

Supplemental Material to:

**Javier A. Menendez, Jorge Joven, Gerard Aragonès,
Enrique Barrajon-Catalán, Raúl Beltrán-Debón, Isabel Borrás-Linares,
Jordi Camps, Bruna Corominas-Faja, Sílvia Cufí, Salvador Fernández-
Arroyo, Anabel Garcia-Heredia, Ana Hernández-Aguilar, María Herranz-
López, Cecilia Jiménez-Sánchez, Eugeni López-Bonet, Jesús Lozano-
Sánchez, Fedra Luciano-Mateo, Begoña Martin-Castillo, Vicente
Martin-Paredero, Almudena Pérez-Sánchez, Cristina Oliveras-Ferraro,
Marta Rierra-Borrull, Esther Rodríguez-Gallego, Rosa Quirantes-Piné,
Anna Rull, Laura Tomás-Menor, Alejandro Vazquez-Martin, Carlos Alonso-
Villaverde, Vicente Micol and Antonio Segura-Carretero**

**Xenohormetic and anti-aging activity of secoiridoid
polyphenols present in extra virgin olive oil: A new family
of gerosuppressant agents**

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Table 1. Gene transcripts differentially up-regulated (red) and down-regulated (green) in JIMT1 human breast cancer cells treated with the secoiridoids-rich EVOO-PE7 (2 µg/mL) for 6 h.

ID	Symbol	Entrez Gene Name	Fold Change
NM_005252	FOS	FBJ murine osteosarcoma viral oncogene homolog	20,027
NM_002422	MMP3	matrix metalloproteinase 3 (stromelysin 1, progelatinase)	17,034
NM_002166	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	16,740
NM_016084	RASD1	RAS, dexamethasone-induced 1	16,320
NM_002923	RGS2	regulator of G-protein signaling 2, 24kDa	15,296
NM_002155	HSPA6	heat shock 70kDa protein 6 (HSP70B')	15,182
NM_002421	MMP1	matrix metalloproteinase 1 (interstitial collagenase)	12,820
NM_001964	EGR1	early growth response 1	12,431
NM_015675	GADD45B	growth arrest and DNA-damage-inducible, beta	11,400
NM_006732	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	11,064
NM_005985	SNAI1	snail homolog 1 (Drosophila)	9,328
NM_004024	ATF3	activating transcription factor 3	9,240
NM_182491	ZFAND2A	zinc finger, AN1-type domain 2A	7,763
NM_006705	GADD45G	growth arrest and DNA-damage-inducible, gamma	7,154
NM_052957	ACRC	acidic repeat containing	7,120
NM_001124	ADM	adrenomedullin	7,070
NM_000076	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	6,852
NM_004417	DUSP1	dual specificity phosphatase 1	6,611
NM_014330	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	6,260
NM_001901	CTGF	connective tissue growth factor	6,144
NM_018602	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	6,120
NM_001965	EGR4	early growth response 4	5,885
NM_025237	SOST	sclerostin	5,817
NM_015193	ARC	activity-regulated cytoskeleton-associated protein	5,765
NM_005261	GEM	GTP binding protein overexpressed in skeletal muscle	5,731
NM_005618	DLL1	delta-like 1 (Drosophila)	5,673
NM_021127	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	5,590
NR_003038	SNHG5	small nucleolar RNA host gene 5 (non-protein coding)	5,538

NM_002928	RGS16	regulator of G-protein signaling 16	5,480
NM_005168	RND3	Rho family GTPase 3	5,480
NM_003311	PHLDA2	pleckstrin homology-like domain, family A, member 2	5,013
BC001892	C1ORF63	chromosome 1 open reading frame 63	4,910
NM_005461	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	4,753
NM_001924	GADD45A	growth arrest and DNA-damage-inducible, alpha	4,731
NM_013262	MYLIP	myosin regulatory light chain interacting protein	4,630
NM_007314	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2	4,567
NM_152608	C1ORF55	chromosome 1 open reading frame 55	4,516
NM_018088	FAM90A1	family with sequence similarity 90, member A1	4,500
NM_006889	CD86	CD86 molecule	4,403
NM_000584	IL8	interleukin 8	4,354
NM_005771	DHRS9	dehydrogenase/reductase (SDR family) member 9	4,318
AA593970	MXD1	MAX dimerization protein 1	4,318
NM_004165	RRAD	Ras-related associated with diabetes	4,310
NM_182597	C7ORF53	chromosome 7 open reading frame 53	4,245
NM_004083	DDIT3	DNA-damage-inducible transcript 3	4,225
NM_005853	IRX5	iroquois homeobox 5	4,205
NM_001300	KLF6	Kruppel-like factor 6	4,000
BC030138	MED26	mediator complex subunit 26	3,940
NM_014905	GLS	glutaminase	3,900
NM_000389	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	3,880
NM_006362	NXF1	nuclear RNA export factor 1	3,824
NM_018661	DEFB103B	defensin, beta 103B	3,813
NM_002970	SAT1	spermidine/spermine N1-acetyltransferase 1	3,790
NM_181726	ANKRD37	ankyrin repeat domain 37	3,778
NM_005842	SPRY2	sprouty homolog 2 (Drosophila)	3,771
NM_021724	NR1D1	nuclear receptor subfamily 1, group D, member 1	3,760
NM_006079	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	3,756
BC020539	FNIP1	folliculin interacting protein 1	3,751
NM_144660	SAMD8	sterile alpha motif domain containing 8	3,747
NM_013376	SERTAD1	SERTA domain containing 1	3,710
NM_013347	RPA4	replication protein A4, 30kDa	3,701
NM_004226	STK17B	serine/threonine kinase 17b	3,681
NM_012328	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	3,655

