# C-terminal tagging, transmembrane domain hydrophobicity, and an ER retention motif influence the secretory trafficking of the inner nuclear membrane protein emerin

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**Abstract:**

The inner nuclear membrane (INM), a subdomain of the endoplasmic reticulum (ER), sequesters hundreds of transmembrane proteins within the nucleus. We previously found that one INM protein, emerin, can evade the INM by secretory transport to the lysosome, where it is degraded. In this work, we used targeted mutagenesis to identify intrinsic sequences that promote or inhibit emerin's secretory trafficking. By manipulating these sequences across several tag and expression level combinations, we now find that emerin's localization is sensitive to C-terminal GFP tagging. While emerin's long, hydrophobic C-terminal transmembrane domain facilitates trafficking to the lysosome, extending its lumenal terminus with a GFP tag biases the protein toward this pathway. In contrast, we identify a conserved ER retention sequence that stabilizes N- and C-terminally tagged emerin by limiting its lysosomal flux. These findings underscore long-standing concerns about tagging artifacts and reveal novel determinants of tail-anchored INM protein targeting.

## Introduction:

Tail-anchored proteins of the inner nuclear membrane (INM) are a unique class of transmembrane proteins with poorly understood biosynthesis, targeting, and degradation. The INM is a specialized extension of the endoplasmic reticulum (ER) membrane, the major site of membrane protein synthesis. Shortly after translation, tail-anchored proteins are embedded by their C-terminal transmembrane domains into the ER[1]. Unlike cytoplasmic tail-anchored proteins, which rapidly traffic out of the ER toward their target membranes, INM proteins must remain in the ER long enough to diffuse through the nuclear pore complex (NPC) and be retained by binding to nuclear structures[2,3]. This process repeats each time the nuclear envelope reforms at the end of mitosis[4]. INM proteins thus spend considerable time in the ER, but how they interact with the ER's secretory or proteostatic functions is unclear.

Our previous work identified emerin (EMD) as a short-lived INM protein in C2C12 mouse myoblasts[5]. While investigating how emerin is degraded, we found that C-terminally GFP-tagged emerin travels by vesicular transport to the Golgi, plasma membrane (PM), and then lysosome during ER stress[5]– an itinerary that closely tracks with the path taken by cargoes of the rapid ER stress-induced export (RESET) pathway[6]. This unexpected secretory trafficking was prevented by the removal of EMD-GFP's N-terminal LEM domain, suggesting that this domain played a role in stress-induced lysosomal degradation. We hypothesized that the INM might dynamically respond to ER stress by shunting emerin through the secretory pathway to the lysosome. However, we now find that N-terminally GFP-tagged emerin traffics at a lower rate than C-terminally tagged emerin, and find no conclusive evidence that untagged emerin traffics to the lysosome. We also show that the secretory trafficking of tagged emerin depends on its unusually hydrophobic transmembrane domain (TMD). In isolation, the TMDs of both emerin and the related tail-anchored protein LAP2β readily traffic to the PM, but trafficking of the full-length tagged proteins is limited by a conserved RXR-type ER retention motif. Our experiments indicate that emerin's trafficking is artifactually expedited by C-terminal GFP tagging. However, these studies identify sequence elements that target emerin to the contiguous nuclear envelope/endoplasmic reticulum (NE/ER) network and highlight the interdependence between protein biogenesis, topology, and localization.

## Results:

After our initial discovery, we aimed to understand the mechanism of emerin's secretory trafficking and its conservation across species, cell types, and expression levels. As our earlier experiments

used C2C12 mouse myoblasts, we first tested whether EMD-GFP trafficking is conserved in human cells. We stably expressed tet-inducible mouse and human GFP fusions in human osteosarcoma (U2OS) cells. When treated with the lysosome blocking agent bafilomycin A1 (BafA1), we found that U2OS cells, unlike C2C12 myoblasts[5], do not rely on ER stress to initiate secretory trafficking of EMD-GFP. Instead, BafA1 alone caused EMD-GFP to accumulate in lysosomal puncta. We used this high secretory flux to differentiate between emerin constructs that could and could not traffic (Figure 1A). Consistent with our C2C12 findings, we verified that WT EMD-GFP could traffic to the lysosome of U2OS cells, while a construct lacking the N-terminal LEM domain (ΔLEM, Figure 1B) could not. Our constructs were tagged with a C-terminal/lumenal GFP, which allowed us to quantify the proportion of EMD-GFP in the secretory pathway using cell surface antibody labeling and flow cytometry (Figure 1C,D). We calculated the trafficking level of each construct by dividing the surface anti-GFP antibody signal by the total EMD-GFP fluorescence. In line with our microscopy experiments, the anti-GFP antibody did not detect any ΔLEM construct at the PM of U2OS cells, while the WT EMD-GFP PM signal was always above background (Figure 1E).

**Emerin's hydrophobic transmembrane domain is necessary and sufficient for trafficking of EMD-GFP**

We further leveraged this U2OS system to examine how emerin's protein sequence facilitates trafficking. Emerin contains three major domains: an N-terminal LEM domain that interacts with the chromatin crosslinker BANF1/BAF, an intrinsically disordered region (IDR) that binds the nuclear lamina, and a C-terminal transmembrane domain (TMD)[7] (Figure 1B). We tested each domain's ability to traffic through the secretory pathway with a series of domain truncation experiments. Having established that removing the LEM domain abolished emerin's ability to traffic, we next deleted the disordered region between the LEM domain and the transmembrane domain (TMD). This construct (termed LEM-TMD) accumulated at the PM 10-fold more than the WT protein, indicating that the TMD, LEM domain, or both together are sufficient for trafficking (Figure 1F). To distinguish between these possibilities, we tested whether emerin's TMD alone can travel to the PM. We removed all but the TMD alpha helix and its surrounding 26 residues (mEMD 212-259), which we found to be required for membrane insertion of the truncated construct (not shown), and appended this TMD-only construct to either the C- or N-terminus of eGFP. Both TMD-GFP and GFP-TMD localized prominently to the ER and PM, and both were evident in the lysosome after BafA1 treatment (Figure 1F-G). These experiments reveal that emerin's TMD alone can traffic to the lysosome, regardless of GFP tag orientation.

We wondered what properties of emerin's TMD mediate its secretion. Tail-anchored proteins can sort via their TMDs along the secretory pathway[8–10]; long and hydrophobic sequences partition to the thicker, more hydrophobic membranes of the late secretory organelles[11] (Figure S2B-C), while tail-anchored proteins with shorter, less hydrophobic TMDs preferentially remain in the ER. We noticed that emerin's TMD is particularly hydrophobic among other NE/ER transmembrane domains (Figure S2A-B), which led us to predict that emerin's TMD is required for its exit from the ER. To test this, we replaced emerin's TMD with that of cytochrome B5, a model ER protein with a modestly hydrophobic TMD[12]. This substitution ablated trafficking through the secretory pathway (Figure 2A-B), indicating that emerin's TMD is indeed necessary for trafficking. We tested whether this depended on the hydrophobic content of the alpha helix by sequentially mutating its aromatic residues to alanine. We divided the TMD into N- and C-terminal halves, mutating three aromatic amino acids in each half (Figure 2C). The N-terminal TMD mutant was slightly less hydrophobic and had a greater effect on secretory trafficking than the C-terminal mutant (Figure 2D-E). Combining the N- and C-terminal mutations additively reduced the surface ratio of EMD-GFP. While these mutations decreased the overall protein expression (Figure S2E), they did not affect the protein's topology (Figure S2F), confirming that the observed loss of surface exposure was due to diminished secretory trafficking and not to defects in membrane insertion. These experiments indicate that manipulating the hydrophobicity and/or aromaticity of the TMD influences EMD-GFP's transit to the cell surface.

**Emerin contains a conserved ER retention signal**

The autonomous trafficking of emerin's TMD challenged our initial hypothesis that emerin's localization relies on the LEM domain. Because EMD ΔLEM-GFP cannot traffic despite containing the TMD, we wondered whether a sequence within the ΔLEM construct inhibits trafficking. We noted that removing the LEM domain exposed a highly charged and conserved motif (QRRR) on the N-terminus of the construct (Figure S2D). Poly-arginine (RXR) motifs are known negative regulators of ER-to-Golgi transit[13]; we therefore tested whether this unprotected RXR could explain the ER-restricted localization of ΔLEM-GFP. Indeed, further truncating the ΔLEM construct by deleting the QRRR (ΔLEMΔQRRR) freed the protein from the ER (Figure 2F-H).

To test whether the RXR motif limits the trafficking of full length EMD-GFP, we mutated the QRRR to AAAA (designated RA) and detected more flux to the PM compared to WT EMD-GFP (Figure 2F-G). Both ΔLEMΔQRRR-GFP and EMD RA-GFP were less abundant at steady-state and were

