

### Supplementary data

**Table S1. The liquid chromatographic separation conditions**

<b>Flow rate</b>	300µl/min
<b>Temp</b>	50 °C
<b>Solvent</b>	Phase A: H <sub>2</sub> O/Hexane/Acetic acid (70:30:0.02, v/v/v)
	Phase B: Hexane/IPA (50:50, v/v)
<b>Gradient(B%)</b>	0 min-0%
	3 min-25%
	11 min-45%
	13 min-60%
	18 min-75%
	18.5 min-90%
	20 min-90%
	21 min-0%
	Held until 25 min

**Table S2. The parameters of the MRM method**

<b>Parameter</b>	<b>Mode</b>
	<b>Negative ion mode</b>
Ion source	Turbo spray
Curtain gas (p.s.i)	10.0 p.s.i
Collisional activated dissociation (CAD)	High(-20V to -45V)
Ion spray voltage	-4500.0V
Temperature	525.0 °C
Ion source gas	40.0 p.s.i
Declustering potential (DP)	-30.0V
Entrance potential (EP)	-15.0V
Collision cell exit potential (CXP)	-15.0

**Table S3. The MRM transitions and the collision energy (CE) values selected for each lipid**

Class	Lipid mediator	Transitions (Q1/Q3)	CE (ev)	Internal standard	Stability RSD%
AA	12-HHT	279/163	-25	12-HETE-d8	0.70
	11-HETE	319.1/167.1	-25	12-HETE-d8	10.53
	12-HETE	319/179	-25	12-HETE-d8	7.74
	15-HETE	319/175	-25	12-HETE-d8	10.24
	20-HETE	319/245	-25	12-HETE-d8	9.56
	5-HETE	319/115	-25	12-HETE-d8	14.64
	8,9-DHET	319/155	-25	11,12-EET-d11	7.26
	8-HETE	319.01/155.01	-25	12-HETE-d8	11.51
	9-HETE	319/151	-25	12-HETE-d8	6.71
	11,12-DHET	337/167	-25	11,12-EET-d11	0.00
	14,15-DHET	337/207	-25	11,12-EET-d11	0.03
	5,6-DHET	337/145	-25	11,12-EET-d11	11.15
	8,9-EET	319/127	-20	11,12-EET-d11	13.89
	11,12-EET	319/167	-20	11,12-EET-d11	12.68
	HXB3	335/183	-20	11,12-EET-d11	14.87
	15-deoxy-PGA2	315/271	-15	PGD2-EA-d4	8.25
	15-deoxy-PGJ2	315.01/271.01	-15	PGD2-EA-d4	14.72
	PGEM	327/291	-15	PGD2-EA-d4	9.08
	PGFM	329/293	-15	PGD2-EA-d4	10.05
	bicyclo PGE2	333/113	-15	PGD2-EA-d4	10.57
PGA2	333/271	-15	PGD2-EA-d4	13.71	
PGB2	333/175	-15	PGD2-EA-d4	7.35	
Class	Lipid mediator	Transitions ( <i>m/z</i> )	CE (ev)	Internal standard	Stability RSD%
AA	PGJ2	333/189	-15	PGD2-EA-d4	3.72
	15d PGD2	333.01/271.01	-15	PGD2-EA-d4	11.26
	15k PGE2	349/113	-15	PGD2-EA-d4	9.60
	PGD2	351/271	-15	PGD2-EA-d4	8.34
	PGE2	351/189	-15	PGD2-EA-d4	0.00
	11 $\beta$ PGE2	351.02/271.02	-15	PGD2-EA-d4	11.05
	dh PGF2a	355/275	-15	PGD2-EA-d4	13.36
	dihomo PGD2	379/299	-15	PGD2-EA-d4	0.00
	LXB5	349/219	-20	LTB4-d4	8.26
	LXA4	351/115	-20	LTB4-d4	2.65
	6R-LXA4	351.01/115.01	-20	LTB4-d4	12.36
	15-HpETE	335/113	-25	12-HETE-d8	13.44
	12-HpETE	335/153	-25	12-HETE-d8	9.99
	5-HpETE	335/155	-25	12-HETE-d8	12.08
	AA	303/259	-20	12-HETE-d8	7.00
	15-oxo-ETE	317/113	-20	12-HETE-d8	11.96

	5-HEPE	317/115	-20	12-HETE-d8	14.08
	5-oxo-EETE	317/203	-25	12-HETE-d8	2.37
	TXB2	369/169	-25	PGD2-EA-d4	13.14
	2,3 dinor-11 $\beta$ -PGF2a	325/145	-15	PGD2-EA-d4	12.82
	15-epi-LXA4	351.02/115.02	-20	LTB4-d4	4.27
LA	9,10-EpOME	295.1/171.1	-20	13-HODE-d4	2.89
	12,13-EpOME	295.01/195.01	-20	13-HODE-d4	5.43
	13-oxoODE	293/113	-25	13-HODE-d4	0.33
	9-oxoODE	293/185	-25	13-HODE-d4	0.00
	9-HODE	295/171	-25	13-HODE-d4	0.00
	13-HODE	295/195	-25	13-HODE-d4	10.74
DGLA	15k PGF1a	353/113	-15	13-HODE-d4	9.24
	TXB1	371/171	-25	13-HODE-d4	2.56
	6,15 dk-,dh-PGF1a	369/113	-15	13-HODE-d4	0.00
EPA	PGD3	349/269	-15	14,15-DiHETrE-d11	11.85
	PGE3	349.01/269.01	-15	14,15-DiHETrE-d11	0.00
	RvE3	333/163	-20	14,15-DiHETrE-d11	18.66
	RvE2	333/199	-20	14,15-DiHETrE-d11	0.00
	18-HEPE	317/259	-25	14,15-DiHETrE-d11	14.08
EPA	TXB3	367/169	-25	14,15-DiHETrE-d11	1.85
DHA	4-HDHA	343/101	-25	14,15-DiHETrE-d11	0.00
	14S-21-diHDHA	359/205	-25	14,15-DiHETrE-d11	13.65
	1-Mar	359/221	-25	14,15-DiHETrE-d11	4.64
	RvD3	375/147	-20	14,15-DiHETrE-d11	0.00

**Table S4. The primers of target genes for qRT-PCR**

Gene	Primers
<i>VSV</i>	Forward: ACGGCGTACTTCCAGATGG Reverse: CTCGGTTCAAGATCCAGGT
<i>HSV-1</i>	Forward: GCTCGAGTGCGAAAAACGTTC Reverse: CGGGGCGCTCGGCTAAC
<i>Ifna2</i>	Forward: TACTCAGCAGACCTTGAACCT Reverse: CAGTCTTGGCAGCAAGTTGAC
<i>Ifn<math>\beta</math>1</i>	Forward: GGCAGTGTAACCTTCTGCAT Reverse: CAGCTCCAAGAAAGGACGAAC
<i>Tnfa</i>	Forward: GACGTGGAAGTGGCAGAAGAG Reverse: TTGGTGGTTTGTGAGTGTGAG