

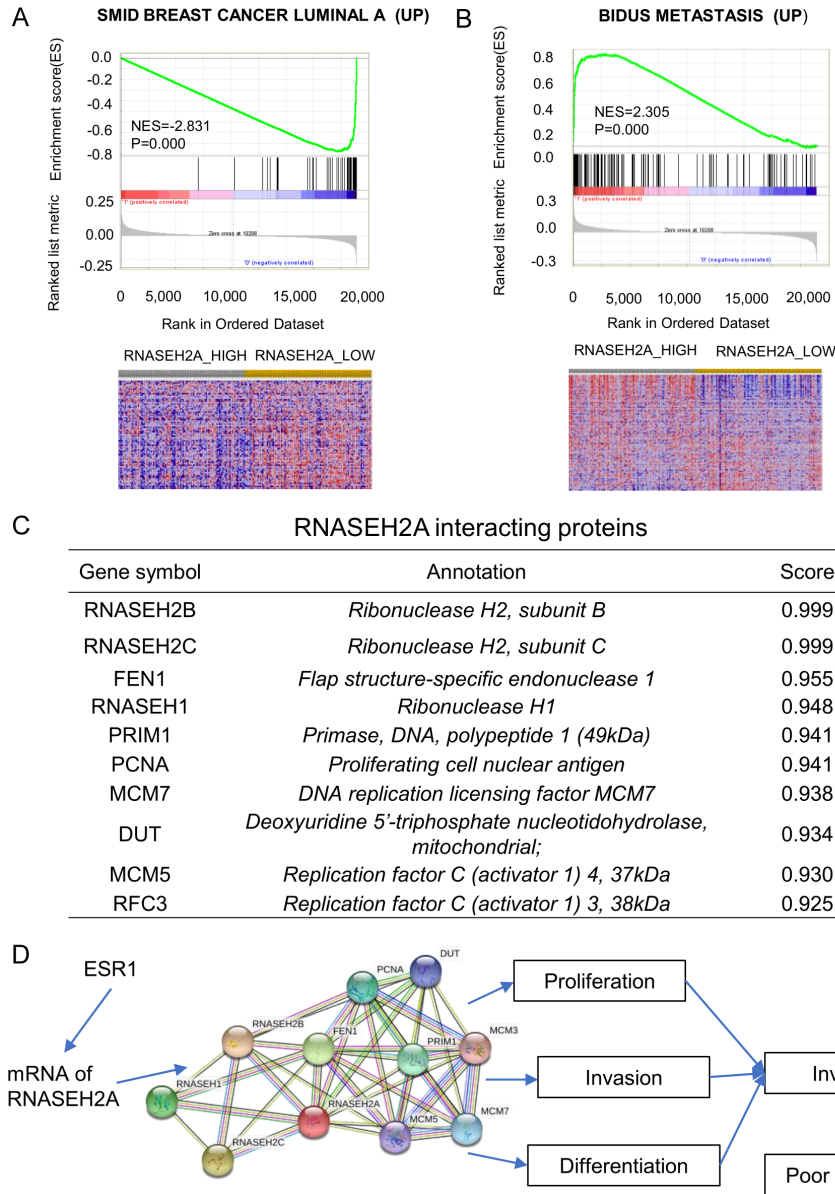
Prognostic value of RNASEH2A in ER+ breast cancer

Supplementary Table 1. Summary of download gene expression data sets

Accession No.	No. of patients	Platforms*	Country	Clinical factors#	OS months	PFS months
GSE7390	198	GPL96	Canada	P	4.9-303.6	4.0-290.4
GSE1456	159	GPL96/GPL97	Sweden	P	2.2-101.9	2.2-101.9
GSE2034	286	GPL96	USA	P	N/A	2.0-171.0
GSE4922	289	GPL96/GPL97	Singapore	P	N/A	0.0-153.0
GSE10885	154	GPL885/GPL887	USA	P	1.0-118.0	1.0-118.0
GSE22226	129	GPL1708/GPL4133	USA	P	9.5-82.0	6.0-84.0
GSE24450	183	GPL6947	Finland	N	22.4-120	0.8-60.0
GSE25066	508	GPL96	USA	P	N/A	1.7-88.3
GSE53031	167	GPL13667	Belgium	P	N/A	2.0-156.0
GSE58812	107	GPL570	France	P	1.0-171.7	1.0-171.7
GSE22220	216	GPL6098	UK	P	N/A	5.0-120.0
GSE3143	158	GPL8300	USA	N	5.7-156.2	N/A
GSE3494	251	GPL96/GPL97	Singapore	P	0.0-153.0	N/A
GSE11121	200	GPL96	Germany	P	N/A	1.0-240.0
GSE12276	204	GPL570	Netherlands	N	N/A	0.0-115.0
GSE6532	244	GPL96/GPL97/GPL570	Canada	P	N/A	0.3-174.4
GSE42568	105	GPL570	Ireland	P	4.5-99.5	4.5-99.5
GSE12093	136	GPL96	USA	P	N/A	7.6-192.6
GSE20624	176	GPL885/GPL887	USA	P	1-118	1-118
GSE20685	327	GPL570	France	P	0-127	4.8-169.2
GSE21653	266	GPL570	France	P	N/A	0-222
GSE7849	78	GPL8300	USA	P	N/A	10.3-157.5
NKI	295	Agilent 25K Chip	Netherlands	A	1.0-220.1	1.0-220.1
TCGA set-1	526	N/A	N/A	P	0-282.7	0-281
TCGA set-2	1904	N/A	N/A	P	0-355	N/A
TCGA set-2	564	N/A	N/A	P	0-216.6	0-214.7

*Platforms: GPL96: [HG-U133A] Affymetrix Human Genome U133A Array; GPL97: [HG-U133B] Affymetrix Human Genome U133B Array; GPL570: [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array; GPL13667: [HG-U219] Affymetrix Human Genome U219 Array; GPL8269: Agilent UNC PerouLab 244K Custom Human Array version 5; GPL1708: Agilent-012391 Whole Human Genome Oligo Microarray G4112A; GPL4133: Agilent-014850 Whole Human Genome Microarray 4x44K G4112F; GPL885: Agilent-011521 Human 1A Microarray G4110A; GPL887: Agilent-012097 Human 1A Microarray (V2) G4110B; GPL6947: Illumina HumanHT-12 V3.0 expression beadchip; GPL6098: Illumina humanRef-8 v1.0 expression beadchip. #Clinical factors: Age at diagnosis, Elson grade, Tumor size, Lymph node, Metastasis, ER status, Molecular subtype. A: all include; P: partial include; N: none.

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Supplementary Figure 1. Bioinformatic analysis of gene signature enrichment and protein-protein interaction networks for RNASEH2A. A. GSEA results of the SMID breast cancer luminal A gene set (upregulation of RNASEH2A mRNA). B. GSEA results of the BIDUS metastasis (upregulation of RNASEH2A mRNA) gene set in the GSE22220 dataset. The functional protein association networks of RNASEH2A. Blue indicates a low level of expression and red indicates a high level of expression. C. The predicted functional partners of RNASEH2A. D. Protein-protein interaction network of RNASEH2A.