NM_198833	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	3,635
NM_003733	OASL	2'-5'-oligoadenylate synthetase-like	3,625
NM_138440	VASN	vasorin	3,622
NM_000565	IL6R	interleukin 6 receptor	3,597
NM_003749	IRS2	insulin receptor substrate 2	3,587
NM_000067	CA2	carbonic anhydrase II	3,492
NM_004561	OVOL1	ovo-like 1(Drosophila)	3,491
NM_004418	DUSP2	dual specificity phosphatase 2	3,490
AK128645	SDCBP	syndecan binding protein (syntenin)	3,384
NM_015000	STK38L	serine/threonine kinase 38 like	3,368
NM_001885	CRYAB	crystallin, alpha B	3,345
BC020867	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	3,340
NM_002130	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	3,340
NM_016270	KLF2	Kruppel-like factor 2 (lung)	3,331
NM_001005217	FRG2	FSHD region gene 2	3,318
NM_016569	TBX3	T-box 3	3,290
NM_014851	KLHL21	kelch-like 21 (Drosophila)	3,288
NM_025201	PLEKHO2	pleckstrin homology domain containing, family O member 2	3,254
NM_002357	MXD1	MAX dimerization protein 1	3,250
NM_012323	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	3,250
NM_014007	ZBTB43	zinc finger and BTB domain containing 43	3,234
NM_183376	ARRDC4	arrestin domain containing 4	3,209
NM_004419	DUSP5	dual specificity phosphatase 5	3,202
NM_152621	SGMS2	sphingomyelin synthase 2	3,174
NM_017664	ANKRD10	ankyrin repeat domain 10	3,156
NM_024616	C3ORF52	chromosome 3 open reading frame 52	3,151
NM_012118	CCR4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	3,145
NM_012342	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	3,137
NM_003811	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	3,090
NM_001514	GTF2B	general transcription factor IIB	3,084
NM_025195	TRIB1	tribbles homolog 1 (Drosophila)	3,080
NM_203339	CLU	clusterin	3,079
NR_002578	GAS5	growth arrest-specific 5 (non-protein coding)	3,076
NM_053044	HTRA3	HtrA serine peptidase 3	3,057
NM_004364	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	3,050

NM_004071	CLK1	CDC-like kinase 1	3,050
NM_002133	HMOX1	heme oxygenase (decycling) 1	3,040
NM_001946	DUSP6	dual specificity phosphatase 6	3,032
NM_020177	FEM1C	fem-1 homolog c (C. elegans)	3,030
NM_000861	HRH1	histamine receptor H1	3,030
NM_198219	ING1	inhibitor of growth family, member 1	3,013
NM_002135	NR4A1	nuclear receptor subfamily 4, group A, member 1	2,973
NM_015472	WWTR1	WW domain containing transcription regulator 1	2,930
NM_001731	BTG1	B-cell translocation gene 1, anti-proliferative	2,914
NM_001008540	CXCR4	chemokine (C-X-C motif) receptor 4	2,910
NM_006572	GNA13	guanine nucleotide binding protein (G protein), alpha 13	2,906
NM_152407	GRPEL2	GrpE-like 2, mitochondrial (E. coli)	2,894
NM_003516	HIST2H2AA3	histone cluster 2, H2aa3	2,880
NM_020127	TUFT1	tuftelin 1	2,877
NM_024640	YRDC	yrdC domain containing (E. coli)	2,871
NM_001006641	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	2,869
XM_942822	LOC646626	hypothetical LOC646626	2,865
NM_013370	OSGIN1	oxidative stress induced growth inhibitor 1	2,857
NM_002632	PGF	placental growth factor	2,855
NM_025090	USP36	ubiquitin specific peptidase 36	2,855
NM_198261	RSRC2	arginine/serine-rich coiled-coil 2	2,850
AY513723	NCRNA00275	non-protein coding RNA 275	2,847
NM_024512	LRRC2	leucine rich repeat containing 2	2,846
NM_152758	YTHDF3	YTH domain family, member 3	2,818
NM_153607	C5ORF41	chromosome 5 open reading frame 41	2,814
NM_005104	BRD2	bromodomain containing 2	2,810
NM_001945	HBEGF	heparin-binding EGF-like growth factor	2,810
NM_006096	NDRG1	N-myc downstream regulated 1	2,808
NM_018700	TRIM36	tripartite motif-containing 36	2,800
NM_022818	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	2,780
NM_003463	PTP4A1	protein tyrosine phosphatase type IVA, member 1	2,780
NM_005524	HES1	hairy and enhancer of split 1, (Drosophila)	2,760
NM_182527	CABP7	calcium binding protein 7	2,752
NM_021979	HSPA2	heat shock 70kDa protein 2	2,743
NM_000399	EGR2	early growth response 2	2,742

