Supplemental Table 1. Chemical constituents in EECP detected using GC-MS

RTs (minute)	Area (%)	Compound
15.61	0.89	1(5)-Guaien-11-ol
16.67	2.64	Beta-Eudesmol
16.78	0.54	Bulnesol
16.91	0.40	Hanamyol
17.12	1.68	Alpha-Bisabolol
19.31	0.23	Ethyl tetradecanoate/Ethyl myristate
19.43	0.41	2-Naphthalenemethanol
20.54	1.65	Cryptomeridiol
24.83	2.78	Ethyl palmitate
28.74	3.60	Elaidic acid, ethyl ester
29.30	0.55	Stearic acid, ethyl ester
29.56	0.87	9-Hexadecenoic acid, ethyl ester
30.95	1.57	Trans-Ferulic acid
33.10	0.39	9-Hexadecenoic acid, eicosyl ester
33.37	2.64	Pinostrobin
33.76	1.16	Cinnamyl cinnamate
35.38	2.87	Benzyl (E)-3-(4-hydroxyphenyl) acrylate
35.69	4.24	Pinocembrin
36.13	1.67	Naringenin 7-methyl ether
36.60	6.85	Tectochrysin
38.44	1.06	Naringin
39.03	1.44	Chrysin
39.77	1.12	Galangin

Supplemental Table 2. Genes and primers' sequences used in qRT-PCR

Gene (symbol)	Primer sequence (5' to 3')	Amplicon
stearoyl-coenzyme A desaturase 2 (*SCD2*)	F: CTGGGGCGAGACTTTTGTAA	197 bp
	R: CGTGGTGGTAGTTGTGGAAG	
NAD(P) dependent steroid dehydrogenase-like (*NSDHL*)	F: CCAGTGTTGTCTTTGAGGGTG	164 bp
	R: AGGACGAATGGCTGCGGTTA	
isopentenyl-diphosphate delta isomerase (*IDI1*)	F: TGGGGCTGACACCAAGAAAA	164 bp
	R: CAGCTCGCCTGGGTTACTTA	
cytochrome P450, family 51 (*CYP51*)	F: TGGAGGTTTTACCCACGCTG	143 bp
	R: GACGCCCGTCCTTGTATGTA	
fatty acid binding protein 5, epidermal (*FABP5*)	F: AACCGAGAGCACAGTGAAGAC	166 bp
	R: CACTCCACGATCATCTTCCCA	
ciliary neurotrophic factor receptor (*CNTFR*)	F: ACAAGGTCTCCATAAGTGTCAGC	188 bp
	R: AGGAAAGGATTCAGGGTCGG	
interleukin 6 receptor, alpha (*IL6RA*)	F: CCTGTATGGTCAAAGGAGTTCA	179 bp
	R: TCTGCTATCCAAGGAGTGCC	
selenoprotein I (*EPT1*)	F: ATAGTGACTGCGGTTGTGGG	185 bp
	R: GCTTCATAGACGGACTTGTGC	
mevalonate (diphospho) decarboxylase (*MVD*)	F: CGAATCCTTATCCTTGTGGTG	166 bp
	R: CCTGAAAGTCCTGCTCTTGG	
glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*)	F: CCTGCACCACCAACTGCTTA	156 bp
	R: CAGGGATGATGTTCTGGGCA	

Supplemental Table 3. Parameters measured in mice from group ET and group EECP-ET

Parameters	Gender	Group ET			Mean ± SEM	Group EECP-ET			Mean ± SEM	*p*
Liver index %	Male	4.404	5.828	6.146	5.46 ± 0.54	5.046	5.552	5.566	5.39 ± 0.17	0.083
	Female	6.850	6.941	6.804	6.86 ± 0.04	5.796	5.766	5.750	5.77 ± 0.01	0.000
Bodyweight	Male	26.0	24.4	21.3	23.9 ± 1.38	21.7	20.1	24.2	22.0 ± 1.19	0.356
(gram)	Female	20.7	20.5	20.4	20.53 ± 0.08	20.1	19.2	19.2	19.50 ± 0.30	0.003
Concentration of TG	Male	0.4254	0.3471	0.3257	0.3661 ± 0.0303	0.3129	0.3047	0.3205	0.3127 ± 0.0046	0.157
(mmol/g)	Female	0.4576	0.4063	0.3515	0.4051 ± 0.0306	0.3219	0.3106	0.3103	0.3143 ± 0.0038	0.042
Concentration of TC	Male	0.2336	0.2775	0.2547	0.2553 ± 0.0127	0.2612	0.2189	0.1805	0.2202 ± 0.0233	0.256
(mmol/g)	Female	0.2830	0.2618	0.2547	0.2665 ± 0.0085	0.2513	0.2459	0.1877	0.2283 ± 0.0203	0.159
Serum AST level	Male	19.4439	17.7045	20.8464	19.3316 ± 0.9087	-	12.5605	12.2764	12.4185 ±0.1420	0.015
(U/L)	Female	17.8459	19.5242	-	18.6851 ± 0.8392	11.1902	-	12.5605	11.8754 ± 0.6852	0.027
Serum ALT level	Male	29.4960	-	28.6554	29.0757 ± 0.4203	26.1237	-	24.6216	25.3726 ± 0.7511	0.075
(U/L)	Female	27.2988	-	27.7000	27.4994 ± 0.2006	-	22.1237	23.3812	22.7525 ± 0.6288	0.062

