

## Supplementary Materials and Methods

**Antibodies.** Anti- $\alpha$ -SMA (1A4) and anti-SDF-1 (79018) monoclonal antibodies for immunocytochemistry were purchased from R&D Systems Inc., Minneapolis, MN, USA. Anti-Pan-Keratin (C11) and anti-vimentin (R28) monoclonal antibodies were obtained from Cell Signaling Technology, Inc., Beverly, Massachusetts, USA. Anti-FAP $\alpha$  anti-collagen I (5D8), were obtained from Abcam Inc., Cambridge, MA, USA. Human cytokine antibody array kits were obtained from RayBiotech, Norcross, GA, USA. Rabbit anti-human Cav-1 (N-20) polyclonal antibody for Western blot and immunohistochemistry, as well as anti- $\beta$ -actin (N-21) for Western blot, were obtained from Santa Cruz Biotechnology Inc., Santa Cruz, CA, USA. Phycoerythrin (PE)-conjugated secondary antibody for flow cytometry and the Alexa Fluor secondary antibody used for immunocytochemistry were purchased from Invitrogen Corp., Carlsbad, Calif., USA.

**Indirect immunocytochemistry of cultured cells.** Cells cultured on the glass cover slips were washed thrice with PBS, fixed in 4% (weight/vol) paraformaldehyde in PBS (PFA/PBS; Sigma-Aldrich, St. Louis, MO, USA) for 10 min at room temperature, and then washed again thrice in PBS after reaching confluence. The cells were permeabilized with 0.1% (vol/vol) Triton X-100/PBS (Amresco Inc., Cleveland, Ohio, USA) for 10 min at room temperature. Afterward, the cells were washed thrice in PBS and incubated with 3% (weight/vol) bovine serum albumin (BSA)/0.3 M glycine in PBS (Sigma-Aldrich) for 2 h at room temperature to reduce the nonspecific binding of primary antibodies. Subsequently, 200  $\mu$ l of the appropriate primary antibody, diluted in 3% (weight/vol) BSA/PBS, was placed on each cover slip, and then incubated overnight at 4°C. The cover slips were then washed thrice for 15 min each with PBS and were incubated with 200  $\mu$ l of the secondary antibody (Alexa Fluor 488) diluted 1:2000 with 3% (weight/vol) BSA/PBS for 2 h at room temperature. Afterward, the cover slips were washed thrice for

5 min each with PBS and counter-stained with DAPI (0.1 µg/ml in PBS; Roche) for 1 min to visualize the nuclei. A final series of three 5 min washes with PBS was performed, after which, the cover slips were mounted on 1.5 µl Bio-Rad FluoroGuard™ Anti-fade Reagent (Bio-Rad, Hercules, CA, USA). The cover slips were sealed with nail polish.

**Proliferation assay.** A total of 3,000 AGS and MKN45 cells per well were seeded in 96-well plates and cultured in RPMI 1640 with 10% FCS. Then the medium was changed to serum-free RPMI for overnight incubation. Concentrated CM of the fibroblasts was added to AGS and MKN45 cells at various concentrations (0.25, 0.5, and 1.0 µg/µL), and serum-free RPMI 1640 or 10% FCS was added to the control wells. The cells were grown in a humidified atmosphere of 5% CO<sub>2</sub> at 37°C. The cell growth of the AGS and MKN45 cell lines was each analyzed at 72 h with the CCK-8 reagent (Sigma-Aldrich) added 1 h before taking the spectrophotometric reading, according to the manufacturer's instructions

**Invasion assay.** BioCoat Matrigel-coated invasion chambers (BD Biosciences) were used to study cell invasiveness. Briefly, 1×10<sup>5</sup> AGS or MKN45 cells in 500 µL serum-free medium was added to the upper chamber. The medium containing RPMI 1640, 10% FCS, or concentrated CM of the fibroblasts (0.25, 0.5, and 1.0 µg/µL) was added into the lower chamber. Serum-free medium was added to the lower chamber of the control wells. The cells were allowed to traverse the Matrigel for 72 h at 37°C in an environment with 5% CO<sub>2</sub>. The non-invading cells on the upper surface of the membrane were removed with a cotton swab, and the filters were fixed in 0.1% glutaraldehyde and stained with 0.2% crystal violet. The number of cells that migrated to the lower side of the filter was counted under an upright microscope (Nikon Optiphot) using Image-Pro Plus 4.5 software (Media Cybernetics, Silver Spring, MD, USA). The whole area was counted per filter.