NM_002341	LTB	lymphotoxin beta (TNF superfamily, member 3)	2,739
NM_014423	AFF4	AF4/FMR2 family, member 4	2,724
NM_001353	AKR1C1	aldo-keto reductase family 1, member C1	2,690
NM_000364	TNNT2	troponin T type 2 (cardiac)	2,682
NM_021065	HIST1H2AD	histone cluster 1, H2ad	2,680
NM_000361	THBD	thrombomodulin	2,674
NM_001657	AREG	amphiregulin	2,672
NM_014504	RABGEF1	RAB guanine nucleotide exchange factor (GEF) 1	2,670
NM_016530	RAB8B	RAB8B, member RAS oncogene family	2,658
NM_012234	RYBP	RING1 and YY1 binding protein	2,640
NM_021958	HLX	H2.0-like homeobox	2,618
NM_006260	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	2,614
NM_025054	VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	2,614
NM_021960	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	2,606
NM_001547	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	2,600
NM_002089	CXCL2	chemokine (C-X-C motif) ligand 2	2,597
NM_005527	HSPA1L	heat shock 70kDa protein 1-like	2,595
NM_001967	EIF4A2	eukaryotic translation initiation factor 4A2	2,590
NM_007207	DUSP10	dual specificity phosphatase 10	2,580
NM_004521	KIF5B	kinesin family member 5B	2,579
NM_002514	NOV	nephroblastoma overexpressed gene	2,570
NM_014650	ZNF432	zinc finger protein 432	2,561
NM_021052	HIST1H2AE	histone cluster 1, H2ae	2,554
NM_173198	NR4A3	nuclear receptor subfamily 4, group A, member 3	2,551
NM_001356	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	2,550
NM_033027	CSRNP1	cysteine-serine-rich nuclear protein 1	2,548
NM_001172	ARG2	arginase, type II	2,546
NM_032717	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	2,541
NM_018064	AKIRIN2	akirin 2	2,540
NM_001955	EDN1	endothelin 1	2,540
BC007524	SPAG9	sperm associated antigen 9	2,537
AB065089	RPS2	ribosomal protein S2	2,536
NM_004281	BAG3	BCL2-associated athanogene 3	2,530
NM_001007245	IFRD1	interferon-related developmental regulator 1	2,530
NM_020307	CCNL1	cyclin L1	2,520

BC063383	LOC400573	hypothetical LOC400573	2,516
BC022205	SNHG12	small nucleolar RNA host gene 12 (non-protein coding)	2,512
NM_001012971	C20ORF106	chromosome 20 open reading frame 106	2,507
NM_020857	VPS18	vacuolar protein sorting 18 homolog (S. cerevisiae)	2,501
NM_022780	RMND5A	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	2,500
NM_005204	MAP3K8	mitogen-activated protein kinase kinase kinase 8	2,498
NM_023940	RASL11B	RAS-like, family 11, member B	2,494
NM_024116	TAF1D	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	2,492
NM_014220	TM4SF1	transmembrane 4 L six family member 1	2,491
NM_002539	ODC1	ornithine decarboxylase 1	2,489
NM_002192	INHBA	inhibin, beta A	2,473
NM_003407	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	2,472
NM_016449	C22ORF43	chromosome 22 open reading frame 43	2,472
NM_006988	ADAMTS1	ADAM metalloproteinase with thrombospondin type 1 motif, 1	2,470
NM_002229	JUNB	jun B proto-oncogene	2,470
NM_003842	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	2,467
NM_030627	CPEB4	cytoplasmic polyadenylation element binding protein 4	2,460
NM_001730	KLF5	Kruppel-like factor 5 (intestinal)	2,460
NM_199188	LARP4	La ribonucleoprotein domain family, member 4	2,460
NM_013453	SPANXA1	sperm protein associated with the nucleus, X-linked, family member A1	2,460
NM_000641	IL11	interleukin 11	2,457
NM_021237	SELK	selenoprotein K	2,457
NM_032199	ARID5B	AT rich interactive domain 5B (MRF1-like)	2,450
NM_021963	NAP1L2	nucleosome assembly protein 1-like 2	2,436
NM_003411	ZFY	zinc finger protein, Y-linked	2,435
NM_012204	GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa	2,434
NM_004235	KLF4	Kruppel-like factor 4 (gut)	2,433
NM_005570	LMAN1	lectin, mannose-binding, 1	2,431
NM_183013	CREM	cAMP responsive element modulator	2,430
NM_003597	KLF11	Kruppel-like factor 11	2,420
NM_020435	GJC2	gap junction protein, gamma 2, 47kDa	2,418
NM_134260	RORA	RAR-related orphan receptor A	2,413
NM_206907	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	2,410
NM_006072	CCL26	chemokine (C-C motif) ligand 26	2,410
NM_001235	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	2,409

