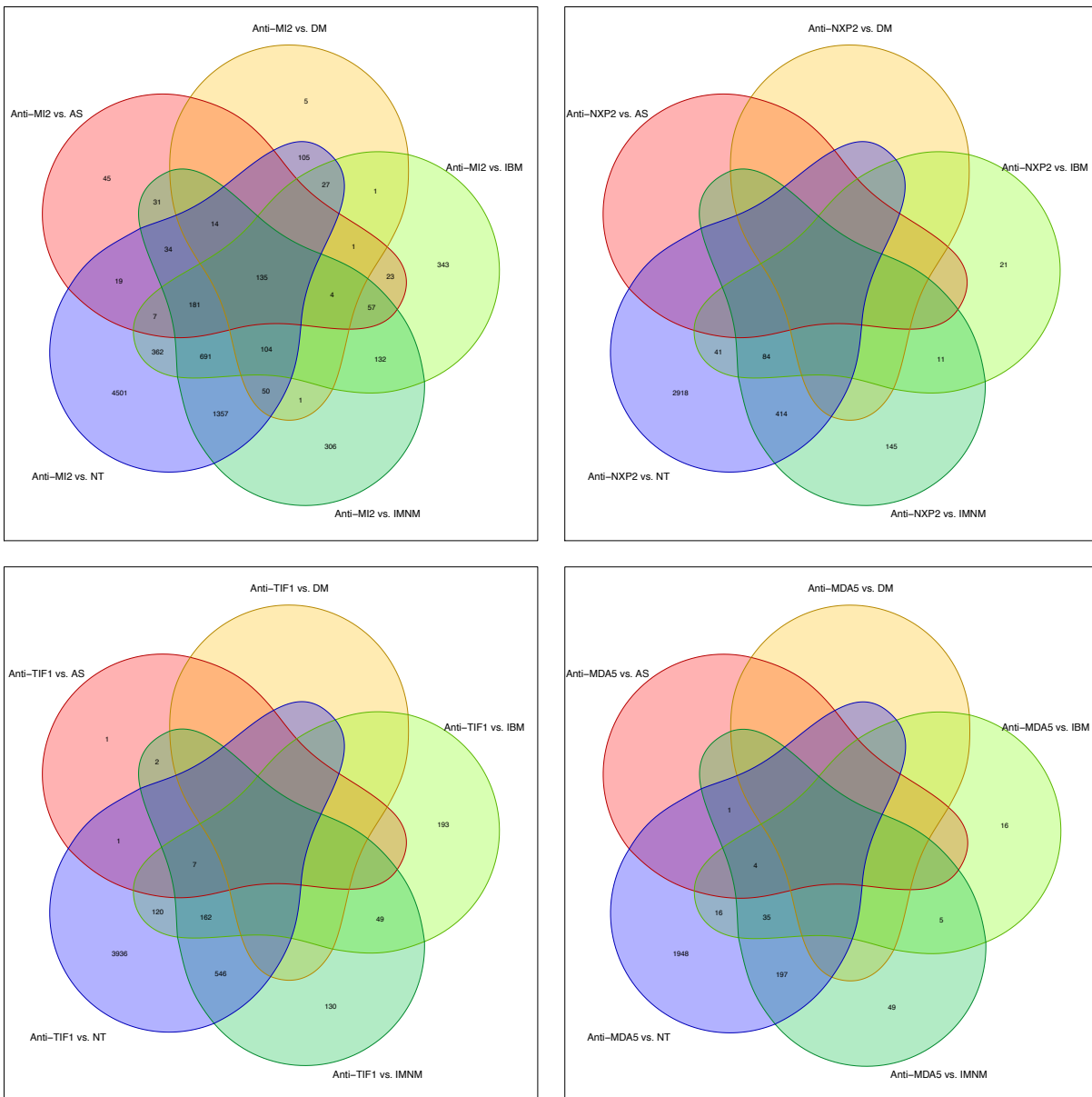
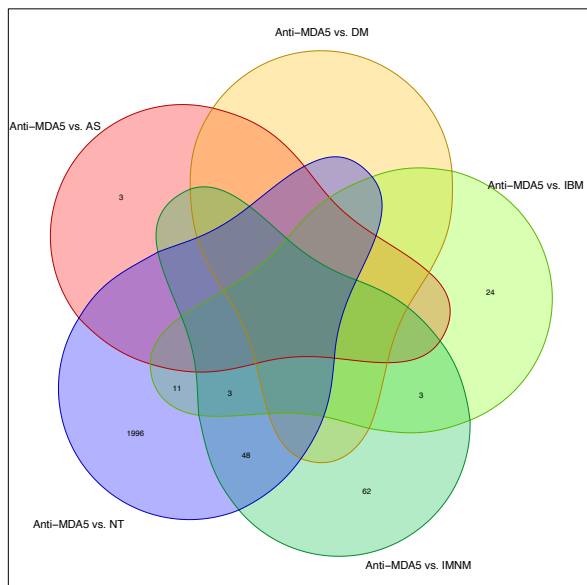
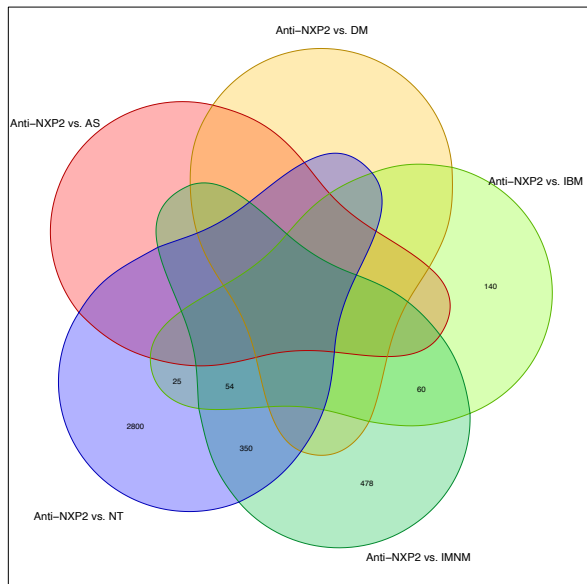


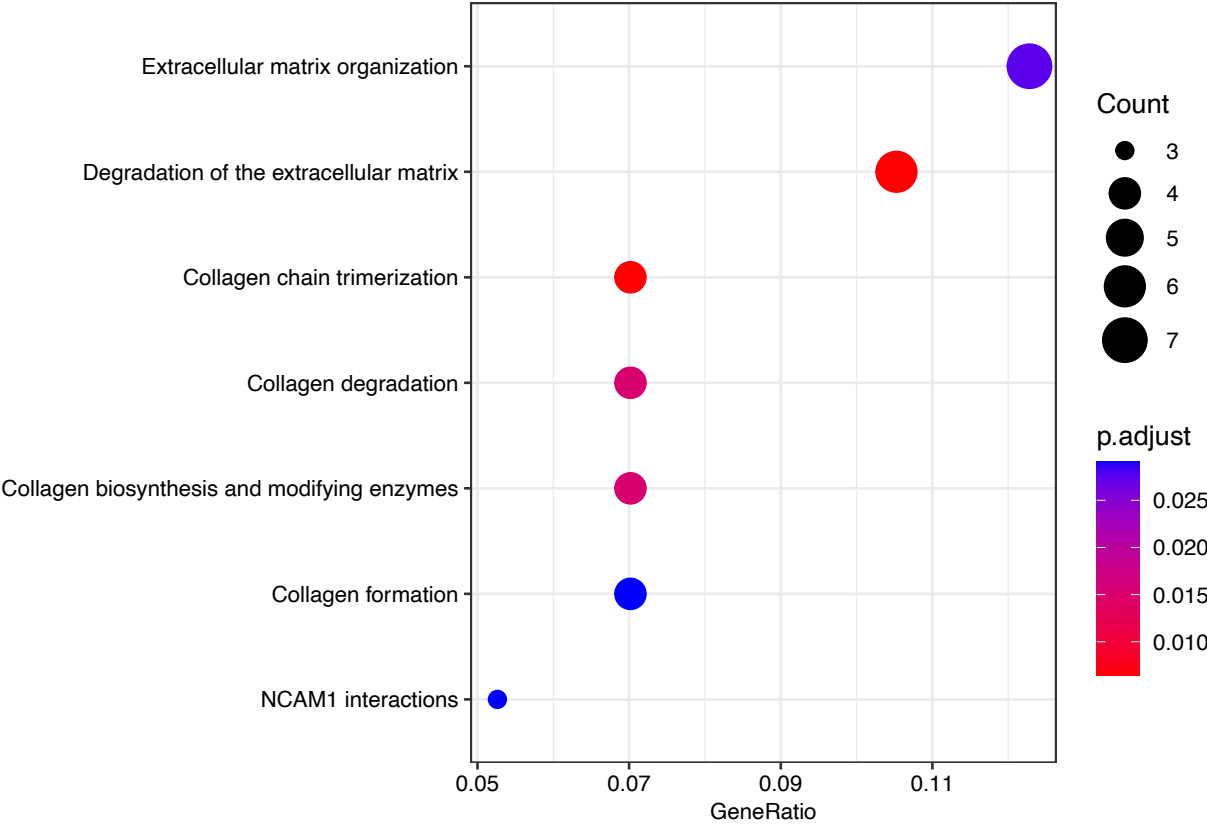
Supplementary Figure 1. Venn diagram showing the number of genes that were differentially overexpressed (q -value < 0.05) in each dermatomyositis subgroup compared to other myositis patients and normal muscle biopsies. DM: dermatomyositis, AS: antisynthetase syndrome, IBM: inclusion body myositis, IMNM: immune-mediated necrotizing myositis, NT: histologically normal biopsies.



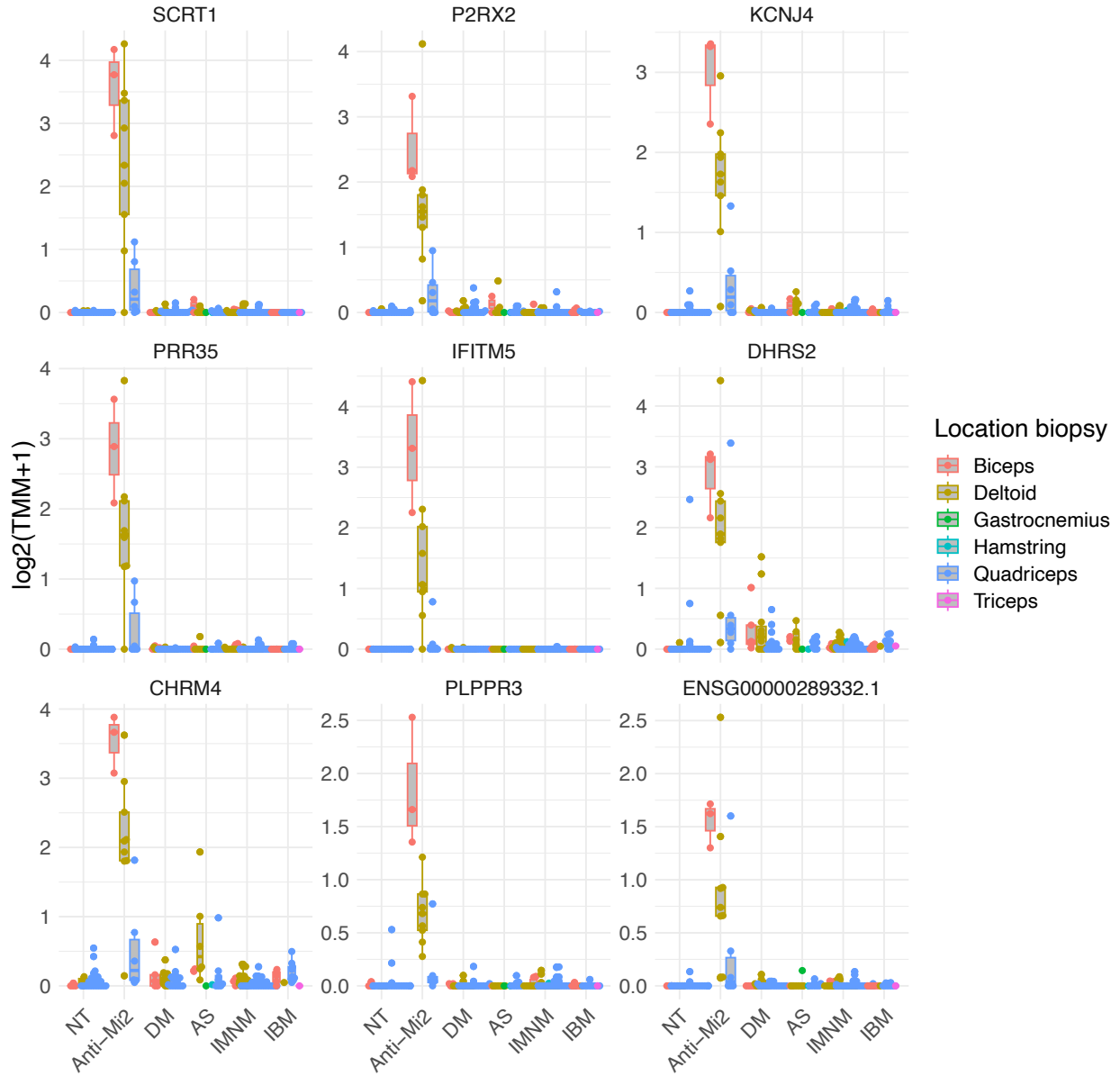
Supplementary Figure 2. Venn diagram showing the number of genes that were differentially underexpressed (q -value < 0.05) in each dermatomyositis subgroup compared to other