

Supporting Information for

Genetically Encoded Aryl Alkyne for Raman Spectral Imaging of Intracellular α -
Synuclein Fibrils

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Table S1. Raman F_{CC} peak positions for **Figure 4**

Figure S1. Raman spectra for F_{CC} in water/DMSO mixture shown in **Figure 2**

Figure S2. Fingerprint region of the Raman spectra for proteins shown in **Figure 4**

Figure S3. Corresponding wide-field fluorescence image of **Figure 5**.

Figure S4. z-Step scans showing cellular internalization of F_{CC} fibrils.

Figure S5. Corresponding Raman spectra for **Figure 7**.

Figure S6. Additional Raman maps collected for internalized Y39F_{CC} fibrils.

Table S1. Raman shifts[‡] of the F_{CC} alkyne stretching band in α -syn constructs in the soluble and aggregated states shown in **Fig. 4**.

Protein	Soluble ν_{max} (cm ⁻¹)	Fibrillar ν_{max} (cm ⁻¹)	$\Delta\nu_{max}$ (cm ⁻¹)
F4F _{CC}	2109.6	2108.9	-0.7
Y39F _{CC}	2109.3	2107.8	-1.5
F94F _{CC}	2108.9	2105.9	-3.0
Y125F _{CC}	2108.7	2107.7	-1.0

[‡] Raman shifts were determined by fitting the alkyne stretching band to a Lorentzian function, which was found to have an accuracy of ± 1 cm⁻¹.

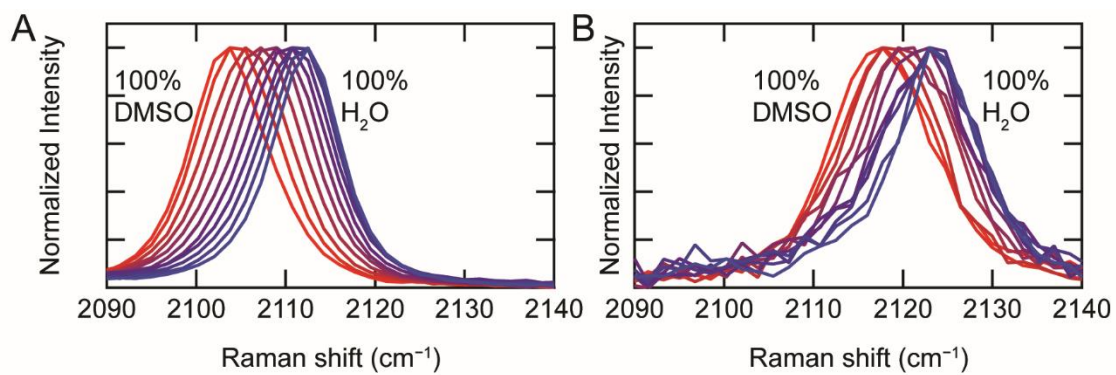


Figure S1. $C\equiv C$ stretching bands of 10 mM (A) FCC and (B) HPG in solvent mixtures from 100% DMSO (red) to 100% phosphate buffer (20 mM sodium phosphate, 100 mM NaCl, pH 7.4, blue).