126 more rapidly degraded after removal of doxycycline from the medium (Figure 2I-J), suggesting
127 increased flux to the lysosome. These data indicate that the RXR motif constitutes an ER retention
128 sequence in EMD-GFP that is strengthened by the removal of the LEM domain. We infer that the
129 presence of the LEM domain modulates the accessibility of the RRR motif; while the LEM domain
130 itself is in fact dispensable for trafficking, its removal constitutively exposes the RRR motif,
131 enhancing emerin's ER localization.
132
133 We next investigated the interplay between emerin's pro-trafficking TMD and its anti-trafficking
134 RXR motif by cloning the RA mutation into our TMD mutant constructs (see Figure 2C-E). The RA
135 mutation generally increased the surface expression of the TMD mutants except for the construct
136 with the lowest hydrophobicity score ($TMD^m$), which was not significantly altered by the RA
137 mutation (Figure 3A-B). We infer from this that the TMD acts upstream of the RXR motif in
138 emerin's secretory trafficking, fitting with the hypothesis that low TMD hydrophobicity suffices to
139 stably retain proteins in the ER[8].
140
141 Emerin is not the only tail-anchored INM protein with a particularly hydrophobic TMD. Another
142 such protein is LAP2β[14], which shares several sequence features with emerin[15] (Figure S2A, 3C).
143 We identified three RXR motifs within the LAP2β N-terminal domain, one of which (designated
144 RXR1) is just downstream of the LEM-like fold—a striking similarity to emerin's RXR motif (Figure
145 3C). To test whether the same localization mechanisms govern LAP2β, we tagged its C-terminus
146 with GFP and expressed it in U2OS cells. LAP2β-GFP was detected at the cell surface, albeit at
147 much lower levels than EMD-GFP (Figure 3D-E, S3A-B). Interestingly, replacing most of the
148 LAP2β N-terminal domain with the soybean ascorbate peroxidase (APEX2) enzyme caused a 20-
149 fold increase in PM expression (Figure 3D, S3B), suggesting that the LAP2β TMD has a similar
150 proclivity for secretory trafficking. Finally, mutating the LAP2β RXR1 to AAA led to a 70% increase
151 in PM accumulation (Figure 3D), mirroring the effect of the EMD RA mutation. Together, these
152 data indicate that the emerin and LAP2β TMDs are insufficient for NE/ER targeting and that both
153 proteins contain retention sequences which counteract TMD-dependent secretion.
154
155 RXR motifs are thought to bind COPI subunits to return escaped proteins to the ER[13,16], though
156 this mechanism is not understood. To test whether the increased trafficking of the RA mutant
157 results from reduced COPI interaction, we immunoprecipitated N-terminally FLAG-tagged mouse
158 emerin constructs from U2OS cells (Figure S3C). Mass spectrometry revealed a robust interaction

between emerin and the COPI coat, with several COPI subunits ranking among the top hits (Figure 3F). Surprisingly however, this interaction was not weakened by the RXR mutation (Figure 3G). We noted that the mouse EMD bait also co-immunoprecipitated endogenous human EMD (Figure 3G), opening the possibility that COPI might indirectly interact with both FLAG constructs via endogenous emerin. Alternatively, the RXR motif's function could depend on protein topology. Importantly, while we were able to detect FLAG-EMD in the lysosome by IF (Figure S3D), FLAG-RA construct was not poorly expressed relative to FLAG-WT (Fig. S3C) in contrast to RA-GFP compared to WT-GFP (Fig. 2I). We also noted that the lysosomal accumulation of N-terminally FLAG-tagged emerin was more subtle than the C-terminally GFP-tagged version (Figures 1A, 2B), indicating that epitope tagging and/or tag orientation influences the extent of emerin protein turnover.

**C-terminal tagging destabilizes emerin via secretory trafficking**

To determine whether tagging and/or overexpression increase the extent of emerin trafficking, we needed a system to better control emerin expression. To this end, we generated a human iPSC line with a dual integrase cassette exchange (DICE) landing pad[17] in the AAVS1 safe harbor locus (Figure 4A), then knocked emerin out of these cells with CRISPR/Cas9 (Figure 4B). Integrating GFP-tagged constructs into the parental and EMD KO DICE landing pads enabled us to measure EMD-GFP trafficking in the presence or absence of the endogenous copy, respectively (Figure 4C). We included an mCherry-P2A upstream of the EMD-GFP to control for minor differences in construct expression (Figure 4A). The GFP-tagged emerin constructs mirrored the trafficking pattern we observed in U2OS cells; the EMD RA-GFP construct accumulated more at the PM, while the TMD mutant did not traffic (Figure 4D-E). The steady state abundance reflected these trafficking patterns. The GFP fluorescence of the TMD mutant accumulated to higher levels, indicating that it was stabilized by its inability to traffic. In contrast, the RA mutant fluorescence was slightly lower, indicating that it was modestly less stable than the WT protein, although this difference is not statistically significant (Figure 4F-G). There was no difference in total or surface expression between integrants in the EMD knockout and WT DICE backgrounds, suggesting that the trafficking of EMD-GFP is comparable both when moderately overexpressed and when expressed at endogenous levels (Figure 4D-E).

Tracking tail-anchored (i.e. untagged/N-terminally tagged) emerin through the secretory pathway is challenging because it lacks a lumenal domain amenable to surface labeling. However, after discovering ways to limit lysosomal flux (via the TMD) or accelerate it (via the RXR motif), we

193 reasoned that the trafficking patterns of tail-anchored mutants could be inferred from their steady
194 state abundance when expressed from the DICE landing pad. To test whether the GFP tag
195 orientation affects protein expression, we compared the steady state fluorescence of N- and C-
196 terminally tagged mutants. Surprisingly, the N-terminally tagged (tail-anchored) GFP fusions were
197 4-5 times more abundant than the C-terminally tagged (single pass) fusions (Figure 4F-G). C-
198 terminal fusions were also more completely relocalized to the lysosome after BafA1 than N-
199 terminal fusions, where NE/ER EMD signal was still apparent (Figure S4A). Unlike the C-terminal
200 fusions, the N-terminally tagged TMD mutant did not accumulate more than the N-terminally
201 tagged WT protein, suggesting that N-terminally tagged emerin is not destabilized by trafficking.
202 We interpret this finding with caution, as we observed a slight decrease in the level of the N-
203 terminally tagged TMD mutant compared to WT (Figure 4G). Since the insertion of tail-anchored
204 proteins relies on TMD hydrophobicity[1,18], improper targeting to the ER membrane due to TMD
205 mutation would confound our conclusion that N-terminally tagged constructs undergo similarly
206 low levels of trafficking. Interestingly, upon treatment with BafA1, the N-terminally tagged WT and
207 RA constructs formed GFP+ lysosomal puncta, while the N-terminally tagged TMD mutant did not
208 (Figure S4A). This suggests that N-terminally tagged emerin does undergo some level of TMD-
209 dependent trafficking. Further, the N-terminal RA fusion was slightly less fluorescent at steady
210 state than WT (Figure 4G), indicating that the RXR motif also stabilizes tail-anchored GFP-EMD.
211
212 Because of the profound differences in the distribution of N and C-terminally tagged constructs,
213 we investigated how lumenal GFP affects emerin's early secretory trafficking by analyzing its
214 enrichment in ER exit sites (ERES). ER cargoes that are actively packaged into ERES can be
215 distinguished from bulk flow secretory cargoes by incubating cells at 10C, where ERES form and
216 cargoes accumulate but cannot progress toward the Golgi[19]. We compared the colocalization of
217 endogenous untagged emerin, WT-GFP, and $TMD^m$-GFP with the ERES marker SEC31 at 37C
218 and 10C (Figure S4B-C). We found that GFP-tagged emerin colocalized with SEC31 at steady-
219 state, while this was not the case for endogenous emerin or the tagged TMD mutant. ERES
220 colocalization was not increased at 10C for any of the emerin variants analyzed, indicating that
221 emerin does not contain specific ER exit signals.
222
223 Collectively, these data indicate that N- and C-terminally tagged emerin constructs travel to the
224 lysosome via their hydrophobic TMDs, although C-terminal tags accelerate this trafficking by
225 encouraging bulk-flow ER exit.
226

227 Finally, we integrated untagged WT, RA, and TMD mutant constructs into EMD KO landing pad
228 cells, then fixed and stained cells for confocal microscopy and flow cytometry. We saw no
229 apparent differences in the localization or intensity of any of the emerin mutants, though the data
230 were considerably noisier than the steady state GFP measurements (Figure 4H). We were also
231 unable to detect untagged emerin in the lysosome after BafA1 treatment (Figure S4D), suggesting
232 it does not traffic through the secretory pathway. However, the sensitivity of these assays may be
233 limited by fixation, permeabilization, and antibody staining; therefore, we cannot rule out the
234 possibility that small differences do exist between untagged emerin variants.
235

236 **Discussion**

237 In this work, we dissected how exogenous epitope tags and intrinsic sequence elements influence
238 the secretory trafficking of the INM resident protein emerin. We discovered that the aromatic
239 amino acids in emerin's 23-residue TMD facilitate its travel to the lysosome. In the absence of
240 other signals, TMD length and hydrophobicity are sufficient to partition tail-anchored proteins
241 along the secretory pathway[8,9]. The biophysical properties of the emerin and LAP2β TMDs
242 resemble PM, rather than ER, resident TMDs (Figure S2, ref.[11]). However, this notable
243 hydrophobicity is likely important for the proteins' biogenesis. Tail-anchored proteins with very
244 hydrophobic transmembrane domains are post-translationally targeted by the TRC40/GET
245 complex, which captures C-terminal alpha helices after they emerge from the ribosome and
246 delivers them to the ER membrane[1]. Emerin and Lap2β are established TRC40 client proteins[20,21],
247 so their hydrophobic TMDs are likely required for TRC40 recognition. However, adding a C-
248 terminal GFP converts a tail-anchored protein to a single-pass transmembrane protein, which will
249 instead be co-translationally targeted to the ER by the SRP pathway[18,22]. Our results indicate that
250 this change in topology displaces emerin, making C-terminally tagged emerin less stable and
251 more prone to lysosomal trafficking than its N-terminally tagged counterpart (Figure 4F-G, S4A).
252 Consistently, we found that only lumenally tagged emerin sampled ER exit sites, and that this was
253 reduced by manipulating the TMD hydrophobicity (Figure S4B-C). This suggests that hydrophobic
254 TMDs are less energetically favored within the ER membrane when attached to a lumenal
255 domain, or that different biogenesis pathways bias cargoes toward ER exit.
256

257 We hypothesize that active ER retention plays a role in INM protein targeting. In interphase,
258 emerin is not entirely sequestered at the INM by the nuclear lamina; a pool of emerin protein
259 remains in the peripheral ER[23,24]. The intrinsic ability of emerin's TMD to traffic from the ER implies
260 that a limiting mechanism must exist to bias the protein toward diffusion to the INM. Emerin could

stably reside in the ER in part by binding to other ER-resident proteins. Interestingly, emerin was reported to interact with the ER tethering protein MOSPD3 via its YEESY (95-99) motif[25], which we previously found to limit trafficking[5]. While both TMDs traffic to the plasma membrane, full-length LAP2β-GFP is more retained in the NE/ER than EMD-GFP (Figure 3D, S3A-B), indicating that the N-terminal domains limit trafficking to different extents.

