

Proteomics of Rimmed Vacuoles Define New Risk Allele in Inclusion Body Myositis

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Objective: Sporadic inclusion body myositis (sIBM) pathogenesis is unknown; however, rimmed vacuoles (RVs) are a constant feature. We propose to identify proteins that accumulate within RVs.

Methods: RVs and intact myofibers were laser microdissected from skeletal muscle of 18 sIBM patients and analyzed by a sensitive mass spectrometry approach using label-free spectral count-based relative protein quantification. Whole exome sequencing was performed on 62 sIBM patients. Immunofluorescence was performed on patient and mouse skeletal muscle.

Results: A total of 213 proteins were enriched by >1.5-fold in RVs compared to controls and included proteins previously reported to accumulate in sIBM tissue or when mutated cause myopathies with RVs. Proteins associated with protein folding and autophagy were the largest group represented. One autophagic adaptor protein not previously identified in sIBM was FYCO1. Rare missense coding *FYCO1* variants were present in 11.3% of sIBM patients compared with 2.6% of controls ($p = 0.003$). *FYCO1* colocalized at RVs with autophagic proteins such as MAP1LC3 and SQSTM1 in sIBM and other RV myopathies. One *FYCO1* variant protein had reduced colocalization with MAP1LC3 when expressed in mouse muscle.

Interpretation: This study used an unbiased proteomic approach to identify RV proteins in sIBM that included a novel protein involved in sIBM pathogenesis. *FYCO1* accumulates at RVs, and rare missense variants in *FYCO1* are over-represented in sIBM patients. These *FYCO1* variants may impair autophagic function, leading to RV formation in sIBM patient muscle. *FYCO1* functionally connects autophagic and endocytic pathways, supporting the hypothesis that impaired endolysosomal degradation underlies the pathogenesis of sIBM.

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Sporadic inclusion body myositis (sIBM) is the most common idiopathic inflammatory myopathy (IIM) in people > 50 years of age. It causes progressive muscle weakness, especially of finger flexion and knee extension.

It is uncertain whether sIBM is a primarily inflammatory or a degenerative myopathy. In contrast to other IIM, conventional immunosuppressants and immunomodulatory regimens have not been found to alter disease

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progression.^{1,2} Typical myopathological features are inflammatory and degenerative changes, accompanied by rimmed vacuoles (RVs) and protein aggregates.^{2–6} The current article intentionally focuses on these “degenerative features” to gain insight into one aspect of sIBM pathogenesis.

RVs are characteristic of the disease and are a useful diagnostic pathological feature; however, their genesis remains enigmatic.^{2,5} They are reported to contain both sarcoplasmic and myonuclear proteins. It has been suggested that the origin of an RV is due to myonuclear breakdown, because both nuclear and nuclear envelope proteins are present in or adjacent to the RV.⁷ Others have identified autophagic, lysosomal, and endosomal protein markers within and surrounding RVs.^{4,8,9} This has led to the hypothesis that impairment of autophagic degradation underlies sIBM pathogenesis. Finally, many proteins present in protein aggregate diseases such as Alzheimer disease, amyotrophic lateral sclerosis, and protein aggregate myopathies are consistently found accumulated in sIBM muscle, suggesting that sIBM is a degenerative proteinopathy akin to neurodegenerative disorders. RVs are typical of sIBM pathology, but they are not specific and are also found in a number of inherited myopathies, including myofibrillar myopathies, hereditary distal myopathies, and rare inherited inclusion body myopathies due to mutations in *GNE* and *VCP*.^{10,11} In these disorders, the disease-associated mutant protein accumulates within degenerating myofibers often within or adjacent to RVs.

Previously we established a combined laser microdissection and label-free proteomic approach to analyze cytoplasmic protein aggregates in myofibrillar myopathies.^{11–13} Using this technique, we identified distinct protein signatures in the muscle of myofibrillar myopathy patients. In the present study, we utilize the same proteomic approach to identify the protein composition of RVs in sIBM. We hypothesize that RV-enriched proteins are pathogenic mediators of disease and will inform both genetic association and sIBM biomarker development.

Subjects and Methods

Patients and Muscle Biopsies

Studies were performed on muscle samples from 18 patients with sIBM (6 women, 12 men, mean age = 66.7 ± 10.7 years, range = 49–93 years) according to local ethics committee regulations (reg. number 3882-10). The diagnosis of sIBM was based on the recently published 2011 European Neuromuscular Center international workshop criteria.⁵ After surgical procedure, skeletal muscle biopsies were divided into 0.5cm³ pieces, embedded into Tissue Freezing Medium (Leica Microsystems, Wetzlar, Germany), and flash frozen in liquid nitrogen.

DNA was collected from 62 patients with a diagnosis of sIBM.⁵ Forty of 62 patients had been previously reported, and targeted sequencing for hereditary causes of muscle disease had been performed.¹⁴ An additional 12 patients were identified from the Washington University Neuromuscular Clinic and 10 patients from Johns Hopkins University. All participants gave written informed consent, and study procedures were approved by the Human Studies Committee at Washington University.

Proteomic Analysis

LASER MICRODISSECTION AND SAMPLE PROCESSING. A combined laser microdissection and label-free mass spectrometry approach was applied as described with modifications.^{13,15} Ten-micrometer-thick frozen skeletal muscle sections were placed on polyethylene terephthalate membranes (Leica Microsystems) and stained with hematoxylin and eosin (H&E). These sections were used to collect (from each patient) a total area of 250,000 μm² of RV and surrounding sarcoplasm (hereinafter referred as RV sample) and the same area of vacuole-free sarcoplasm in normal-looking muscle fibers (control sample) by laser microdissection (LMD 6500, Leica Microsystems) into tubes containing 40 μl of 98 to 100% formic acid. After incubation for 30 minutes and sonification (35kHz) for 5 minutes (RK31; BANDELIN electronic, Berlin, Germany), samples were centrifuged at 12,000 × *g* for 10 minutes at 4 °C and frozen at –80 °C. The in-solution digestion and sample processing were performed as described.^{13,15}

NANO HIGH-PERFORMANCE LIQUID CHROMATOGRAPHY–MASS SPECTROMETRY. High-performance liquid chromatography (HPLC)–mass spectrometry (MS) analysis was performed on a nano-HPLC system (UltiMate 3000 RSLCnano; Dionex, Idstein, Germany) interfaced to a quadrupole orbitrap mass spectrometer (Q Exactive; Thermo Fischer Scientific, Darmstadt, Germany). HPLC analysis was performed as described before.¹³ After nano-HPLC separation, peptides were ionized in a nano-electrospray ionization source (ESI) and analyzed in data-dependent scan mode in the Q Exactive mass spectrometer. Full MS spectra were scanned between 350 and 1,400 *m/z* with a resolution of 70,000 at 200 *m/z* (automatic gain control [AGC] target = 3e6, maximum injection time = 80 milliseconds). The capillary temperature was set at 250 °C and the spray voltage at 1,600V (+). Lock mass polydimethylcyclodioxane (*m/z* = 445.120) was used for internal recalibration. The *m/z* values initiating MS/MS were set on a dynamic exclusion list for 30 seconds, and the 10 most intensive ions (charge = +2, +3, +4) with intensity > 1.7e3 were selected for fragmentation. Tandem MS fragments were generated by higher-energy collision–induced dissociation, and the fragmentation was performed with 27% normalized collision energy. The first MS/MS mass was fixed at 130.0 *m/z* and isolation window at 2.2 *m/z*. The fragments were injected into the orbitrap analyzer with 35,000 resolution at 2,000 *m/z* (AGC = 1e6, maximum injection time = 120 milliseconds).

