

## Supplemental Data

# A new ultrasensitive bioluminescence-based method for assaying Monoacylglycerol lipase

Matteo Miceli<sup>a</sup>, Silvana Casati<sup>a</sup>, Pietro Allevi<sup>b</sup>, Silvia Berra<sup>a</sup>, Bruce R. Branchini<sup>c</sup>, Roberta Ottria<sup>a</sup>, Paola Rota<sup>b</sup>, and Pierangela Ciuffreda<sup>a\*</sup>

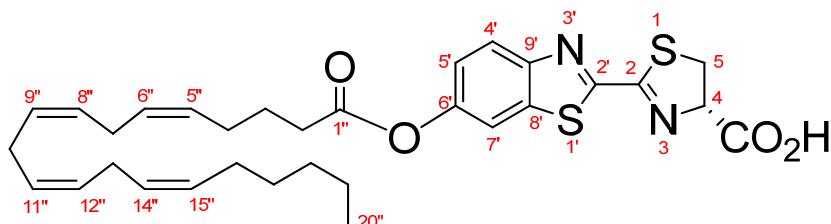
- a. *Dipartimento di Scienze Biomediche e Cliniche “Luigi Sacco”, Università degli Studi di Milano, Via G.B. Grassi 74, 20157 Milano, Italy.*
- b. *Dipartimento di Scienze Biomediche, Chirurgiche e Odontoiatriche, Dipartimento di Scienze Biomediche, Università degli Studi di Milano, Via della Commenda 10, 20122 Milano, Italy.*
- c. *Department of Chemistry, Connecticut College, New London, CT 06320, United States*

