

Supplementary Information

## **Avellanin A Has an Antiproliferative Effect on TP-Induced RWPE-1 Cells via the PI3K-Akt Signalling Pathway**

## List of Supporting Information

**Figure S1.** HR-ESI-MS spectrum of avellanin A.

**Figure S2.**  $^1\text{H}$  NMR (d<sub>4</sub>-methanol, 600 MHz) spectrum of Avellanins A.

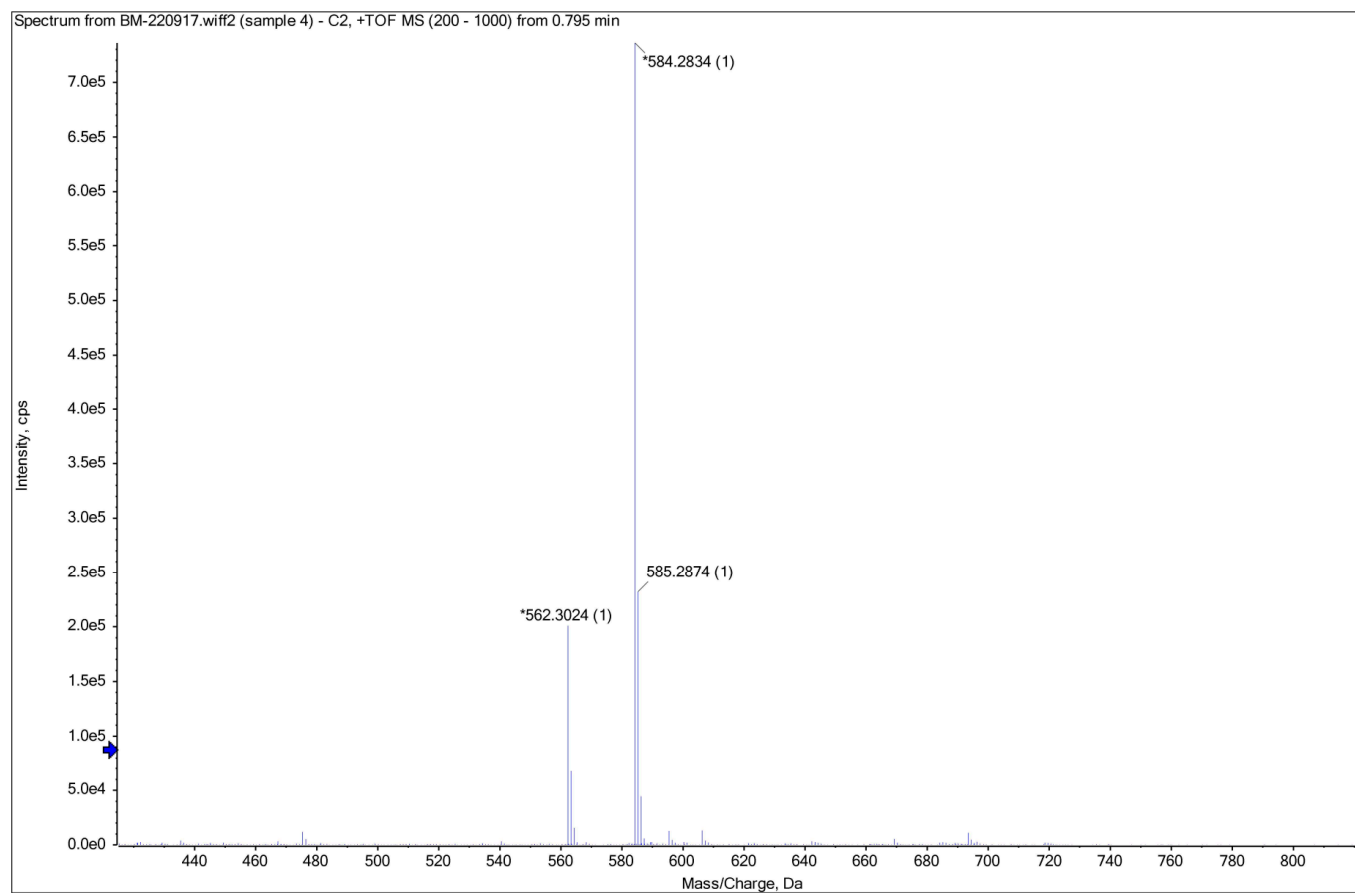
**Figure S3.**  $^{13}\text{C}$  NMR (d<sub>4</sub>-methanol, 150 MHz) spectrum of Avellanins A.