myositis patients and normal muscle biopsies. DM: dermatomyositis, AS: antisynthetase syndrome, IBM: inclusion body myositis, IMNM: immune-mediated necrotizing myositis, NT: histologically normal biopsies.



Supplementary Figure 3. Pathway enrichment analysis of the set of genes specifically overexpressed in anti-Mi2 using the Reactome database.



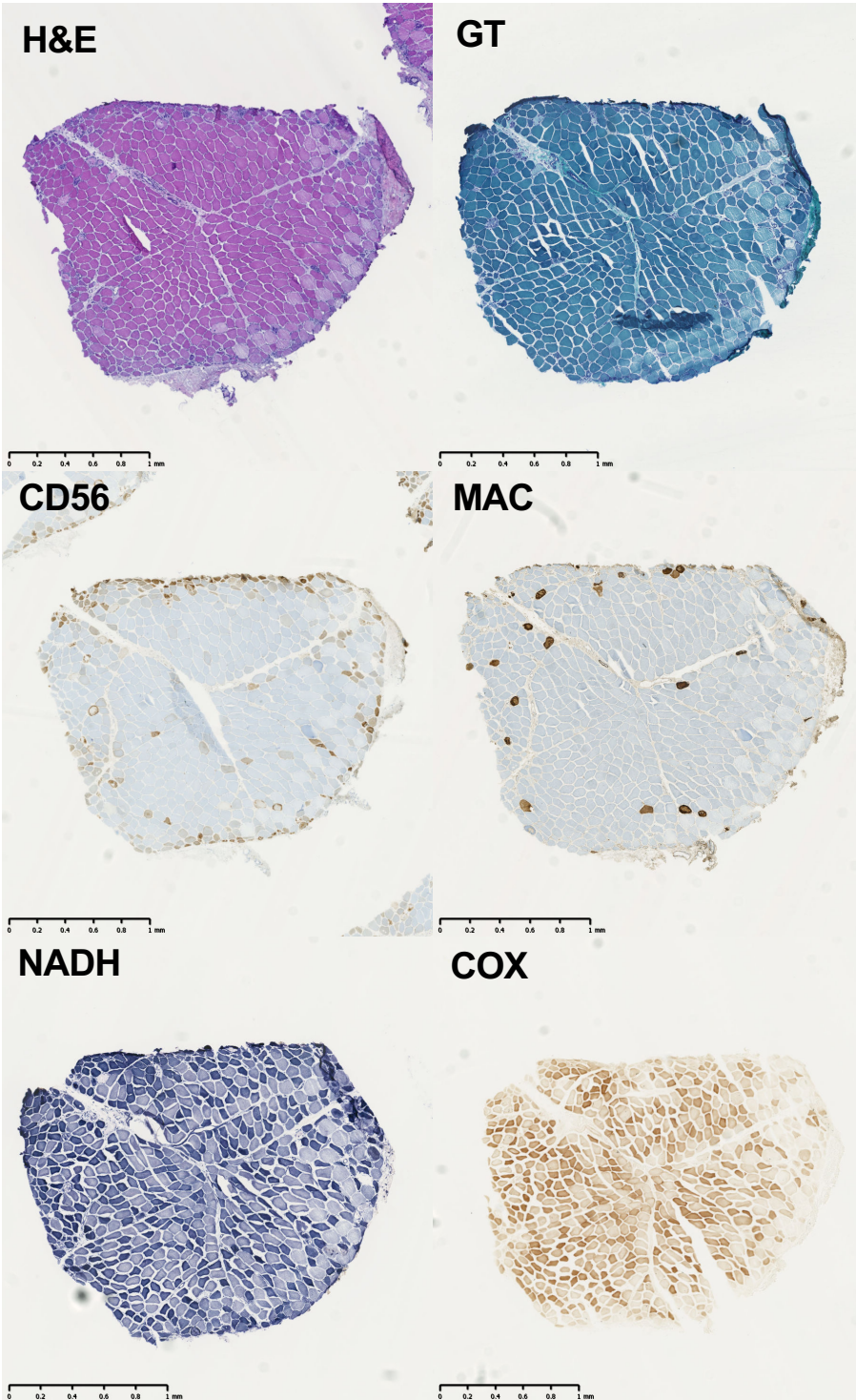
Supplementary Figure 4. Most differentially overexpressed genes in anti-Mi2 dermatomyositis muscle compared to all the other muscle biopsies included in the study according to the location of the muscle biopsy (histologically normal muscle biopsies [NT], non-anti-Mi2 dermatomyositis [DM], antisynthetase syndrome [AS], immune-mediated necrotizing myositis [IMNM], and inclusion body myositis [IBM]).