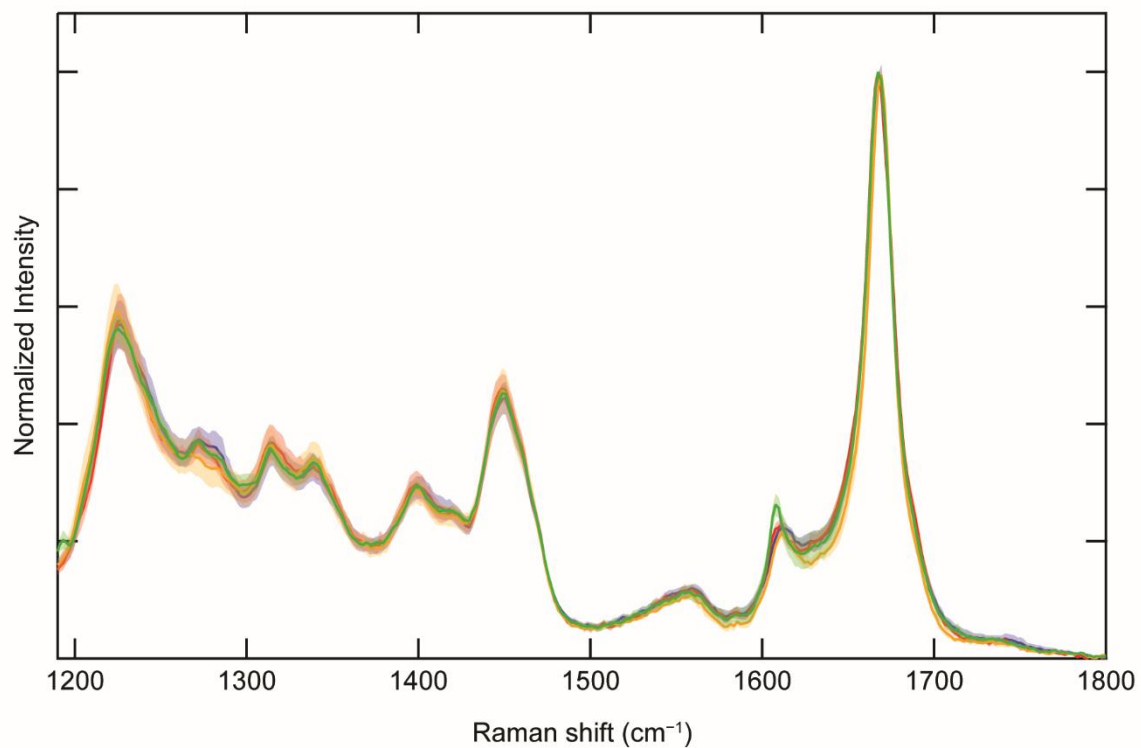


Figure S2. Fingerprint region from the Raman spectra of fibrillar F4F_{CC} (blue), Y39F_{CC} (green), F94F_{CC} (orange), and Y125F_{CC} (red). Solid lines represent averages across multiple aggregates with shaded areas indicating the standard deviation ($n = 8$).

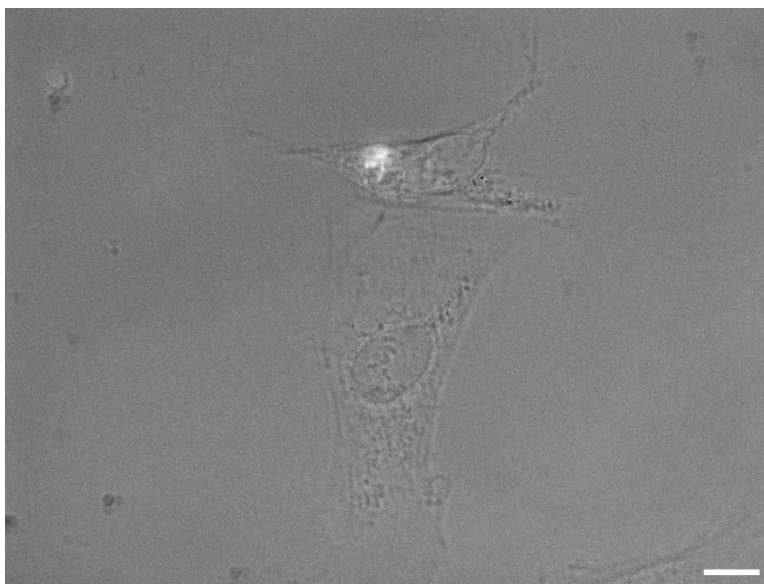


Figure S3. Combined bright-field and wide-field fluorescence image of the cell shown in **Figure 5**. The fluorescence signal represents ThT emission from internalized FCC fibrils.

