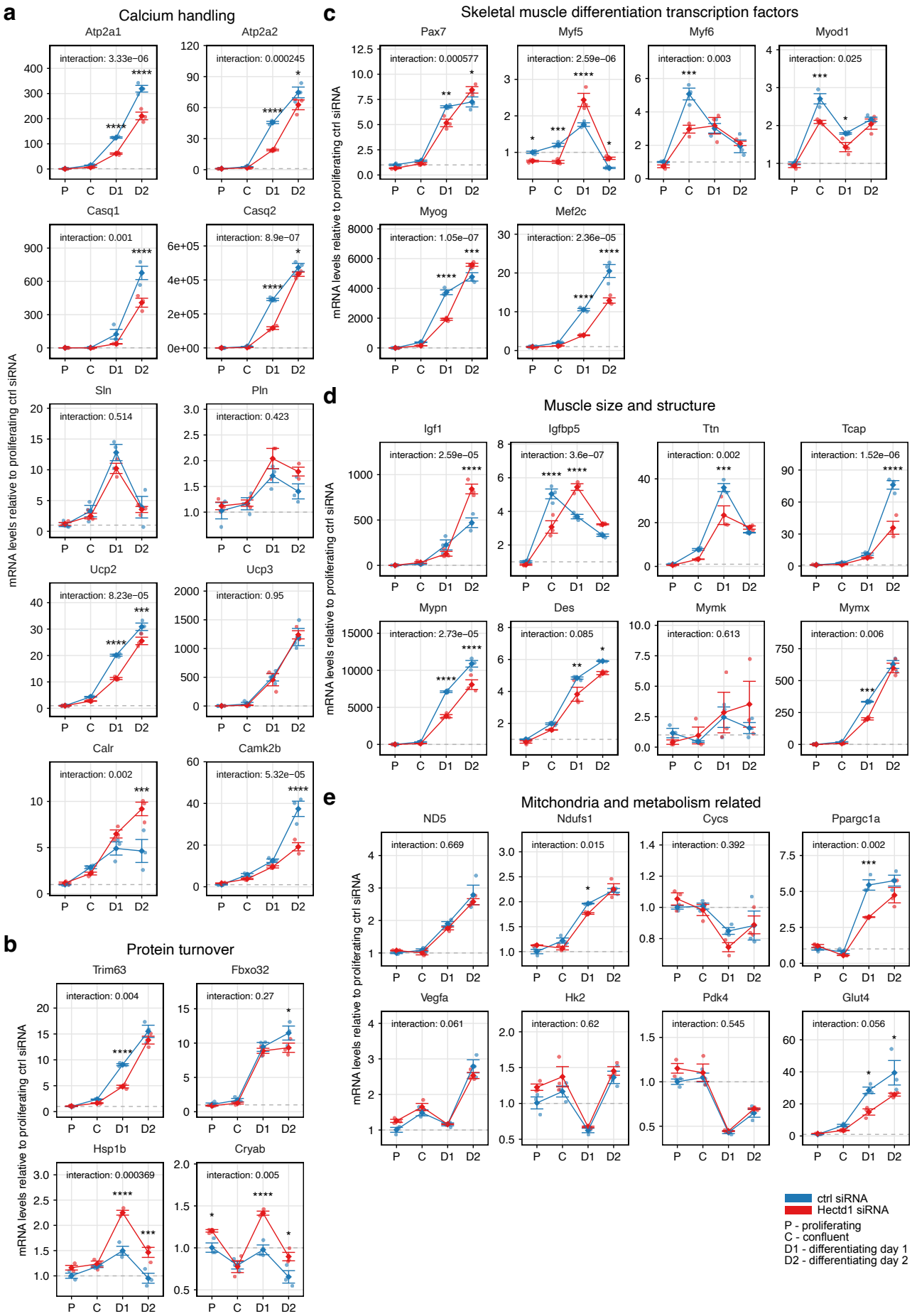
a
Calcium handling
Atp2a1
interaction: 3.33e−06
Atp2a2
interaction: 0.000245
Casq1
interaction: 0.001
Casq2
interaction: 8.9e−07
Sln
interaction: 0.514
Pln
interaction: 0.423
Ucp2
interaction: 8.23e−05
Ucp3
interaction: 0.95
Calr
interaction: 0.002
Camk2b
interaction: 5.32e−05
mRNA levels relative to proliferating ctrl siRNA
P C D1 D2
b
Protein turnover
Trim63
interaction: 0.004
Fbxo32
interaction: 0.27
Hsp1b
interaction: 0.000369
Cryab
interaction: 0.005
c
Skeletal muscle differentiation transcription factors
Pax7
interaction: 0.000577
Myf5
interaction: 2.59e−06
Myf6
interaction: 0.003
Myod1
interaction: 0.025
Myog
interaction: 1.05e−07
Mef2c
interaction: 2.36e−05
d
Muscle size and structure
Igf1
interaction: 2.59e−05
Igfbp5
interaction: 3.6e−07
Ttn
interaction: 0.002
Tcap
interaction: 1.52e−06
Mypn
interaction: 2.73e−05
Des
interaction: 0.085
Mymk
interaction: 0.613
Mymx
interaction: 0.006
e
Mitchondria and metabolism related
ND5
interaction: 0.669
Ndufs1
interaction: 0.015
Cycs
interaction: 0.392
Ppargc1a
interaction: 0.002
Vegfa
interaction: 0.061
Hk2
interaction: 0.62
Pdk4
interaction: 0.545
Glut4
interaction: 0.056
ctrl siRNA
Hectd1 siRNA
P - proliferating
C - confluent
D1 - differentiating day 1
D2 - differentiating day 2

Supplementary Fig. 2.

Quantification of gene expression of selected gene sets during differentiation of C2C12 myotubes after control or Hectd1 siRNA transfection. The following gene sets are shown: **a**, calcium handling, **b**, protein turnover, **c**, transcription factors involved in skeletal muscle differentiation, **d**, skeletal muscle size and structure, **e**, mitochondrial bioenergetics and metabolism (n = 3). All data are represented as mean ± sd. Data were analyzed with two-way ANOVA, P-value for interaction between differentiation timepoint and genotype is indicated in the graph. Comparison of individual time points was analyzed by pairwise t-test with Holm-Bonferroni correction. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.0001$.