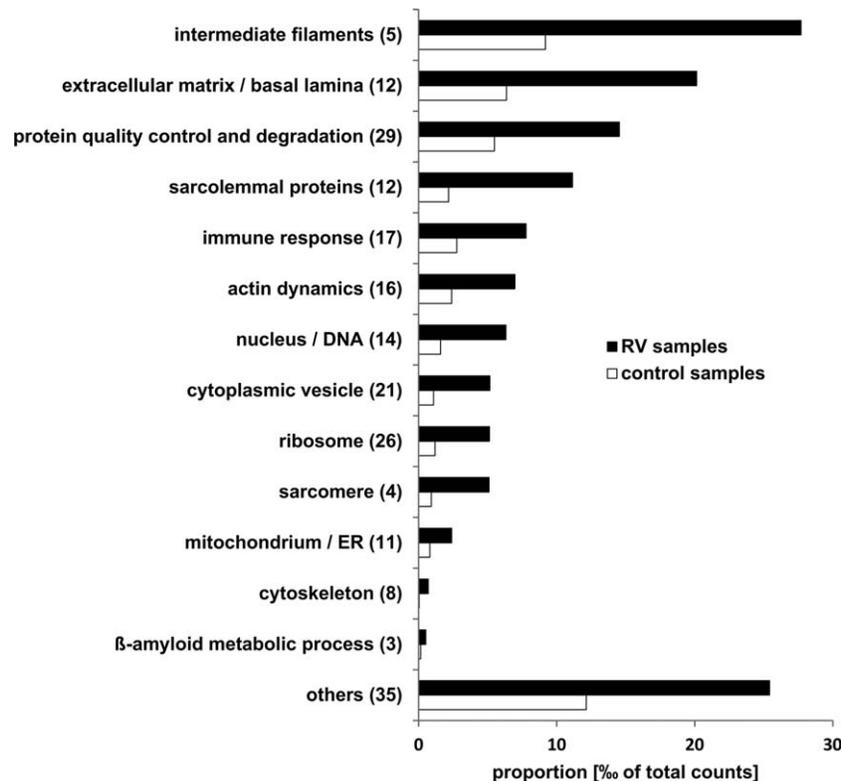


FIGURE 1: Functional classification of proteins identified as overrepresented in rimmed vacuole (RV) samples by proteomic analysis. A bar chart showing the sum of the mean proportion of proteins assigned to a subgroup is given for RV and control samples in per mill of total spectral counts. The number of detected proteins is given in parentheses after the subgroup name. Black bars show the proportion in RV samples, and white bars the proportion in control samples. Details of proteins assigned to the different subgroups are provided in Supplementary Table 1. ER = endoplasmic reticulum.

DATABASE SEARCH AND RELATIVE PROTEIN QUANTIFICATION. After ESI-MS/MS analysis, mass spectrometric data were searched against a human protein database containing the entire UniProt/Swiss-Prot (May 28, 2014 release, 20,265 curated entries) using Mascot (v2.5)¹⁶ and label-free relative protein quantification based on spectral counting was performed as described¹³ using PIA.¹⁷ To identify proteins that were overrepresented in RV within muscle fibers in sIBM, the ratios between the averaged proportions of proteins in RV and control samples were calculated and a 2-tailed unpaired *t* test (equal variances assumed) was performed for each protein. A protein was accepted as significantly overrepresented if the RV/control ratio was > 1.5 and $p < 0.05$.

VALIDATION OF PROTEOMIC FINDINGS BY IMMUNOFLUORESCENCE STUDIES. Immunofluorescence studies were performed on muscle samples from 5 sIBM patients to validate the proteomic findings as described.^{6,13} Serial frozen skeletal muscle sections were incubated overnight at 4°C with primary antibodies against 21 proteins (Supplementary Table 1), followed by washing steps and incubation with isotope-specific secondary antibodies conjugated with Alexa Fluor 488 (Dianova, Hamburg, Germany; dilution = 1:1,000) or Texas Red (Dianova, dilution = 1:400). Nuclei were visualized by 4',6-diamidino-2-phenylindole staining (Roche Diagnostics, Indianapolis, IN; dilution = 1:10,000).

Whole Exome Sequencing

Indexed genomic DNA libraries were prepared from genomic DNA using TruSeq DNA Preparation Kit (Illumina, San Diego, CA) and exome capture using TruSeq Exome Enrichment Kit (Illumina), according to the manufacturer's protocol. Sequencing was performed with 100bp paired-end reads on a HiSeq2000 (Illumina). Reads were aligned to the human reference genome with NovoAlign (Novocraft Technologies, Selangor, Malaysia) or Burrows–Wheeler Aligner.¹⁸ Variants were called with SAMtools¹⁹ and annotated with SeattleSeq. Coverage across genomic intervals was calculated using BEDTools.²⁰ Genomic coordinates for regions targeted by the whole exome capture kit were provided by Illumina. Whole exome sequences from 62 sIBM patients were filtered for variants that (1) had a minor allele frequency of ≤ 0.001 in the ExAC database, (2) generated a loss of function variant or a nonsynonymous change, and (3) fulfilled a strict sequence quality as defined by Genesis 2.0 software.