NM_053067	UBQLN1	ubiquilin 1	2,400
NM_001621	AHR	aryl hydrocarbon receptor	2,398
NM_006718	PLAGL1	pleiomorphic adenoma gene-like 1	2,395
NM_022117	TSPYL2	TSPY-like 2	2,394
NM_019116	UBFD1	ubiquitin family domain containing 1	2,390
AK002097	FLJ11235	hypothetical FLJ11235	2,390
NM_139160	DEPDC7	DEP domain containing 7	2,388
NM_018948	ERRFI1	ERBB receptor feedback inhibitor 1	2,388
NM_033514	LIMS3	LIM and senescent cell antigen-like domains 3	2,387
NM_015428	ZNF473	zinc finger protein 473	2,383
NM_025040	ZNF614	zinc finger protein 614	2,381
NM_020354	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	2,380
NM_002268	KPNA4	karyopherin alpha 4 (importin alpha 3)	2,380
BC036699	LOC654433	hypothetical LOC654433	2,372
NM_005126	NR1D2	nuclear receptor subfamily 1, group D, member 2	2,362
NM_032895	C17ORF91	chromosome 17 open reading frame 91	2,357
NM_001100	ACTA1	actin, alpha 1, skeletal muscle	2,355
NM_000640	IL13RA2	interleukin 13 receptor, alpha 2	2,352
NM_005066	SFPQ	splicing factor proline/glutamine-rich	2,350
NM_003359	UGDH	UDP-glucose 6-dehydrogenase	2,340
NM_003338	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	2,338
NM_014931	PPP6R1	protein phosphatase 6, regulatory subunit 1	2,333
NM_020651	PELI1	pellino homolog 1 (Drosophila)	2,331
NM_173354	SIK1	salt-inducible kinase 1	2,330
NM_175065	HIST2H2AB	histone cluster 2, H2ab	2,326
NM_170744	UNC5B	unc-5 homolog B (C. elegans)	2,324
BC038983	USP36	ubiquitin specific peptidase 36	2,322
NM_021217	ZNF77	zinc finger protein 77	2,318
NM_006644	HSPH1	heat shock 105kDa/110kDa protein 1	2,315
NM_012325	MAPRE1	microtubule-associated protein, RP/EB family, member 1	2,314
NM_002448	MSX1	msh homeobox 1	2,311
NM_006033	LIPG	lipase, endothelial	2,311
NM_004831	MED26	mediator complex subunit 26	2,305
NM_007039	PTPN21	protein tyrosine phosphatase, non-receptor type 21	2,304
NM_001321	CSRP2	cysteine and glycine-rich protein 2	2,304

NM_003533	HIST1H3I	histone cluster 1, H3i	2,302
NM_003745	SOCS1	suppressor of cytokine signaling 1	2,300
NM_004093	EFNB2	ephrin-B2	2,299
NM_022041	GAN	gigaxonin	2,297
NM_032145	FBXO30	F-box protein 30	2,295
NM_015394	ZNF10	zinc finger protein 10	2,293
AK090405	KDM4B	lysine (K)-specific demethylase 4B	2,291
NM_015723	PNPLA8	patatin-like phospholipase domain containing 8	2,290
NM_003655	CBX4	chromobox homolog 4	2,289
AI570240	ERRFI1	ERBB receptor feedback inhibitor 1	2,289
NM_002041	GABPB1	GA binding protein transcription factor, beta subunit 1	2,283
NM_004241	JMJD1C	jumonji domain containing 1C	2,280
NM_017798	YTHDF1	YTH domain family, member 1	2,278
NM_004040	RHOB	ras homolog gene family, member B	2,276
AK023803	ARF1	ADP-ribosylation factor 1	2,276
NM_025209	EPC1	enhancer of polycomb homolog 1 (Drosophila)	2,270
NM_014587	SOX8	SRY (sex determining region Y)-box 8	2,265
NM_018445	SELS	selenoprotein S	2,264
NM_006086	TUBB3	tubulin, beta 3	2,260
NM_015247	CYLD	cyliindromatosis (turban tumor syndrome)	2,246
NM_198077	C1ORF52	chromosome 1 open reading frame 52	2,241
NM_007350	PHLDA1	pleckstrin homology-like domain, family A, member 1	2,240
NM_018169	C12ORF35	chromosome 12 open reading frame 35	2,239
NM_145254	TMEM170A	transmembrane protein 170A	2,237
NM_032596	C9ORF24	chromosome 9 open reading frame 24	2,231
NM_019891	ERO1LB	ERO1-like beta (S. cerevisiae)	2,230
NM_000214	JAG1	jagged 1	2,227
NM_006322	TUBGCP3	tubulin, gamma complex associated protein 3	2,225
NM_152699	SENP5	SUMO1/sentrin specific peptidase 5	2,222
NR_002307	MSX2P	msh homeobox 2 pseudogene 1	2,222
AK090585	SNHG7	small nucleolar RNA host gene 7 (non-protein coding)	2,220
NM_019600	KIAA1370	KIAA1370	2,220
AI652920	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	2,216
NM_004864	GDF15	growth differentiation factor 15	2,214
NM_025106	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	2,210

