Figure S1. Database search analysis of GO 'Biological process' category on Uniprot. HDAC2 was found to be associated with 'histone H3 deacetylation' and histone acetylation sites (H3K14) regulated by HDAC2. HDAC2, histone deacetylase 2; GO, Gene Ontology.

GO-Biological process [i]

- behavioral response to ethanol Source: RGD
- cardiac muscle cell development Source: RGD
- cardiac muscle hypertrophy Source: RGD
- cellular response to dopamine Source: RGD
- cellular response to heat Source: RGD
- cellular response to hydrogen peroxide Source: RGD
- cellular response to retinoic acid Source: RGD
- cellular response to transforming growth factor beta stimulus Source: RGD
- cellular response to trichostatin A Source: RGD
- circadian regulation of gene expression Source: RGD
- dendrite development Source: RGD
- embryonic digit morphogenesis Source: RGD
- epidermal cell differentiation Source: RGD
- eyelid development in camera-type eye Source: RGD
- fungiform papilla formation Source: RGD
- hair follicle placode formation Source: RGD
- hippocampus development Source: RGD
- histone deacetylation Source: RGD
- histone H3 deacetylation Source: RGD
- histone H3-K27 methylation Source: RGD
- histone H4 deacetylation Source: RGD

Child Terms

This table lists all terms that are direct descendants (child terms) of GO:0070932

Child Term		Relationship to GO:0070932
GO:1990619	histone H3-K9 deacetylation	is_a
GO:0071572	histone H3-K56 deacetylation	is_a
GO:0031078	histone deacetylase activity (H3-K14 specific)	part_of
GO:1990596	histone H3-K4 deacetylation	is_a

Figure S2. Prediction of c-Myc binding sites at the miR-30a-5p gene promoter region. Location of the predicted c-Myc binding sites at the miR-30a-5p gene proximal promoter region. The miR-30a-5p gene promoter (-2000/+71) was analyzed using the JASPAR database, which gave the relative score. Five c-Myc binding sites at the miR-30a-5p gene promoter are highlighted in red text and gray shadow, and the transcriptional start site is labeled. miR, microRNA.

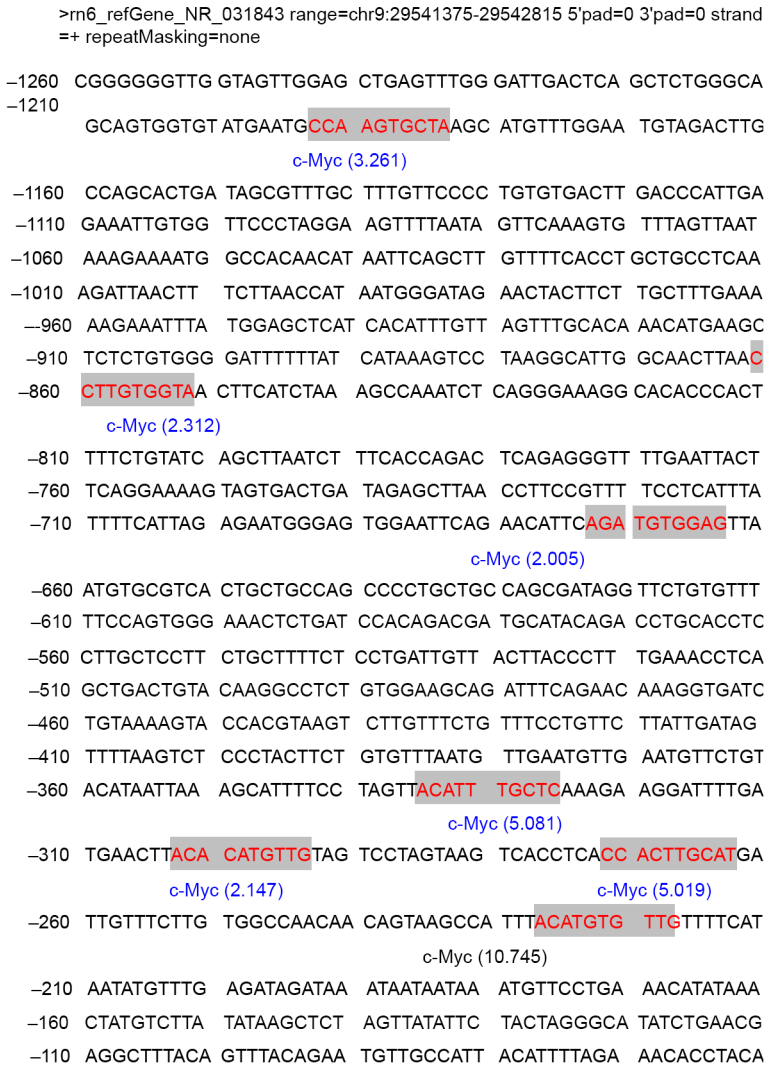

Figure S3. Expression of c-Myc and HDAC2 in senescent cardiomyocytes. c-Myc and HDAC2 expression levels were measured via reverse transcription-quantitative PCR and western blotting after cells were transfected with three different Ad-shRNAs of c-Myc or HDAC2 in senescent H9C2 cells. Data are presented as the mean ± SD from three independent experiments. *P<0.05 vs. Ad-shNC group. HDAC2, histone deacetylase 2; Ad-, adenovirus; sh, short hairpin RNA; NC, negative control.