## <sup>1</sup>H and <sup>13</sup>C-NMR data

### Instruments

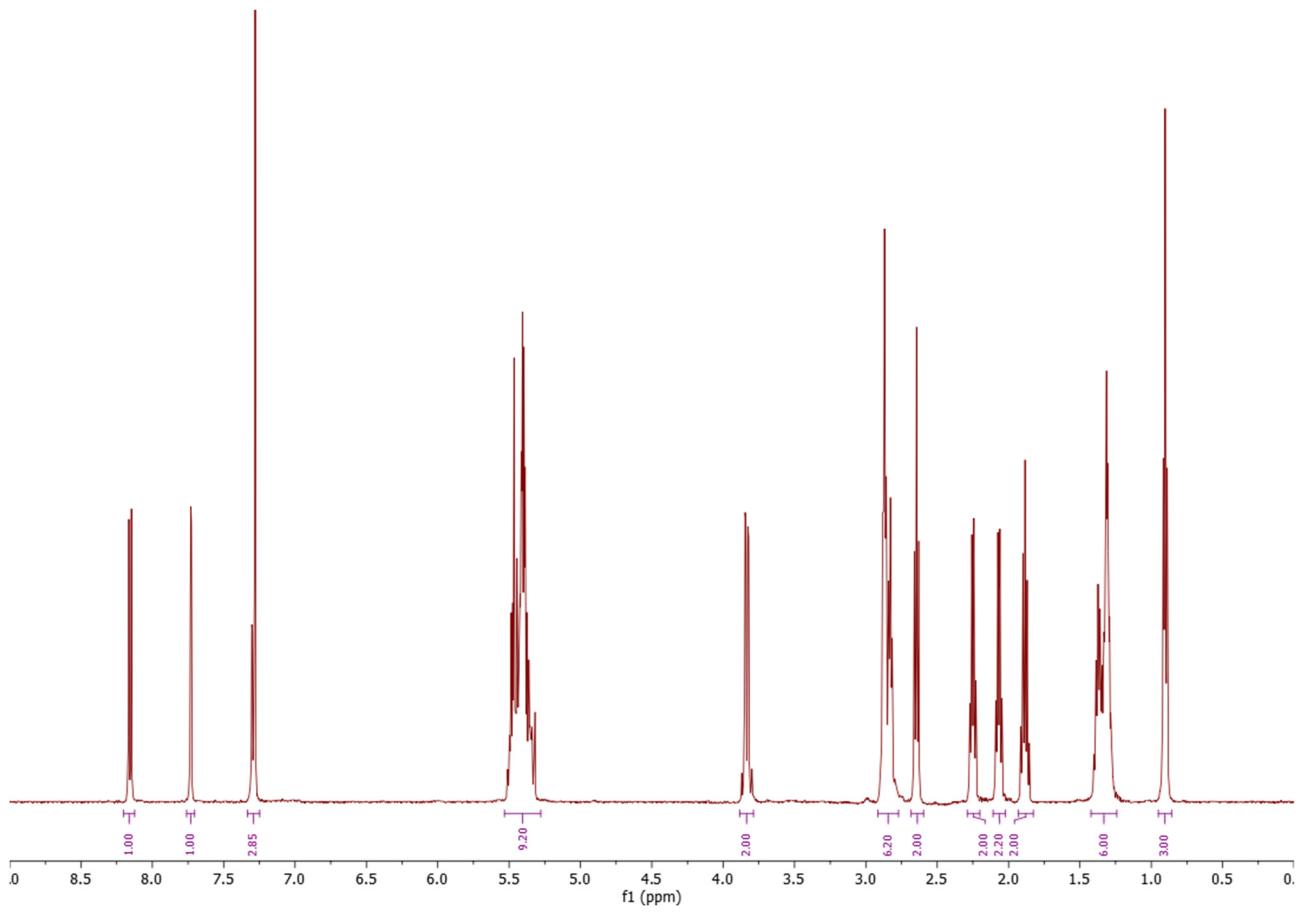
<sup>1</sup>H-NMR spectra were recorded in CDCl<sub>3</sub> (isotopic enrichment 99.95%) solutions at 300 K using a Bruker AVANCE 500 instrument (500.13 MHz for <sup>1</sup>H, 125.76 MHz for <sup>13</sup>C) using 5 mm inverse detection broadband probes and deuterium lock. Chemical shifts (*d*) are given as parts per million relative to the residual solvent peak (7.26 ppm for <sup>1</sup>H and 77.0, central line, for <sup>13</sup>C) and coupling constants (*J*) are in Hertz. The experimental error in the measured <sup>1</sup>H-<sup>1</sup>H coupling constants is  $\pm 0.5$  Hz. The splitting pattern abbreviations are as follows: s, singlet; d, doublet; t, triplet; q, quartet; m, multiplet, and bs, broad peak. For two-dimensional experiments, Bruker microprograms using gradient selection (gs) were applied. Acquisition parameters for 1D were as follows: <sup>1</sup>H spectral width of 5000 Hz and 32 K data points providing a digital resolution of ca. 0.305 Hz per point, relaxation delay 2 s; <sup>13</sup>C spectral width of 29412 Hz and 64 K data points providing a digital resolution of ca. 0.898 Hz per point, relaxation delay 2.5 s.

For two-dimensional experiments, standard Bruker microprograms using gradient selection (gs) were applied. COSY-45 experiments were acquired with 512 t1 increments; 2048 t2 points; spectral/spectrum width 10.0 ppm. The acquisition data for HSQC and HMBC experiments were obtained with 512 t1 increments; 2048 t2 points; spectral/spectrum width 10.0 ppm for <sup>1</sup>H and 220 ppm for <sup>13</sup>C. Delay values were optimized for <sup>1</sup>J<sub>C,H</sub> 140.0 Hz and <sup>1</sup>J<sub>C,H</sub> 3.0 Hz. Zero filling in F1 to 1 K,  $\pi/2$  shifted sine-bell squared (for gHSQC) or sinebell (for gHMBC) apodization functions were used for processing.

