

Table S6. Significant GO categories for the top 300 H3K9ac genes.

Category	Term	Count	%	P-Value	Benjamini
GOTERM_CC_FAT	contractile fiber	17	5.7	2.4E-11	2.7E-09
GOTERM_CC_FAT	myofibril	17	5.7	1.5E-11	3.4E-09
SP_PIR_KEYWORDS	muscle protein	13	4.3	3.6E-11	9.4E-09
GOTERM_CC_FAT	sarcomere	15	5.0	5.7E-10	4.3E-08
GOTERM_CC_FAT	contractile fiber part	15	5.0	1.3E-09	7.5E-08
GOTERM_MF_FAT	calcium ion binding	31	10.3	5.9E-08	2.0E-05
GOTERM_CC_FAT	I band	10	3.0	1.2E-06	5.5E-05
SP_PIR_KEYWORDS	calcium	25	8.3	1.3E-06	1.8E-04
GOTERM_CC_FAT	actin cytoskeleton	14	4.7	4.9E-05	1.8E-03
GOTERM_CC_FAT	myosin complex	7	2.3	2.6E-04	8.4E-03
GOTERM_CC_FAT	Z disc	7	2.3	3.6E-04	1.0E-02
KEGG_PATHWAY	Cardiac muscle contraction	8	2.7	1.3E-04	1.3E-02
KEGG_PATHWAY	Hypertrophic cardiomyopathy (HCM)	8	2.7	2.9E-04	1.4E-02
GOTERM_CC_FAT	myosin filament	4	1.3	1.2E-03	3.0E-02
GOTERM_BP_FAT	muscle organ development	13	4.3	3.3E-05	3.7E-02
INTERPRO	Immunoglobulin subtype 2	9	3.0	5.6E-04	4.5E-02
GOTERM_CC_FAT	integral to plasma membrane	12	4.0	2.3E-03	5.0E-02
INTERPRO	Immunoglobulin I-set	8	2.7	5.2E-04	5.1E-02
SP_PIR_KEYWORDS	glycoprotein	54	18.0	6.2E-04	5.3E-02
SMART	IGc2	9	3.0	9.0E-04	5.5E-02
INTERPRO	Calcium-binding EF-hand	9	3.0	4.6E-04	5.6E-02
INTERPRO	EF-HAND 2	11	3.7	2.5E-04	6.0E-02
KEGG_PATHWAY	Dilated cardiomyopathy	7	2.3	1.8E-03	6.0E-02
INTERPRO	EF-HAND 1	11	3.7	4.0E-04	6.4E-02
GOTERM_CC_FAT	intrinsic to plasma membrane	12	4.0	3.5E-03	6.9E-02
INTERPRO	EF-Hand type	12	4.0	1.5E-04	7.3E-02
SP_PIR_KEYWORDS	skeletal muscle	4	1.3	1.2E-03	7.5E-02
GOTERM_BP_FAT	muscle contraction	7	2.3	3.0E-04	8.2E-02
INTERPRO	EGF-like calcium-binding. conserved site	7	2.3	1.6E-03	8.7E-02
SMART	EGF_CA	7	2.3	2.2E-03	8.7E-02
INTERPRO	EGF-like calcium-binding	7	2.3	1.5E-03	8.8E-02

SMART	EFh	9	3.0	7.5E-04	8.9E-02
INTERPRO	EGF-type aspartate/asparagine hydroxylation conserved site	7	2.3	1.3E-03	9.0E-02
UP_SEQ_FEATURE	domain:EF-hand 1	10	3.3	2.3E-04	9.3E-02
