

Table S2. Synbindin regulates the ERK/MAPK, which is activated gastric cancers.

ERK/MAPK related genes					
Gene Symbol	Synbindin expression		Gastric cancer		Relevance to MAPK pathway and cell survival
	P-value*	FC*	P-value	FC***	
ACTG2	0.033	2.590	0.017	1.563	phosphorylated by ERK
DUSP5	0.040	1.680	0.001	1.577	phosphorylated by ERK
SEPT7L	0.049	1.950	0.008	1.072	phosphorylated by ERK
HNRNPA3	0.017	2.360	0.033	1.117	putative ERK-regulated gene
IGFBP3	0.046	1.570	0.002	1.629	expression regulated by ERK
TLR4	0.003	1.640	0.041	1.765	dependent on MSK, downstream of ERK
SRP19	0.013	1.880	0.225	0.892	ribonucleoprotein regulated by ERK
PPM1H	0.019	2.020	0.438	0.796	affects HER phosphorylation, downstream of ERK
OLR1	0.046	1.540	0.000	2.120	initiates ERK activation
RNASEL	0.047	2.300	0.025	1.631	required for ERK activation by LPS
EDN1	0.038	1.870	0.401	1.147	activates ERK
RSU1	0.029	1.620	0.434	0.791	enhances ERK activation and inhibits JNK
EDN2	0.030	1.510	0.683	1.138	chemotaxis towards EDN2 is via ERK
NRG1	0.021	1.510	0.024	1.602	activates ERK
COL8A1	0.003	1.860	0.025	1.402	promotes proliferation and ERK phosphorylation
RASAL2	0.048	1.830	0.394	0.774	activates Ras
EREG	0.016	2.090	0.709	0.895	MEK-dependent expression
TCP1	0.031	1.650	0.000	1.749	targets for RSK in the Ras-MAPK Pathway
ZMYND11	0.025	1.540	0.030	0.847	interacts with MAP3K7IP1
GBP1	0.002	1.780	0.313	1.569	p38-dependent expression
ATF3	0.028	2.230	0.180	0.848	p38-dependent expression
SH3RF2	0.026	1.690	0.209	0.718	promotes cell survival
ADAM12	0.021	1.810	0.003	0.749	confer proliferation advantage
MICAL1	0.028	1.870	0.587	0.921	inhibits apoptosis
<i>GADD45G</i>	0.003	0.420	0.037	0.709	<i>Induces cell cycle arrest</i>
<i>PTPN5</i>	0.021	0.370	0.000	0.322	<i>Induces apoptosis, inhibited by ERK2</i>
<i>TNFSF10</i>	0.012	0.660	0.014	1.353	<i>Induces apoptosis</i>

Genes related to neuronal cell function and Golgi structure					
Gene Symbol	Synbindin expression		Gastric cancer		Relevance to neuronal cell function and Golgi structure
	P-value	FC	P-value	FC	
VAMP1	0.031	1.510	0.875	1.050	transport of synaptic vesicles
NAV1	0.006	1.560	0.907	1.018	involved in axon guidance
RSPO3	0.038	1.770	0.305	0.745	binds to syndecan and induces Wnt signaling
NF2	0.025	1.660	0.578	1.147	affects development of Schwann cells
SERPINI1	0.021	1.530	0.159	0.610	regulates neuronal survival, tumor associated
CEP350	0.030	1.890	0.436	1.101	stabilises Golgi-associated microtubules
<i>NPSR1</i>	0.020	0.660	0.086	0.895	<i>Inhibits cell growth</i>
<i>CALY</i>	0.045	0.470	0.087	2.325	<i>Neuron-specific vesicular protein</i>
<i>TACR1</i>	0.001	0.300	0.090	0.486	<i>G protein receptor in nervous system</i>