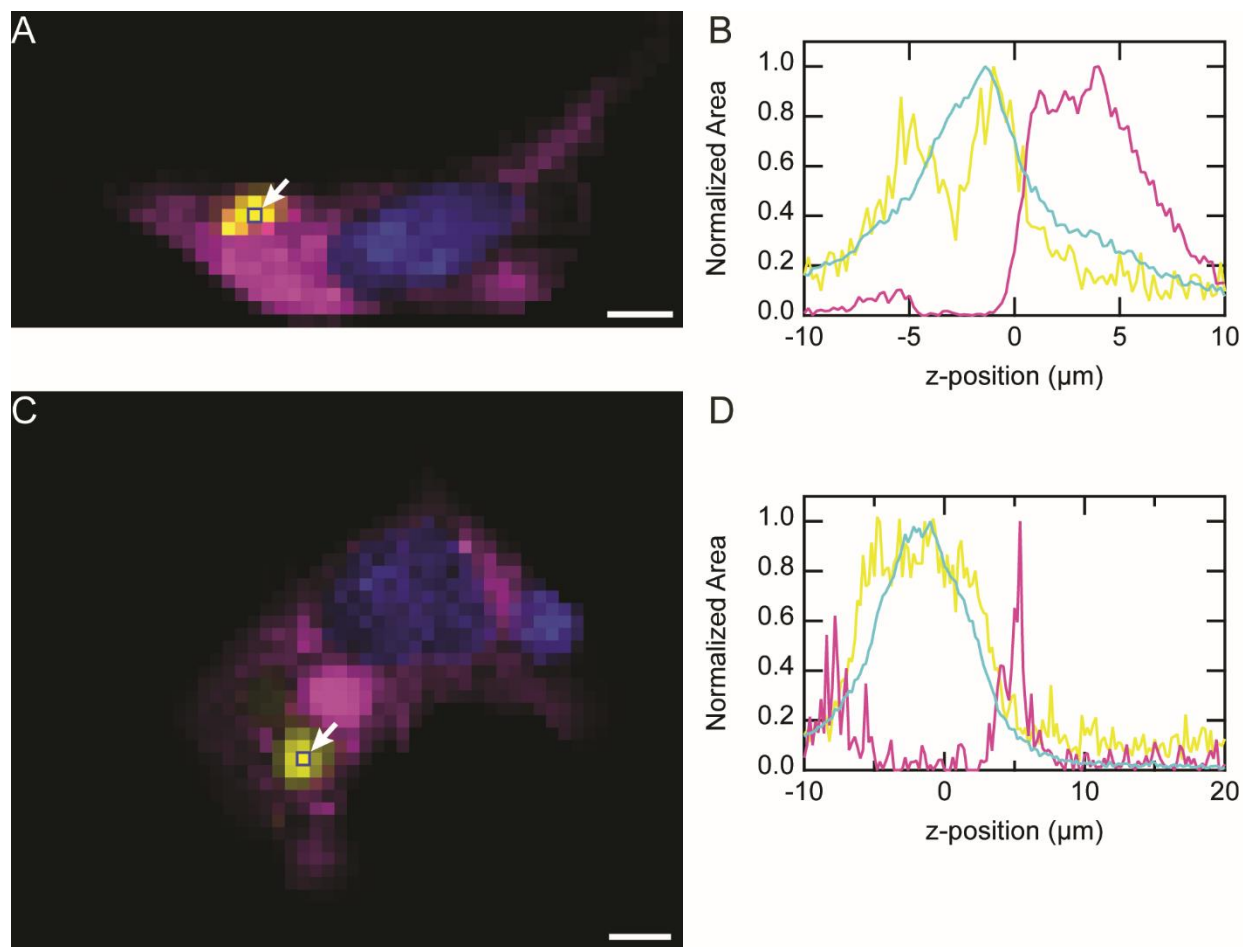


Figure S4. Fibril clusters are fully internalized within SH-SY5Y cells. **(A, C)** Raman maps of lipids (magenta, methylene C–H stretching band $2825\text{--}2860\text{ cm}^{-1}$), nucleotides (blue, nucleotide ring breathing mode $1557\text{--}1587\text{ cm}^{-1}$), and F94F_{CC} fibrils (yellow, $\text{C}\equiv\text{C}$ stretching band $2090\text{--}2130\text{ cm}^{-1}$). Scale bars are $5\text{ }\mu\text{m}$. **(B, D)** z-Position scans recorded at the fibril clusters marked in **(A)** and **(C)** at a single location (blue squares indicated by white arrows) showing lipids (magenta, $2825\text{--}2860\text{ cm}^{-1}$), proteins (cyan, $2900\text{--}2950\text{ cm}^{-1}$), and F94F_{CC} fibrils (yellow, $2090\text{--}2130\text{ cm}^{-1}$). Data were collected with 1-s accumulation at each z-position with $0.2\text{ }\mu\text{m}$ steps. The cell in **(A)** is the same cell shown in **Figure 5**.

