

HDAC4 regulates satellite cell proliferation and differentiation by targeting P21 and Sharp1 genes

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## Supplementary Information

### Supplementary Figure Legends

**Supplementary Figure S1. HDAC4 expression is reduced in HDAC4 KO satellite cells.** HDAC4 expression in HDAC4 KO and control satellite cells, analyzed by (a) real-time PCR (n=6 each sample) and (b) western blot (cropped blots) analyses, with relative densitometry (n=3 each sample).  $\alpha$ -Tubulin was used as a loading control. Full-length blots are presented in Supplementary Figure S2A. Data are presented as mean  $\pm$  SEM. \*p<0.05; \*\*p<0.005 (Student's t-test).

**Supplementary Figure S2. Full-length western blots.** Uncropped gels showing the expression of (a) HDAC4 and (b) MHC in HDAC4 KO (KO) and control (C) satellite cells.  $\alpha$ -Tubulin was used as a loading control.

**Supplementary Figure S3. HDAC4 intrinsically regulate satellite cell differentiation.** (a) Immunofluorescence for MHC in wild-type satellite cells cultured with conditioned medium from HDAC4 KO or control satellite cells. Conditioned media from n=3 mice, per each condition. Scale bar: 100  $\mu$ m. (b) Quantification of the differentiation and fusion indexes in wild-type satellite cells cultured with conditioned medium from HDAC4 KO or control satellite cells. n=3 each condition. Data are presented as mean  $\pm$  SEM. (c) HDAC4 expression in satellite cells treated with vehicle or 4OH-TMX, analyzed by real-time PCR. n=4 each sample. Data are presented as mean  $\pm$  SEM. \*p<0.05 (Student's t-test).

**Supplementary Figure S4. HDAC4 does not affect apoptosis in satellite cells.** (a) TUNEL assay and quantification of apoptotic cells in control, HDAC4 KO samples, and positive controls of the assay. Scale bar: 50 and 100  $\mu$ m. n=5 per genotype; n=3 for the positive controls. \*\*p<0.005 (Student's t-test). (b) Expression of indicated apoptotic markers in control and HDAC4 KO satellite cells. n=4 for each sample. Data are presented as mean  $\pm$  SEM.

**Supplementary Figure S5. Overexpression of HDAC4 in HDAC4 S/A overexpressing muscle cells.** HDAC4 expression in primary myotubes infected with adenovirus expressing HDAC4 S/A or GFP, as control. n=5 GFP, n=7 HDAC4 S/A. Data are presented as mean  $\pm$  SEM. \*\*\*p<0.001 (Student's t-test).

**Supplementary Figure S6. Downregulation of P21 in HDAC4 KO satellite cells.** (a) Immunofluorescence for P21 in HDAC4 KO satellite cells treated with UC2288 or

vehicle for 24 hours. Scale bar: 50  $\mu\text{m}$ . **(b)** Expression of P21 in HDAC4 KO satellite cells transfected with a pool of four siRNA against P21 (P21) or a pool of non-targeting siRNA (Scr), as control. n=5 Scr and n=7 P21. Data are presented as mean  $\pm$  SEM. \*p<0.05 (Student's t-test).

**Supplementary Figure S7. Downregulation of Sharp1 in muscle cells.** Sharp1 expression in C2C12 cells transfected with Sharp1 shRNA or scramble (shScr) expression vector, as control. n=4 each sample. Data are presented as mean  $\pm$  SEM. \*p<0.05 (Student's t-test).