NM_002641	PIGA	phosphatidylinositol glycan anchor biosynthesis, class A	2,209
S72869	CCDC6	coiled-coil domain containing 6	2,209
NM_152829	TES	testis derived transcript (3 LIM domains)	2,205
NM_175839	SMOX	spermine oxidase	2,202
NM_001002233	RAB11FIP1	RAB11 family interacting protein 1 (class I)	2,199
NM_003629	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	2,196
NM_024700	SNIP1	Smad nuclear interacting protein 1	2,192
NM_138800	TRIM43	tripartite motif-containing 43	2,191
NM_016006	ABHD5	abhydrolase domain containing 5	2,188
NM_206866	BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	2,186
NM_003537	HIST1H3B	histone cluster 1, H3b	2,183
NM_006832	FERMT2	fermitin family member 2	2,181
NM_000574	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	2,180
NM_005345	HSPA1A	heat shock 70kDa protein 1A	2,180
NM_016120	RLIM	ring finger protein, LIM domain interacting	2,180
NM_015046	SETX	senataxin	2,180
NM_005994	TBX2	T-box 2	2,179
NM_144606	FLCN	folliculin	2,174
NM_004582	RABGGTB	Rab geranylgeranyltransferase, beta subunit	2,170
NM_032829	C12ORF34	chromosome 12 open reading frame 34	2,167
NM_022826	MARCH7	membrane-associated ring finger (C3HC4) 7	2,161
NM_024708	ASB7	ankyrin repeat and SOCS box-containing 7	2,160
NM_007034	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	2,160
NM_005749	TOB1	transducer of ERBB2, 1	2,158
NM_006912	RIT1	Ras-like without CAAX 1	2,157
BG980953	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	2,154
NM_004947	DOCK3	dedicator of cytokinesis 3	2,154
NM_017447	C21ORF91	chromosome 21 open reading frame 91	2,150
NM_194285	SPTY2D1	SPT2, Suppressor of Ty, domain containing 1 (<i>S. cerevisiae</i>)	2,149
NM_138459	NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (<i>S. cerevisiae</i>)	2,146
BU731317	HSPA8	heat shock 70kDa protein 8	2,146
NM_006504	PTPRE	protein tyrosine phosphatase, receptor type, E	2,145
NM_018143	KLHL11	kelch-like 11 (<i>Drosophila</i>)	2,144
NM_001032281	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	2,144
NM_015092	SMG1	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (<i>C. elegans</i>)	2,144

NM_005238	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	2,142
NM_003622	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	2,141
NM_015683	ARRDC2	arrestin domain containing 2	2,140
NM_006007	ZFAND5	zinc finger, AN1-type domain 5	2,140
NM_017633	FAM46A	family with sequence similarity 46, member A	2,139
NM_004420	DUSP8	dual specificity phosphatase 8	2,139
NM_012421	RLF	rearranged L-myc fusion	2,138
NM_005156	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	2,137
CR622681	FLJ43663	hypothetical LOC378805	2,137
NM_007076	FICD	FIC domain containing	2,137
NM_006186	NR4A2	nuclear receptor subfamily 4, group A, member 2	2,132
NM_012238	SIRT1	sirtuin 1	2,130
NM_001005464	HIST2H3A	histone cluster 2, H3a	2,130
NM_015277	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	2,130
NM_006241	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	2,130
NM_006425	SLU7	SLU7 splicing factor homolog (S. cerevisiae)	2,128
NM_015161	ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	2,128
NM_012110	CHIC2	cysteine-rich hydrophobic domain 2	2,127
NM_133496	SLC30A7	solute carrier family 30 (zinc transporter), member 7	2,126
NM_000958	PTGER4	prostaglandin E receptor 4 (subtype EP4)	2,125
NM_014997	KLHDC10	kelch domain containing 10	2,125
NM_004405	DLX2	distal-less homeobox 2	2,123
NM_181453	GCC2	GRIP and coiled-coil domain containing 2	2,120
NM_005054	RGPD5	RANBP2-like and GRIP domain containing 5	2,117
NM_152718	VWCE	von Willebrand factor C and EGF domains	2,113
NM_015866	PRDM2	PR domain containing 2, with ZNF domain	2,111
NM_033083	EAF1	ELL associated factor 1	2,110
NM_004429	EFNB1	ephrin-B1	2,110
NM_020801	ARRDC3	arrestin domain containing 3	2,109
BC000527	EWSR1	Ewing sarcoma breakpoint region 1	2,103
NM_012257	HBP1	HMG-box transcription factor 1	2,099
NM_014395	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	2,098
NM_017548	CDV3	CDV3 homolog (mouse)	2,098
NM_001008394	EID3	EP300 interacting inhibitor of differentiation 3	2,097
NM_032417	SPANXD	SPANX family, member D	2,094