We identified the RXR motif as a shared negative regulator of TMD-dependent trafficking, prompting us to revise our original model: the exposure of this motif, not the absence of the LEM domain, prevents ER exit of EMD-GFP (Figure 2F-G). This suggests that the sequences around the RXR motif influence its activity by steric occlusion or other mechanisms. RXR motifs prevent the ER exit of some PM-resident proteins until they are masked by oligomerization, thus coupling ER exit to folding and/or assembly[13]. Like the canonical ER retrieval motif KKXX, RXR motifs are thought to engage COPI subunits to return escaped ER membrane proteins from the early Golgi[13,26]. Yeast-2-hybrid experiments predicted RXR signals to interact with the beta and delta subunits of the COPI coat[16], though the molecular details are still unclear. Contrary to KKXX motifs, found only on C-termini, RXR motifs may be on N-termini or within a poly-peptide chain[13]. Truncated, lumenally tagged variants of Sun2, another tail-anchored INM protein, require a poly-arginine motif to prevent mislocalization to the Golgi[27]. Turgay et al[27]. observed purified Sun2 RXR mutants losing interaction with COPI subunits in GST pull-down assays. In contrast, we did not observe loss of COPI binding in our RXR mutant immunoprecipitations. This discrepancy may be explained by differences in methods (purified recombinant protein binding assays vs. native IP), or by oligomerization of tagged emerin with endogenous emerin to indirectly bind COPI in lysate[28]. Emerin's interaction with the COPI coat was recently detected by proximity biotinylation in mouse P19 cells[29]. Interestingly, emerin was the only non-Golgi resident protein identified in the gamma-COP subunit interactome, indicating that endogenous emerin might be a COPI cargo. While we predict this interaction occurs via emerin's RXR motif, we cannot exclude the possibility of other COPI-interacting mechanisms.

Our previous work identified EMD as an unstable protein subject to significant lysosomal flux[5]. However, we have now discovered that emerin's trafficking is markedly promoted by C-terminal GFP tagging, likely influencing many of our initial observations. While we used C-terminal tags to avoid disrupting emerin's N-terminal interactions with chromatin and lamins, this approach inadvertently altered its localization. We did detect trafficking of N-terminally tagged emerin, but found that it occurs at a much lower rate. We conclude that hydrophobic tail-anchored

transmembrane domains are readily dislocated by C-terminal tags, and echo the warnings raised by generations of cell biologists regarding tag-induced localization artifacts[30–32]. We did not detect trafficking of the untagged emerin constructs. Nonetheless, because trafficking is detectable at or below endogenous levels with different tags and orientations, we cannot rule out the possibility that emerin traffics under specific conditions. We note poor correlation of emerin transcript and protein across tissues[33] (Figure S4E), which suggests protein-level regulation that may dynamically regulate emerin levels. While we still do not know whether emerin's ability to travel beyond the NE/ER influences its function, our experiments reveal an unanticipated connection between the topology and localization of INM proteins and raise new questions about the balance between secretion and retention of INM-destined proteins.

**Methods:**

**Cell culture and cell line generation:**

U2OS cells were obtained from the UCSF Cell and Genome Engineering Core and were cultured in McCoy's 5A medium supplemented with 10% FBS and penicillin/streptomycin. To generate EMD-GFP cell lines, U2OS were seeded into 6-well plates at a density of 300,000 cells per well. The next day, a transfection mix of 0.5 ug EMD-GFP donor plasmid, 0.25 ug PB200A-1 PiggyBac Transposase plasmid, 3.5 uL Lipofectamine 2000, and 300 uL Optimem was added to each well. After 24 hours, cells were split 1:2 and selected in 5 ug/mL blasticidin for 1 week, then maintained in 5 ug/mL blasticidin thereafter. Prior to an experiment, cells were split into media without blasticidin and induced with 1 ug/mL doxycycline for 24-48 hours. To generate FLAG-EMD cell lines, 2 ug CMV-FLAG-EMD plasmid was transfected without PiggyBac Transposase. Cells were selected with 400 ug/mL G418 for one week, then maintained in 200 ug/mL G418.

WTC-11 hiPSCs were obtained from the Berkeley Stem Cell Center. Cells were maintained on Matrigel-coated vessels in mTeSR+ without penicillin/streptomycin. Cells were passaged as clumps (using ReLeSR) for routine culture and as single cells (using Accutase) for counting and electroporating. Cells were plated in ROCK inhibitor Y-27632, then changed to fresh mTeSR+ after 24 hours. CRISPR editing was performed by electroporating 12.5 pmol pure Cas9-NLS and 12.5 pmol sgRNA into 1 million cells using a 100 uL Neon electroporator set to 1300 V, 30 ms, and 1 pulse. For DICE landing pad installation, we included 2 ug cassette-containing HDR template plasmid in the transfection mix. Landing pad cells were selected in 0.25 ug/mL puromycin for 3 days. Single clones were isolated by limiting dilution in 96 well plates, then expanded and genotyped for heterozygous insertion using primers spanning the AAVS1

329 homology arms. Emerin knockouts were generated from one landing pad clone using two sgRNAs
330 targeting the start and end of the coding sequence. Clones were genotyped by PCR to verify the
331 entire region was deleted, then by Western blot to confirm the loss of protein. To integrate emerin
332 constructs into the DICE landing pad, we electroporated 1 million cells with 2 ug attB-containing
333 donor plasmid and 500 ng BxbI-P2A-PhiC31 integrase plasmid. After letting cells recover, we
334 isolated landing pad BFP–/donor+ cells using a SONY SH800 cell sorter. Cells were checked for
335 mycoplasma every 3-4 months and were found to be negative.
336
337 **Plasmid cloning:**
338 All U2OS constructs except FLAG-EMD were expressed in the XLone all-in-one Tet-ON Piggybac
339 plasmid[34]. Mouse emerin sequences were cloned into XLone from plasmids used in our previous
340 study. Human emerin and LAP2β were amplified from Hek293T and WTC-11 cDNA using primers
341 with overhangs to XLone. Mouse cytochrome B5 was amplified from E14 mESC cDNA. cDNA
342 was synthesized using NEB MMLV reverse transcriptase. FLAG-EMD constructs were expressed
343 from the CMV promoter in a Neo/Kan resistant vector.
344

345 **Emerin constructs:**

| Designation | Gene | Species | Uniprot ID | Mutation |
|---|---|---|---|---|
| LAP2β RXR1 | LAP2β | Human | P42167 | 48-50 -> AAA |
| LAP2β APEX2-TMD | LAP2β | Human | P42167 | 1-280 -> APEX2 |
| hEMD RA | EMD | Human | P50402 | 44-47 -> AAAA |
| hEMD ΔLEM | | Human<br>Mouse | P50402<br>O08579 | D1-43 |
| hEMD ΔLEM<br>ΔQRRR | EMD | Human<br>Mouse | P50402<br>O08579 | D1-47 |
| hEMD Cyb5 TM | EMD | Human | P50402 (EMD)<br>P56395 (Cyb5) | EMD 1-224 + mouse cyb5a 95-134 |
| mEMD Cyb5 TM | EMD | Mouse | O08579 (EMD)<br>P56395 (Cyb5) | EMD 1-225 + mouse Cyb5a 95-134 |
| TMD-GFP | EMD | Mouse | O08579 | 212-259 |
| N-TMD$^{m}$ | EMD | Human | P50402 | W226A ,F232A, F235A |
| C-TMD$^{m}$ | EMD | Human | P50402 | F240A, F241A, Y243A |
| Full TMD$^{m}$ | EMD | Human | P50402 | W226A ,F232A, F235A, F240A, F241A, Y243A |

346

347 Small emerin mutations were generated using the NEB site-directed mutagenesis kit, while larger
348 fusions were assembled using the NEB HiFi Assembly kit.
349 The DICE landing pad cassette contained a PGK promoter driving HSV thymidine kinase-P2A-
350 TagBFP, all flanked by BxbI and PhiC31 attP sites. This cassette was built into an AAVS1 targeting
351 vector (a generous gift from Dr. Tom Nowakowski) containing a splice acceptor-P2A-puro. DICE
352 donor constructs contained Bxb1 and PhiC31 attB sites flanking the CAGGS promoter and an
353 mCherry-P2A-EMD.
354 Plasmids were prepped using the ZymoPURE II midiprep kit. All plasmids were verified by Sanger
355 or whole plasmid nanopore sequencing before transfection.
356

357 **Transmembrane domain hydrophobicity calculations:**
358 Transmembrane segments were obtained for EMD, LAP2β, STX3, and CYB5 from Uniprot
359 annotations. DG-ins was calculated using the DGprediction algorithm[35]. Median DG-transfer and

360 TM length values for secretory membranes were obtained from the human Membranome
361 database[14,36]. Data obtained from the Membranome database were plotted in GraphPad Prism.
362
363 **Surface labeling and flow cytometry:**
364 The surface staining assay was adapted from Welch et al[37]. Briefly, cells were washed with PBS,
365 lifted for 3-5 minutes with accutase, then quenched with cold complete media. Cells were
366 transferred to microfuge tubes and placed on ice for the duration of staining and washing. Cells
367 were pelleted 800g for 3 minutes at 4C, then washed once in 2% FBS/PBS. Cells were stained
368 in 80 uL anti-GFP 647 (1:20 in 2% FBS/PBS) or anti-rabbit IgG Alexa Fluor 647 secondary
369 antibody (1:200 in 2% FBS/PBS) as a negative control. The cells used for the anti-IgG controls
370 were WT EMD-GFP (for all EMD comparisons) or WT LAP2β-GFP (for LAP2β comparisons). After
371 staining for 30 minutes, cells were diluted with 200 uL 2% FBS/PBS, pelleted and washed twice
372 with 400 uL 2% FBS/PBS, and then optionally fixed in 4% PFA/PBS for 10 minutes at room
373 temperature. Fixed cells were washed twice and then stored at 4C until being resuspended in
374 PBS and strained into round bottom FACS tubes before analysis.
375
376 For flow analysis of antibody-stained proteins, cells were lifted with accutase, washed with PBS,
377 and fixed by rotating in 4% PFA/PBS for 10 minutes. After washing twice in PBS, cells were
378 permeabilized in IF buffer (0.1% Tx100, 0.02% SDS, 10 mg/ml BSA in PBS) for 30 minutes before
379 incubating in primary antibody solution for 1-2 hours at room temperature. Cells were washed
380 three times in IF buffer, incubated with fluorescent secondary antibodies for 1 hour, and then
381 washed three more times before being strained into FACS tubes.
382
383 Cells were analyzed on a BD FACSVerse or a ThermoFisher Attune NxT. At least 50,000 cells
384 were analyzed per sample. Flow cytometry data were analyzed in FlowJo. Surface antibody:GFP
385 ratio was obtained using the “derive parameters” function and applied to the GFP+ populations.
386 Histograms are normalized to the mode of each sample for visualization.
387
388 **Immunofluorescence microscopy:**
389 Cells were seeded in Ibidi culture chambers (Matrigel-coated for hiPSCs) prior to an IF
390 experiment. For lysosome colocalization analysis, cells were treated with 100 nM bafilomycin A1
391 for 16-18 hours. Cells were washed in PBS, then fixed in 4% paraformaldehyde in PBS for 5
392 minutes at room temperature. For LAMP1 staining, cells were permeabilized in 0.1%
393 digitonin/PBS at 4 C for 10 minutes, then blocked in 2% FBS/PBS. LAMP1 antibody was diluted