**Figure S4.** The original Western Blot image of Figure 4C.

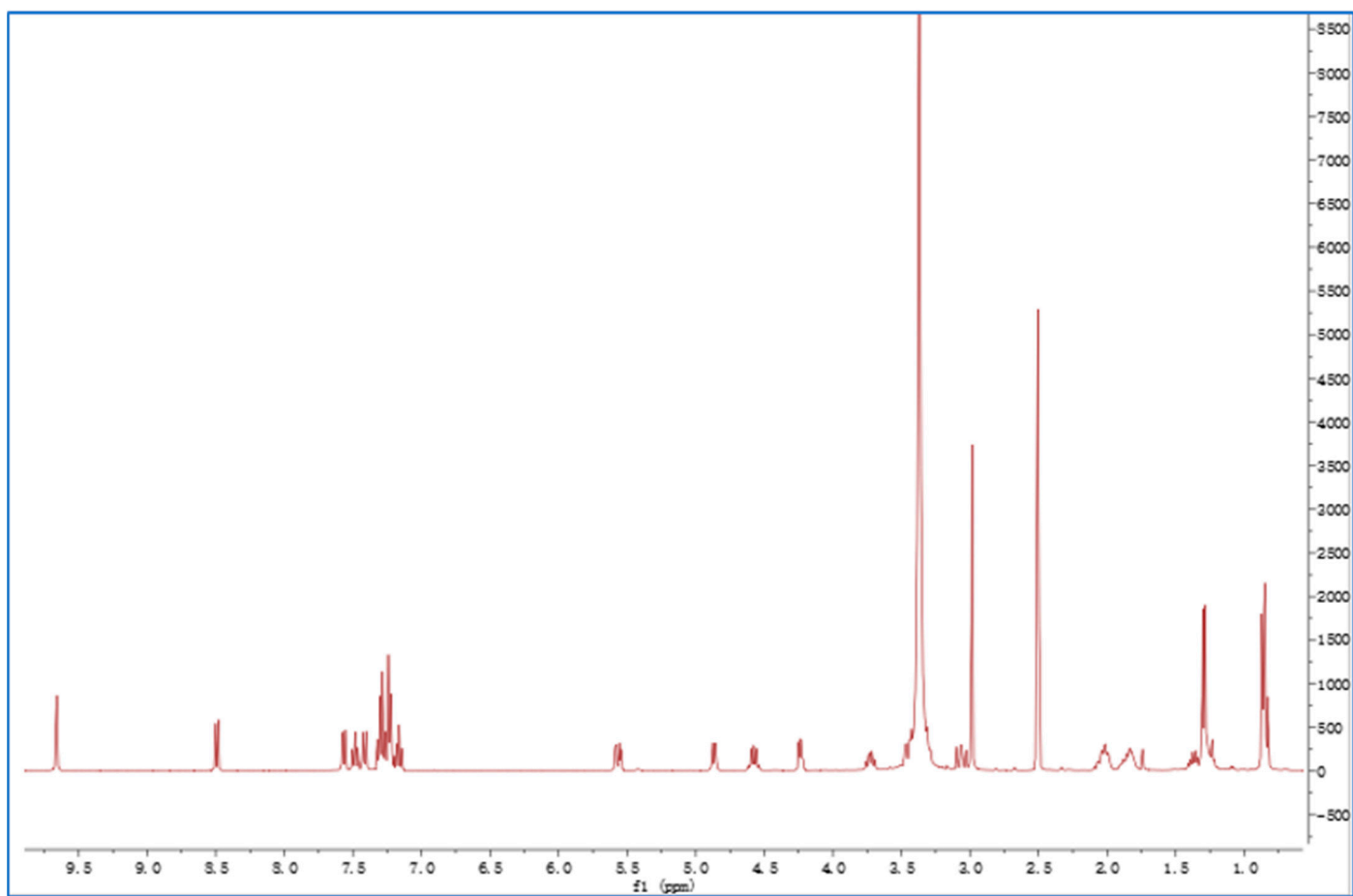
**Figure S5.** The original Western Blot image of Figure 5.