Supplementary Table S1. Basic characteristics of 120 gastric cancer patients.

Variables	Number (%)	5-year survival rate (%)
Age (y)		
<60	49 (41)	50
≥60	71 (59)	43
Sex		
Male	74 (68)	51
Female	36 (32)	30
H pylori infection*		
negative	53 (58)	49
positive	38 (42)	52
Size(cm)		
<5	60 (50)	54
≥5	60 (50)	35
Histologic type		
Well and moderately	74 (62)	57
Poorly and others*	46 (38)	25
Lauren classification		
Intestinal type	73 (61)	53
Diffuse and Mixed type	47 (35)	32
Location		
GEJ	14 (12)	48
Stomach	96 (88)	23
Lymphatic invasion		
negative	31 (26)	58
positive	79 (74)	39
Depth of tumor(T)		
T1+ T2	28 (23)	81
T3+ T4	92 (77)	35
Lymph node metastasis (N)		
No+ N1	52 (43)	57
N2+ N3	68 (57)	35
Distant metastasis(M)		
M0	107 (89)	48
M1	13 (11)	20
TNM stage		
I+II	52 (43)	58
III+IV	68 (57)	35

Note : \**H. pylori* status was determined histologically and/or serologically. GEJ: gastroesophageal junction. The TNM stage of GC was determined according to the classification system of the International Union Against Cancer (7th edition). \*Other histologic types of gastric cancer mainly included mucinous adenocarcinomas and signet-ring cell carcinomas, according to the World Health Organization (WHO) classifications.

**Supplementary Table S2. Patient Characteristics of Primary Fibroblast Cultures**

NO.	Sex	Age (y)	Histological Type	Location	Lauren Classification	Tumor Stage			Adjacent Tissue	
						T	N	M	Histology	H.p Status
1	Male	79	P	Antrum	IGC	T4a	N2	M0	CG with IM	Neg
2	Male	61	P	Corpus	IGC	T3	N0	M0	CG	Pos
3	Male	52	P	Antrum	MGC	T3	N3b	M0	CG	Neg
4	Male	58	M	Antrum	DGC	T3	N2	M1	CG	Neg
5	Male	54	M	Antrum	IGC	T3	N3a	M0	CG	Pos
6	Male	48	P	Corpus	IGC	T3	N0	M0	CG	ND
7	Female	67	M	Corpus	DGC	T3	N3a	M1	CG	Neg
8	Male	59	M	Antrum	MGC	T4	N1	M0	CG	Neg
9	Male	84	M	Antrum	IGC	T4b	N1	M0	CG with IM	ND
10	Female	47	M	GEJ	DGC	T2	N2	M0	CG	Neg

Note: M-moderately differentiated; P-poorly differentiated; ; IGC- Intestinal gastric cancer; DGC-diffuse gastric cancer; MGC-mixed gastric cancer; T-tumor; N-lymph node; M- metastasis. IM-Intestinal metaplasia; CG-Chronic gastritis; Neg, negative; Pos, positive; ND, not determined;

Supplementary Table S3. Expression difference of soluble mediators in the Media of  
GCAFs and GIAFs

Protein Name	Ratio of GCAFs/GIAFs	Official Gene Name
Cytokines		
IL-1alpha	1.04	interleukin 1, alpha
IL-2	1.24	interleukin 2
IL-3	1.25	interleukin 3
IL-4 *	1.60	interleukin 4
IL-5	1.29	interleukin 5
IL-6 **	2.07	interleukin 6
IL-7 *	1.60	interleukin 7
IL-8 **	3.57	interleukin 8
IL-12P70	1.19	interleukin 12A
IL-12P40 *	1.53	interleukin 12B
IL-13	1.30	interleukin 13
IL-15	1.23	interleukin 15
IL-1ra	1.15	interleukin 1 receptor antagonist
IL-2sRa *	1.33	interleukin 2 receptor, alpha
GM-CSF	1.06	colony stimulating factor 2
G-CSF	1.03	colony stimulating factor 3
TNF-alpha	1.12	tumor necrosis factor, alpha
TNF-beta	1.35	tumor necrosis factor, beta
MIF *	1.41	macrophage migration inhibitory factor
TIMP-1	1.02	tissue inhibitor of metalloproteinase 1
TIMP-2 *	1.69	tissue inhibitor of metalloproteinase 2
IFN-gamma	1.37	interferon, gamma
TPO	1.22	thrombopoietin
Signal Proteins		
BMP-4 *	1.53	bone morphogenetic protein 4
BMP-6 *	1.63	bone morphogenetic protein 6
Angiogenin **	1.53	angiogenin, ribonuclease, RNase A family, 5
IGFBP-1	1.17	insulin-like growth factor binding protein 1
IGFBP-3 *	1.39	insulin-like growth factor binding protein 3
IGFBP-4 *	1.57	insulin-like growth factor binding protein 4
IGFBP-6 *	1.66	insulin-like growth factor binding protein 6
Leptin	1.05	Leptin
SCF	1.34	stem cell factor
Fas	1.22	Fas (TNF receptor superfamily, member 6)
Osteoprotegerin	1.18	tumor necrosis factor receptor superfamily, member 11b

