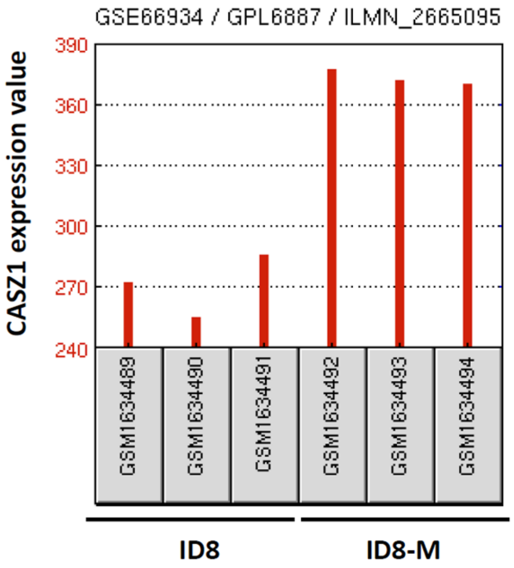
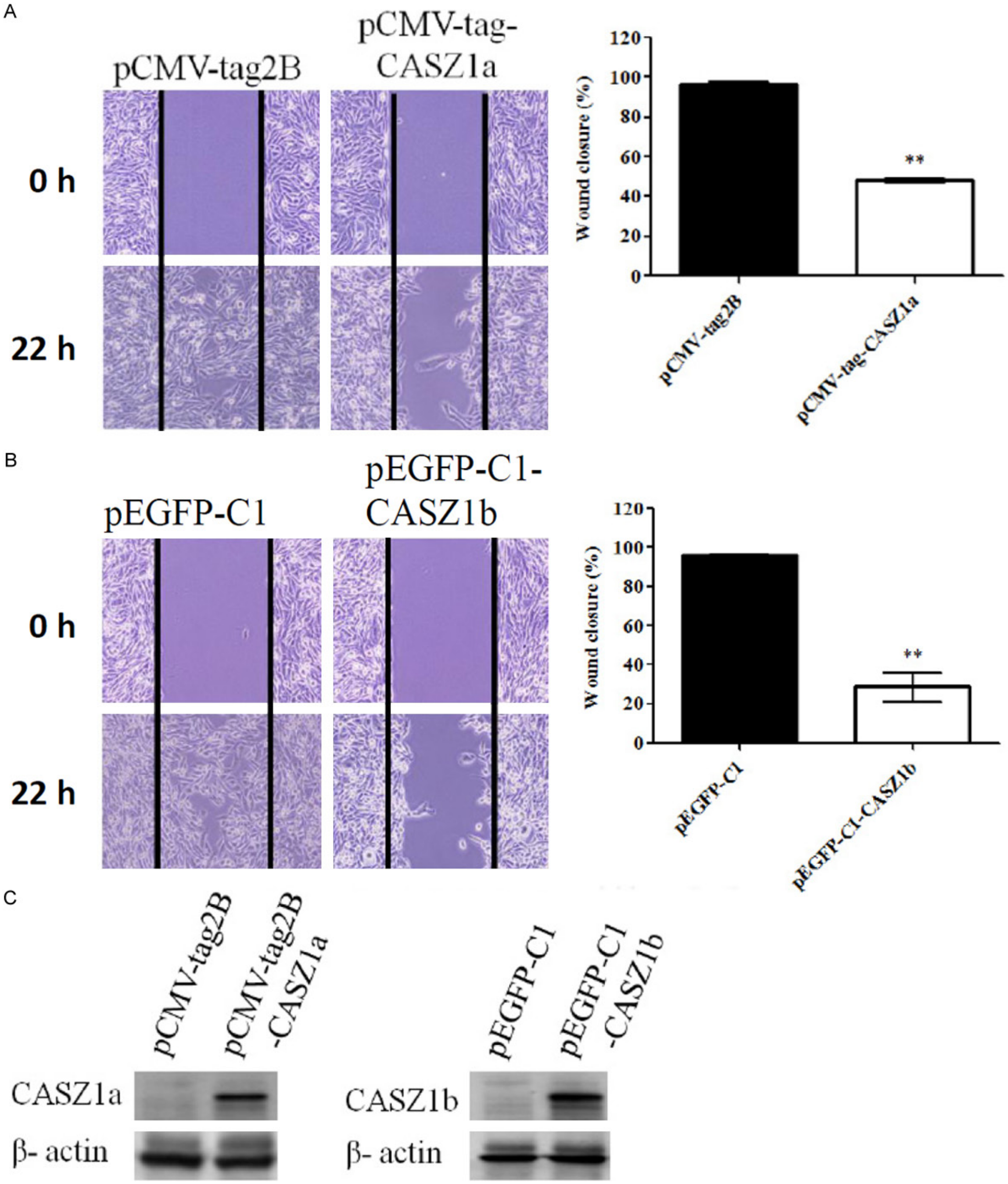
Supplementary Table 1. Top 10 up-and down-regulated genes and other metastasis-related genes in MCAS cells with sh-CASZ1 (2) and sh-CASZ1 (3), compared to that in sh-luc cells by the analysis of microarray data

