

Table S6. Most of the pro- or anti-apoptotic genes that were dysregulated in FSHD vs. control myotubes were apparently up- or downregulated in FSHD myotubes because of dampening of their normal myogenesis-associated changes in expression

Gene	Gene description	Fold change ^a	
		FSH myot / Ctl myot	Ctl myot/ Non-muscle
Inducer of apoptotsis, GO:000691			
<i>NUPR1</i>	nuclear protein, transcriptional regulator, 1	3.4	-1.5
<i>INHBA</i>	inhibin, beta A	3.1	1.9
<i>EI24</i>	etoposide induced 2.4 mRNA	2.2	-1.2
<i>TRADD</i>	TNFRSF1A-associated via death domain	2.2	-2.0
<i>NDUFS3</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	2.1	-1.6
<i>NUDT2</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 2	2.1	-1.6
<i>TGFB1</i>	transforming growth factor, beta 1	2.0	-2.2
<i>PLEKHF1</i>	pleckstrin homology domain containing, family F (with FYVE domain) member 1	1.9	-1.3
<i>NME3</i>	non-metastatic cells 3, protein expressed in	1.8	-1.9
<i>PML</i>	promyelocytic leukemia	1.8	-1.5
<i>PYCARD</i>	PYD and CARD domain containing	1.7	-2.1
<i>BAD</i>	BCL2-associated agonist of cell death	1.6	-1.9
<i>TNFRSF25</i>	tumor necrosis factor receptor superfamily, member 25	1.6	-1.1
<i>PRUNE2</i>	prune homolog 2 (Drosophila)	-3.3	65.5
<i>DAPK1</i>	death-associated protein kinase 1	-2.6	4.3
<i>TGFB3</i>	transforming growth factor, beta 3	-2.2	5.0
<i>FEM1B</i>	fem-1 homolog b (C. elegans)	-1.7	1.5
<i>ZMAT3</i>	zinc finger, matrin type 3	-1.6	5.1
Anti-apoptosis, GO:000691			
<i>CCL2</i>	chemokine (C-C motif) ligand 2	7.0	1.53
<i>GSTP1</i>	glutathione S-transferase pi 1	2.9	-0.84
<i>CLU</i>	clusterin	2.5	-1.61
<i>VEGFA</i>	vascular endothelial growth factor A	2.5	-0.56
<i>UBA52</i>	ubiquitin A-52 residue ribosomal protein fusion product 1	2.5	-1.26
<i>ANGPT1</i>	angiopoietin 1	2.4	1.57
<i>DAD1</i>	defender against cell death 1	2.1	-0.32
<i>IGF1</i>	insulin-like growth factor 1 (somatomedin C)	2.0	-0.19
<i>VEGFB</i>	vascular endothelial growth factor B	2.0	-0.89
<i>HBXIP</i>	hepatitis B virus x interacting protein	1.9	-0.60
<i>SOD1</i>	superoxide dismutase 1, soluble	1.9	-0.52
<i>HSPB1</i>	heat shock 27kDa protein 1	1.9	-0.68
<i>SPHK1</i>	sphingosine kinase 1	1.8	-0.95
<i>ANXA5</i>	annexin A5	1.7	0.96
<i>API5</i>	apoptosis inhibitor 5	1.7	-0.33
<i>TXNDC5</i>	thioredoxin domain containing 5 (endoplasmic reticulum)	1.7	-0.60
<i>TRAF6</i>	TNF receptor-associated factor 6	-2.4	1.24
<i>HIPK3</i>	homeodomain interacting protein kinase 3	-2.3	3.09
<i>NGFR</i>	nerve growth factor receptor	-2.1	1.70

^a The genes associated with the above two GO terms that were significantly dysregulated in FSHD vs. control myotubes are shown. Similar results were obtained for genes in these two GO terms dysregulated in FSHD vs. control myoblasts. Fold changes in RNA signal for FSHD cells vs. non-muscle cells were determined by identical expression profiling of FSHD and control myogenic cells and 19 non-muscle cell types (See Additional File 1 and Additional File 2 for details about cell samples). Green highlighting, significant FSHD downregulation ($p < 0.01$); pink, significant FSHD upregulation ($p < 0.01$ or, if in italics, $p < 0.001$).