394 1:200 in 2% FBS/PBS. For emerin and FLAG immunostaining, fixed cells were permeabilized in
395 IF buffer for 30 minutes, then incubated in primary antibodies (diluted 1:250 and 1:1000 in IF
396 buffer, respectively) for 1 hour at room temperature. After washing, cells were incubated with
397 Alexa-Fluor-conjugated secondary antibodies and Hoechst 33342 (both 1:1000) for 30 minutes
398 at room temperature. Emerin/FLAG staining is incompatible with LAMP1 staining because of
399 differential permeabilization requirements. In these cases, we had to rely on the formation of
400 EMD+ puncta after bafilomycin treatment to infer lysosome localization.
401
402 Selective permeabilization and ERES co-localization temperature blocks were performed as
403 previously described[38]. For selective permeabilization topology analysis, U2OS cells were
404 induced with doxycycline for 24 hours, washed with cold PBS, and incubated with cold 0.0025%
405 digitonin/PBS or PBS only for 5 minutes at 4C. Cells were then fixed with 4% PFA for 5 minutes
406 at RT. To permeabilize all endomembranes, cells were incubated with IF buffer (0.1% Tx100,
407 0.02% SDS, 10 mg/ml BSA in PBS for 30 minutes, then stained with anti-EMD and anti-GFP
408 antibodies diluted in 2% FBS/PBS.
409
410 For ERES co-localization, EMD-GFP U2OS cells were were induced with doxycycline for 4
411 hours or left uninduced to analyze newly synthesized or endogenous emerin, respectively. Cells
412 were then placed on a metal platform submerged in a 10C water bath or continued incubation at
413 37C for 2 hours, then fixed and stained for endogenous emerin and Sec31a to mark ERES.
414 Images were acquired using a Nikon CSU-X1 spinning disk confocal microscope with 40x/1.3
415 NA or 60x/1.4 NA oil objectives. 20-30 Z-slices were imaged per cell with a step size of 0.3
416 microns. 16-bit images were saved as ND2 files using the Nikon Elements 5.02 build 1266
417 software. Representative slices were selected and cropped in FIJI. Pearson correlation was
418 calculated using the FIJI PSC colocalization plugin.
419
420 **Protein stability measurement and Western blotting:**
421 For doxycycline washout experiments, 300,000 U2OS cells were seeded in 12 well plates with 2
422 ug/mL doxycycline. After 48 hours, half the wells were washed twice with PBS and incubated in
423 fresh medium without doxycycline for 18 hours. Cells were washed twice with PBS and lysed in
424 the wells by scraping in 80 uL RIPA buffer (50mM Tris, 150mM NaCl, 1% TritonX-100, 0.5%
425 deoxycholate, 0.1% SDS) plus protease inhibitors and benzonase. Lysates were spun 17,000g
426 at 4C for 10 minutes, then supernatants were mixed with sample buffer and boiled for 10

427 minutes. 12 uL of each sample was loaded onto homemade 10% SDS-PAGE gels, then
428 transferred onto nitrocellulose membranes. Blots were incubated at 4C overnight in primary
429 antibody diluted with 5% milk/TBST, then washed and incubated in HRP-conjugated secondary
430 antibodies for 1 hour at room temperature. Blots were developed using Pierce ECL Western
431 blotting substrate and imaged using the GelDoc imaging system. Band intensity was quantified
432 in Fiji.
433
434 **FLAG-EMD immunoprecipitation and mass spectrometry**
435 FLAG-EMD, FLAG-RA, and parental U2OS (non-expressing negative control) cells were grown
436 to confluence in 3 10cm plates per cell line, then harvested by scraping and transferring to a
437 microfuge tube. Cells were pelleted and lysed in 1 mL lysis buffer (50 mM Tris-HCl pH 7.4, 150
438 mM NaCl, 0.3% TritonX-100, 1 mM DTT, 2 mM EDTA, 5 mM MgCl2, 1x protease inhibitor cocktail,
439 1x PhosSTOP, benzonase), then incubated for 30 minutes end over end at 4C. Lysates were
440 probe sonicated in 6 rounds of 10 second pulses at 20% power, then spun 17,000g at 4C for 25
441 minutes. The supernatant was added to 40 uL FLAG M2 magnetic beads which had been
442 calibrated in 500 uL lysis buffer and separated on a magnetic stand. Samples were incubated end
443 over end at room temperature for 1 hour, then magnetically separated and washed 3 times with
444 1 mL wash buffer (100 mM HEPES-KOH pH 7.5, 100 mM KCl, 5% glycerol, 0.1% NP-40, protease
445 inhibitors). After the final wash, the supernatant was discarded and the beads were resuspended
446 in 200 uL elution buffer (100 ug/mL 3x FLAG peptide in wash buffer) and eluted for 1 hour at room
447 temperature. Eluates were precipitated with 4 volumes ice cold acetone overnight at -20C, spun
448 at max speed for 5 minutes, then air dried. Pellets were processed for mass spectrometry using
449 a PreOmics iST kit according to manufacturer's instructions.
450
451 **Mass spectrometry and analysis**
452 A nanoElute was attached in line to a timsTOF Pro equipped with a CaptiveSpray Source
453 (Bruker, Hamburg, Germany). Chromatography was conducted at 40°C through a 25 cm
454 reversed-phase C18 column (PepSep) at a constant flowrate of 0.5 µL $min^{-1}$. Mobile phase A
455 was 98/2/0.1% water/MeCN/formic acid (v/v/v) and phase B was MeCN with 0.1% formic acid
456 (v/v). During a 108 min method, peptides were separated by a 3-step linear gradient (5% to 30%
457 B over 90 min, 30% to 35% B over 10 min, 35% to 95% B over 4 min) followed by a 4 min
458 isocratic flush at 95% for 4 min before washing and a return to low organic conditions.
459 Experiments were run as data-dependent acquisitions with ion mobility activated in PASEF
460 mode. MS and MS/MS spectra were collected with $m/z$ 100 to 1700 and ions with $z$ = +1 were

excluded. Raw data files are available on the Mass Spectrometry Interactive Virtual Environment (MassIVE), a full member of the Proteome Xchange consortium under the identifier: MSV000096858.

Raw data files were searched using PEAKS Online Xpro 1.6 (Bioinformatics Solutions Inc., Waterloo, Ontario, Canada). The precursor mass error tolerance and fragment mass error tolerance were set to 20 ppm and 0.03 respectively. The trypsin digest mode was set to semi-specific and missed cleavages was set to 2. The human Swiss-Prot reviewed (canonical) database (downloaded from UniProt) totaling 20,385 entries or a custom database using human and mouse emerin (downloaded from uniprot, EMD_human P50402, EMD_mouse O08579) was used. Carbamidomethylation (C) was selected as a fixed modification. Oxidation (M) was selected as a variable modification.

Resulting datasets were subjected to the following filtration criteria: (1) Database search ($-10\log(p\text{-value}) \geq 20$, 1% peptide and protein FDR). (2) Identified proteins with less than 3% coverage, 3 unique peptides, or spectral areas less than 5000 were discarded. (4) Spectral counts for each protein were normalized to corresponding counts from the negative control IP, and then to the protein length. (5) The ratio of normalized counts to the mouse emerin bait was plotted to obtain relative co-immunoprecipitation efficiency.