Mouse Expression Studies

Plasmid constructs expressing GFP-FYCO-WT and mCherry-LC3 were obtained from Dr Terje Johansen. The LIRmut (F1280A/I1283A), T1270A, and P1302L point mutations were generated via site-directed mutagenesis. For electroporation, mice were anesthetized using inhaled isoflurane. The skin overlying the tibialis anterior muscle was shaved, and the animals were coinjected with 30 μg endotoxin-free expression plasmid, diluted

TABLE. Rare Missense Variants in >2 of 62 sIBM Patients Compared with ALS Patients

Gene Name	sIBM Patients with Rare Variant			ALS Patients with Rare Variant			Statistical Significance
	Number	Total	%	Number	Total	%	
<i>AHNAK</i>	7	62	11.3	77	680	11.3	1
<i>ALDH3A2</i>	2	62	3.2	6	680	0.88	0.14
<i>ASAH1</i>	2	62	3.2	4	680	0.59	0.08
<i>C3</i>	2	62	3.2	8	680	1.2	0.2
<i>COL4A2</i>	2	62	3.2	14	680	2.1	0.64
<i>DMD</i>	4	62	6.5	29	680	4.3	0.51
<i>DYSF</i>	4	62	6.5	28	680	4.1	0.51
<i>FYCO1</i>	7	62	11.3	18	680	2.6	0.003 ^a
<i>GSN</i>	2	62	3.2	10	680	1.5	0.61
<i>HSPG2</i>	10	62	16.1	56	680	8.2	0.06
<i>LAMA2</i>	2	62	3.2	24	680	3.5	1
<i>LAMC1</i>	2	62	3.2	16	680	2.4	0.45
<i>NRAP</i>	5	62	8.1	17	680	2.5	0.03
<i>SPTAN1</i>	2	62	3.2	9	680	1.3	0.23
<i>SPTB</i>	4	62	6.5	33	680	4.9	0.8
<i>UNC45B</i>	3	62	4.8	9	680	1.3	0.07
<i>XIRP2</i>	4	62	6.5	48	680	7.1	1

^aStatistically significant.
ALS = amyotrophic lateral sclerosis; sIBM = sporadic inclusion body myositis.

in sterile phosphate-buffered saline to a volume of 50 μ l by using a 0.5ml syringe fitted with a 29-gauge needle. Two-needle array electrodes (450121; Harvard Apparatus, Holliston, MA) were inserted into the muscle immediately after DNA delivery for electroporation. The distance between the electrodes was 5mm, and the array was inserted longitudinally relative to the muscle fibers. In vivo electroporation parameters were the following: voltage = 75V, pulse length = 50 milliseconds, number of pulses = 6, pulse interval = 200 milliseconds, desired field strength = 200V/cm, given by a BTX ECM830 Electro Square Porator (Harvard Apparatus). Animals were allowed to recover for 7 days prior to muscle isolation; muscle was frozen in liquid nitrogen-cooled isopentane and processed into 10 μ m sections. Slides were examined using a fluorescent microscope (80i upright; Nikon, Tokyo, Japan) and charge-coupled device camera (EZ monochrome; Roper Industries, Sarasota, FL) with deconvolution software analysis (NIS Elements, Nikon). Image processing and analysis were performed with NIS Elements 4.0 software and Photoshop CS3 (Adobe Systems, San Jose, CA). All images were taken on fixed tissue at room temperature using Prolong Gold mounting solution (Invitrogen, Carlsbad, CA). Objectives used for immunofluorescence were Apochromat \times 20 and \times 40.

For colocalization analysis, 40 random fibers from 3 experiments were selected. The Pearson colocalization coefficient was determined for each fiber using NIS Elements 4.0 software. All images were taken at the same gain and exposure intensity.

Results

Proteomic Analysis

In total, 3,873 different proteins were identified by mass spectrometric analysis, including 213 proteins that

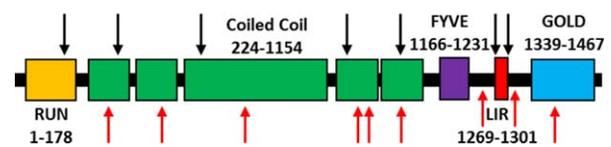


FIGURE 2: Scheme of *FYCO1*. Black arrows denote sites of missense variants identified in patients with sporadic inclusion body myositis. Red arrows denote mutations previously identified in patients with congenital cataracts. Domains include RUN (GTPase interacting motif), coiled coil (dimerization motif), FYVE (phospholipid binding region), LIR (LC3 interacting region), and GOLD (Golgi dynamics domain).