**Table S1.**  $^1\text{H}$  and  $^{13}\text{C}$  NMR assignments for avellanin A in DMSO-*d*<sub>6</sub>.

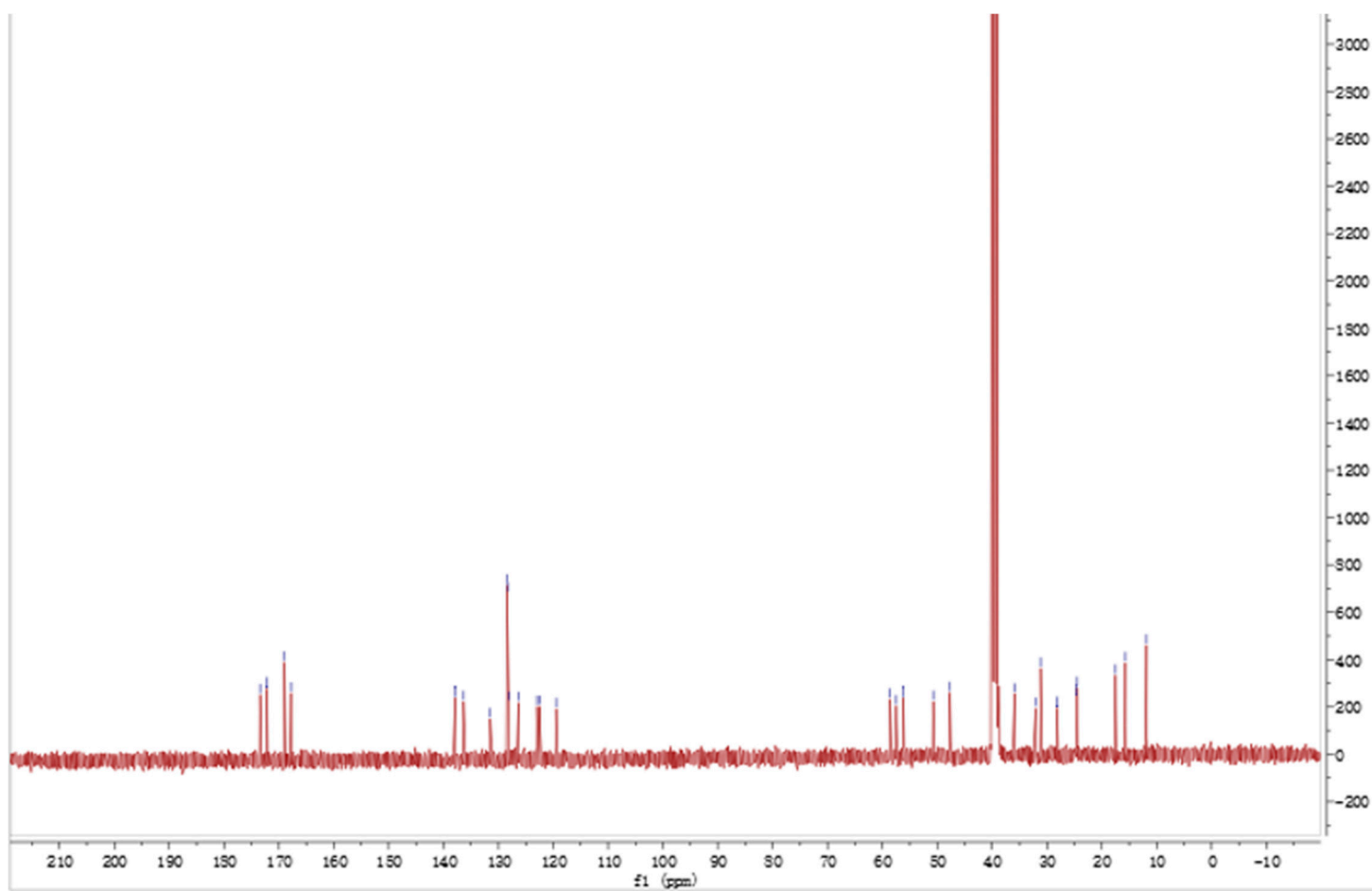
**Table S2.** Sequences of qPCR primers.



