% (1.2 < ratio < 0.8) considering a statistical significant p-value < 0.05. Functional networks: (A) cellular movement; (B) drug metabolism; (C) protein synthesis; (D) skeletal and muscular system development and function, tissue morphology; (E) cellular development, embryonic development, cellular assembly and organization; (F) small molecule biochemistry, gene expression.

| Accession number | Description | Fold change Mjd siRNA/ mock | Functional network |
|---|---|---|---|
| **gi\|6680229** | high mobility group box 2 | **3.076** | **D** |
| **gi\|31981035** | dynein light chain LC8-type 1 | **2.611** | **D** |
| **gi\|31981327** | proteasome (prosome, macropain) subunit, beta type 2 | **2.259** | **D** |
| **gi\|84042521** | barrier to autointegration factor 1 | **2.233** | **D** |
| **gi\|13542867** | non-metastic cells 1, protein (NM23A) | **1.775** | **A , E** |
| **gi\|114326546** | phosphoglycerate mutase 1 | **1.774** | **A** |
| **gi\|37700232** | nucleoside-diphosphate kinase 1 | **1.736** | **-** |
| **gi\|84875544** | LIM domain binding 3 isoform c | **1.574** | **B** |
| **gi\|21886811** | S100 calcium binding protein A11 (calizzarin) | **1.559** | **F** |
| **gi\|50263046** | glutathione S-transferase, alpha 2 (Yc2) | **1.540** | **B** |
| **gi\|61098065** | glutathione S-transferase, alpha 1 (Ya) | **1.475** | **-** |
| **gi\|125656173** | acetyl-Coenzyme A carboxylase alpha | **1.470** | **A** |
| **gi\|33859580** | galectin 3 | **1.463** | **A** |
| **gi\|115385968** | transportin 1 isoform 1 | **1.443** | **B** |
| **gi\|6681079** | cathepsin B preproprotein | **1.440** | **C , F** |
| **gi\|31982030** | Rho GDP dissociation inhibitor (GDI) alpha | **1.401** | **A** |
| **gi\|96975138** | hypoxanthine guanine phosphoribosyl transferase 1 | **1.399** | **C** |
| **gi\|56605979** | basic transcription factor 3 | **1.391** | **B** |
| **gi\|83921595** | diazepam binding inhibitor isoform 1 | **1.387** | **A** |
| **gi\|9790141** | actin related protein 2/3 complex, subunit 3 | **1.362** | **A** |
| **gi\|6677833** | S100 calcium binding protein A10 | **1.360** | **C** |
| **gi\|61743961** | AHNAK nucleoprotein isoform 1 | **1.338** | **E** |
| **gi\|83921612** | thioredoxin domain containing 5 | **1.337** | **E** |
| **gi\|13384778** | 6-phosphogluconolactonase | **1.336** | **-** |
| **gi\|94378322** | PREDICTED: similar to ribosomal protein L38 | **1.331** | **C** |
| **gi\|6680840** | calumenin isoform 1 | **1.316** | **F** |
| **gi\|6679439** | peptidylprolyl isomerase A | **1.304** | **B , C** |
| **gi\|10092608** | glutathione S-transferase, pi 1 | **1.303** | **B** |
| **gi\|149270774** | PREDICTED: similar to Myoferlin (Fer-1-like protein 3) isoform 2 | **1.302** | **D** |
| **gi\|6753364** | cell division cycle 42 homolog | **1.302** | **A** |
| **gi\|6754082** | glutathione S-transferase, alpha 4 | **1.297** | **B** |
| **gi\|6997239** | poly(rC) binding protein 2 | **1.297** | **-** |
| **gi\|116517336** | four and a half LIM domains 1 isoform 2 | **1.287** | **B** |
| **gi\|6681219** | dihydropyrimidinase-like 3 | **1.284** | **F** |
| **gi\|19527026** | leucine rich repeat containing 59 | **1.272** | **-** |
| **gi\|12963737** | chromosome segregation 1-like | **1.264** | **D** |
| **gi\|21313144** | GTP-binding protein PTD004 isoform a | **1.262** | **-** |
| **gi\|31559990** | torsin family 1, member B | **1.252** | **-** |
| **gi\|6755152** | prolyl endopeptidase | **1.247** | **C** |
| **gi\|22094111** | solute carrier family 2 (facilitated glucose transporter), member 1 | **1.246** | **A** |
| **gi\|6681069** | cysteine and glycine-rich protein 1 | **1.234** | **E** |
| **gi\|31982186** | malate dehydrogenase 2, NAD (mitochondrial) | **1.225** | **A** |
| **gi\|6754696** | macrophage migration inhibitory factor | **1.223** | **A , F** |
| **gi\|31981302** | annexin A6 | **1.221** | **F** |
| **gi\|126012517** | small inducible cytokine subfamily E, member 1 | **1.220** | **A** |
| **gi\|6755392** | S100 calcium binding protein A6 (calcyclin) | **1.219** | **C** |
| **gi\|93102409** | fatty acid synthase | **1.219** | **B** |
| **gi\|6754256** | heat shock protein 9 | **1.218** | **-** |

| | | | |
|---|---|---|---|
| **gi\|113680348** | fascin homolog 1, actin bundling protein | **1.213** | **A** |
| **gi\|6677777** | ribosomal protein L26 | **1.206** | **C** |