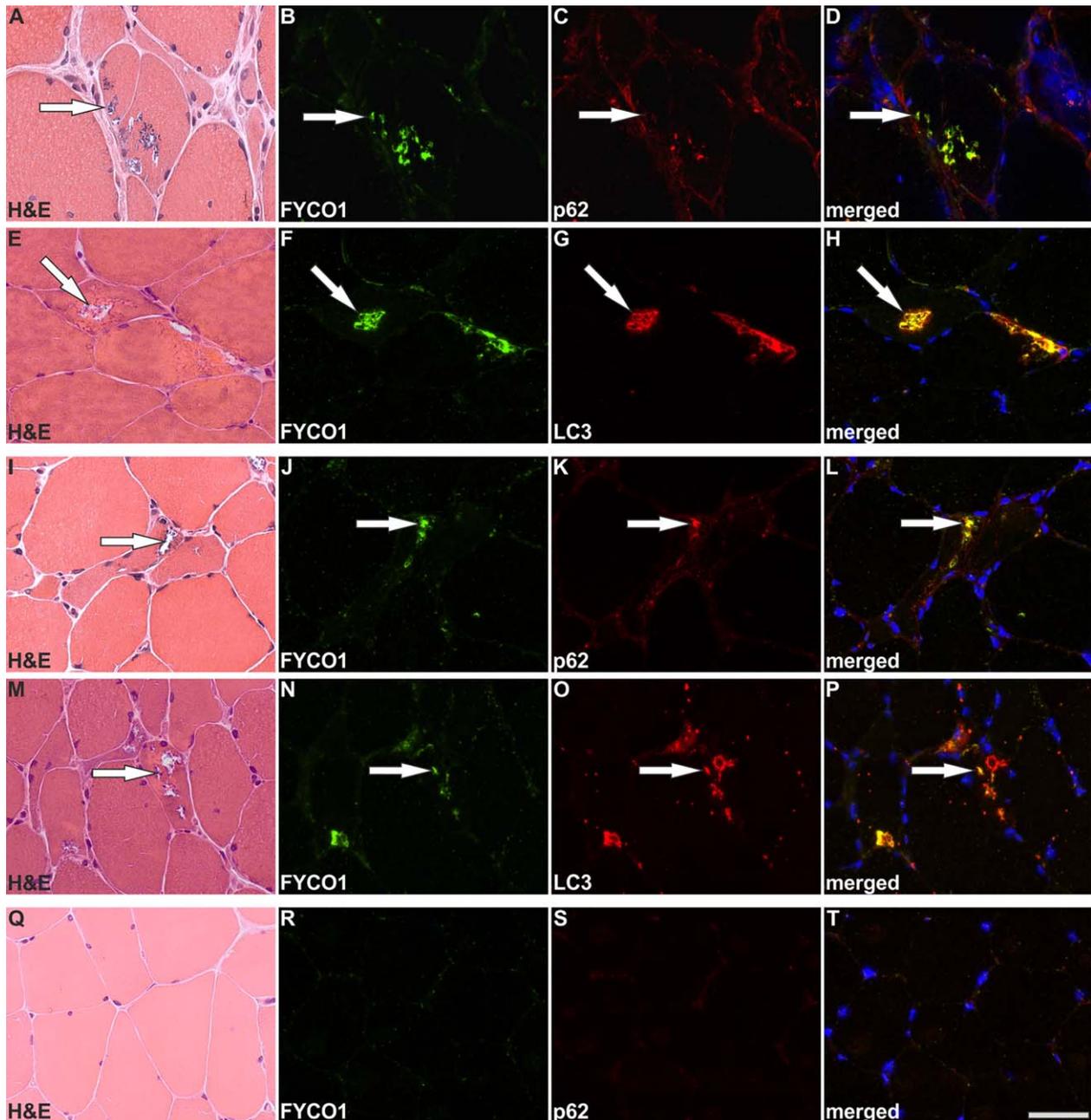


FIGURE 3: Colocalization of FYCO1, p62, and LC3 in rimmed vacuoles (RVs) of sporadic inclusion body myositis (sIBM) patients. Serial skeletal muscle sections from 2 sIBM patients (Patient 1: A–H, Patient 2: I–P) and from a healthy control (Q–T) were stained with hematoxylin and eosin (H&E) and double-immunostained with primary antibodies directed against FYCO1 (green) and p62 or LC3 (red). Nuclei were stained with 4',6-diamidino-2-phenylindole (blue). For each sIBM patient, 2 different RV containing areas of the muscle samples are displayed. All RVs show a strong immunoreactivity for FYCO1, p62, and LC3. The colocalization of FYCO1 with p62 and LC3 is indicated by yellow in the merged images. Scale bar = 50 μ m.

showed a statistically significant overrepresentation in RV samples compared to controls (see Supplementary Table 1). The proteins were assigned to subgroups based on their main physiological cell function. The proportion of each subgroup related to the sum of spectral counts is shown in Figure 1. Intermediate filaments were the most abundant overrepresented proteins, followed by proteins of the extracellular matrix and by

proteins involved in cell stress response, protein quality control, and protein degradation (see Fig 1). The latter group contains 29 different proteins, including 3 proteins that were detected in >50% of RV samples but in none of the control samples: transaldolase (an enzyme of the pentose–phosphate pathway), p62 (SQSTM1), and FYVE and coiled-coil domain-containing protein 1 (FYCO1).

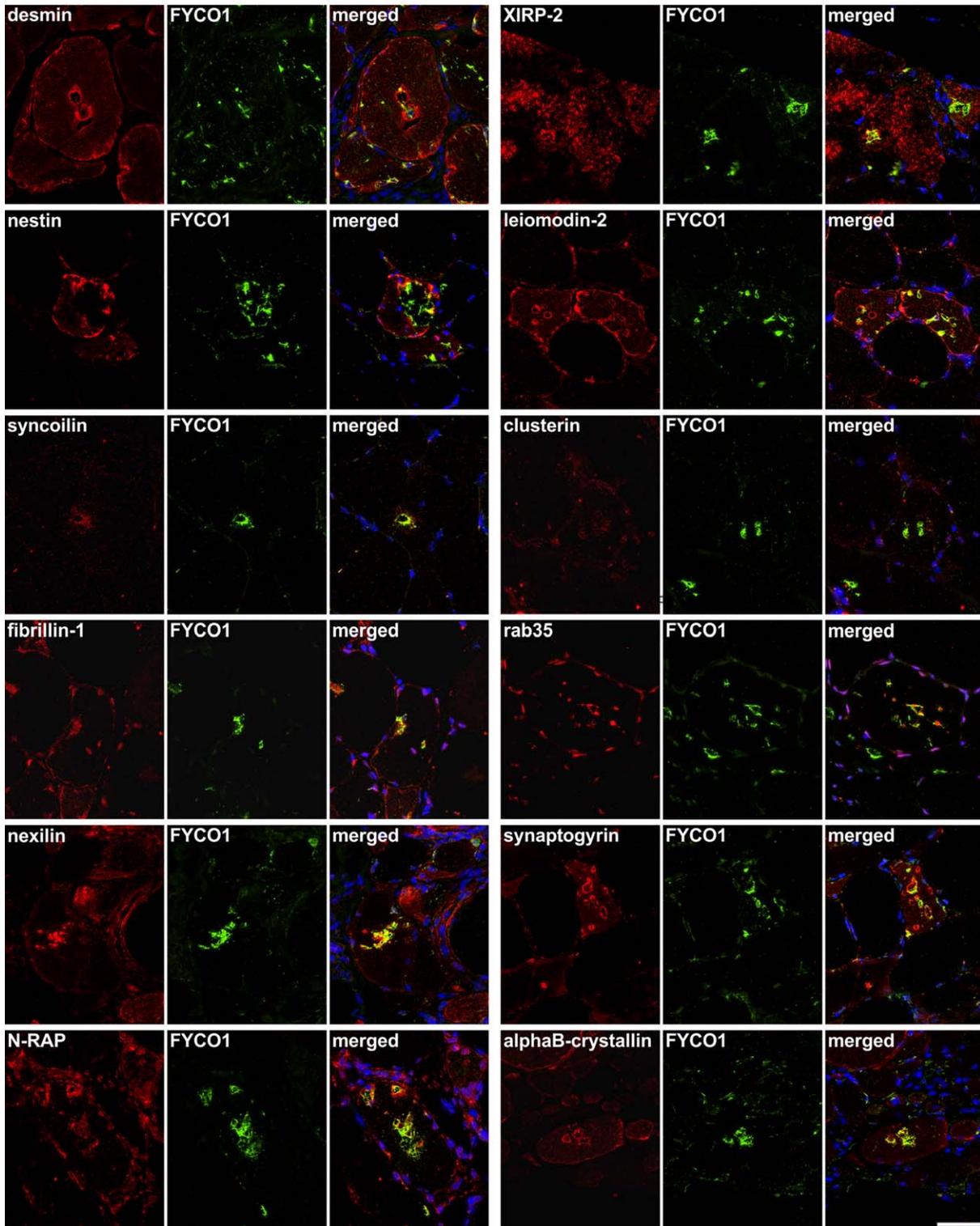


FIGURE 4: Validation of proteomic findings by immunolocalization studies I. Serial sections from 2 sporadic inclusion body myositis patients were double-immunostained with antibodies recognizing desmin, nestin, syncoilin, fibrillin-1, nexilin, N-RAP, XIRP-2, leiomodlin-2, clusterin, rab35, synaptogyrin, and alphaB-crystallin (red) and FYCO1 (green) as a positive control to localize RVs. Nuclei were stained with 4',6-diamidino-2-phenylindole (blue). All proteins showed an accumulation in RV areas. Scale bar = 50 μ m.

