

Supplementary Table S1. Description of over-expressed genes associated with chromatin modifications in skeletal muscle included in the present study

Gene ID	Symbol	Name	Locus	Function
2145	EZH1	Enhancer of zeste 1 polycomb repressive complex 2 subunit	17q21.2	It facilitates methylation of H3K27 and it is involved in embryonic stem-cell pluripotency and plasticity maintenance.
4297	KMT2A	Lysine methyltransferase 2A	11q23.3	It regulates gene expression throughout hematopoiesis and early development. Its H3K4 methyltransferase activity is involved in chromatin modifications and the consequent epigenetic transcriptional activation.
8085	KMT2D	Lysine methyltransferase 2D	12q13.12	It methylates H3K4. It contributes as a transcriptional regulator of estrogen receptor and beta-globin genes.
23081	KDM4C	Lysine demethylase 4C	9p24.1	It regulates gene expression and chromosome segregation by converting specific trimethylated histone residues to the dimethylated form.
7403	KDM6A	Lysine demethylase 6A	Xp11.3	It catalyzes demethylation of tri/dimethylated H3.
1387	CREBBP	CREB binding protein	16p13.3	It has intrinsic histone acetyltransferase activity, and it participates in the transcriptional coactivation of transcription factors.
83933	HDAC10	Histone deacetylase 10	22q13.33	Its function of deacetylate histones modulates chromatin structure, contributing to cell cycle, and developmental event.
9759	HDAC4	Histone deacetylase 4	2q37.3	It has histone deacetylase activity and inhibits transcription when bound to a promoter.
29947	DNMT3L	DNA methyltransferase 3 like	21q22.3	It promotes de novo methylation by DNA cytosine methyltransferase 3 alpha, contributing to the establishment of maternal genomic imprints. It facilitates transcriptional inhibition by interacting with histone deacetylase 1.

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3014	H2AX	H2A.X histone	variant	11q23.3	It produces two transcripts using the conserved stem-loop termination and the polyA addition motifs
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