Oncostatin M	1.11	Oncostatin M
IL-6 sR	1.06	interleukin 6 receptor
TRAIL R4 *		tumor necrosis factor receptor
	1.43	superfamily, member 10d, decoy with truncated death domain
EGFR		epidermal growth factor receptor
	1.24	(erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
IL-1R4	1.11	interleukin-1 receptor 4
GITR	1.14	tumor necrosis factor receptor superfamily, member 18
TNFR-1	1.26	tumor necrosis factor receptor superfamily, member 1A
Sgp130	1.12	interleukin 6 signal transducer (gp130, oncostatin M receptor)
IL-1 R-like 1	1.03	interleukin 1 receptor-like 1
Growth Factors		
TGF- $\beta$ 1 *#	2.04	transforming growth factor, beta 1
IGF-1 *#	2.24	insulin-like growth factor 1
HGF *#	2.07	hepatocyte growth factor (hepapoietin A scatter factor)
GDNF *	1.32	glial cell derived neurotrophic factor
FGF-4	1.10	fibroblast growth factor 4
FGF-7	1.06	fibroblast growth factor 7
FGF-9	1.09	fibroblast growth factor 9
bFGF	1.06	basic fibroblast growth factor
Chemokines		
CCL1/I-309 *	1.88	chemokine (C-C motif) ligand 1
CCL2/MCP-1 *#	2.87	chemokine (C-C motif) ligand 2/ macrophage chemotactic protein-1
CCL3/MIP-1 $\alpha$	1.08	chemokine (C-C motif) ligand 3/ macrophage inflammatory protein 1 $\alpha$
CCL4/MIP-1 $\beta$	1.01	chemokine (C-C motif) ligand 4/ macrophage inflammatory protein 1 $\beta$
CCL5/RANTES *#	2.01	chemokine (C-C motif) ligand 5/ regulated upon activation, normal T cells expressed and secreted
CCL11/Eotaxin	1.47	chemokine (C-C motif) ligand 11
CCL16/LEC*#	2.15	chemokine (C-C motif) ligand 16/ liver-expressed chemokine
CCL20/MIP-3	1.05	chemokine (C-C motif) ligand 20/ macrophage inflammatory protein 3
CCL23/CKb8-1	1.35	chemokine (C-C motif) ligand 23
CCL24/Eotaxin-2	1.18	chemokine (C-C motif) ligand 24
CCL26/Eotaxin-3	1.01	chemokine (C-C motif) ligand 26
CCL-28*#	3.09	chemokine (C-C motif) ligand 28

CXCL9/MIG*#	3.10	chemokine (C-X-C motif) ligand 9/ monokine induced by IFN
CXCL11/I-TAC	1.06	chemokine (C-X-C motif) ligand 11/Interferon-inducible T-cell alpha chemoattractant
CXCL12/SDF-1*#	2.09	chemokine (C-X-C motif) ligand 12/Stromal cell-derived factor-1
Lymphotactin	1.163341912	lymphotactin

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\*GCAFs/GIAFs ratio of more than 1.3 folds; # confirmation by ELISA.

