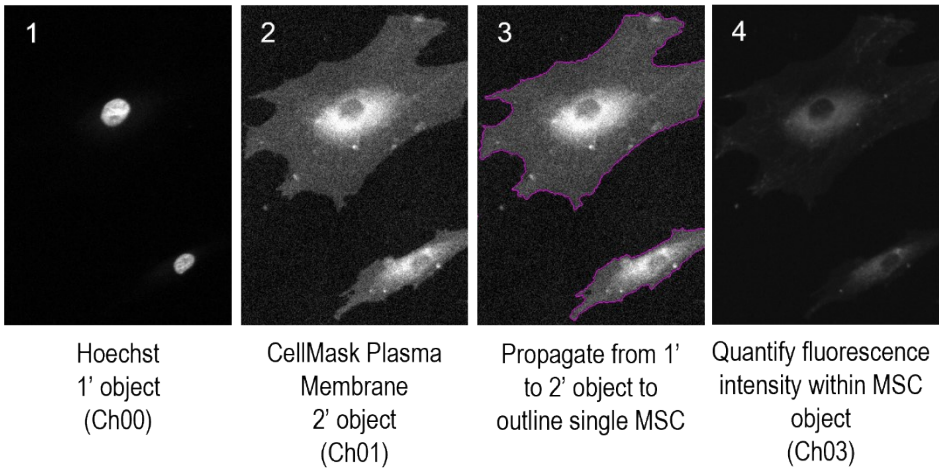
Electronic Supplementary Material (ESI) for Nanoscale.

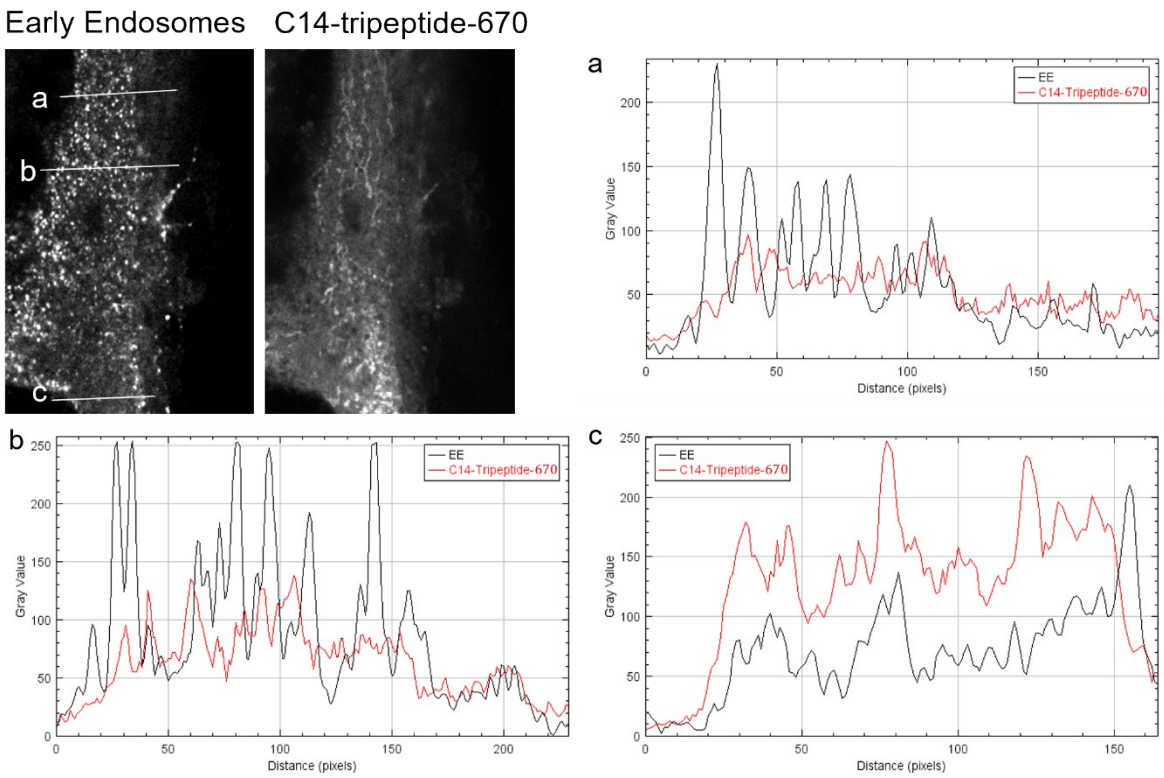
Supporting Information

CellProfiler pipeline:

https://drive.google.com/file/d/1SfiC-a2UbvkdfxMQDKkuOiK7IKoXtyMK/view?usp=sharing



S 1. Image analysis methodology. Representative images of each image processing step performed by CellProfiler. Images 1 (Hoechst, Ch00) and 2 (CellMask PlasmaMembrane, Ch01) were pre-processed in ImageJ to remove fluorescent background. Image 4 (C14-tripeptide-670, Ch03) was pre-processed with flatfield correction. In CellProfiler, Image 1 was used to segment primary objects (nuclei), then Image 2 was used to segment secondary objects (total cell) by global propagation from primary objects to the cell border (Image 3). The fluorescent intensity in Image 4 (Ch03) was quantified within the primary, secondary, and tertiary (secondary subtract primary i.e., cytoplasm) objects.



S 2. C14-tripeptide-670 does not co-localise with early endosomes. Representative intensity (gray value) line plots of CellLights Early Endosomes (Black) and C14-tripeptide-670 (Red) fluorescence micrographs at three locations across the MSC cytoplasm (lines a,b,c).