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584

*Figure 1*

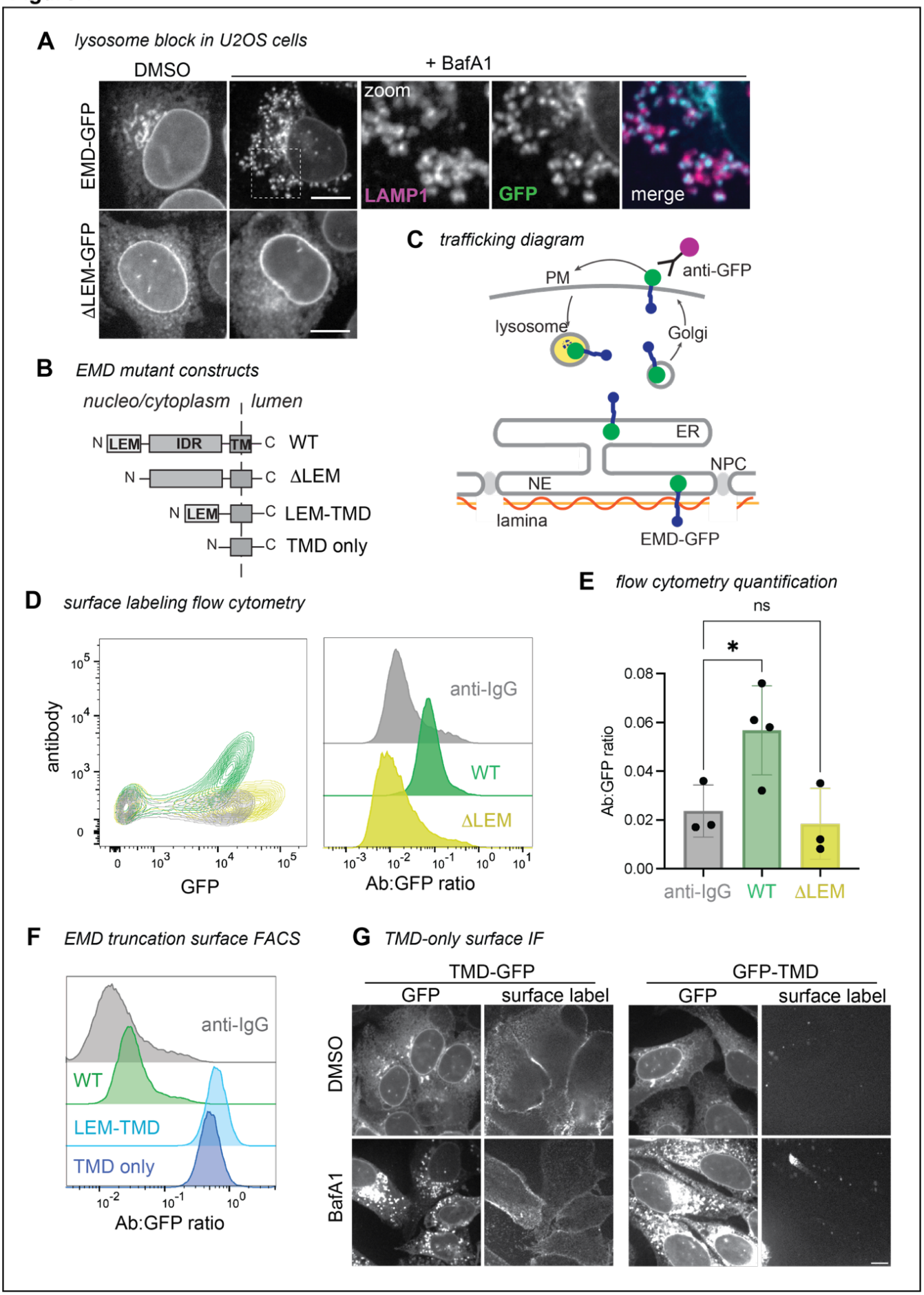

A
lysosome block in U2OS cells
DMSO
+ BafA1
EMD-GFP
ΔLEM-GFP
zoom
LAMP1
GFP
merge
B
EMD mutant constructs
nucleo/cytoplasm
lumen
N LEM IDR TM C WT
N C ΔLEM
N LEM C LEM-TMD
N C TMD only
C
trafficking diagram
PM
anti-GFP
lysosome
Golgi
ER
NPC
NE
lamina
EMD-GFP
D
surface labeling flow cytometry
antibody
GFP
anti-IgG
WT
ΔLEM
Ab:GFP ratio
E
flow cytometry quantification
ns
*
Ab:GFP ratio
anti-IgG
WT
ΔLEM
F
EMD truncation surface FACS
anti-IgG
WT
LEM-TMD
TMD only
Ab:GFP ratio
G
TMD-only surface IF
TMD-GFP
GFP-TMD
GFP
surface label
DMSO
BafA1

**Figure 1. EMD ΔLEM does not traffic in U2OS cells, while the TMD alone does.**

**A)** U2OS cells expressing mouse EMD-GFP and ΔLEM-GFP were induced with 1 ug/mL doxycycline for 24 hours, treated with 100nM lysosome blocking agent Bafilomycin A1 (BafA1) overnight, and fixed and stained for lysosome marker Lamp1. Scale bar, 10 um.

**B)** Summary of EMD domains and truncation mutants.

**C)** EMD enriches at the INM by binding to the nuclear lamina, or exits the ER into the secretory pathway. Before reaching the lysosome, EMD transiently accesses the cell surface where lumenal GFP is exposed to anti-GFP antibody.

**D)** Example FACS plot of mouse WT vs ΔLEM surface labeling; fluorescent anti-IgG secondary antibody included as background control. Antibody signal is divided by total GFP+ signal to yield histograms on the right.

**E)** Quantification of the antibody:GFP ratio from 4 independent experiments, with error bars representing SD. * indicates adjusted P-value = 0.0451 by one-way ANOVA with Šídák's multiple comparisons test.

**F)** U2OS cells expressing mouse TMD-GFP (lumenal tag) or GFP-TMD (cytosolic tag) were treated overnight with BafA1, then fixed and stained with an anti-GFP antibody.

**G)** Example surface labeling FACS histogram of U2OS cells expressing WT, LEM-TMD-GFP, or TMD-GFP.

## Figure 2

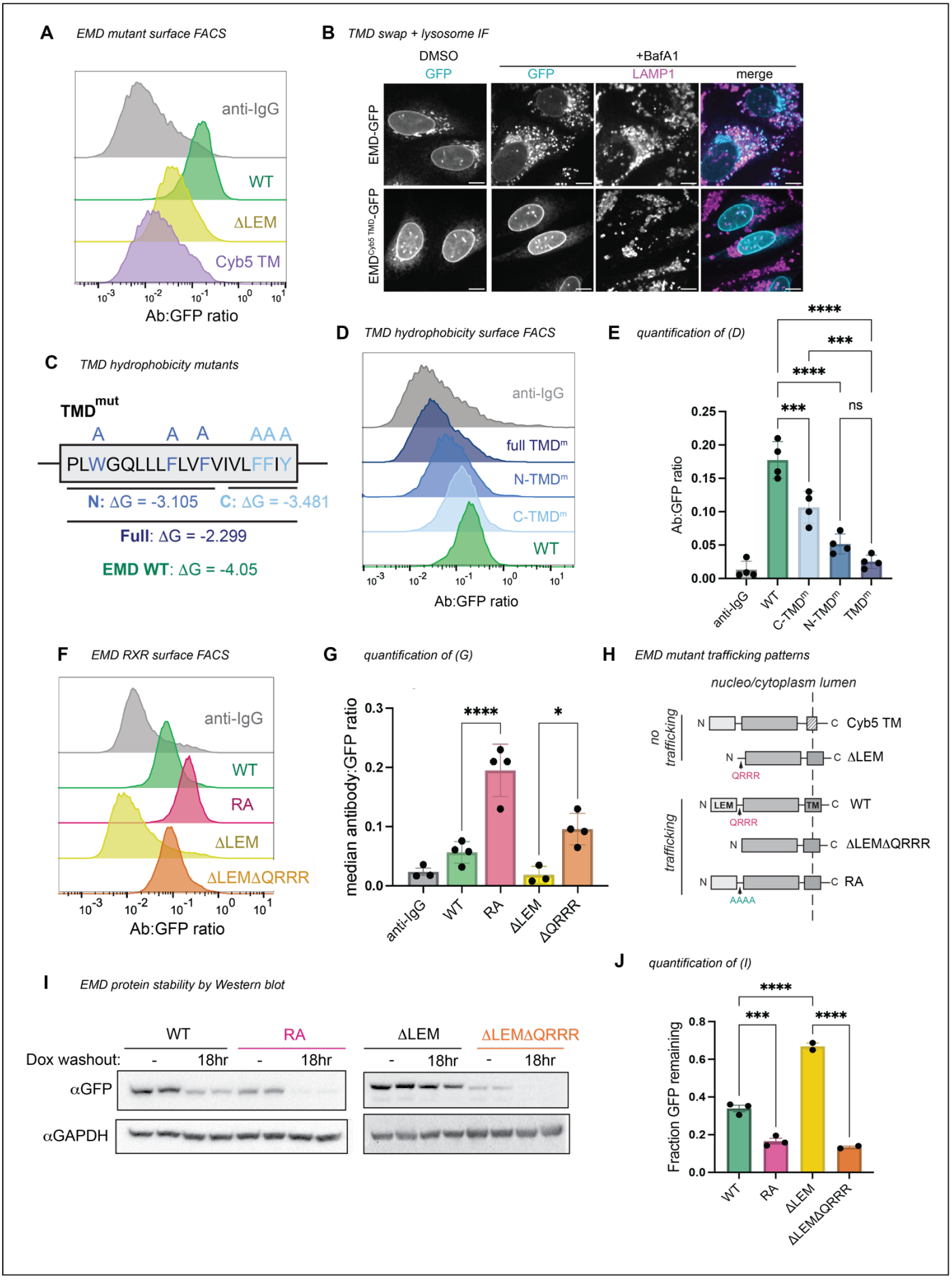

A
EMD mutant surface FACS
anti-IgG
WT
ΔLEM
Cyb5 TM
Ab:GFP ratio
B
TMD swap + lysosome IF
DMSO
+BafA1
GFP
GFP
LAMP1
merge
EMD-GFP
EMDCyb5 TMD-GFP
C
TMD hydrophobicity mutants
TMDmut
A A A AAA
PLWGQLLLFLVFVIVLFFIY
N: ΔG = -3.105
C: ΔG = -3.481
Full: ΔG = -2.299
EMD WT: ΔG = -4.05
D
TMD hydrophobicity surface FACS
anti-IgG
full TMDm
N-TMDm
C-TMDm
WT
Ab:GFP ratio
E
quantification of (D)
Ab:GFP ratio
anti-IgG
WT
C-TMDm
N-TMDm
TMDm
ns
F
EMD RXR surface FACS
anti-IgG
WT
RA
ΔLEM
ΔLEMΔQRRR
Ab:GFP ratio
G
quantification of (G)
median antibody:GFP ratio
anti-IgG
WT
RA
ΔLEM
ΔQRRR
H
EMD mutant trafficking patterns
nucleo/cytoplasm lumen
no trafficking
trafficking
Cyb5 TM
ΔLEM
QRRR
LEM
TM
WT
ΔLEMΔQRRR
RA
AAAA
I
EMD protein stability by Western blot
WT
RA
ΔLEM
ΔLEMΔQRRR
Dox washout:
18hr
αGFP
αGAPDH
J
quantification of (I)
Fraction GFP remaining
WT
RA
ΔLEM
ΔLEMΔQRRR

**Figure 2. Emerin's trafficking depends on its TMD, not on the LEM domain.**

**A)** Surface anti-GFP antibody:GFP histogram of human WT EMD, ΔLEM, and EMD with mouse cytochrome B5 TMD ($EMD^{Cyb5\ TMD}$) chimera.

**B)** U2OS cells expressing mouse EMD-GFP and $EMD^{Cyb5\ TMD}$-GFP were induced with 1 ug/mL doxycycline for 24 hours, treated with 100nM lysosome blocking drug bafilomycin A1 (BafA1) overnight, and fixed and stained for lysosome marker Lamp1. Scale bars, 10 um.

**C)** TMD mutation strategy. The TM alpha helix of human EMD was divided into N-terminal and C-terminal halves, and the aromatic residues in each half were mutated to alanine to generate mutants with similar ΔG-insertion values. For the full TMD mutant, all aromatic residues were mutated to alanine, yielding a predicted ΔG-insertion of -2.299.