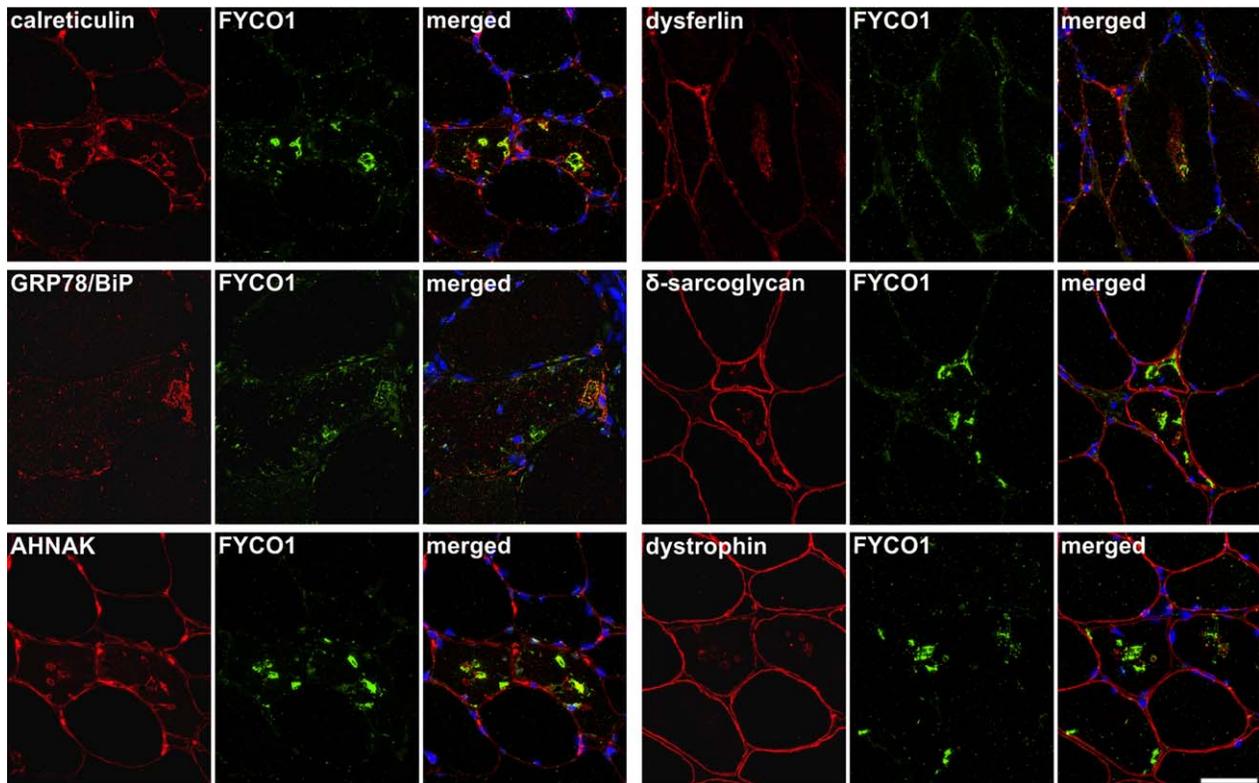


FIGURE 5: Validation of proteomic findings by immunolocalization studies II. Serial sections from 2 sporadic inclusion body myositis patients were double-immunostained with antibodies recognizing calreticulin, GRP78/BiP, AHNAK, dysferlin, δ -sarcoglycan, and dystrophin (red) and FYCO1 (green) as a positive control to localize RVs. Nuclei were stained with 4',6-diamidino-2-phenylindole (blue). RV areas showed an increased immunoreactivity for all proteins studied. Scale bar = 50 μ m.

Genetic Analysis

We reasoned that the proteins overrepresented in RVs may facilitate the identification of potential genetic risk alleles for sIBM. To test this, we identified rare missense or loss of function (LoF) variants in genes that encoded proteins that were present in $\geq 50\%$ of RV samples (131 genes; see Supplementary Table 1) using whole exome sequencing (WES) of 62 patients with sIBM. This analysis identified 100 variants from 52 genes. Seventeen genes had variants in ≥ 2 sIBM patients (Table). To see whether the burden of variants within a single gene was increased in other diseased control populations, or whether this enrichment was specific to sIBM, we determined the number of rare missense or LoF variants within these 17 genes in sporadic amyotrophic lateral sclerosis (ALS) patients from an existing WES dataset. Using these data, we found that variants in only 1 gene were statistically enriched in sIBM patients with a p value < 0.01 . Specifically, 7 of 62 (11.3%) sIBM patients carried a rare missense or LoF *FYCO1* variant as compared with 18 of 680 (2.6%) ALS patients ($p = 0.0029$; see Table). Similarly, the burden of *FYCO1* variants in sIBM was significantly enriched ($p = 0.011$) when compared

with ethnically matched patient genomes within the 1000 Genomes database, with 17 of 503 carrying a rare missense or LoF variant in *FYCO1*. sIBM-associated *FYCO1* rare variants were present throughout the protein, although 2 variants were adjacent to or within the LC3-interacting region (LIR) domain (Supplementary Table 2, Fig 2).²¹

Validation of Proteomic Data by Double Immunofluorescence Staining

Our proteomic and genetic data suggested that FYCO1 was an intriguing candidate protein to explore further. FYCO1 binds to LC3 and other vesicular cargo, facilitating autophagic degradation.²² We found that RVs displayed immunoreactivity for FYCO1, the autophagic adaptor p62, and the autophagosome protein MAP1LC3 in sIBM patients, with a slightly stronger immunoreactivity for FYCO1 (Fig 3). Therefore, we used FYCO1 as a marker for RV in double immunofluorescence analyses to evaluate 18 additional proteins from different subgroups identified as enriched in RV samples by our proteomic analyses (Figs 4 and 5). The immunoreactivity for these proteins was increased inside RVs or very closely around