Other genes					
Gene Symbol	Synbindin expression		Gastric cancer		Description
	P-value	FC	P-value	FC	
CHST11	0.039	1.599	0.150	1.238	Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), transcript variant 1, mRNA
PAFAH2	0.041	1.660	0.203	0.829	Homo sapiens platelet-activating factor acetylhydrolase 2, 40kDa (PAFAH2), mRNA [NM_000437]
HS3ST3B1	0.041	1.641	0.639	0.905	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 [Source:HGNC Symbol;Acc:5198]
BTN3A1	0.039	1.522	0.754	0.936	Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, mRNA [NM_007048]
LNPEP	0.042	1.569	0.381	0.564	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), transcript variant 1, mRNA [NM_005575]
LRRC15	0.045	1.700	0.088	0.621	Homo sapiens leucine rich repeat containing 15 (LRRC15), transcript variant 2, mRNA [NM_130830]
RBBP9	0.042	1.555	0.152	1.161	Homo sapiens retinoblastoma binding protein 9 (RBBP9), mRNA [NM_006606]
ATP1A1OS	0.045	1.668	0.009	0.530	Homo sapiens ATP1A1 opposite strand (ATP1A1OS), transcript variant 3, non-coding RNA [NR_024126]
C11orf96	0.041	1.522	0.310	0.822	Homo sapiens chromosome 11 open reading frame 96 (C11orf96), mRNA [NM_001145033]
LOC728431	0.042	1.552	0.694	0.910	Homo sapiens hypothetical LOC728431 (LOC728431), non-coding RNA [NR_038842]
RFX3	0.046	1.602	0.854	1.030	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, mRNA [NM_134428]
LOC147670	0.045	1.627	0.361	0.761	Homo sapiens hypothetical protein LOC147670 (LOC147670), mRNA [NM_001193628]
SLC44A2	0.048	1.629	0.000	0.510	Homo sapiens solute carrier family 44, member 2 (SLC44A2), transcript variant 1, mRNA [NM_020428]
SPINK13	0.048	1.640	0.000	0.327	Homo sapiens serine peptidase inhibitor, Kazal type 13 (putative) (SPINK13), mRNA [NM_001040129]
CROT	0.048	1.652	0.001	0.611	Homo sapiens carnitine O-octanoyltransferase (CROT), transcript variant 2, mRNA [NM_021151]
MTMR11	0.045	1.512	0.096	1.310	Homo sapiens myotubularin related protein 11 (MTMR11), transcript variant 2, mRNA [NM_181873]
USP32	0.027	1.619	0.907	1.010	Homo sapiens ubiquitin specific peptidase 32 (USP32), mRNA [NM_032582]
IL27RA	0.024	1.659	0.754	0.914	Homo sapiens interleukin 27 receptor, alpha (IL27RA), mRNA [NM_004843]
CDV3	0.039	1.612	0.091	0.876	Homo sapiens CDV3 homolog (mouse) (CDV3), transcript variant 2, mRNA [NM_017548]
SHROOM1	0.039	1.609	0.510	0.872	Homo sapiens shroom family member 1 (SHROOM1), transcript variant 2, mRNA [NM_133456]
WHSC1L1	0.049	1.600	0.910	0.981	Homo sapiens Wolf-Hirschhorn syndrome candidate 1-like 1 (WHSC1L1), transcript variant long, mRNA [NM_023034]
TCTE3	0.029	1.598	0.001	0.485	Homo sapiens t-complex-associated-testis-expressed 3 (TCTE3), mRNA [NM_174910]
LOC100233156	0.032	1.589	0.013	0.688	Homo sapiens tektin 4 pseudogene (LOC100233156), transcript variant 1, non-coding RNA [NR_037871]
C20orf112	0.045	1.588	0.066	0.730	Homo sapiens chromosome 20 open reading frame 112 (C20orf112), mRNA [NM_080616]
SNORA73A	0.046	1.588	0.454	0.543	Homo sapiens small nucleolar RNA, H/ACA box 73A (SNORA73A), small nucleolar RNA [NR_002907]