**D)** Surface antibody:GFP FACS histogram and **E)** quantification of the mutants diagramed in (C). *N* = 4 independent experiments

**F)** Surface antibody:GFP FACS histogram and **G)** quantification of mouse WT EMD, RA, ΔLEM, and ΔLEMΔQRRR truncation surface expression. *N* = 4 independent experiments.

**H)** Summary of emerin constructs that do or do not traffic.

**I)** Western blot analysis of emerin constructs induced with 2 ug/mL doxycycline for 48 hours, then washed and incubated for an 18 hour chase.

**J)** Quantification of Western blot band intensity from (I). GFP antibody signal after washout was divided by the respective unwashed condition to yield the fraction GFP remaining after doxycycline washout across 3 independent replicates.

For all panels: *** indicates adjusted P-value <0.0005, * indicates P = 0.0104. All P-values were obtained by one-way ANOVA with Šídák's or Tukey's multiple comparisons tests.

*Figure 2 supplement*

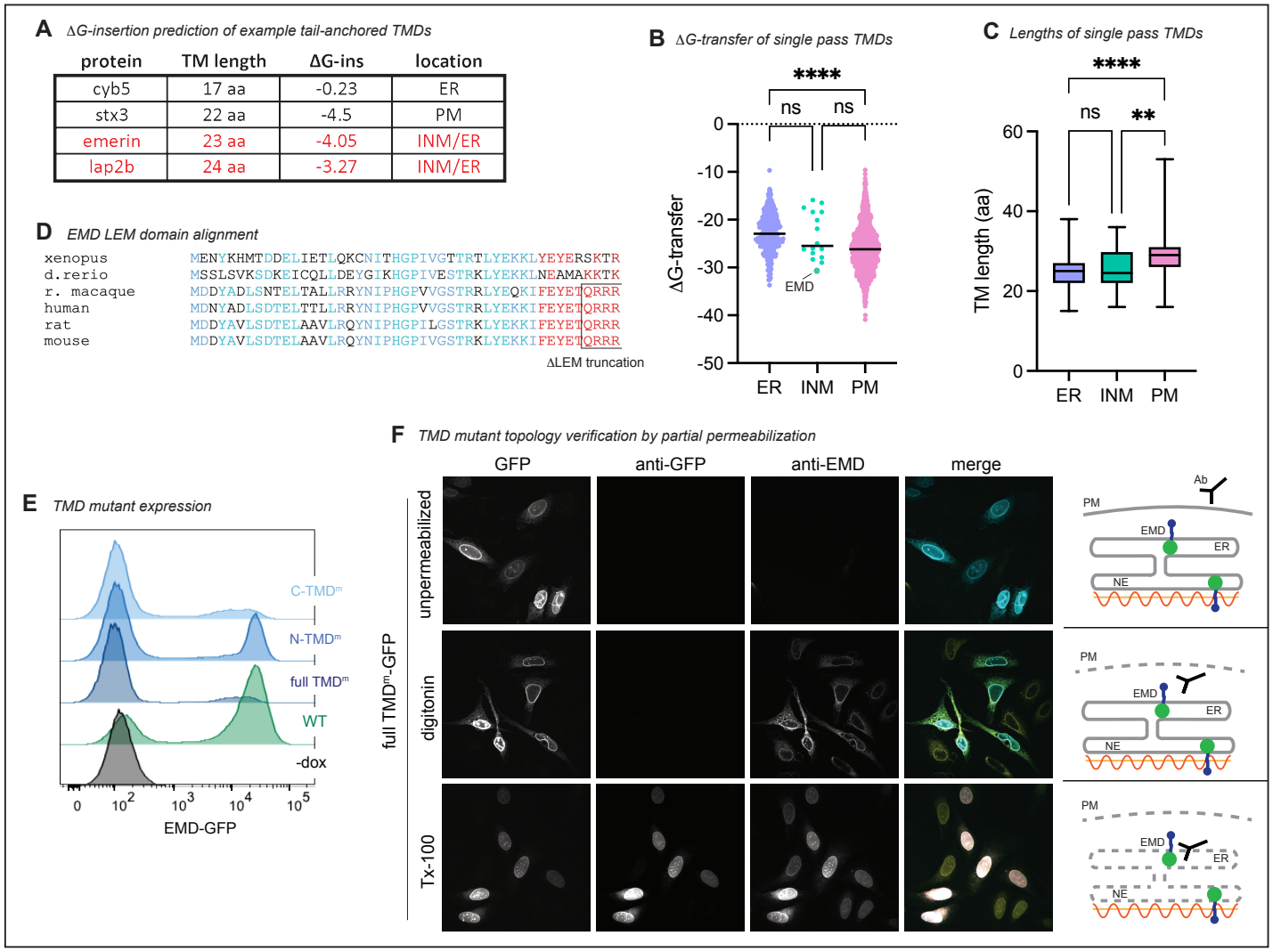



**Figure 2 supplement: A)** Lengths and predicted ΔG-insertion values of ER protein cytochrome B5, PM protein syntaxin 3, and emerin INM proteins emerin and Lap2β.
**B)** Single pass human transmembrane proteins from Membranome database plotted by free energy of transfer into a lipid bilayer. Lines represent median; **** indicates P < 0.0001 by one-way Anova with Tukey's multiple comparisons test.
**C)** Transmembrane domain length (by amino acid count) of the proteins in (B). ** indicates P = 0.0028; **** indicates P < 0.0001.
**D)** Protein sequence alignment of emerin's LEM domain across species. Conserved LEM domain amino acid class indicated in blue. QRRR motif is conserved in mammals and is exposed in the ΔLEM construct.
**E)** FACS plots of WT EMD-GFP and TMD mutant expression upon dox induction. Fewer cells express C-TMD$^m$ and full TMD$^m$, though topology of constructs that are expressed is not altered (see (F).
**F)** Antibody accessibility upon differential permeabilization of U2OS cells expressing full TMD$^m$. Cells were incubated with digitonin to permeabilize the plasma membrane, TritonX-100 to permeabilize all internal membranes, or left unpermeabilized, then stained with antibodies against emerin (cytosolic epitope) and GFP (lumenal epitope).

## Figure 3

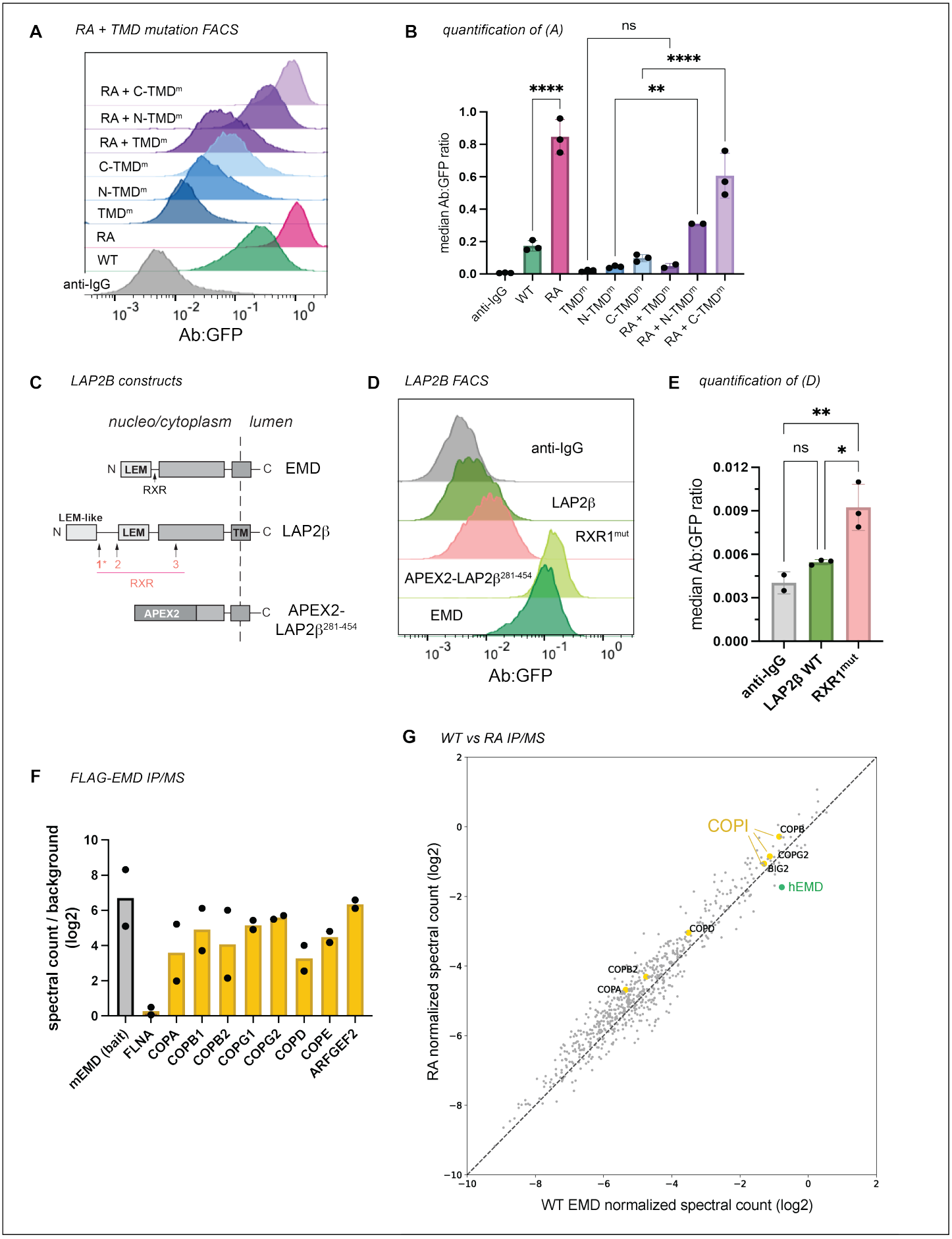

A
RA + TMD mutation FACS
RA + C-TMDm
RA + N-TMDm
RA + TMDm
C-TMDm
N-TMDm
TMDm
RA
WT
anti-IgG
Ab:GFP
B
quantification of (A)
ns
****
****
**
median Ab:GFP ratio
anti-IgG
WT
RA
TMDm
N-TMDm
C-TMDm
RA + TMDm
RA + N-TMDm
RA + C-TMDm
C
LAP2B constructs
nucleo/cytoplasm
lumen
N
LEM
RXR
C
EMD
LEM-like
LAP2β
TM
1*
2
3
APEX2
APEX2-LAP2β281-454
D
LAP2B FACS
anti-IgG
LAP2β
RXR1mut
APEX2-LAP2β281-454
EMD
Ab:GFP
E
quantification of (D)
**
ns
*
median Ab:GFP ratio
anti-IgG
LAP2β WT
RXR1mut
F
FLAG-EMD IP/MS
spectral count / background (log2)
mEMD (bait)
FLNA
COPA
COPB1
COPB2
COPG1
COPG2
COPD
COPE
ARFGEF2
G
WT vs RA IP/MS
COPI
COPB
COPG2
BIG2
hEMD
COPD
COPB2
COPA
RA normalized spectral count (log2)
WT EMD normalized spectral count (log2)

