Supplementary Material

The Clinicopathological Significance and Correlative Signaling Pathways of an Autophagy-Related Gene, Ambra1, in Breast Cancer: a Study of 25 Microarray RNA-Seq Datasets and in-House Gene Silencing

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	E-GECOD-28117 (13) E-GECOD-27103 (22) E-GECOD-27103 (22) E-GECOD-27103 (22) E-GECOD-27103 (22) E-GECOD-27103 (22) E-GECOD-27103 (22) E-GECOD-27103 (22) E-GECOD-27103 (22) E-GECOD-27103 (22) E-GECOD-27104 (5) E-GECOD-27104 (5) E-GECOD-27104 (5) E-GECOD-27104 (5) E-GECOD-27104 (5) E-GECOD-27105 (22) E-GECOD-27105 (22)	rank 1		last sd 0
AMBRA1 SUPT6H		5.17e-46	AMBRA1 SUPT6H	234237_S_AT 1554311_a_at
MAU2 TEE2		2.28e-42	MALI2 TEE2	210920_s_at
FOXK2		1.43e-39	FOXK2	242938 s at
MCMBAP		499e-39	MCMBAP	215581_s_at
VARS		473e-36	VARS	201796_s_at
MFN2		1.2e-35	MFN2	216205_s_at
CRKL		2.57e-35	CRKL	206184_at
KLAA0430		1.188-34	KIAA0430	1536097_a_at
PHF12 RFM33		1.388-34	PHF12 RBM33	239801 at
CNOT4		3.5Be-34	CNOT4	210866 s at
HSF1		1.51e-33	HSF1	213756_s_at
WDR8		1.7e-33	WDR6	233573_s_at
CANT1		2.88e-33	CANT1	1554327_a_at
PT BP1		438e-33	PT BP1	212016_s_at
RNF38 7NE217		1.148-32	KNF38 7NE247	1555337 a at
ZRTB45		7816-32	ZRTB45	240551 at
UPF1		8.89e-32	UPF1	208947 s at
MTMR3		2.24e-31	MTMR3	211507_s_at
TMEM2 59		2.7e-31	TMEM2 59	212575_at
RBM14		4.57e-31	RBM14	1555639_a_at
MTMR1		584e-31	MTMR1	214975_s_at
CEO DENDE		6.14e-31	CODESOF	21030/_S_8t
GIVR1		6.780-31	GIVR1	221628 s at
KCT D20		9.06e-31	KCT D20	214849 at
COPA		2.09e-30	COPA	214336_s_at
AC009487		3.01e-30	AC009487.	_1580224_at
SMURF1		3.45e-30	SMURF1	215458_s_at
RAB35		9.58e-30	RAB35	205461_at
SMG7		1.48e-29	SMG7	21/189_5_8t
REPIN1		4310-29	REPINI	222501 s at
MED1		6.13e-29	MED1	1555611 s at
GGA3		6.57e-29	GGA3	211815_s_at
NUP133		1.03e-28	NUP133	233421_s_at
SP1		2.26e-28	SP1	214732_at
YTHDF3		3.53e-28	YTHDF3	1564053_a_at
MIER3		3.81e-28	MIER3	1553336_a_at
TMEND 50		2.048-27	TMENDER	213986 s at
ARHGAPI		2.540-27	ARHGAPI	216689 x at
CTDS PL2		2.9e-27	CTDSPL2	1555106_a_at
RAD51L3		3.25e-27	RAD51L3-	1552649_a_at
WIZ		3.26e-27	WIZ	221785_at
DDX42		3.63e-27	DDX42	1559954_s_at
ZDHHC5 NFRKB		4.42e-27 5.76e-27	ZDHHC5 NFRKB	224868_at 206968_s_at