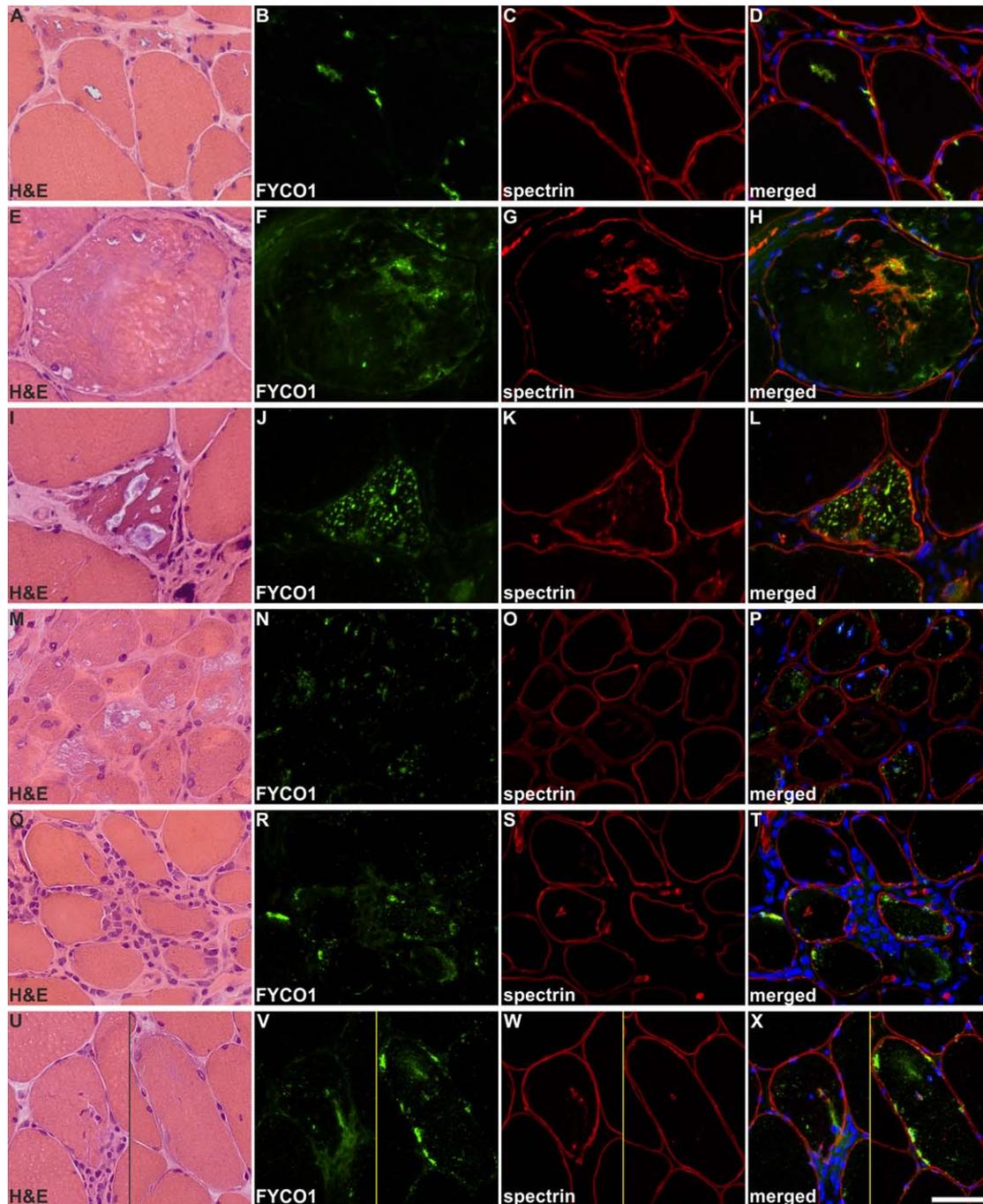


FIGURE 6: Localization of FYCO1 in hereditary myopathies with rimmed vacuoles (RVs) and in idiopathic inflammatory myopathies. Shown are findings in patients with: *GNE*-related hereditary inclusion body myopathy (A–D), myofibrillar myopathy caused by *FLNC* mutation (E–H), glycogen storage disease type II (I–L), dermatomyositis (M–P), polymyositis (Q–T), and a morphological diagnosis of polymyositis but a typical sporadic inclusion body myositis (sIBM) clinical phenotype (U–X). Serial skeletal muscle sections were stained with hematoxylin and eosin (H&E) and double-immunostained with antibodies recognizing FYCO1 (green) and the constituent muscle protein spectrin (red). Nuclei were stained with 4',6-diamidino-2-phenylindole (blue). RVs in hereditary inclusion body myopathy, myofibrillar myopathy, and glycogen storage disease type II showed a strong immunoreactivity for FYCO1. In myofibrillar myopathy, FYCO1 was also located in cytoplasmic protein aggregates. In dermatomyositis, some perifascicular muscle fibers showed an increased immunoreactivity for FYCO1, but "punched-out" areas of myofibrillar loss were not rimmed or markedly filled with FYCO1. In polymyositis and in sIBM with a morphological phenotype of polymyositis, muscle fibers surrounded by inflammatory cells displayed a diffuse/punctate immunoreactivity for FYCO1. In addition, some fibers showed FYCO1 accumulations in subsarcolemmal areas similar to that found in RV areas in sIBM. These areas were basophilic in H&E staining. Scale bar = 50 μ m.

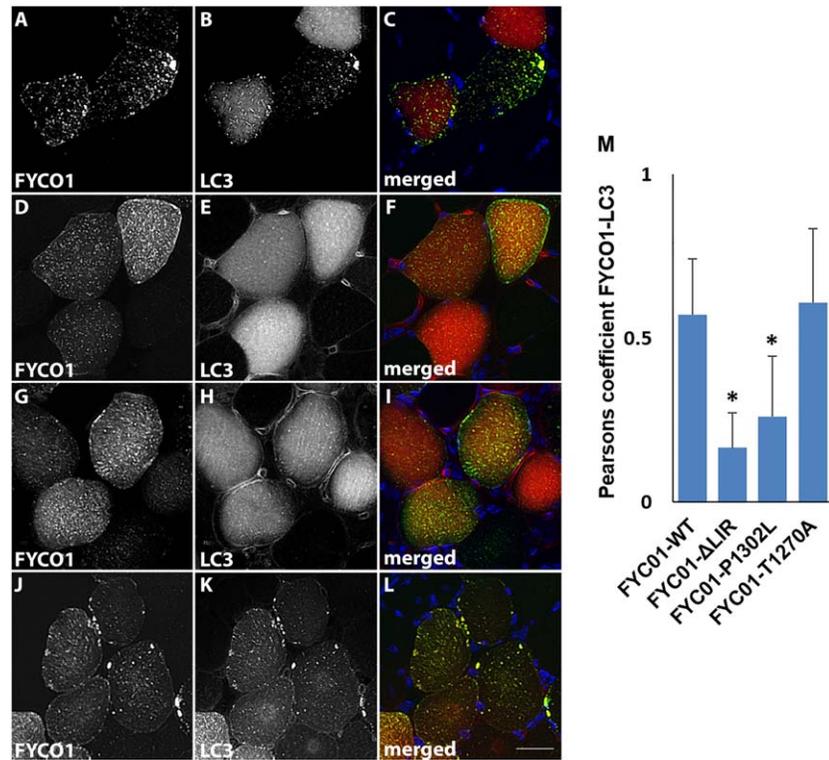


FIGURE 7: Localization of GFP-FYCO1 and mCherry-LC3 in mouse tibialis anterior muscle. GFP-FYCO1-WT (A–C), GFP-FYCO1-LIRmut (D–F), GFP-FYCO1-P1302L (G–I) and GFP-FYCO1-T1270A (J–L) were coexpressed with mCherry-LC3 and visualized via fluorescence microscopy for FYCO1 (A, D, G, J in green on merged), LC3 (B, E, H, K in red on merged) and 4',6-diamidino-2-phenylindole for nuclei (C, F, I, L in blue on merged). Scale bar = 25 μ m. (M) Quantitation of the Pearson colocalization coefficient for FYCO1 and LC3 in 40 fibers from 3 independent experiments. Error bars are standard deviation; * $p < 0.001$.

them, matching the area that has been collected by laser microdissection and thus confirming our mass spectrometric data.