**Figure 3. RXR motif limits TMD-dependent trafficking of emerin and LAP2β without influencing COPI binding.**
**A)** Surface anti-GFP:GFP histogram and **B)** quantification of indicated RA + TMD mutant combinations. ** indicates P = 0.0021. *N* = 3 independent experiments.
**C)** Diagram of LAP2β domain structure and position of RXR motifs. APEX2 fusion contains no RXR motifs.
**D)** Antibody:GFP histogram and **E)** quantification of the highest 25% GFP-expressing cells diagramed in (C). RXR$^{mut}$ : LAP2β RXR1 mutated to AAA. * indicates P = 0.0173; ** indicates P = 0.0072
**F)** Spectral counts of COPI proteins immunoprecipitated by WT FLAG-EMD normalized to negative control IP. Spectral counts of the mouse EMD bait and common contaminant filamin A (FLNA) plotted for comparison. *N* = 2 independent experiments.
**G)** Spectral counts of proteins immunoprecipitated by FLAG-WT and FLAG-RA mouse EMD normalized to each respective bait. Dotted line represents equal co-immunoprecipitation with the two constructs. COPI proteins and endogenous human EMD highlighted in yellow and green, respectively.
All P-values were obtained by one-way ANOVA with Šídák's or Tukey's multiple comparisons tests.

***Figure 3 supplement***

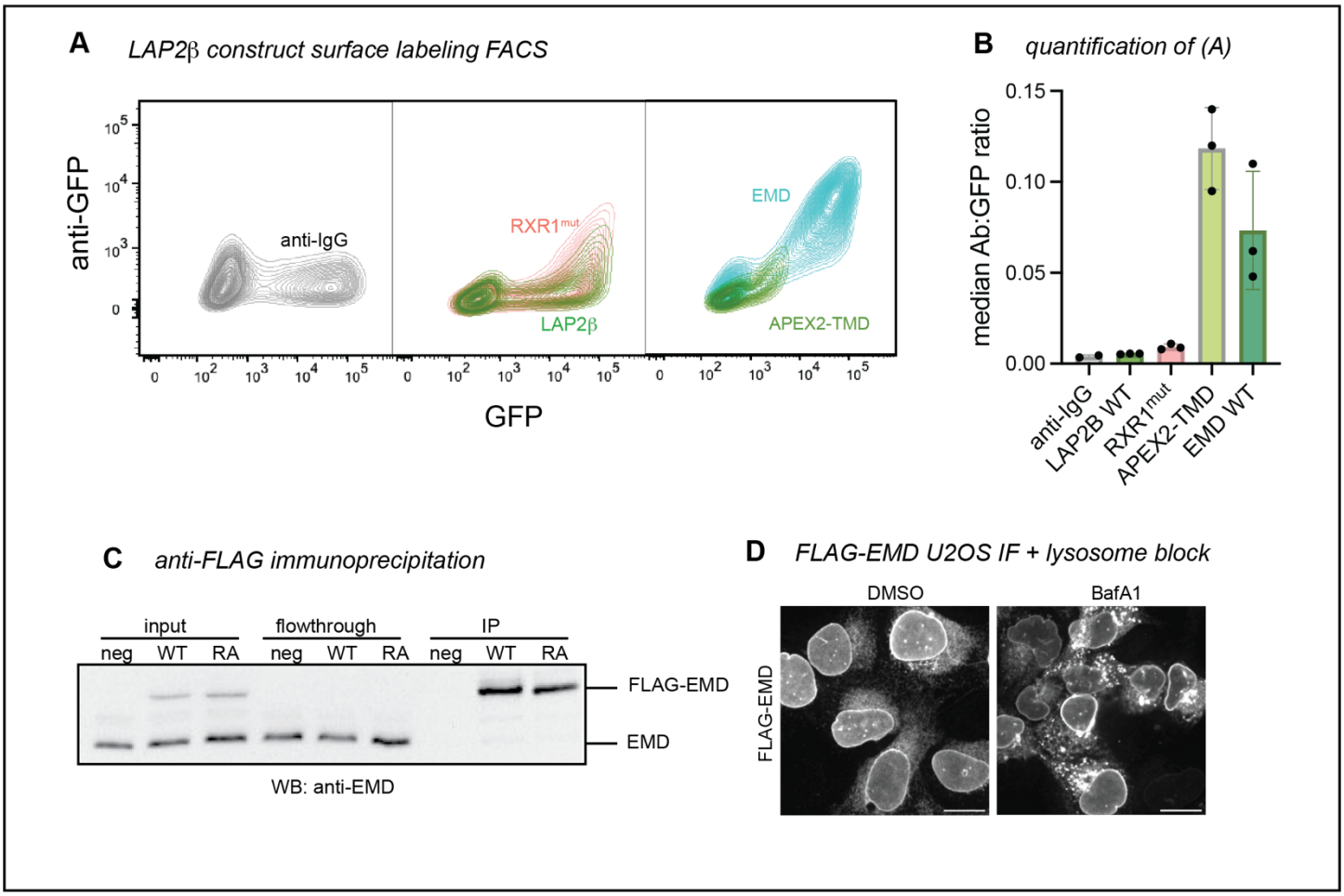
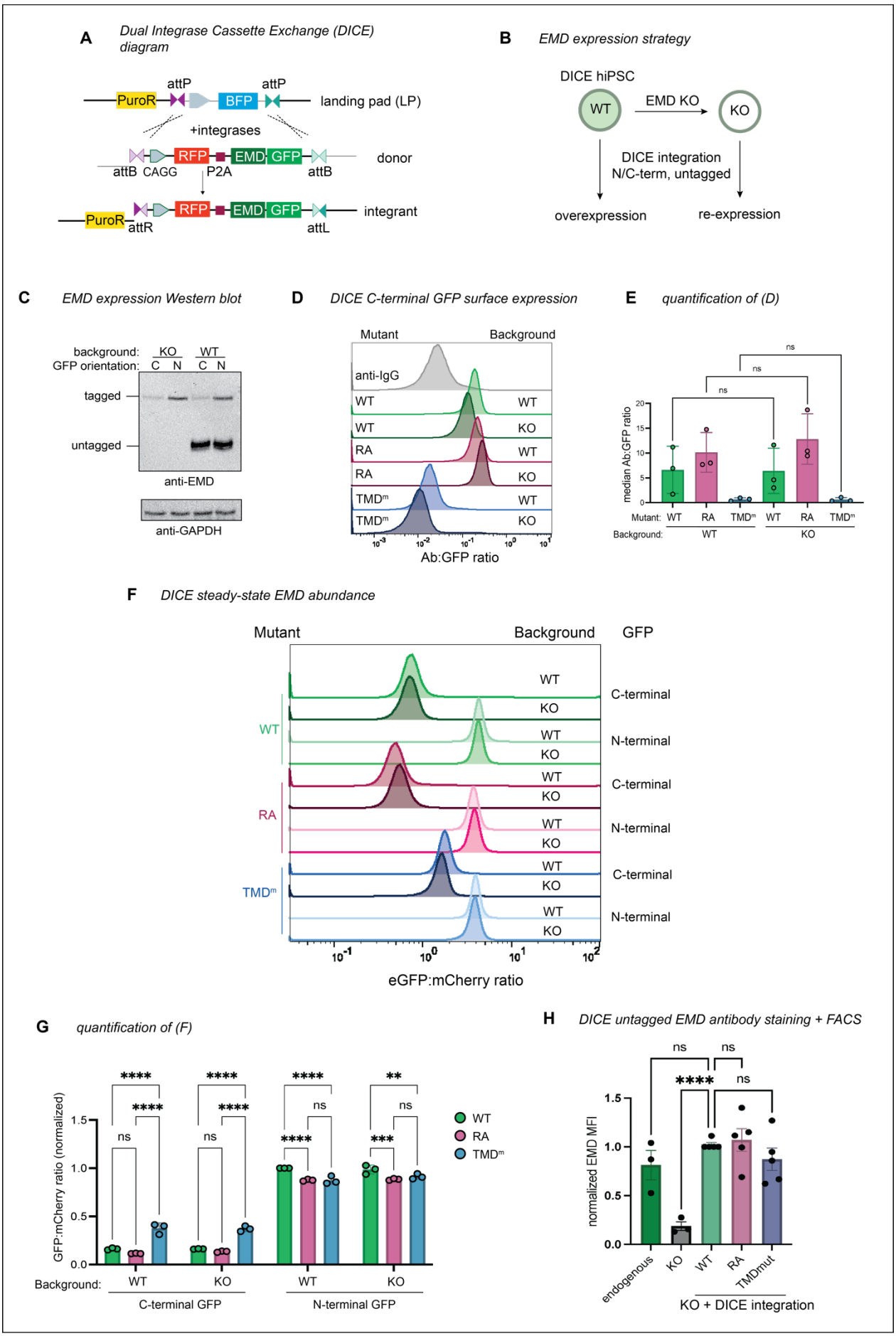



**Figure 3 supplement: A)** GFP versus surface anti-GFP FACS plots of negative control anti-IgG, WT LAP2β / RXR1mut, and WT EMD / LAP2β APEX2-TMD.
**B)** Median anti-GFP antibody:GFP ratio of the highest 25% GFP-expressing cells in (A).
**C)** Western blot analysis of anti-FLAG immunoprecipitations. U2OS cells expressing no FLAG construct (neg), FLAG-WT mouse EMD, and FLAG-RA mutant were lysed and incubated with anti-FLAG magnetic beads. Equal volume equivalents were separated by SDS-PAGE and blotted with an anti-EMD antibody to visualize tagged and untagged EMD.
**D)** U2OS cells expressing FLAG-EMD were incubated with lysosome blocker bafilomycin A1 (BafA1) overnight, then fixed and permeabilized with 0.1% Triton-X-100, 0.02% SDS, 10 mg/ml BSA in PBS. Cells were stained with anti-FLAG antibody to visualize relocalization during BafA1 treatment. Scale bars, 20 um.