NM_152342	CDYL2	chromodomain protein, Y-like 2	2,094
NM_016040	TMED5	transmembrane emp24 protein transport domain containing 5	2,093
NM_003534	HIST1H3G	histone cluster 1, H3g	2,091
NM_000331	SAA1	serum amyloid A1	2,091
NM_032793	MFSD2A	major facilitator superfamily domain containing 2A	2,088
NM_001011713	NAA30	N(alpha)-acetyltransferase 30, NatC catalytic subunit	2,085
NM_020933	ZNF317	zinc finger protein 317	2,083
NM_173582	PGM2L1	phosphoglucomutase 2-like 1	2,081
NM_020119	ZC3HAV1	zinc finger CCCH-type, antiviral 1	2,080
NM_015368	PANX1	pannexin 1	2,080
NM_032228	FAR1	fatty acyl CoA reductase 1	2,080
NM_002852	PTX3	pentraxin 3, long	2,080
NM_018456	EAF2	ELL associated factor 2	2,079
NM_006577	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	2,079
NM_001040440	CCDC112	coiled-coil domain containing 112	2,078
X90978	RUNX1	runt-related transcription factor 1	2,075
NM_002184	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	2,074
NM_006509	RELB	v-rel reticuloendotheliosis viral oncogene homolog B	2,073
NM_014999	RAB21	RAB21, member RAS oncogene family	2,073
NM_144653	NACC2	NACC family member 2, BEN and BTB (POZ) domain containing	2,068
NM_017709	FAM46C	family with sequence similarity 46, member C	2,067
NM_002090	CXCL3	chemokine (C-X-C motif) ligand 3	2,067
NM_013360	ZNF222	zinc finger protein 222	2,065
AK125902	QSER1	glutamine and serine rich 1	2,059
NM_016379	VCX3A	variable charge, X-linked 3A	2,059
NM_002061	GCLM	glutamate-cysteine ligase, modifier subunit	2,056
NM_013452	VCX	variable charge, X-linked	2,056
NM_003531	HIST1H3C	histone cluster 1, H3c	2,054
NM_016378	VCX2	variable charge, X-linked 2	2,053
NM_004926	ZFP36L1	zinc finger protein 36, C3H type-like 1	2,049
BC011923	RBM33	RNA binding motif protein 33	2,049
NM_015878	AZIN1	antizyme inhibitor 1	2,044
NR_003098	SNHG1	small nucleolar RNA host gene 1 (non-protein coding)	2,042
NM_020414	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	2,040
NM_178815	ARL5B	ADP-ribosylation factor-like 5B	2,040

NM_021599	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	2,040
NM_002065	GLUL	glutamate-ammonia ligase	2,039
NM_138771	CCDC126	coiled-coil domain containing 126	2,038
NM_002167	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	2,038
NM_001197	BIK	BCL2-interacting killer (apoptosis-inducing)	2,038
NM_006275	SRSF6	serine/arginine-rich splicing factor 6	2,036
NM_032505	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	2,036
NM_005078	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	2,036
NM_182580	CYB561D1	cytochrome b-561 domain containing 1	2,034
NM_203411	TMEM88	transmembrane protein 88	2,032
NM_003290	TPM4	tropomyosin 4	2,030
NM_018047	RBM22	RNA binding motif protein 22	2,030
NM_007355	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	2,027
NM_015633	FGFR1OP2	FGFR1 oncogene partner 2	2,026
NM_032315	SLC25A33	solute carrier family 25, member 33	2,026
NM_003799	RNMT	RNA (guanine-7-) methyltransferase	2,022
NM_003921	BCL10	B-cell CLL/lymphoma 10	2,022
NM_020390	EIF5A2	eukaryotic translation initiation factor 5A2	2,021
NM_001025366	VEGFA	vascular endothelial growth factor A	2,020
NM_016605	FAM53C	family with sequence similarity 53, member C	2,020
NM_144975	SLFN5	schlafen family member 5	2,018
NM_058241	CCNT2	cyclin T2	2,018
NM_024018	BTN2A3	butyrophilin, subfamily 2, member A3	2,018
BF475893	TRIB1	tribbles homolog 1 (Drosophila)	2,015
NM_014701	SECISBP2L	SECIS binding protein 2-like	2,013
NM_005470	ABI1	abl-interactor 1	2,010
NM_003543	HIST1H4H	histone cluster 1, H4h	2,009
NM_005335	HCLS1	hematopoietic cell-specific Lyn substrate 1	2,008
NM_004907	IER2	immediate early response 2	2,007
NM_001558	IL10RA	interleukin 10 receptor, alpha	2,006
NM_002359	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	2,005
NM_021968	HIST1H4J	histone cluster 1, H4j	2,004
NM_020755	SERINC1	serine incorporator 1	2,004
NM_058229	FBXO32	F-box protein 32	2,002
NM_021945	SLC22A23	solute carrier family 22, member 23	2,001