**Supplementary Table S1.** List of genes in each gene ontology category of the RNA-seq results.

Biological Process	Genes
Response to stimulus	<p>fas, taok1, fap, ccl2, srpk3, hmga2, fh11, hspb3, dact2, pdgfb, mapkapk3, f3, spint1, ctsh, sema3c, nod1, evalc, penk, slit2, cxcl5, lif, fbn1, ndrg1, hk1, ngf, abcc9, map3k2, itgb7, igha, ptgir, gabre, cgregf1, sema3e, anxa8, gpx3, cxcl3, ttc1, itgb5, il20rb, tie1, txndc2, hspb8, gpx3, plet1, mxipl, gpr97, tnfaip3, wnt11, pak6, csf1, gria3, nkd2, tll1, pamr1, pdk1, slc30a4, inhba, pik3c2a, trp53inp1, arhgap23, slc39a4, tnfrsf1b, atg9b, tshr, cryab, gpx7, sqstm1, clec4d, ubxn2b, xiap, ptk2b, gal, sema7a, tek, kpna3, cripl, angpt4, anpep, wnt5a, cma1, il12rb2, fzd6, ccl9, bdkrb1, zfp385a, cxcl2, gpr3711, cd55, p2rx6, sod3, mapk13, procr, icam1, ppp3cb, tfpi2, hspb7, neto2, cyr61, rcan2, timp3, pik3r3, crlf1, cdc42ep1, ppap2b, cxcl14, hmga1, tec, klk8, il11, adrb2, def6, rom1, nuak2, ccl7, phldb3, fcgrt, il21r, fign1, pdzd2, ndrg2, sgk1, osmr, blnk, itgb3, efna5, cxcl16, wnt10b, ikbke, hspb1, cx3cl1, eda2r, pgf, p2rx7, klk8, ncf2, itpr3, ttc12, rad1, wnt7b, psme1, tec, trib3, hfe2, adat1, ctgf, dusp6, mocos, tmx3, slc38a3, ngfr, il4ra, cd99</p>
Developmental process	<p>scube1, fas, taok1, mier3, fgf1, plxna4, numbl, myo7a, lce1g, csrp3, bmpr2, fh11, mbp, micall1, mef2c, slit2, phex, fgf11, cdh5, cidea, fgf5, vat1, mical2, fbn1, ngf, cdh19, myh11, adamts1, tpm1, map3k2, lmod2, notch4, traf1, fubp1, olfml2a, fgd3, lce1f, tie1, tmeff2, dusp1, rbp1, maob, spdef, phactr1, plet1, myh3, gpr97, wnt11, pak6, foxo3, cgnl1, csf1, dtx4, tll1, b3galt5, inhba, crabp1, tnfrsf1b, ldb3, tshr, myh9, myh8, pacsin1, clec3b, neurl3, adam3, xiap, ptk2b, pvalb, arhgef28, col4a1, lama2, tmp3-rs7, bhlhe22, tek, ier3, cripl, arhgef3, angpt4, wnt5a, tnc, myom2, il12rb2, myf6, fabp4, itm2b, cd80, bhlhe40, col16a1, zfp385a, mbnl2, gpr3711, myl2, mybpc2, ptgis, ntn4, olfml3, tgfb1i1, ppp3cb, neto2, cyr61, pcdh7, cdh11, syne4, plekhh1, tlr9, ankrd2, map6, tec, klk8, phldb3, mcam, il21r, acp5, plxnb3, myod1, fmod, intm2c, utr, pdzd2, neurl3, dmp1, ndrg2, fat1, mylpf, vdr, sgk1, osmr, tnmd, lamc3, efna5, myo1e, atoh8, wt10b, scube3, adam12, lingo2, pcdh20, myh7, crabp2, foxd3, eda2r, pgf, gli2, creb3l1, jag2, clip1, lce1h, gdnf, wnt7b, tec, lrn1, adat1, plp1, ctgf, dusp6, myog, hoxa10, bhlhe41, ngfr, mybpc1, hoxb2, col5a3, tgfb1</p>
Metabolic process	<p>isg15, elovl6, rpl39l, cyb5a, mier3, hk1, aebp1, rbpj, h2afj, ak1, plxna4, lce1g, fap, ccl2, hmga2, fh11, larp7, hspb3, pddc1, ass1, anxa5, anxa3, apobec1, g2e3, upf3a, ube3a, mapkapk3, hist1h1c, spint1, pck2, fbp2, ctsh, selt, adh7, ptma, pdk1, cox6a2, aim1, nod1, atp9a, ptms, gfpt2, phex, naa50, hmgs1, gm20939, ppp1r3c, psmc1, ndufs7, cpeb2, ugcg, prrg1, pcna-ps2, mt-nd2, adamts1, enpp1, hebp2, slc1a2, igha, tbc1d2, pgam2, s100a16, ptpre, cpt1c, adprhl1,</p>