## Figure 4

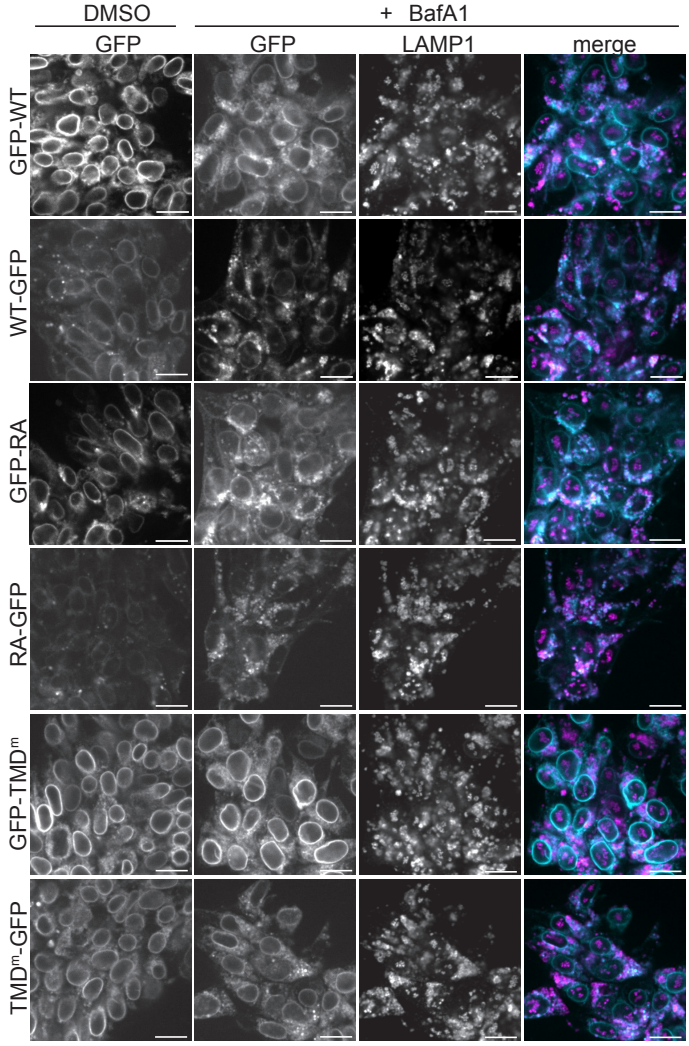


A
Dual Integrase Cassette Exchange (DICE) diagram
attP
attP
PuroR
BFP
landing pad (LP)
+integrases
RFP
EMD
GFP
donor
attB
CAGG
P2A
attB
PuroR
RFP
EMD
GFP
integrant
attR
attL
B
EMD expression strategy
DICE hiPSC
WT
EMD KO
KO
DICE integration
N/C-term, untagged
overexpression
re-expression
C
EMD expression Western blot
background:
KO
WT
GFP orientation:
C N
C N
tagged
untagged
anti-EMD
anti-GAPDH
D
DICE C-terminal GFP surface expression
Mutant
Background
anti-IgG
WT
WT
WT
KO
RA
WT
RA
KO
TMDm
WT
TMDm
KO
Ab:GFP ratio
E
quantification of (D)
ns
ns
ns
median Ab:GFP ratio
Mutant:
WT
RA
TMDm
WT
RA
TMDm
Background:
WT
KO
F
DICE steady-state EMD abundance
Mutant
Background
GFP
WT
KO
C-terminal
WT
KO
N-terminal
WT
KO
C-terminal
RA
WT
KO
N-terminal
WT
KO
C-terminal
TMDm
WT
KO
N-terminal
eGFP:mCherry ratio
G
quantification of (F)
GFP:mCherry ratio (normalized)
****
****
****
****
****
**
ns
ns
ns
ns
****
***
WT
RA
TMDm
Background:
WT
KO
WT
KO
C-terminal GFP
N-terminal GFP
H
DICE untagged EMD antibody staining + FACS
ns
ns
****
ns
normalized EMD MFI
endogenous
KO
WT
RA
TMDmut
KO + DICE integration

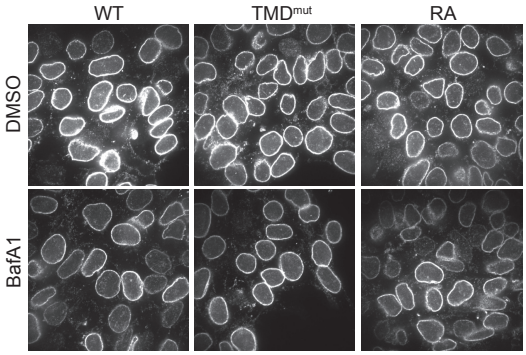
**Figure 4. Safe harbor expression reveals that C-terminal GFP destabilizes emerin**. **A)** Diagram of emerin integration into the AAVS1 locus. Landing pad BFP is exchanged for mCherry-P2A-emerin +/- GFP via Bxb1 and PhiC31 integrases. Integrases irreversibly recombine landing pad attP and donor attB sites into attR and attL sites.
**B)** Strategy to compare overexpressed emerin to knockout (KO) rescue.
**C)** Western blot analysis WT and EMD KO DICE hiPSCs expressing N- and C-terminally GFP-tagged emerin. Untagged endogenous EMD and GFP-tagged EMD are detected by the same anti-EMD antibody.
**D)** Anti-GFP surface labeling histogram and **E)** quantification of C-terminally tagged emerin integrants from (B-C). Statistical significance was determined using one-way ANOVA with Šídák's multiple comparisons test. *N* = 3 independent experiments.
**F)** FACS plot and **G)** quantification of steady state GFP abundance. Data were normalized to the GFP-EMD signal in the EMD WT background. *N* = 3 independent experiments. ** indicates P = 0.0079 by two-way ANOVA with Tukey's multiple comparisons test.
**H)** DICE landing pad WT, EMD KO, and KO re-integrated with untagged constructs were lifted, fixed, and stained with anti-EMD antibody. Fluorescence was quantified by flow cytometry and normalized to the WT DICE integrant. MFI, median fluorescence intensity of antibody signal. *N* = 5 replicates over 4 independent experiments. **** indicates P <0.0001 by mixed effects analysis.

## *Figure 4 supplement*

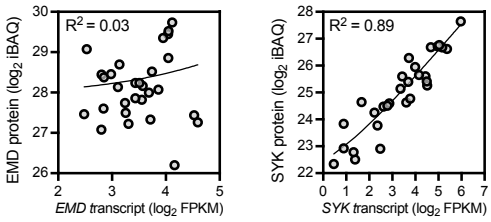
**A** *GFP-tagged EMD in KO background + lysosome IF*



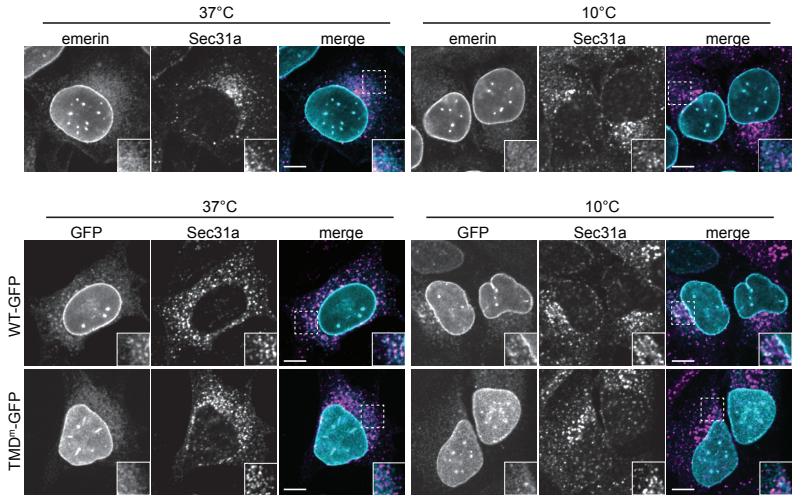

**D** *untagged EMD in KO background*




**E** *EMD transcript vs protein abundance*




**B** *ERES colocalization with temperature block*




**C** *quantification of (B)*

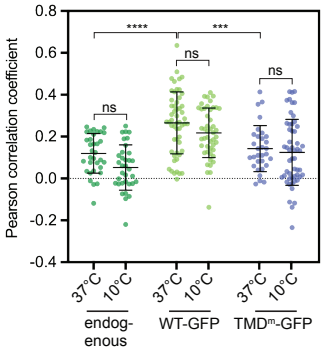


**Figure 4 supplement: A)** EMD KO DICE hiPSCs were integrated with GFP-tagged EMD constructs. Cells were treated with vehicle or lysosome blocker bafilomycin A1 (BafA1) overnight, then fixed and stained with anti-LAMP1 antibody.
**B)** U2OS cells expressing indicated constructs were induced with doxycycline for 4 hours (bottom panels) or left uninduced (top panels). Cells were then shifted to 10C or continued incubation at 37C for 2 hours. Cells were then fixed and stained for endogenous emerin (top panel) and Sec31a to mark ERES.
**C)** Pearson correlation coefficient was calculated between endogenous emerin or EMD-GFP and Sec31a. *N* = 31-54 cells over 3 independent experiments. *** indicates P = 0.0006 by one-way ANOVA with Tukey's multiple comparisons test.
**D)** EMD KO DICE hiPSCs were integrated with untagged EMD WT, TMD mutant, or RA mutant. Cells were treated overnight with BafA1, then fixed and stained with anti-EMD antibody. Scale bars, 20 um.
**E)** We mined a dataset of matched RNAseq and quantitative protein abundances across 29 human tissues to evaluate EMD transcript and protein abundances. EMD protein and transcript abundance are largely uncorrelated (R2 ~ 0), while, for comparison, the enzyme spleen tyrosine kinase (SYK) has well-correlated protein and RNA levels (R2 = 0.89)