NM_005266	GJA5	gap junction protein, alpha 5, 40kDa	-2,002
NM_002764	PRPS1	phosphoribosyl pyrophosphate synthetase 1	-2,003
NM_182513	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-2,005
NM_021824	NIF3L1	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	-2,008
NM_020190	OLFML3	olfactomedin-like 3	-2,012
NM_032015	RNF26	ring finger protein 26	-2,014
NM_032637	SKP2	S-phase kinase-associated protein 2 (p45)	-2,017
NM_021643	TRIB2	tribbles homolog 2 (Drosophila)	-2,019
CR594281	METTL3	methyltransferase like 3	-2,024
NM_005502	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	-2,025
NM_032831	ORAI2	ORAI calcium release-activated calcium modulator 2	-2,029
NM_005374	MPP2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	-2,036
NM_002034	FUT5	fucosyltransferase 5 (alpha (1,3) fucosyltransferase)	-2,037
NM_003119	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	-2,040
NM_006455	LEPREL4	leprecan-like 4	-2,041
NM_005576	LOXL1	lysyl oxidase-like 1	-2,046
NM_198580	SLC27A1	solute carrier family 27 (fatty acid transporter), member 1	-2,048
NM_000481	AMT	aminomethyltransferase	-2,048
NM_152308	C16ORF75	chromosome 16 open reading frame 75	-2,050
NM_005951	MT1H	metallothionein 1H	-2,050
NM_022167	XYLT2	xylosyltransferase II	-2,057
BC004287	ZNF704	zinc finger protein 704	-2,061
NM_021137	TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	-2,064
NM_173508	SLC35F3	solute carrier family 35, member F3	-2,064
AF495725	SLC25A37	solute carrier family 25, member 37	-2,067
NM_030641	APOL6	apolipoprotein L, 6	-2,069
NM_006876	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	-2,073
NM_004990	MARS	methionyl-tRNA synthetase	-2,087
NM_014897	ZNF652	zinc finger protein 652	-2,089
NM_000190	HMBS	hydroxymethylbilane synthase	-2,090
NM_207446	FAM174B	family with sequence similarity 174, member B	-2,103
NM_021198	CTDSP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	-2,107
NM_145294	WDR90	WD repeat domain 90	-2,119
NR_002791	EMX2OS	EMX2 opposite strand (non-protein coding)	-2,121
NM_138375	CABLES1	Cdk5 and Abl enzyme substrate 1	-2,125

NM_032854	CORO6	coronin 6	-2,127
AK098787	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	-2,135
NM_004613	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	-2,140
NM_000930	PLAT	plasminogen activator, tissue	-2,140
NM_017712	PGPEP1	pyroglutamyl-peptidase I	-2,142
NM_006113	VAV3	vav 3 guanine nucleotide exchange factor	-2,145
AK023606	ADAMTSL4	ADAMTS-like 4	-2,146
NM_001567	INPPL1	inositol polyphosphate phosphatase-like 1	-2,148
NM_000149	FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	-2,159
NM_057161	KLHDC3	kelch domain containing 3	-2,160
NM_181832	NF2	neurofibromin 2 (merlin)	-2,163
NM_005952	MT1X	metallothionein 1X	-2,170
NM_176798	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	-2,178
NM_005325	HIST1H1A	histone cluster 1, H1a	-2,179
NM_005479	FRAT1	frequently rearranged in advanced T-cell lymphomas	-2,179
NM_138370	PKDCC	protein kinase domain containing, cytoplasmic homolog (mouse)	-2,182
NM_175617	MT1E	metallothionein 1E	-2,192
NM_005434	MALL	mal, T-cell differentiation protein-like	-2,192
NM_032883	TOX2	TOX high mobility group box family member 2	-2,194
NM_175709	CBX7	chromobox homolog 7	-2,194
X97261	MT1L	metallothionein 1L (gene/pseudogene)	-2,206
	LOC10013119		
AL359605	9	transmembrane protein 178-like	-2,211
NM_018205	LRRC20	leucine rich repeat containing 20	-2,228
NM_002692	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	-2,237
NM_138768	MYEOV	myeloma overexpressed (in a subset of t(11;14) positive multiple myelomas)	-2,241
NM_001874	CPM	carboxypeptidase M	-2,250
NM_001039651	C6ORF26	chromosome 6 open reading frame 26	-2,254
NM_005322	HIST1H1B	histone cluster 1, H1b	-2,272
NM_005397	PODXL	podocalyxin-like	-2,274
NM_005947	MT1B	metallothionein 1B	-2,304
NM_001001522	TAGLN	transgelin	-2,309
NM_000693	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	-2,309
AK056534	LOC145757	hypothetical LOC145757	-2,314