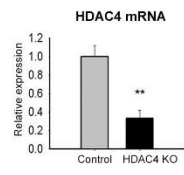
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Cellular process	<p>scube1, tbkbp1, fas, taok1, tnfaip2, elovl6, rpl39l, spink2, mier3, arhgdib, hk1, aebp1, actg2, fgf1, h2afj, plxna4, numbl, myo7a, cotl1, lce1g, fap, gprc5a, ccl2, srpk3, tmem202, gng11, hmga2, pddc1, daam2, ass1, dact2, mbp, capg, pdgfb, mapre3, eube3a, mapkapk3, hist1h1c, cd36, ctsh, pdk1, pls3, rap1a, synm, atp9a, palm3, evalc, scn1b, penk, mgarp, mgmt1, slit2, cxcl5, gfpt2, phex, fgf11, ccnd2, slco2a1, cidea, lif, mzt1, mpz, rbp1, orai2, fgf5, naa50, gm20939, fbn1, akap2, ndrg1, hk1, psmc1, cpeb2, ugcg, ngf, caq1, appl1, slc4a7, tnxb, pcna-ps2, myh11, adamts1, tmp1, zfyve1, stx16, map3k2, lmod2, itgb7, slc1a2, igha, tbc1d2, pgam2, s100a16, adprhl1, traf1, fubp1, olfml2a, atp11b, clta, lce1f, adamts15, has2, azin2, mterf1b, aatk, cxcl3, arhgap36, cltb, itgb5, ucp1,</p>

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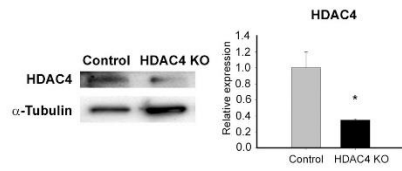
**Supplementary Table S2.** Primer used for real-time PCR

Gene	Primer Forward	Primer Reverse
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Cyclin E1	GGCGAGGATGAGAGCAG TTC	CGATCAAAGAAGAAGTCC TGTGCC
Cyclin A2	CCCTGCATTTGGGTGTG AAC	GGTGCTCCATTCTCAGAAC C
Pax7	TCCCCCTGGAAGTGTCC A	TGGGAAACACGGAGCTGA
e-MHC	TGGTCGTAATCAGCAGC A	TCGTCTCGCTTTGGCAA
P21	AGCGCGTTCGGAGCCTA	CCGTTTTTCGGCCCTGAGA
Sharp1	GGAGCTTGAAGCGAGACGAT	GAGCGCTCCCCATTCTGTAA
Bax	GCCTCCTCTCCTACTTCG GG	TGAGGACTCCAGCCACAA AGA
Bcl-2	AAGCTGTCACAGAGGGG CTA	TCTCAGGCTGGAAGGAGA AG

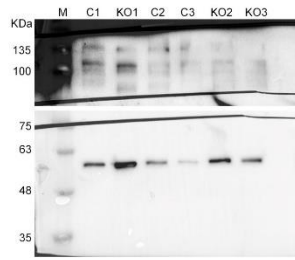
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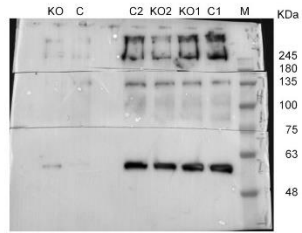
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**a**

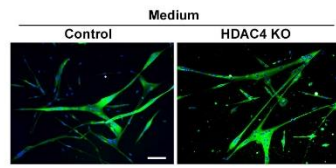


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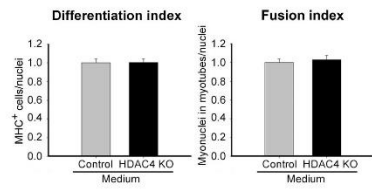




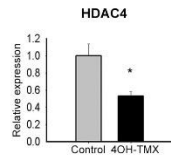
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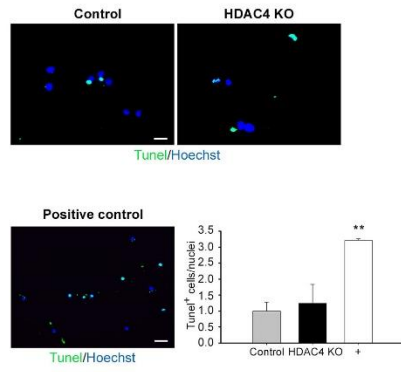
**b**



**c**



**a**



**b**