Supplementary Table 2. Association between the set of anti-Mi2-specific genes and genes previously proposed to be regulated by the CHD4/NuRD complex in skeletal or cardiac muscle using five different publicly available datasets from different animal models deficient in CHD4. CHD4-mck, CHD4-myh6, CHD4-corin, and CHD4-nkx_E10.5 were obtained from PMID 27166947, whereas CHD4-nkx_E9.5, and CHD4-nkx_E10 were obtained from PMID 29891665 (GSE109012). The list of mouse genes was restricted to those having a human homolog and the mouse homologs of the anti-Mi2 specific genes (n=114) were used for the analysis. The composite analysis of upregulated and downregulated genes contains more genes than the global composite analysis because some genes were underexpressed in one dataset and overexpressed in another.

	All the genes			Upregulated genes			Downregulated genes		
	Mi2	No Mi2	p-value	Mi2	No Mi2	p-value	Mi2	No Mi2	p-value
Composite	54% (61)	26% (4804)	6e-10	49% (56)	15% (2828)	5e-17	7% (8)	12% (2161)	1
CHD4-mck	18% (20)	7% (1352)	3e-04	17% (19)	5% (827)	1e-06	1% (1)	3% (525)	1
CHD4-myh6	11% (12)	3% (571)	3e-04	9% (10)	2% (351)	8e-05	2% (2)	1% (220)	0.4
CHD4-corin	12% (14)	3% (635)	5e-05	11% (13)	3% (479)	1e-05	1% (1)	1% (156)	0.6
CHD4-nkx_E9.5	32% (37)	15% (2833)	5e-06	28% (32)	8% (1468)	3e-10	4% (5)	7% (1365)	0.9
CHD4-nkx_E10	21% (24)	7% (1254)	8e-07	21% (24)	5% (861)	7e-10	0% (0)	2% (393)	1
CHD4-nkx_E10.5	4% (5)	1% (238)	0.02	4% (5)	1% (217)	0.01	0% (0)	0% (21)	1

Supplementary Figure 5. Representative stainings of the muscle biopsy sections used for Figure 7 and panel B of Figure 6 including H&E (hematoxylin and eosin) for general morphology, Gomori trichrome (GT), NADH (nicotinamide adenine dinucleotide) and COX (cytochrome c oxidase), as well as immunohistochemical stains for CD56 and membrane attack complex (MAC).



Supplementary Figure 6. Result of the confocal immunofluorescence analysis, showing the separate fluorescent channels of the regions of interest depicted in Figure 7. MAdCAM-1 and SCRT1 were visualized in the red channel, while human IgG (IGG) was detected in the green channel. The blue channel corresponds to Hoechst staining, which was used to visualize nuclei, and the magenta channel corresponds to laminin (LMN) staining.