		mov 1		last
	Control Contro Control Control Control Control Control Control Control Control Co	Fight Inc.		>3
	1119 1119 1119 1119 1119 1119 1119 111			0
	(112) (112)			
AMBRA1			AMBRA1	52731_AT
AMBRA1		8.85e-82	AMBRA1	219141_s_at
ELMO2 BRD1		3.91e-39	BRD1	215460 x at
BRD1		1.66e-38	BRD1	204520_x_at
KBTBD4		6.67e-38	KBTBD4	218570_at
MTMR3		8.29e-38	MTMR3	202197_at
ZNF/64		2.408-3/	ZNF/04	219433 at
SART3		6.4e-37	SART3	200069_at
FOXJ3		3.35e-36	FOX.J3	206015_s_at
ZNF410		427e-36	ZNF410	209944_at
CIAPINI		8.83e-36	CIAPINI	208424_s_at
SI KJO RARGAPI		1.10e-35 2.82a-35	RARGAPI	213313 at
CRKL		4748-35	CRKL	212180_at
TLK2		1.27e-34	TLK2	212997_s_at
GAPVD1		1.72e-34	GAPVD1	212802_s_at
CST F1		2.648-34	CSTF1	32125_8t
PSEN1		2.946-34	PS EN 1	203460 s at
CNOT4		5.57e-33	CNOT4	203291_at
PT PRA		6.07e-33	PTPRA	213795_s_at
SAP130		8.66e-33	SAP130	220367_s_at
CTORF55		1.110-32	CTORF55-	_21/842_at
KPNA8		2.48a-30	KPNA8	226976 at
RTF1		2.728-32	RTF1	212301_at
ASXL1		3.93e-32	ASXL1	212234_at
EHMT1		4.06e-32	EHMT1	22.5461_at
SP2 NCOA6		4./30-32	SP2 NCOAR	204307_at 208070_at
CHERP		3.81e-31	CHERP	202230 s at
RNF169		57e-31	RNF169	226739_at
RBM33		6.08e-31	RBM33	226732_at
ELMO2		7.74e-31	ELMO2	221528_s_at
KTMDA		9.03e-31	KUNDA	208988 at
DYRK1A		9.68e-31	DYRK1A	209033_s_at
GGNBP2		9.89e-31	GGNBP2	233936_s_at
TRRAP		1.37e-30	TRRAP	202642_s_at
RBM10		1.78e-30	RBM10	208984_x_at
SNAP47		2.398-30	SNAP47	22 5244 at
CSNK2A1		3.82e-30	CSNK2A1	212072_s_at
UBR7		4.39e-30	UBR7	218108_at
UXS1		6.13e-30	UDS1	22,5583_at
MED29		6.85e-30	MED29	15558.41 e et
WDR92		9.49-30	WDR92	201934 at
AFTPH		1.08e-29	AFTPH	222472 at

	E-GECOD - 19882 (5) E-GECOD - 223375 (5) E-GECOD - 223476 (8) E-GECOD - 23476 (8) E-GECOD - 23477 (11) E-GECOD - 23476 (8) E-GECOD - 23477 (11) E-GECOD - 23476 (8) E-GECOD - 23477 (12) E-GECOD - 23476 (8) E-GECOD - 23476 (8) E-GECOD - 23476 (8) E-GECOD - 27482 (8) E-GECOD - 27483 (12) E-GECOD - 27494 (14) E-GECOD - 27494 (14) E-GECOD - 27494 (14) E-GECOD - 27494 (14)	rank 1		last > 3 = 50 0
AMBRA1 (242862 (239959 SMG1 TCTN2 RP11-717 (216702 (241632)		1.28e-29 6.14e-28 1.42e-26 6.42e-26 7.38e-26 1.65e-25 2.36e-25	AMBRA1 (242862 (239959 SMG1 TCTN2 RP11-717_ (216702 (241632	234236_AT 242862_x_at 239959_x_at 1558534_at 206438_x_at 234773_x_at 216702_x_at 241632_x_at
(238701		2.52e-25	(238701	238701_x_at
(1553498		4.52e-25	(1553498	1553498_at
(1566145.		7.35e-25	(1566145	1566145_s_at
TRIM4		1.39e-24	TRIMH	224159_x_at
(215278		1.61e-24	(215278	215278_at
(220725		2.09e-24	(220725	220725_x_at
(220691		2.53e-23	(220891	220691_at
220874		2.64e-22	(220874)	200874_at
(1566581		446e23	(1506581	1566581_at
[240002		771e23	(240002	240002_at
[233810		1.55e22	(233810	233810_x_at
C100 RF67		2.31e22	C100 RF67	1553843_at
[234494		474e22	(234494	234494_x_at
[241615		497e22	(241615	241615_x_at
[216704		581e22	(216704	216704_at
CD054]		7.55e22	CF05	20005_x_at
(236389		8.07e-22	(236389	236389_x_at
(217054		1.13e-21	(217054	217054_at
(234805		1.17e-21	(234805	234805_at
(231527		1.29e-21	(231527	231527_at
(215182		1.53e-21	(215182	215182_x_at
(222329		1.62e-21	(222329	222329_x_at
(224276		1.83e-21	(222329)	224276_at
(234906		2.71e-21	(234906	234906_at
(242266		2.96e-21	(242266	242266_x_at
(210741		3.38e-21	(210741	210741_at
(240988		3.98e-21	(240988	240988_x_at
(232917		4.46e-21	(232917	232917_at
RP11-755		5.46e-21	RP11-756.	15661102_at
(1566452		6.04e-21	(1566452.	1566452_at
(214019		1.06e-20	(214019	214019_at
ZNF445		1.07e-20	ZNF445	233992_x_at
(1566644		1.19e-20	(1566644.	1566644_at
(216153		1.22e-20	(216153	216153_x_at
(232495		1.36e-20	(232495	232495_x_at
RIMS2		1.54e-20	RIMS2	215478_at
KLF13		1.54e-20	KLF13	1564463_at
(220877		1.87e-20	(220877	220877_at
(1564208		2.12e-20	(1564208	1564306_at
EPPIN		2.3e-20	EPFIN	206318_at
(211585		2.72e-20	(211585	211585_at
(233891		2.83e-20	(233891	233891_at
(232556		2.97e-20	(232558	232556_at