SPINK5	0.023	1.583	0.000	0.282	Homo sapiens serine peptidase inhibitor, Kazal type 5 (SPINK5), transcript variant 1, mRNA [NM_001127698]
LOC286071	0.048	1.574	0.029	0.585	Homo sapiens cDNA FLJ34440 fis, clone HLUNG2001214. [AK091759]
LOC100128402	0.038	1.568	0.560	0.847	Homo sapiens cDNA FLJ42583 fis, clone BRACE3009090. [AK124574]
PRUNE2	0.048	1.565	0.250	0.820	Homo sapiens prune homolog 2 (Drosophila) (PRUNE2), mRNA [NM_015225]
SATL1	0.029	1.561	0.230	0.770	Homo sapiens spermidine/spermine N1-acetyl transferase-like 1 (SATL1), mRNA [NM_001012980]
PSG8	0.038	1.558	0.340	0.890	Homo sapiens pregnancy specific beta-1-glycoprotein 8 (PSG8), transcript variant 1, mRNA [NM_182707]
BTBD7	0.017	1.558	0.100	0.648	Homo sapiens BTB (POZ) domain containing 7 (BTBD7), transcript variant 1, mRNA [NM_001002860]
BHLHE23	0.016	1.550	0.200	0.417	Homo sapiens basic helix-loop-helix family, member e23 (BHLHE23), mRNA [NM_080606]
ZBTB26	0.034	1.548	0.352	1.229	Homo sapiens zinc finger and BTB domain containing 26 (ZBTB26), mRNA [NM_020924]
PTGES	0.032	1.546	0.563	1.096	Homo sapiens prostaglandin E synthase (PTGES), mRNA [NM_004878]
HSPA2	0.026	1.545	0.475	0.917	Homo sapiens heat shock 70kDa protein 2 (HSPA2), mRNA [NM_021979]
HNRNPUL2	0.037	1.545	0.895	0.975	Homo sapiens heterogeneous nuclear ribonucleoprotein U-like 2 (HNRNPUL2), mRNA [NM_001079559]
C1orf106	0.033	1.541	0.089	1.298	Homo sapiens chromosome 1 open reading frame 106 (C1orf106), transcript variant 1, mRNA [NM_018265]
TMCC2	0.020	1.540	0.519	0.842	Homo sapiens transmembrane and coiled-coil domain family 2 (TMCC2), transcript variant 1, mRNA
RAB9BP1	0.046	1.537	0.289	0.694	Homo sapiens RAB9B, member RAS oncogene family pseudogene 1 (RAB9BP1), non-coding RNA
ARHGAP42	0.042	1.532	0.200	0.391	Homo sapiens Rho GTPase activating protein 42 (ARHGAP42), mRNA [NM_152432]
C6orf35	0.046	1.531	0.897	0.980	Homo sapiens chromosome 6 open reading frame 35 (C6orf35), mRNA [NM_018452]
KLHL13	0.013	1.530	0.001	0.393	Homo sapiens kelch-like 13 (Drosophila) (KLHL13), transcript variant 1, mRNA [NM_033495]
LOC339988	0.020	1.530	0.086	0.675	Homo sapiens cDNA clone IMAGE:5217034. [BC041468]
FERMT3	0.021	1.528	0.266	0.779	Homo sapiens fermitin family member 3 (FERMT3), transcript variant URP2LF, mRNA [NM_178443]
AVL9	0.034	1.524	0.893	1.018	Homo sapiens AVL9 homolog (S. cerevisiae) (AVL9), mRNA [NM_015060]
C3orf35	0.050	1.520	0.080	0.621	Homo sapiens chromosome 3 open reading frame 35 (C3orf35), transcript variant B, mRNA [NM_178339]
TPD52L1	0.007	1.510	0.000	0.398	Homo sapiens tumor protein D52-like 1 (TPD52L1), transcript variant 4, mRNA [NM_001003397]
INVS	0.021	1.510	0.160	1.313	Homo sapiens inversin (INVS), transcript variant 2, mRNA [NM_183245]
VKORC1	0.024	1.506	0.098	1.164	Homo sapiens cDNA FLJ43630 fis, clone SPLEN2030479. [AK125618]

*P value: student t-test.

** The higher fold change values (FC) are marked by darker red color.

*** The fold change of genes in gastric cancers are calculated according to published microarray dataset (GSE13911 and GSE15460). The yellow color highlights significantly altered genes.