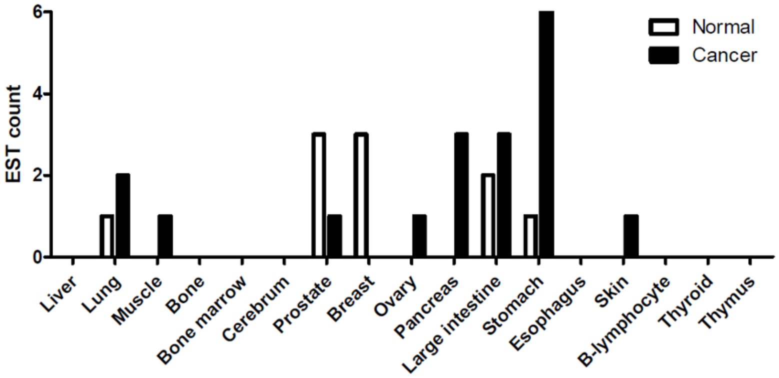
Gene symbol	Accession No.	Gene description	Log2 fold-change (sh-CASZ1 (2)/sh-luc)	Log2 fold-change (sh-CASZ1 (3)/sh-luc)
IL8	NM_000584.2	Homo sapiens interleukin 8	-2.97	-2.84
SERPINA3	NM_001085.4	Homo sapiens serpin peptidase inhibitor, clade A, member 3	-2.32	-2.19
GDF15	NM_004864.1	Homo sapiens growth differentiation factor 15	-2.22	-2.39
CXCL2	NM_002089.3	Homo sapiens chemokine (C-X-C motif) ligand 2	-2.12	-2.10
SAA1	NM_000331.3	Homo sapiens serum amyloid A1	-2.10	-1.98
CXCL1	NM_001511.1	Homo sapiens chemokine (C-X-C motif) ligand 1	-2.10	-2.13
C15ORF48	NM_032413.2	Homo sapiens chromosome 15 open reading frame 48	-2.05	-2.12
FST	NM_006350.2	Homo sapiens follistatin	-1.92	-1.96
PHGDH	NM_006623.2	Homo sapiens phosphoglycerate dehydrogenase	-1.85	-1.76
RARRES3	NM_004585.3	Homo sapiens retinoic acid receptor responder 3	-1.84	-1.78
CCL20	NM_004591.1	Homo sapiens chemokine (C-C motif) ligand 20	-1.76	-1.82
TNF	NM_000594.2	Homo sapiens tumor necrosis factor	-1.24	-1.33
MMP7	NM_002423.3	Homo sapiens matrix metallopeptidase 7	-1.05	-1.05
SAA4	NM_006512.1	Homo sapiens serum amyloid A4	-0.78	-0.82
IL6	NM_000600.1	Homo sapiens interleukin 6	-0.72	-0.80
S100A4	NM_019554.2	Homo sapiens S100 calcium binding protein A4	-0.68	-0.74
SAA2	NM_030754.2	Homo sapiens serum amyloid A2	-0.62	-0.59
DHRS9	NM_005771.3	Homo sapiens dehydrogenase/reductase member 9	1.41	1.41
SNAPC4	NM_003086.2	Homo sapiens small nuclear RNA activating complex, polypeptide 4	1.43	1.49
INTS1	NM_001080453.1	Homo sapiens integrator complex subunit 1	1.45	1.11
NTSR1	NM_002531.2	Homo sapiens neurotensin receptor 1	1.49	1.48
IL1RL1	NM_016232.4	Homo sapiens interleukin 1 receptor-like 1	1.60	1.53
TXNIP	NM_006472.2	Homo sapiens thioredoxin interacting protein	1.63	1.65
ZDHHC11	NM_024786.1	Homo sapiens zinc finger, DHHC-type containing 11	1.75	1.66
HAS3	NM_005329.2	Homo sapiens hyaluronan synthase 3	1.80	1.72
KRT6A	NM_005554.3	Homo sapiens keratin 6A	1.89	1.92
MMP1	NM_002421.2	Homo sapiens matrix metallopeptidase 1	2.03	2.13