Supplementary Table S4. Differentially Expressed Proteins in GCAFs and GIAFs by 2D-Nano-LC-ESI-MS/MS

Accession number	Symbol	Description	Fold change		
			(GCAF/GIAF) 1	(GCAF/GIAF) 2	(GCAF/GIAF) 3
Seventy-six down-regulated proteins in GCAFs					
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	0.14	0.12	0.13
O43852	CALU	Calumenin	0.17	0.12	0.08
P21266	GSTM3	Glutathione S-transferase Mu 3	0.14	0.13	0.18
P07099	EPHX1	Epoxide hydrolase 1	0.1	0.19	0.21
Q00688	FKBP3	FK506-binding protein 3	0.22	0.11	0.18
P10599	TXN	Thioredoxin	0.16	0.18	0.25
Q03135	CAV1	Caveolin-1	0.16	0.14	0.25
O96008	TOMM40	Mitochondrial import receptor subunit TOM40 homolog	0.22	0.27	0.28
P20700	LMNB1	Lamin-B1	0.28	0.16	0.25
P09429	HMGB1	High mobility group protein B1	0.15	0.24	0.29
P62158	CALM1	Calmodulin	0.11	0.29	0.19
P13645	KRT10	Keratin, type I cytoskeletal 10	0.29	0.19	0.17
Q99733	NAP1L4	Nucleosome assembly protein 1-like 4	0.34	0.12	0.25
Q8TDZ2	MICAL1	NEDD9-interacting protein with calponin homology and LIM domains	0.35	0.23	0.36
Q92597	NDRG1	Protein NDRG1	0.37	0.29	0.26
P28482	MAPK1	Mitogen-activated protein kinase 1	0.37	0.13	0.33
P47755	CAPZA2	F-actin-capping protein subunit alpha-2	0.39	0.15	0.18
P26038	MSN	Moesin	0.39	0.31	0.39
Q99715	COL12A1	Collagen alpha-1(XII) chain	0.42	0.2	0.07
P19338	NCL	Nucleolin	0.27	0.3	0.42
P80303	NUCB2	Nucleobindin-2	0.24	0.22	0.42
P43121	MCAM	Cell surface glycoprotein MUC18	0.42	0.35	0.4



Q14914	PTGR1	Prostaglandin reductase 1	0.43	0.21	0.23
P58546	MTPN	Myotrophin	0.29	0.43	0.32
P35527	KRT9	Keratin, type I cytoskeletal 9	0.16	0.25	0.43
O76074	PDE5A	cGMP-specific 3',5'-cyclic phosphodiesterase	0.43	0.16	0.35
Q9UNM6	PSMD13	26S proteasome non-ATPase regulatory subunit 13	0.42	0.37	0.43
P53992	SEC24C	Protein transport protein Sec24C	0.45	0.22	0.42
Q9P0K7	RAI14	Ankyrin	0.45	0.25	0.19
O60888	CUTA	Protein CutA	0.42	0.46	0.42
O95816	BAG2	BAG family molecular chaperone regulator 2	0.35	0.1	0.48
	TXNDC1				
Q9BRA2	7	Thioredoxin domain-containing protein 17	0.24	0.2	0.48
P05387	RPLP2	60S acidic ribosomal protein P2	0.19	0.37	0.49
P21964	COMT	Catechol O-methyltransferase	0.5	0.25	0.27
Q14152	EIF3A	Eukaryotic translation initiation factor 3 subunit A	0.51	0.42	0.14
P42224	STAT1	Signal transducer and activator of transcription 1-alpha/beta	0.5	0.51	0.43
P60228	EIF3E	Eukaryotic translation initiation factor 3 subunit E	0.44	0.32	0.52
Q15181	PPA1	Inorganic pyrophosphatase	0.39	0.41	0.52
O00116	AGPS	Alkyldihydroxyacetonephosphate synthase, peroxisomal	0.53	0.45	0.37
P00441	SOD1	Superoxide dismutase [Cu-Zn]	0.24	0.34	0.53
P00750	PLAT	Tissue-type plasminogen activator	0.41	0.33	0.53
Q7L2H7	EIF3M	Eukaryotic translation initiation factor 3 subunit M	0.54	0.42	0.44
P61604	HSPE1	10 kDa heat shock protein, mitochondrial	0.49	0.54	0.44
P15311	EZR	Ezrin	0.31	0.54	0.35
Q9UL46	PSME2	Proteasome activator complex subunit 2	0.13	0.54	0.38
Q01105	SET	Protein SET	0.55	0.5	0.28
P20290	BTF3	Transcription factor BTF3	0.21	0.55	0.54
P61981	YWHAG	14-3-3 protein gamma	0.55	0.43	0.42
	PRKCDB				
Q969G5	P	Protein kinase C delta-binding protein	0.4	0.49	0.55
Q14444	CAPRIN1	Caprin-1	0.4	0.56	0.2
O43399	TPD52L2	Tumor protein D54	0.41	0.32	0.56