***FYCO1* Localization in Other Vacuolar Myopathies and IIMs**

To assess the specificity of FYCO1 for RV, we performed immunofluorescence staining on skeletal muscle sections from patients with hereditary inclusion body myopathy caused by *GNE* mutations, filaminopathy associated with a myofibrillar myopathy phenotype, and glycogen storage disorder type II (Pompe disease), as well as normal control muscle tissue. The sarcolemma was marked with an antibody to spectrin (Fig 6). FYCO1 was associated with RVs in hereditary inclusion body myopathy, glycogen storage disorder type II, and filaminopathy. In filaminopathy, immunoreactivity for FYCO1 was increased in RV and in sarcoplasmic aggregates (see Fig 6). In dermatomyositis, some perifascicular muscle fibers showed an increased immunoreactivity for FYCO1, but “punched-out” areas of myofibrillar loss were not rimmed or markedly filled with FYCO1. In polymyositis and in sIBM with a morphological phenotype of polymyositis, muscle fibers surrounded by inflammatory cells displayed a diffuse/punctate immunoreactivity for FYCO1. In addition,

some fibers showed FYCO1 accumulations in subsarcolemmal areas similar to that found in RV areas in sIBM. These areas were basophilic in H&E staining. FYCO1 immunostaining and its colocalization to autophagic proteins (LC3 and p62) at RVs were similar in 3 sIBM patients carrying *FYCO1* variants as compared with colocalization in sIBM patients not carrying a *FYCO1* variant (data not shown).

***FYCO1* Variant Localization in Mouse Muscle**

FYCO1 is reported to facilitate the transport of autophagosomes along microtubules via its association with LC3.²² Two identified missense variants, FYCO1-T1270A and FYCO1-P1302L, are adjacent to or within the LIR domain, suggesting they may alter LC3 interaction (see Supplementary Table 2, Fig 2). We coelectroporated a plasmid expressing mCherry-tagged LC3 with a plasmid expressing green fluorescent protein-tagged FYCO1-WT in mouse tibialis anterior muscle. After 7 days, muscle was sectioned and visualized via fluorescent microscopy. GFP-FYCO1-WT was present as small puncta throughout the sarcoplasm that colocalized with mCherry-LC3 (Fig 7). Expression of FYCO1 with 2 point mutations within the LIR domain that abolish

LC3 interaction, GFP-FYCO1-LIRmut, demonstrated a similar pattern of GFP-FYCO1 puncta but diffuse mCherry-LC3 with reduced colocalization. This pattern of reduced FYCO1/LC3 colocalization was also seen with the sIBM variant GFP-FYCO1-P1302L but not with GFP-FYCO1-T1270A. The degree of GFP-FYCO1/mCherry-LC3 colocalization was quantified from coexpressing fibers/condition from 3 independent experiments and was significantly reduced in GFP-FYCO1-P1302L-expressing fibers compared to GFP-FYCO1-WT controls.

Discussion

In this study, we applied for the first time a highly sensitive proteomic approach to analyze the composition of a characteristic histopathological feature in sIBM. We used laser microdissection to collect RV and intraindividual control samples from muscle sections of sIBM patients. Mass spectrometric analysis and relative protein quantification allowed us to identify 213 proteins accumulated in RV samples compared to controls. Forty of these overrepresented proteins have already been described in sIBM (see Supplementary Table 1). Thus, the results of these previous studies validate our method and findings. Many of the proteins overlap with those identified in other protein aggregate myopathies,^{11–13} making most of the identified proteins not specific for sIBM, but highlighting converging pathogenic mechanisms with other muscle diseases. We also identified 173 proteins that have not been described in sIBM previously, which provides a basis for future studies to further investigate disease mechanisms. Our approach of label-free proteomic analysis combined with next generation sequencing has enabled us to identify a possible new genetic risk factor for sIBM.

We categorized the overrepresented RV proteins by their main cellular function and performed extensive immunofluorescence studies to further evaluate selected members of the different protein subgroups. These analyses confirmed and validated our proteomic data. We found that intermediate filaments were the most abundant overrepresented components in RV samples, and immunolocalization analysis proved that distinct intermediate filaments accumulate in RV areas. Very few studies have investigated intermediate filaments in sIBM.^{23–26} Olivé et al showed an accumulation of desmin in muscle fibers from patients with sIBM.²³ One proteomic study revealed an increase of vimentin in whole muscle biopsies,²⁴ and 2 studies described nestin and vimentin in regenerating muscle fibers.^{25,26} The surprising abundance of intermediate filaments in RVs is new, but their exact role in RV genesis needs further investigation.

Intermediate filaments are engaged in the formation and organization of aggregated and misfolded proteins.²⁷ Intracellular protein aggregates are transported along microtubules to form larger aggresomes finally removed by autophagic degradation.^{27,28} The intermediate filament protein vimentin forms a cage-like structure around aggresomes and is also responsible for lysosome organization and transport.^{28,29} The abundance of intermediate filaments around RVs may suggest that they support autophagic degradation in muscle fibers of sIBM patients. It is notable that mutations in the intermediate filament desmin cause a myopathy with rimmed vacuoles.¹⁰

