

Accepted Manuscript

Integrated omics approaches to characterize a nuclear receptor corepressor-associated histone deacetylase in mouse skeletal muscle

Yingyun Gong, Rui Cao, Guolian Ding, Sungguan Hong, Wenjun Zhou, Wenyun Lu, Manashree Damle, Bin Fang, Chuhan C. Wang, Justin Qian, Natasha Lie, Cristina Lanzillotta, Joshua D. Rabinowitz, Zheng Sun

PII: S0303-7207(17)30293-9

DOI: [10.1016/j.mce.2017.05.024](https://doi.org/10.1016/j.mce.2017.05.024)

Reference: MCE 9955

To appear in: *Molecular and Cellular Endocrinology*

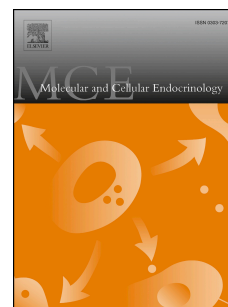
Received Date: 4 May 2017

Revised Date: 9 May 2017

Accepted Date: 23 May 2017

Please cite this article as: Gong, Y., Cao, R., Ding, G., Hong, S., Zhou, W., Lu, W., Damle, M., Fang, B., Wang, C.C., Qian, J., Lie, N., Lanzillotta, C., Rabinowitz, J.D., Sun, Z., Integrated omics approaches to characterize a nuclear receptor corepressor-associated histone deacetylase in mouse skeletal muscle, *Molecular and Cellular Endocrinology* (2017), doi: 10.1016/j.mce.2017.05.024.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



Integrated Omics Approaches to Characterize a Nuclear Receptor Corepressor-associated Histone Deacetylase in Mouse Skeletal Muscle

Yingyun Gong¹, Rui Cao¹, Guolian Ding¹, Sungguan Hong¹, Wenjun Zhou¹, Wenyun Lu², Manashree Damle³, Bin Fang³, Chuhan C Wang¹, Justin Qian¹, Natasha Lie¹, Cristina Lanzillotta³, Joshua D Rabinowitz², and Zheng Sun^{1,#}

¹ Division of Diabetes, Endocrinology and Metabolism, Department of Medicine; Department of Molecular and Cellular Biology, Baylor College of Medicine, Houston, TX 77030

² Lewis-Sigler Institute for Integrative Genomics; Princeton University, Princeton, NJ 08544

³ Division of Endocrinology, Diabetes, and Metabolism, Department of Medicine; the Institute for Diabetes, Obesity, and Metabolism, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104

Correspondence: zheng.sun@bcm.edu

ABSTRACT

Nuclear receptors regulate gene expression by differential binding to coactivators or corepressors in a ligand-dependent manner, which further recruits a set of epigenome-modifying enzymes that remodel chromatin conformation. Histone acetylation is a major epigenomic change controlled by histone acetyltransferases (HATs) and histone deacetylases (HDACs). HDAC3 is the only HDAC that confers the enzymatic activity to the complexes nucleated by nuclear receptor corepressors NCoR and SMRT. To address the metabolic function of HDAC3, we have deleted it specifically in mouse skeletal muscles. We have performed the following omics profiling in skeletal muscles of these mice: (1) RNA-seq profiling of total RNA; (2) Global nuclear run-on (GRO-seq) analysis of nascent RNAs; (3) Chromatin immuno-precipitation (ChIP-seq) of HDAC3 at both early evening and early morning; (4) proteomics profiling with mass spectrometry; (5) snap-shot metabolomics profiling of water-soluble metabolites at the basal condition; (6) snap-shot metabolomics profiling of lipid species at the basal condition; (7) kinetic fluxomics analysis of glucose utilization using ¹³C₆-glucose *in vivo* during treadmill running exercise. These approaches have provided several novel insights into how nuclear receptors regulate circadian rhythm of skeletal muscle fuel metabolism, which has been published elsewhere. Here we present the original datasets and technical details during the execution, analysis, and interpretation of these omics studies.

Download English Version:

<https://daneshyari.com/en/article/8476365>

Download Persian Version:

<https://daneshyari.com/article/8476365>

[Daneshyari.com](https://daneshyari.com)