NM_001067	TOP2A	topoisomerase (DNA) II alpha 170kDa	-2,317
NM_005730	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	-2,323
NM_005950	MT1G	metallothionein 1G	-2,326
NM_000674	ADORA1	adenosine A1 receptor	-2,359
NM_005071	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	-2,368
NM_015346	ZFYVE26	zinc finger, FYVE domain containing 26	-2,370
NM_017637	BNC2	basonuclin 2	-2,411
NM_000430	PAFAH1B1	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	-2,449
NM_018706	DHTKD1	dehydrogenase E1 and transketolase domain containing 1	-2,522
NM_153840	GPR110	G protein-coupled receptor 110	-2,611
NM_032865	TNS4	tensin 4	-2,686
AK022110	GPX8	glutathione peroxidase 8 (putative)	-2,695
NM_005566	LDHA	lactate dehydrogenase A	-2,716
AK095678	LOC151009	hypothetical LOC151009	-2,745
NM_015035	ZHX3	zinc fingers and homeoboxes 3	-2,818
NM_002318	LOXL2	lysyl oxidase-like 2	-3,160

Table 2. Significantly over-represented biological processes in the whole transcriptome signature of EVOO secoiridoids-treated human breast cancer cells

Gene Expression	Significantly Over-represented BIOLOGICAL PROCESS	ES
Down-regulated		
EVOO-PE7	Hexose Catabolic Process	1.63
	Cell Cycle (M phase)	1.30
	Cellular Component Assembly	1.20
	Cellular Metabolic Process	1.05
	Cellular Carbohydrate Metabolic Process	1.00
	Regulation of Cell Adhesion	1.00
	DNA Metabolic Process	1.00
Up-regulated		
EVOO-PE7	Developmental Process	9.16
	Positive Regulation of Biological Process	8.17
	Biological Regulation (Regulation of Gene Expression)	7.68
	Biopolymer Metabolic Process	7.16
	Negative Regulation of Biological Process (Transcription)	6.68
	Response to Stress	6.33
	Regulation of Cell Cycle	6.17
	Organ Morphogenesis	5.73
	Response to Chemical Stimulus (Unfolded Protein)	5.31
	Regulation of Cell Differentiation (Hemopoiesis)	3.87
	Regulation of Biological Quality (Cell Growth/Cell Size)	3.62
	Positive Regulation of Metabolic Process (Transcription)	3.41
	Regulation of a Molecular Function (MAP Kinase Activity)	3.04
	Regulation of Apoptosis (Induction of Cell Death)	2.73
	Response to Wounding	2.59
	Embryonic Pattern Specification (Tube Development)	2.53
	Chromatin Assembly	2.45
	Muscle Development (Myoblast Differentiation)	2.34
	Nitric Oxide Biosynthetic Process	2.34
	Signal Transduction	2.14
	Post-Translational Protein Modification (Ubiquitin)	2.09
	Reproduction (Gamete Generation)	1.98
	Embryonic Pattern Specification (Cell Fate Commitment)	1.85
	Tissue Development (Epidermis)	1.84
	Tube Development (Lung)	1.74
	Regulation of Body Fluid Levels (Hemostasis)	1.72
	Lymphocyte Differentiation (T cell activation)	1.58
	Mast Cell Cytokine Production	1.57
	Cell Migration	1.56
	Cell Activation (B cell activation)	1.48
	Protein Ubiquitination	1.37
	Skeletal Development (Bone Remodeling)	1.28
	Negative Regulation of Phosphorylation (Lymphocyte Activation)	1.27
	Inflammatory Response	1.09
	Protein Digestion (Collagen Catabolic Process)	1.07
	Negative Regulation of Hormone Secretion	1.06
	mRNA Metabolic Process	1.00
	Polyamine Metabolic Process	1.00

DAVID (Database for Annotation, Visualization and Integrated Discovery) provides tools and statistical methods for discovering enriched processes and pathways within diverse and disparate gene lists. We used the DAVID functional annotation tool, which provides Gene Ontology (GO) term enrichment analysis, to highlight the most relevant GO terms associated with the gene list generated by treatment of JIMT1 breast cancer cells with EVOO secoiridoids. We used extended annotation coverage that not only included GO terms but also protein-protein interactions, disease associations, bio-pathways, gene functional summaries, gene tissue expression, and relevant literature. Gene functional classifications of EVOO secoiridoid-responsive gene expression changes in human breast cancer cells were evaluated in terms of enrichment scores (for each gene cluster), which were calculated as the geometric mean of all the enrichment p-values (EASE [ES] scores) for each annotation term associated with the gene members in the group. The geometric mean is a relative score instead of an absolute p-value, and therefore, minus log transformation is applied on the average p-values. A higher score for a group indicates that the gene members in the group are involved in more important (enriched) terms and, consequently, more attention should be given to them. An enrichment score of 1.3 is equivalent to non-log scale 0.5. Thus, more attention should be given to groups with scores ≥ 1.3 .