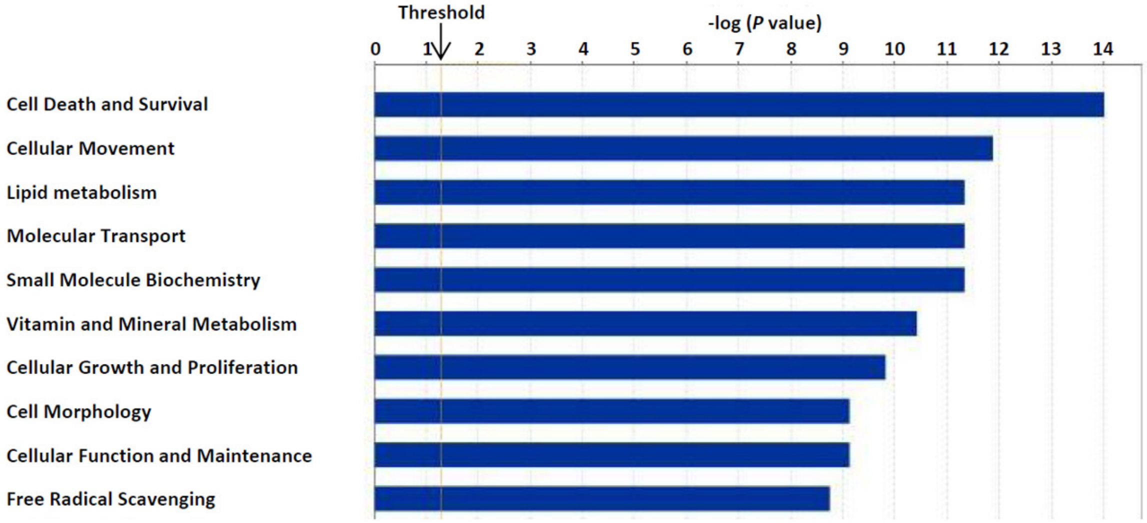
Supplementary Figure 1. CASZ1 expression is higher in mouse ovarian cancer cells with accelerated metastatic phenotype. CASZ1 expression is analyzed in a GEO dataset, GSE66934. ID8-M cells is *in vivo* selected from ascites in mice intraperitoneally injected parental ID8 cells, a mouse ovarian epithelial papillary serous adenocarcinoma cell line. ID8-M exhibits a rapid metastatic phenotype.



Supplementary Figure 2. Overexpression of CASZ1 inhibits the migration abilities in SHSY5Y cells. SH-SY5Y cells were transfected with pCMV-tag2B vector or pCMA-tag-CASZ1a (A), and pEGFP-C1 vector or pEGFP-C1-CASZ1b (B). The migration ability was examined by wound healing assay. Error bars represent SEM. **, $P < 0.005$ by Student's t-test. (C) The expression of CASZ1a or CASZ1b in CASZ1-overexpressed SH-SY5Y cells was analyzed by immunoblotting. β-actin was used as the internal control.



Supplementary Figure 3. CASZ1 is highly expressed in ovarian cancer tissues analyzed by *in silico* data mining. The EST expression analysis of the CASZ1 gene in different normal and cancerous tissues was modified from the ECgene database (http://genome.ewha.ac.kr/ECgene/).



Supplementary Figure 4. Ingenuity Pathways Analysis (IPA) for microarray data of MCAS cells with sh-luc, sh-CASZ1 (2), and sh-CASZ1 (3).