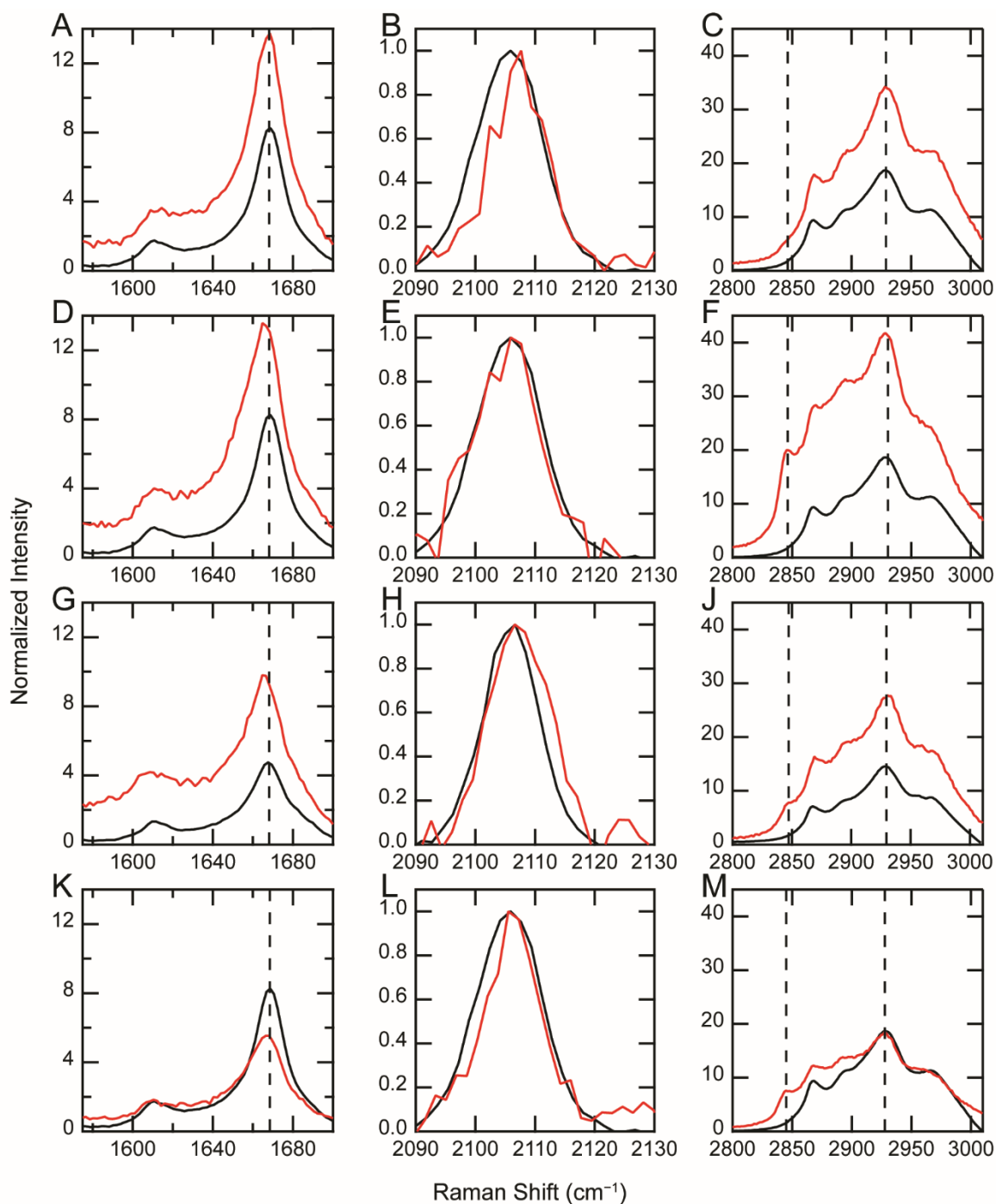


Figure S5. Raman spectra from the individual pixels (blue boxes) as indicated in the corresponding panels in **Figure 7 A, D, G, and K**. Amide-I (**A, D, G, K**), C≡C stretching (**B, E, H, L**), and C–H stretching (**C, F, J, M**) regions are shown as red curves. The *in vitro* fibril spectrum is also shown as a reference (black curves) in each panel. Dashed lines serve as guides for comparison.

