



Supplementary Fig. 3.

a,b, Differentially regulated GO-MF identified from proteins with a increased and b decreased expression in C2C12 myotubes after knockdown of Hectd1, numbering to the right indicates rank of the pathway when sorted by enrichment fold-change. **c**, Immunoblot showing increased stabilization of nebulin fragment after co-expression of Klhl40, arrow indicates nebulin fragment band. **d**, Immunoblot showing increased stabilization of nebulin fragment after co-expression of Klhl41. **e**, Immunoblot detection and quantification of KLHL40 stabilization after co-expression of wild-type (wt) or catalytically inactive Hectd1 (n = 3). **f**, Immunoprecipitation of KLHL40 followed by immunoblot detection and quantification of KLHL40 ubiquitination after co-expression of wt or catalytically inactive Hectd1 (n = 3). **g**, Immunoblot detection of nebulin fragment stabilization after co-expression of wt or catalytically inactive Hectd1 and Klhl40. All data are represented as mean \pm sd. Immunoblot data in e were normalized to loading control and analyzed by one-way ANOVA. Immunoblot data for KLHL40 in f were normalized to corresponding KLHL40 input and analyzed by one-way ANOVA. GO – Gene Ontology, MF – molecular function, ORA – overrepresentation analysis.