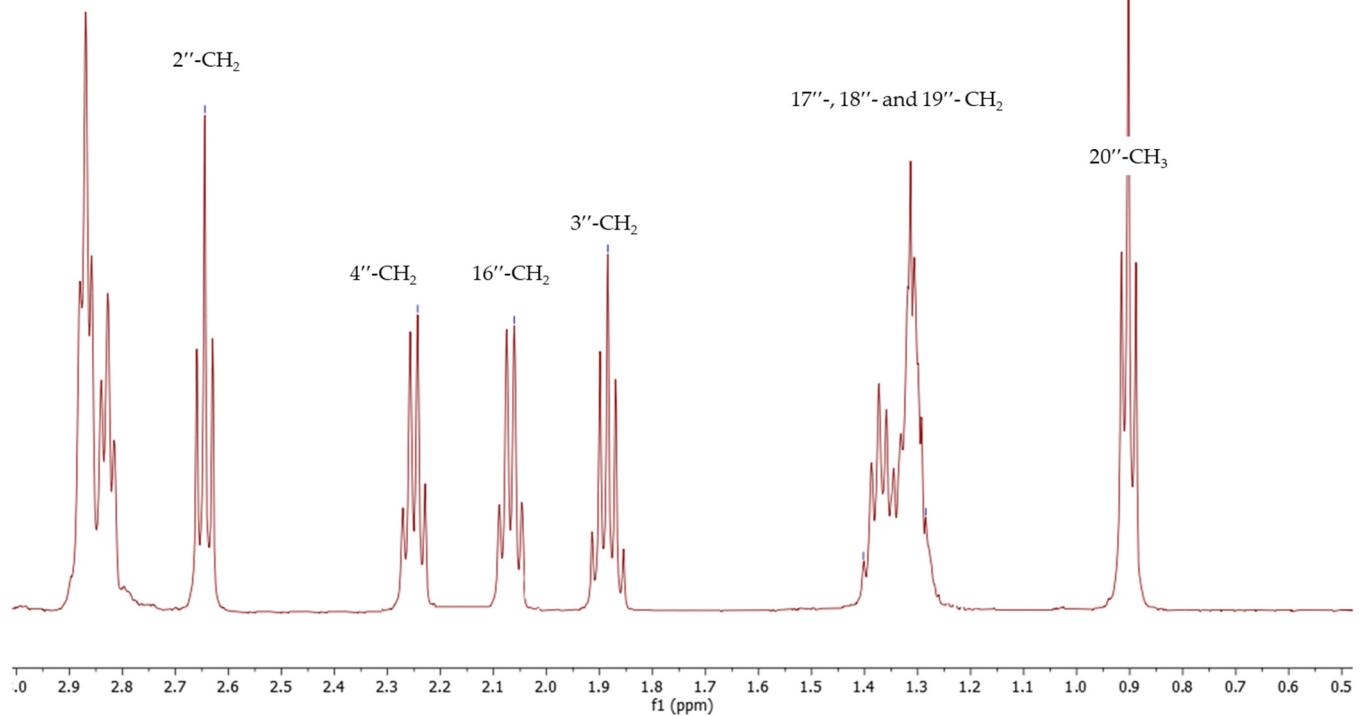


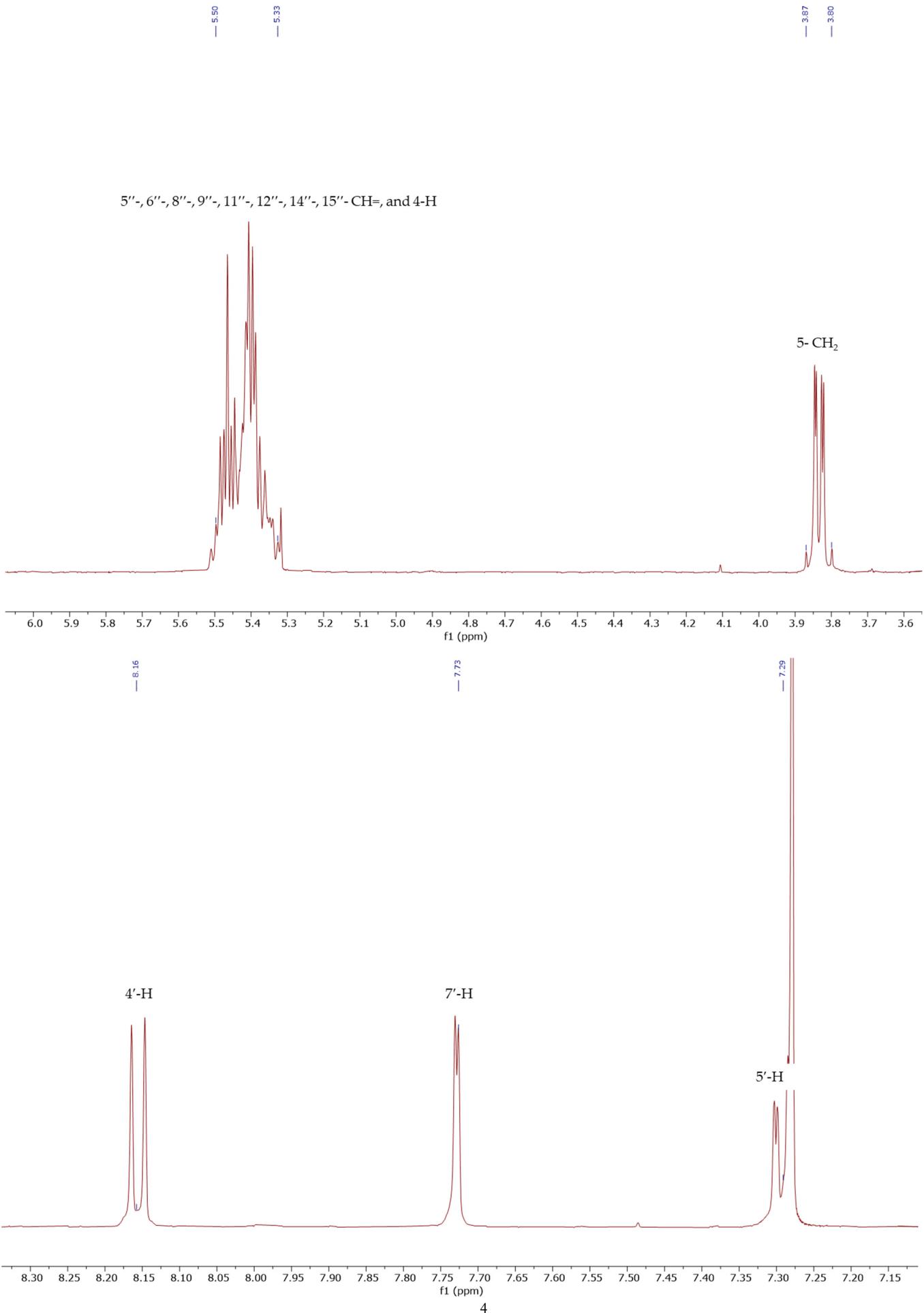
**Figure S1.** IUPAC numbering of 6-O-arachidonoylluciferin (**1**)

<sup>1</sup>H spectrum of 6-O-arachidonoylluciferin (**1**)