The largest group of proteins identified as overrepresented in RV areas is those associated with protein folding and degradation. Protein homeostasis or “proteostasis” likely plays an important role in sIBM pathogenesis and is thus a tractable therapeutic target.³⁰ Our study reveals that several new chaperone components may be relevant and may refine therapeutic strategies. Small heat shock proteins and other molecular chaperones are of particular interest, because they facilitate proper protein folding and degradation of misfolded and aggregated proteins. α B-Crystallin, 78kDa glucose-regulated protein, and calreticulin have already been described in sIBM.^{31–34} A new finding is the enrichment of components of the TCP-1 ring complex (TRiC; also called CCT for chaperonin-containing TCP1). Interestingly, an overrepresentation of these proteins was not detected in other protein aggregate myopathies (Kley et al,¹¹ Maerkens et al,^{12,13} and unpublished data), and it may therefore be a specific feature of sIBM that needs further investigation. TRiC is a central chaperonin complex that interacts with approximately 5 to 10% of cytosolic proteins³⁵ and seems to be important for the prevention of protein aggregation and toxicity.^{35–37} Moreover, TRiC is a regulator of the heat shock transcription factor 1 (HSF1) in muscle fibers.^{38,39} It directly interacts with HSF1 and represses HSF1 activity.³⁸ It would be interesting to know if TRiC affects the efficacy of arimoclomol, a pharmacological agent that prolongs the activation of HSF1. Arimoclomol is currently in clinical trials for the treatment of sIBM.³⁰

Of the 213 proteins found enriched at RVs, disease mutations in 22 of these proteins lead to muscle-related phenotypes, including 9 proteins associated with myopathies containing prominent RV pathology. This may not be surprising, because several studies have demonstrated the utility of proteomics for the identification of accumulated proteins that are ultimately found to be the genetic cause of the disease.^{40,41} These previous reports led us to evaluate the burden of rare coding variants in RV-

accumulated proteins in sIBM patients. Current genetic studies in sIBM are limited. Some studies have performed targeted genetic mutation analysis in small cohorts of sIBM patients,¹⁴ whereas other studies have focused on modifier genes within populations of sIBM patients such as human leukocyte antigen subtypes as means to correlate *MHC* gene alleles with sIBM severity and prognosis.⁴² However, no studies have identified a clear risk allele for sIBM. One challenge to sIBM genetics relates to the rarity of the disease and its late onset, which usually precludes obtaining parental DNA. Therefore, obtaining patient samples with the statistical power necessary to perform genome-wide associations is difficult. To circumvent this, the current study uses proteomic candidates to explore potential genetic risk factors. Rare variants in *FYCO1* were found in 11.3% of sIBM patients as compared with 2.6% of disease controls and 3.4% of population controls. We suggest that rare variants in *FYCO1* are associated with risk of developing sIBM. This would be similar to other recently identified genetic risk variants such as *TREM2* and *TBK1* in sporadic ALS, where there is an overrepresentation of rare missense and LoF variants in cases as compared to matched controls.^{43,44} It is important to note several limitations of our genetic study, in particular the small sample size of 62 sIBM patients. Future studies will be necessary to explore whether *FYCO1* remains a risk factor for sIBM in larger cohorts. It will also be interesting to see whether *FYCO1* variants explain the pathogenesis or modify the phenotype of other myopathies with RVs.

FYCO1 belongs to an emerging group of autophagic adaptor proteins.⁴⁵ These adaptors facilitate autophagic cargo loading, autophagosome to lysosome maturation, or in the case of *FYCO1*, autophagosome/endosome trafficking.⁴⁵ *FYCO1* binds to LC3 and Rab7 on the surface of autophagosomes and endosomes, respectively, links them to microtubules via kinesin, and enables transport of autophagosomes along microtubules to acidic lysosomes.^{22,46} Depletion of *FYCO1* or point mutations within its LIR domain lead to the accumulation of autophagosomes and autophagic cargo that have failed to mature to autolysosomes and be degraded.²¹ We identified 2 rare *FYCO1* variants (T1270A and P1302L) that resided in or adjacent to the LIR domain. In mouse skeletal muscle, *FYCO1*-WT colocalizes with LC3 puncta. In contrast, deletion of the LIR domain or expression of the *FYCO1*-P1302L variant failed to recruit and localize to LC3 puncta, suggesting that this sIBM-associated *FYCO1* missense variant may disrupt its function. Missense variants in *FYCO1* have been previously identified in rare patients with congenital cataracts.⁴⁷ Interestingly, expression of these variants did not

disrupt *FYCO1*'s association with LC3, suggesting that loss of LC3 interaction is not the only mechanism by which *FYCO1* mutations can disrupt its function. The role of *FYCO1* in normal skeletal muscle is currently unknown. That *FYCO1* localizes throughout the myofiber in control mouse muscle and in myopathies lacking RVs such as dermatomyositis and polymyositis supports a role for *FYCO1* in processes unrelated to its pathologic accumulation at RVs.

Our study identified an overrepresentation of rare missense coding variants in *FYCO1* in sIBM patients and suggests that a failure in autophagosome/endosome trafficking may underlie sIBM pathogenesis. The role of impaired vesicular trafficking along microtubules in vacuolar myopathies is further supported by patients and animals treated with colchicine, a microtubule-destabilizing agent. Mice chronically treated with colchicine develop an autophagic vacuolar myopathy with the accumulation of LC3, p62, and late endosomal markers such as Lamp2.⁴⁸ This also occurs in patients receiving toxic doses of colchicine.⁴⁸ Similarly, RVs in sIBM seem to agglomerate, which hints at ineffective or inadequate transport mechanisms along the cytoskeleton. It is intriguing that dominantly inherited mutations in 2 other proteins (*VCP* and *p62/SQSTM1*) also responsible for autophagosome maturation/degradation lead to RV myopathies.^{49–52} Notably, *VCP* and *p62* were both identified as RV-enriched proteins in the current study. Moreover, rare missense pathogenic variants in both *VCP* and *SQSTM1* have been found in patients with sIBM.^{14,53}

The pathogenesis of sIBM is uncertain and likely due to multiple contributing factors. Specifically, a combination of environmental, genetic, and age risk factors needs to be present for disease manifestation. Although our study has identified a potential risk allele in a gene associated with autophagic degradation, this does not preclude the possibility that a primary immune process instigates sIBM pathogenesis. A *FYCO1* missense variant is not sufficient for disease pathogenesis, because all of our sIBM patients lacked a family history of sIBM or weakness. However, it is intriguing that several genes associated with autophagosome-lysosome processing are emerging as risk alleles in sIBM.^{14,53} Future therapies aimed at improving autophagic function may be beneficial in sIBM patients, especially when used in conjunction with other therapies addressing immune dysfunction.

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Author Contributions

A.-K.G., S.B., A.M., A.S., M.T., J.L.H., M.V., C.C.W., K.M., and R.A.K. contributed significantly to the conception and design of the study. A.K.G., S.B., K.K., A.M., J.U., M.E., A.S., S.G., J.M.-R., M.B.H., T.E.L., M.V., C.C.W., K.M., and R.A.K. contributed significantly to data acquisition and analysis. A.-K.G., S.B., K.K., A.M., M.V., C.C.W., and R.A.K. contributed significantly to drafting the manuscript or figures. M.V., C.C.W., K.M., and R.A.K. contributed equally to authorship.

Potential Conflicts of Interest

Nothing to report.

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