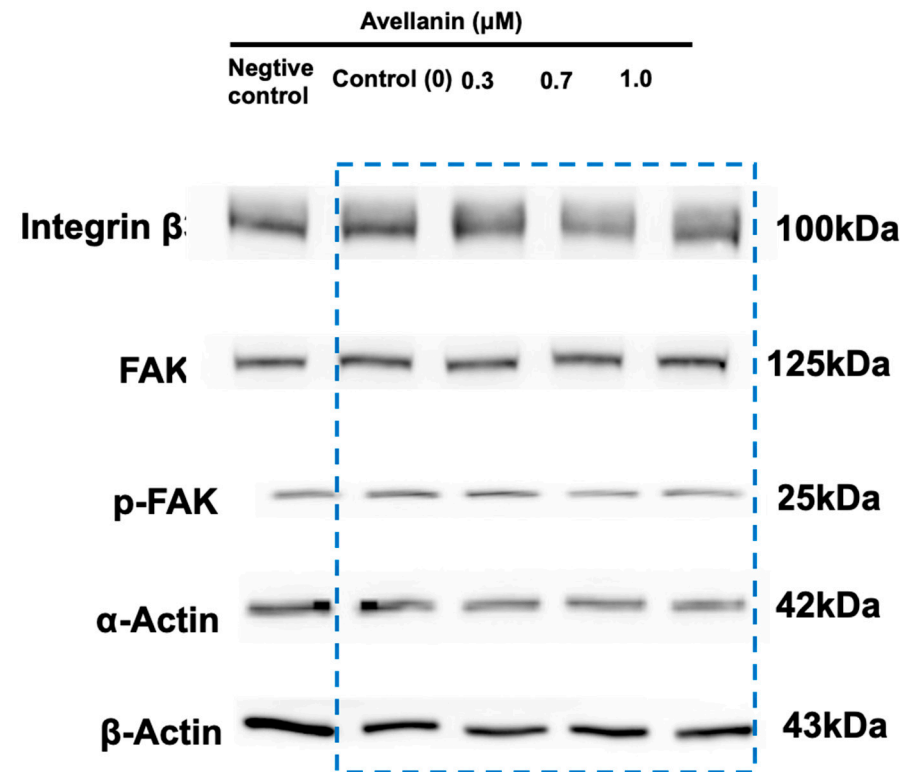
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**Figure S4.** The original Western Blot image of Figure 4C.