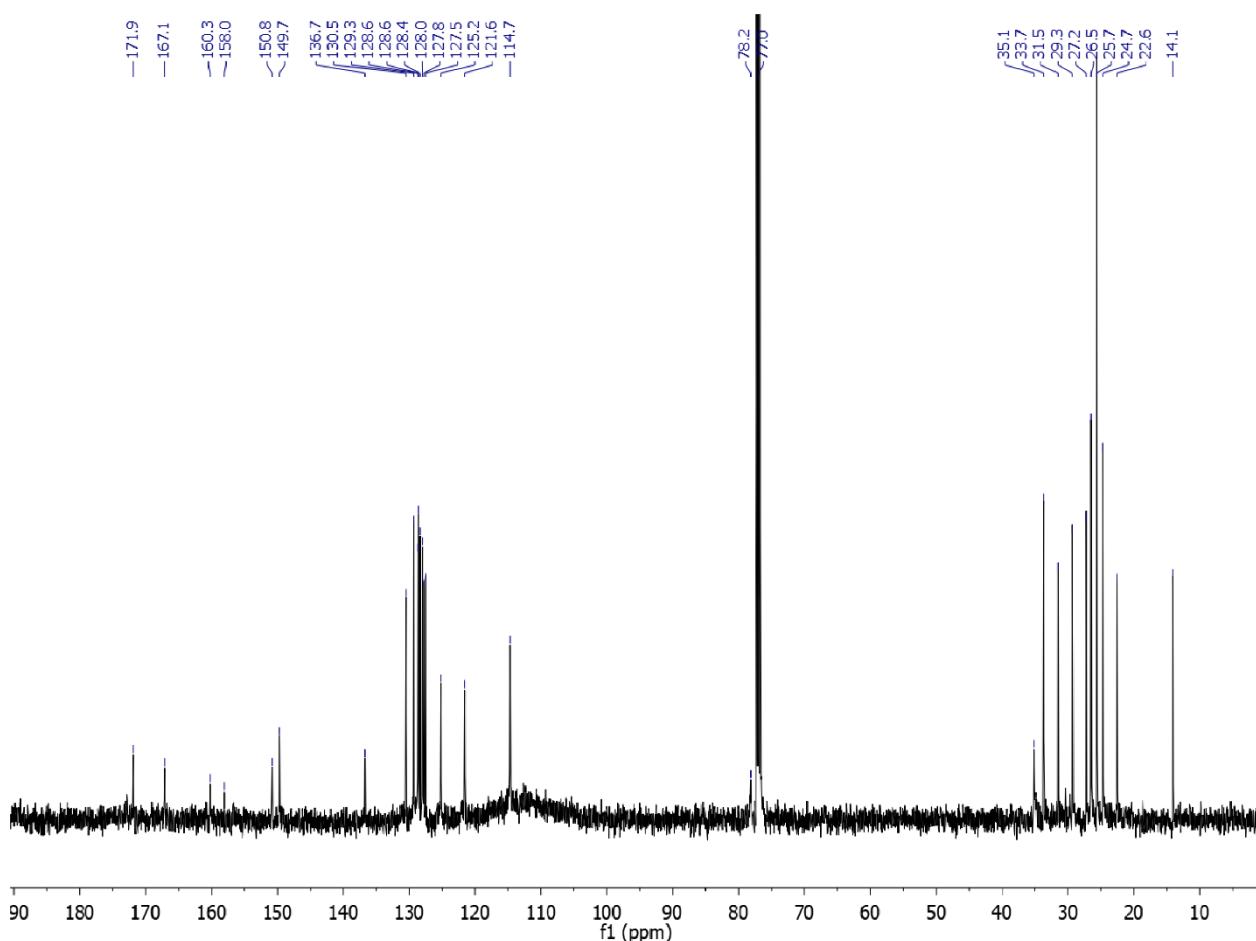
7'', 10''- and 13''-CH<sub>2</sub>





<sup>1</sup>H NMR (CDCl<sub>3</sub>, 500 MHz): δ (ppm) 0.90 (3H, t, J=7.6, 20''-CH<sub>3</sub>), 1.28-1.40 (6 H, m, 17''-, 18''-, 19''- CH<sub>2</sub>), 1.88 (2H, tt, J=7.0, 7.6 Hz, 3''-CH<sub>2</sub>), 2.06 (2H, dt, J=7.6, 7.6 Hz, 16''-CH<sub>2</sub>), 2.24 (2H, dt, J=7.0, 7.4 Hz, 4''-CH<sub>2</sub>), 2.64 (2H, t, J=7.0 Hz, 2''-CH<sub>2</sub>), 2.82-2.88 (6H, m, 7''- 10''- and 13''-CH<sub>2</sub>), 3.80-3.87 (2H, AB part of ABX system, 5a- and 5b-H), 5.32-5.50 (9H, m, 5''- 6''- 8''- 9''- 11''- 12''- 14''- 15''-CH and 4-H), 7.29 (1H, dd, J=2.3, 8.9 Hz, 5'-H), 7.73 (1H, d, J=2.3 Hz, 7'-H), 8.16 (1H, d, J=8.9 Hz, 4'-H).

<sup>13</sup>C NMR spectrum of 6-O-arachidonoylluciferin (**1**)



<sup>13</sup>C NMR (CDCl<sub>3</sub>, 125.76 MHz): δ (ppm) 14.1 (20''), 22.6 (19''), 24.7 (3''), 25.7 (7'', 10'', 13''), 26.5 (4''), 27.2 (16''), 29.3 (17''), 31.5 (18''), 33.7 (2''), 35.1 (5), 78.2 (4), 114.7 (7'), 121.6 (5), 125.2 (4), 127.5, 127.8, 128.0, 128.4, 128.6, 128.6, 129.3, 130.5 (5', 6', 8', 9', 11', 12', 14', 15'), 136.7 (8'), 149.7 (6'), 150.8 (9'), 158.0 (2), 160.3 (2'), 167.1(1''), 171.9 (COOH).