Supplemental Table 4. Significantly GO BPs and KEGG pathways compared between groups ET and ET-EECP

	Term	Count	*P*-value
GO:0035634	Response to stilbenoid	12	7.98E-11
GO:0006695	Cholesterol biosynthetic process	13	1.05E-10
GO:0006629	Lipid metabolic process	44	1.70E-10
GO:0055114	Oxidation-reduction process	53	2.47E-09
GO:0008202	Steroid metabolic process	17	6.44E-09
GO:0006694	Steroid biosynthetic process	14	5.12E-08
GO:0002548	Monocyte chemotaxis	11	3.13E-07
GO:0071347	Cellular response to interleukin-1	14	1.16E-06
GO:0016126	Sterol biosynthetic process	9	1.18E-06
GO:0042759	Long-chain fatty acid biosynthetic process	6	3.41E-06
GO:0006636	Unsaturated fatty acid biosynthetic process	7	3.68E-06
GO:0048247	Lymphocyte chemotaxis	9	6.26E-06
GO:0006633	Fatty acid biosynthetic process	12	1.85E-05
GO:0045638	Negative regulation of myeloid cell differentiation	8	1.94E-05
GO:0019373	Epoxygenase P450 pathway	8	3.16E-05
GO:0030595	Leukocyte chemotaxis	7	4.54E-05
GO:0071346	Cellular response to interferon-gamma	11	4.88E-05

GO:0070374	Positive regulation of ERK1 and ERK2 cascade	18	9.44E-05
GO:0008203	Cholesterol metabolic process	12	1.06E-04
GO:1903966	Monounsaturated fatty acid biosynthetic process	4	1.20E-04
mmu03320	PPAR signaling pathway	16	5.09E-07
mmu01100	Metabolic pathways	85	8.92E-07
mmu01040	Biosynthesis of unsaturated fatty acids	9	7.06E-06
mmu00830	Retinol metabolism	15	1.06E-05
mmu01130	Biosynthesis of antibiotics	24	1.46E-05
mmu00100	Steroid biosynthesis	7	6.98E-05
mmu01212	Fatty acid metabolism	10	1.66E-04
mmu00140	Steroid hormone biosynthesis	13	1.69E-04
mmu04152	AMPK signaling pathway	15	5.90E-04
mmu00590	Arachidonic acid metabolism	12	8.18E-04

Supplemental Table 5. The top 20 most significant GO BPs in female mice

	Term	Count	*P*-value
GO:0006695	Cholesterol biosynthetic process	12	1.88E-11
GO:0055114	Oxidation-reduction process	41	1.50E-09
GO:0006629	Lipid metabolic process	31	2.09E-08
GO:0035634	Response to stilbenoid	9	2.18E-08
GO:0016126	Sterol biosynthetic process	9	4.32E-08
GO:0071346	Cellular response to interferon-gamma	12	1.16E-07
GO:0008202	Steroid metabolic process	13	1.28E-07
GO:0048247	Lymphocyte chemotaxis	9	2.43E-07
GO:0042759	Long-chain fatty acid biosynthetic process	6	4.00E-07
GO:0006694	Steroid biosynthetic process	11	4.53E-07

GO:0071347	Cellular response to interleukin-1	12	6.38E-07
GO:0045638	Negative regulation of myeloid cell differentiation	8	1.12E-06
GO:0002548	Monocyte chemotaxis	9	1.19E-06
GO:0030595	Leukocyte chemotaxis	7	3.86E-06
GO:0006636	Unsaturated fatty acid biosynthetic process	6	8.63E-06
GO:0030593	Neutrophil chemotaxis	10	1.05E-05
GO:0008203	Cholesterol metabolic process	11	1.32E-05
GO:0070098	Chemokine-mediated signaling pathway	9	1.44E-05
GO:0071356	Cellular response to tumor necrosis factor	12	1.51E-05
GO:0006633	Fatty acid biosynthetic process	10	1.87E-05

Supplemental Table 6. The top 20 most significant GO BPs in male mice

	Term	Count	*P*-value
GO:0008202	Steroid metabolic process	8	1.36E-04
GO:0006629	Lipid metabolic process	18	1.67E-04
GO:0042327	Positive regulation of phosphorylation	5	6.63E-04
GO:0043406	Positive regulation of MAP kinase activity	6	7.78E-04
GO:0006695	Cholesterol biosynthetic process	5	8.51E-04
GO:0098609	Cell-cell adhesion	10	0.001063
GO:0016477	Cell migration	10	0.001143
GO:0006694	Steroid biosynthetic process	6	0.001459
GO:0030855	Epithelial cell differentiation	6	0.002063
GO:0051005	Negative regulation of lipoprotein lipase activity	3	0.002604
GO:0043410	Positive regulation of MAPK cascade	7	0.002808
GO:0007166	Cell surface receptor signaling pathway	10	0.002896
GO:0003382	Epithelial cell morphogenesis	4	0.004431
GO:0035634	Response to stilbenoid	4	0.004431
GO:0001666	Response to hypoxia	9	0.004516
GO:0030335	Positive regulation of cell migration	9	0.006288
GO:0008284	Positive regulation of cell proliferation	16	0.006739
GO:0001701	In utero embryonic development	11	0.007387
GO:0019373	Epoxygenase P450 pathway	4	0.007446
GO:0001558	Regulation of cell growth	5	0.007654