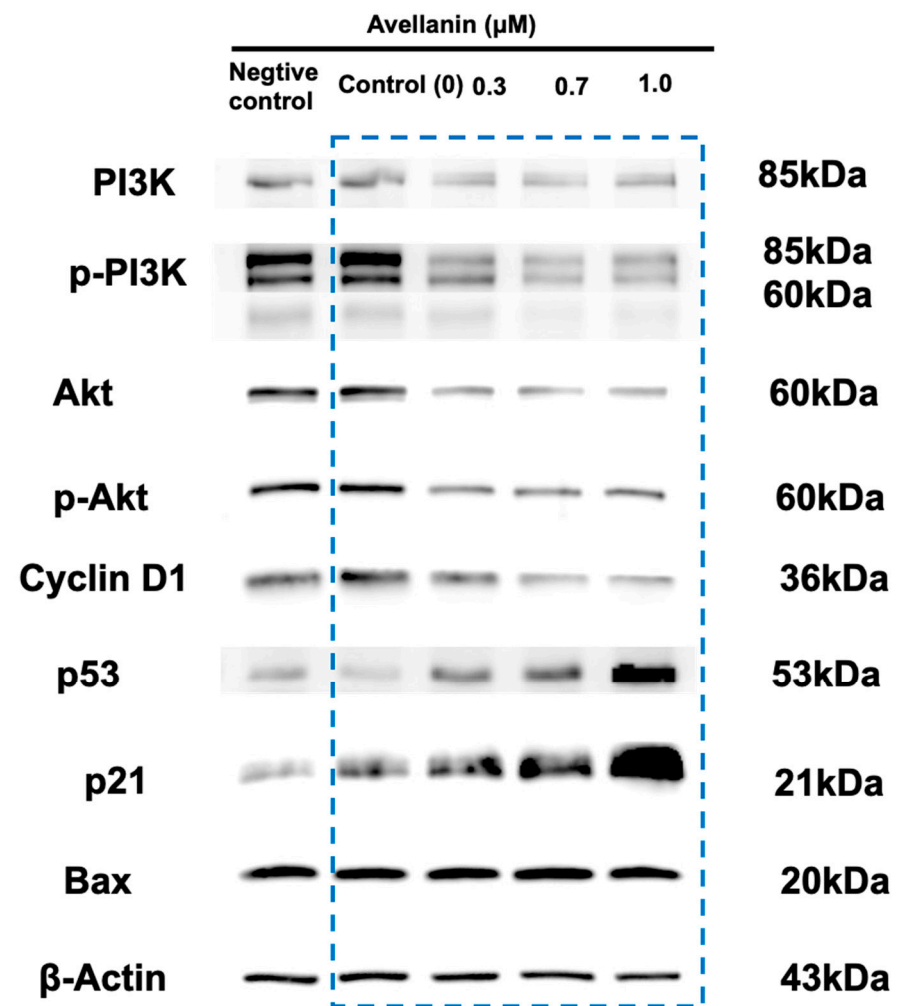


Figure S5. The original Western Blot image of Figure 5.

**Table S1.**  $^1\text{H}$  and  $^{13}\text{C}$  NMR assignments for avellanin A in  $\text{DMSO-}d_6$ 

Residue	Position	avellanin A ( $\text{DMSO-}d_6$ )		Reported avellanin A ( $\text{DMSO-}d_6$ )	
		$\delta_{\text{H}}$ , mult. ( $J$ in Hz)	$\delta_{\text{C}}$ , Type	$\delta_{\text{H}}$ , mult. ( $J$ in Hz)	$\delta_{\text{C}}$ , Type
Ala	1		172.1 (C)		172.0 (qC)
	2	4.58, m	47.6 (CH)	4.72, dd (7.3, 2.6)	48.5 (CH)
	3	1.29, d (7.2)	17.5 ( $\text{CH}_3$ )	1.52, d (6.8)	18.1 ( $\text{CH}_3$ )
	NH			7.43, d (7.7)	
Ile	1		168.9 (C)		169.5 (C)
	2	4.24, dd (7.2, 4.0)	57.4 (CH)	4.69, dd (9.4, 3.4)	57.5 (CH)
	3	2.02, m	35.9 (CH)	2.00, m	36.2 (CH)
	4	1.38, dt (12.9, 6.1)	24.5 ( $\text{CH}_2$ )	1.46, m	24.4 ( $\text{CH}_2$ )
				1.48, m	
	5	0.85, t (4.8)	11.8 ( $\text{CH}_3$ )	0.93, t (7.7)	12.2 ( $\text{CH}_3$ )
	3'	0.86, d (7.2)	15.7 ( $\text{CH}_3$ )	0.97, d (6.8)	16.3 ( $\text{CH}_3$ )
Ant	1		168.9 (C)		169.5 (C)
	2		136.3 (C)		136.6 (C)
	3	7.57, dd (8.0, 1.2)	128.1 (CH)	7.32, m	128.2 (CH)
	4	7.16, td (7.6, 0.8)	126.3 (CH)	7.08, t (7.7)	127.3 (CH)
	5	7.48, t (1.6)	131.4 (CH)	7.44, t (7.7)	131.7 (CH)
	6	8.49, d (7.6)	119.4 (CH)	8.45, d (7.7)	121.4 (CH)
	7		122.9 (C)		123.0 (C)
	NH	9.66, s		9.79, s	
Pro	1		173.4 (C)		174.0 (C)
	2	4.87, dd (10.8, 2.0)	56.1 (CH)	4.89, m	56.4 (CH)
	3	2.03, m	28.1 ( $\text{CH}_2$ )	2.10, m	28.6 ( $\text{CH}_2$ )