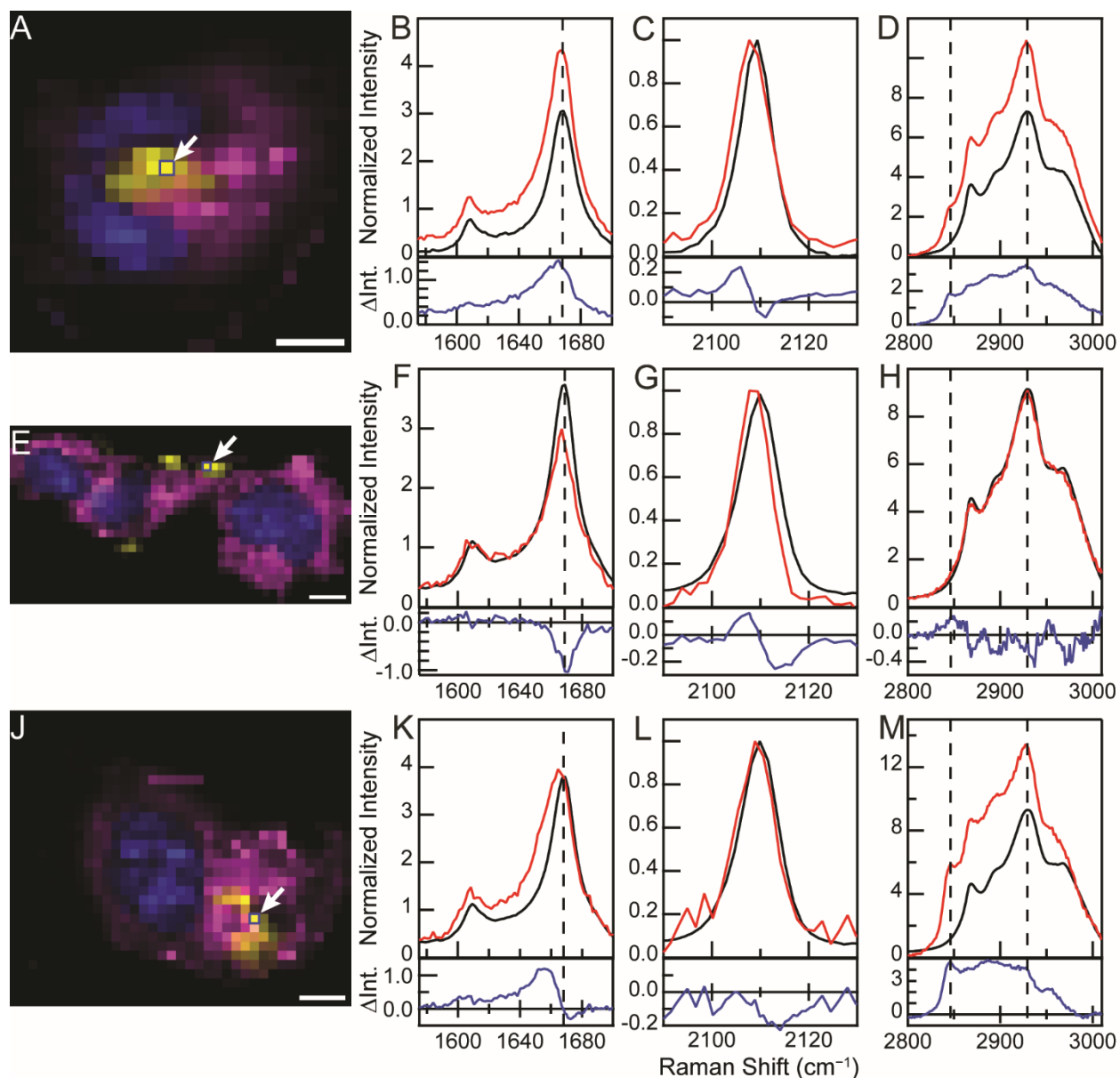


Figure S6. Cellular treatments with Y39F_{CC} fibrils. (A, E, J) Raman maps of lipids (magenta, methylene C–H stretching band 2825–2860 cm⁻¹), nucleotides (blue, nucleotide ring breathing mode 1557–1587 cm⁻¹), and Y39F_{CC} fibrils (yellow, C≡C stretching band 2090–2130 cm⁻¹). Scale bars are 5 μm. Raman spectra (red) of the amide-I (B, F, K), C≡C stretching (C, G, L), and C–H stretching regions (D, H, M) collected from the individual pixels in (A, E, and J, blue boxes indicated by white arrows) are shown. Raman spectra collected for *in vitro* Y39F_{CC} fibrils are also shown for comparison (black) with the difference spectra (cell–*in vitro* fibril, blue) shown below. Data are normalized to the intensity of the C≡C stretching band. Dashed lines are shown as guides for comparison.