	EGECD - 2877 EGECD - 2789 EGECD - 11299 EGECD - 11299 EGEC	rank 1		last sd 0
				2101.41 S AT
AMBRA1		572e-122	AMBRA1	52731 at
PRKD2		3.24e-30	PRKD2	38269_at
TRIM11		3.36e-29	TRIM11	226566_at
SEC24C		7.93e-29	SEC24C	202361_at
RHED D3		9.45e-28	RHED D3	204402_at
DH030		2.25e-28	DHX30	204355_at
PRKD2		4.62e-28	PRKD2	209282_at
DNASE1L2		6.74e-26	DNASE1L2	218524_at 38308_at
SART1		3.58e-25	SART1	200051 at
CSNK1D		4.5e-2.5	CSNK1D	208774_at
ARFGAP2		3.82e-24	ARFGAP2	211975_at
ZNF282		1.49e-23	ZNF282	212892_at
SE3R2		2.68a-23	SE3R2	200619 at
KCT D2		3.38e-23	HCT D2	212564_at
FAM193A		3.43e-23	FAM193A	203600_s_at
DH030		3.68e-23	DHX30	212674_s_at
ZBTR17		9200-23	ZBTR17	200904_x_at 203602 s at
PRCC		7.95e-23	PRCC	208938_at
PRPF31		8.17e-23	PRPF31	202408_s_at
PUF60		1.11e-22	PUF60	209899_s_at
COPS7B		1.12e-22	COPS78	219997_s_at 2263.57_at
ARFGAPI		1.48e-22	AREGAPI	217888 s at
AAMP		1.48e-22	AAMP	201511_at
MADD		3.04e-22	MADD	210252_s_at
MFSD10		3.24e-22	MFSD 10	209215_at
RBM10		3.82e-22 486e-22	RRMID	205419_at 215089_s_at
PI4KB		6.44e-22	FI4KB	206138 s_at
BAP1		7.16e-22	BAP1	201419_at
UPF1		7.170-22	UPF1	211168_s_at
ATG2A		9.29e-22 0.34a.22	ATG2A	213300 at
IP6K1		1.36e-21	IP6K1	212439_at
BUD13		1.39e-21	BUD13	224504_s_at
GTF3C1		1.61e-21	GTF3C1	35671_at
ATG13		1.71e-21	ATG13	203364_s_at
KCT D2		3.7e-21	KCT D2	34858 at
CRTC2		443e-21	CRTC2	226307_at
TMEM2 59		462e-21	TMEM2 59	22.5247_at
RBM		473e-21	RBMA	200997_at
PHRP 1 BANP		498a-21	PANP	233186 s at
HRAS		7.37e-21	HRAS	212983_at
PAF1		7.66e-21	PAF1	202093_s_at



Supplementary materials

Figure S1: Bioinformatics analysis of 181 overlapping genes of differentially expressed genes (DEGs) in breast cancer (BC) and Ambra1 co-expressed genes. (A) DEGs following Ambra1 knock-down in BC cells presented as a volcano plot. DEGs are marked in blue. (B) DEGs following Ambra1 knock-down in BC cells presented as a heatmap. (C) Venn diagram for 183 overlapping genes of DEGs in BC and Ambra1 co-expressed genes. (D) Most enriched biological process terms of 183 overlapping genes of DEGs and Ambra1 co-expressed genes. (E) Most enriched cellular component terms of 183 overlapping genes. (F) Most enriched molecular function terms of 183 overlapping genes. (G) The significant Kyoto Encyclopedia of Genes and Genomes pathways of the 183 overlapping genes. (H) Protein–protein interaction network of 183 overlapping genes. Disconnected nodes were hidden in the network. Each circle represents a protein encoded by the corresponding gene. Each line represents a protein–protein association. The node size changes gradually from small to large in ascending order according to the combined score between two neighbored genes. FC: fold change; KD: knock-down; NC: negative control.

Figure S2: Co-expressed genes of Ambra1 downloaded from MEM database based on probe 234237_S_AT.

Figure S3: Co-expressed genes of Ambra1 downloaded from MEM database based on probe 52731_AT.

Figure S4: Co-expressed genes of Ambra1 downloaded from MEM database based on probe 234236_AT.

Figure S5: Co-expressed genes of Ambra1 downloaded from MEM database based on based on probe 219141_S_AT.

Figure S6: Gene set enrichment analysis of 12 overlapping genes of differentially expressed genes (DEGs) in breast cancer (BC), Ambra1 co-expressed genes, and Ambra1

similar genes. (A) Venn diagram for 12 overlapping genes of DEGs in BC, Ambra1 coexpressed genes, and Ambra1 similar genes. (B) Expression patterns of 12 overlapping genes in various human tissues based on the GSEA database. (C) Expression patterns of 12 overlapping genes in 60 cell lines based on the GSEA database.