Phe		1.29, m		1.18, m	
	4	1.85, m	24.7 (CH <sub>2</sub> )	1.88, m	25.0 (CH <sub>2</sub> )
	5	3.31, m	50.7 (CH <sub>2</sub> )	3.50-3.70, m	51.4 (CH <sub>2</sub> )
		3.73, m			
	1		167.8 (C)		169.7 (C)
	2	5.57, dd (12.4, 4.4)	58.5 (CH)	5.78, dd (12.8, 4.7)	58.5 (CH)
	3	3.44, dd (15.2, 4.0)	32.0 (CH <sub>2</sub> )	3.83, dd (16.2, 4.7)	33.1 (CH <sub>2</sub> )
		3.06, dd (15.6, 12.8)		2.97, dd (16.2, 12.8)	
	4		137.8 (C)		137.1 (C)
	5,9	7.26 <sup>d</sup>	128.2 (CH)	7.21 <sup>d</sup>	128.2 (CH)
	6,8	7.26 <sup>d</sup>	128.4 (CH)	7.30-7.31 <sup>d</sup>	128.6 (CH)
	7	7.29 <sup>d</sup>	126.3 (CH)	7.24 <sup>d</sup>	126.8 (CH)
	NMe	2.98, s	31.1 (CH <sub>3</sub> )	3.02, s	31.1 (CH <sub>3</sub> )

**Table S2.** Sequences of qPCR primers

Gene	Forward primer	Reverse primer
COL1A1	5'-CATCTCCATTCTTCCAGGG-3'	5'-TTCAGTGGTTTGGATGGTG-3'
COL1A2	5'-CATAACCACCACCGCTTAC-3'	5'-TCTTACTCCTGAAGGCTCTAG-3'
COL5A2	5'-CAGGCTCCATAGGAATCAGAG-3'	5'-CAGCATTTCTGCTTCTCCAG-3'
COL6A3	5'-ACCGGAAGTGTC AATTCGCA-3'	5'- CAATGACTTGTGTGACAATG-3'
ITGA2	5'-GCCATTGTATATAACATCACA-3'	5'-TTTGTTTTGGTTGCTGACAAT- 3'
ITGB3	5'-CACTCTGCTTCTTCACTTCC-3	5'-TTTACCACTGATGCCAAGAC-3'
MMP2	5'-GAAGAAGAAGATCTCACCAC-3'	5'-GATTGATGCGGTATACGAGG-3'
MMP9	5'-CATCCAGTTTGGTGTCGCG-3'	5'-AAGATGAATGGAAGTGGCAG-3'
FGF2	5'-ATCCGTGAACCCCAGGTCC-3'	5'-GGAAGGCGCCGCTGCCGCCAT-3'
VWF	5'CCAGGGCGACGACTTCCTTAC3'	5'TCCGAGCAGGAGCACACGTCG3'
$\beta$ -actin	5'-CATGTACGTTGCTATCCAGGC-3'	5'-CTCCTTAATGTCACGCACGAT-3'