| **gi\|7106303** | EH-domain containing 1 | **1.201** | **E** |
| **gi\|6753320** | chaperonin subunit 3 (gamma) | **-1.251** | **B** |
| **gi\|21281687** | deoxyuridine triphosphatase | **-1.254** | **F** |
| **gi\|126723461** | chaperonin subunit 8 (theta) | **-1.261** | **B** |
| **gi\|94377390** | PREDICTED: similar to insulinoma protein (rig) | **-1.261** | **-** |
| **gi\|31982755** | vimentin | **-1.263** | **A** |
| **gi\|6678419** | tripeptidyl peptidase II | **-1.265** | **C** |
| **gi\|82965849** | PREDICTED: hypothetical protein | **-1.266** | **E** |
| **gi\|116089273** | guanosine diphosphate (GDP) dissociation inhibitor 2 | **-1.272** | **D** |
| **gi\|21312298** | serine hydroxymethyltransferase 2 (mitochondrial) | **-1.276** | **C** |
| **gi\|22165392** | non-SMC condensin I complex, subunit D2 | **-1.276** | **B** |
| **gi\|13385408** | ribosomal protein L11 | **-1.280** | **E** |
| **gi\|31981679** | heat shock protein 1 (chaperonin) | **-1.281** | **A** |
| **gi\|27883844** | small nuclear ribonucleoprotein E | **-1.284** | **D** |
| **gi\|15426055** | coatomer protein complex, subunit beta 1 | **-1.289** | **E** |
| **gi\|149269890** | PREDICTED: similar to ribosomal protein L11 | **-1.289** | **E** |
| **gi\|41322931** | plectin 1 isoform 6 | **-1.300** | **A** |
| **gi\|112363072** | actin related protein 2/3 complex, subunit 2 | **-1.303** | **A** |
| **gi\|93102415** | phosphoribosylglycinamide formyltransferase | **-1.310** | **C** |
| **gi\|149234051** | PREDICTED: similar to ribosomal protein L10a | **-1.313** | **-** |
| **gi\|149254252** | PREDICTED: similar to vesicle associated protein | **-1.319** | **B** |
| **gi\|6755364** | RNA polymerase II transcriptional coactivator | **-1.328** | **B** |
| **gi\|33468885** | calcyclin binding protein | **-1.330** | **A** |
| **gi\|33859482** | eukaryotic translation elongation factor 2 | **-1.330** | **A** |
| **gi\|47271396** | GNAS complex locus isoform a | **-1.341** | **B** |
| **gi\|6680047** | guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 | **-1.346** | **B** |
| **gi\|27229277** | threonyl-tRNA synthetase | **-1.346** | **-** |
| **gi\|149262992** | PREDICTED: similar to Protein disulfide isomerase associated 6 | **-1.390** | **-** |
| **gi\|56699434** | eukaryotic translation initiation factor 4, gamma 1 isoform b | **-1.393** | **A** |
| **gi\|38348472** | adaptor-related protein complex 2, sigma 1 subunit | **-1.406** | **C** |
| **gi\|6677813** | ribosomal protein S8 | **-1.424** | **E** |
| **gi\|58037465** | Ribosomal protein L18A | **-1.428** | **E** |
| **gi\|31981534** | proteasome (prosome, macropain) subunit, alpha type 3 | **-1.437** | **D** |
| **gi\|6753620** | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked | **-1.447** | **B** |
| **gi\|88853578** | adaptor protein complex AP-1, beta 1 subunit | **-1.470** | **D** |
| **gi\|94395563** | PREDICTED: hypothetical protein isoform 2 | **-1.482** | **-** |
| **gi\|6753882** | FK506 binding protein 4 | **-1.506** | **B** |
| **gi\|78190507** | exportin 1, CRM1 homolog | **-1.517** | **F** |
| **gi\|25742730** | ribosomal protein L32 | **-1.520** | **C** |
| **gi\|10242373** | minichromosome maintenance complex component 7 | **-1.527** | **D** |
| **gi\|6755198** | proteasome (prosome, macropain) subunit, alpha type 6 | **-1.545** | **D** |
| **gi\|6754616** | mago-nashi homolog, proliferation-associated | **-1.551** | **C** |
| **gi\|31982143** | WW domain binding protein 11 | **-1.554** | **-** |
| **gi\|82953132** | PREDICTED: hypothetical protein | **-1.605** | **-** |
| **gi\|8393150** | carboxyl terminal LIM domain protein 1 | **-1.607** | **B** |
| **gi\|6755698** | surfeit gene 4 | **-1.612** | **E** |
| **gi\|22122515** | AHA1, activator of heat shock 90kDa protein ATPase homolog 1 | **-1.621** | **C** |
| **gi\|34328185** | prosaposin | **-1.629** | **D** |
| **gi\|6755206** | proteasome (prosome, macropain) subunit, beta type 7 | **-2.225** | **D** |
| **gi\|94378251** | PREDICTED: similar to histone H4 | **-2.282** | **-** |
| **gi\|84619697** | sterol O-acyltransferase 1 | **-2.555** | **F** |
| **gi\|149269808** | PREDICTED: similar to Eukaryotic translation initiation factor 3, subunit 1 alpha | **-2.557** | **-** |
| **gi\|149272386** | PREDICTED: similar to thymosin beta-4 | **-2.630** | **-** |