P63010	AP2B1	AP-2 complex subunit beta-1	0.57	0.4	0.47
P25789	PSMA4	Proteasome subunit alpha type-4	0.26	0.57	0.39
P62195	PSMC5	26S protease regulatory subunit 8	0.5	0.58	0.28
Q9NQC3	RTN4	Reticulon-4	0.48	0.58	0.37
P05455	SSB	Lupus La protein	0.55	0.59	0.4
O95336	PGLS	6-phosphogluconolactonase	0.26	0.59	0.24
Q9NVD7	PARVA	Alpha-parvin	0.36	0.6	0.54
P30085	CMPK1	UMP-CMP kinase	0.39	0.6	0.53
P05556	ITGB1	Integrin beta-1	0.6	0.53	0.6
P46459	NSF	Vesicle-fusing ATPase	0.52	0.61	0.17
Q5T4S7	UBR4	E3 ubiquitin-protein ligase UBR4	0.32	0.52	0.61
P55209	NAP1L1	Nucleosome assembly protein 1-like 1	0.61	0.37	0.41
P27487	DPP4	Dipeptidyl peptidase 4	0.45	0.57	0.62
Q562R1	ACTBL2	Beta-actin-like protein 2	0.08	0.63	0.49
Q13561	DCTN2	Dynactin subunit 2	0.35	0.49	0.63
P55769	NHP2L1	NHP2-like protein 1	0.63	0.23	0.61
O95340	PAPSS2	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2	0.63	0.56	0.39
Q9HDC9	APMAP	Adipocyte plasma membrane-associated protein	0.5	0.63	0.41
P16070	CD44	CD44 antigen	0.65	0.44	0.51
P21589	NT5E	5'-nucleotidase	0.65	0.57	0.51
P48163	ME1	NADP-dependent malic enzyme	0.31	0.43	0.66
	PPP1R12				
O14974	A	Protein phosphatase 1 regulatory subunit 12A	0.66	0.54	0.24
Q9H3H3	C11orf68	UPF0696 protein C11orf68	0.38	0.5	0.66
Q96D15	RCN3	Reticulocalbin-3	0.65	0.52	0.66
Q9BT78	COPS4	COP9 signalosome complex subunit 4	0.66	0.56	0.29
Forty-five up-regulated proteins in GCAFs					
Q15084	PDIA6	Protein disulfide-isomerase A6	2.22	2.01	2.32
	SERPINE				
P07093	2	Glia-derived nexin	2.78	2.35	2.46

P05067	APP	Amyloid beta A4 protein	2.16	2.79	2.42
Q9HBL0	TNS1	Tensin-1	2.29	2.82	2.74
O95571	ETHE1	Protein ETHE1, mitochondrial	2.1	2.39	2.93
P09486	SPARC	SPARC	2.94	1.62	1.77
P07814	EPRS	Bifunctional aminoacyl-tRNA synthetase	3.13	2.02	2.47
Q9Y570	PPME1	Protein phosphatase methylesterase 1	2.94	2.71	3.16
	GSPT2	Eukaryotic peptide chain release factor GTP-binding subunit			
Q8IYD1		ERF3B	2.58	2.05	3.2
P61254	RPL26	60S ribosomal protein L26	2.2	2.83	3.39
P26373	RPL13	60S ribosomal protein L13	3.42	2.4	2.43
P40429	RPL13A	60S ribosomal protein L13a	2.98	2.96	3.48
P42677	RPS27	40S ribosomal protein S27	3.55	2.2	2.23
Q9Y5M8	SRPRB	Signal recognition particle receptor subunit beta	3.63	3.48	2.44
P09619	PDGFRB	Beta-type platelet-derived growth factor receptor	2.15	2.33	3.71
P56134	ATP5J2	ATP synthase subunit f, mitochondrial	2.4	3.83	3.32
Q16851	UGP2	UTP--glucose-1-phosphate uridylyltransferase	2.11	2.4	3.94
P07996	THBS1	Thrombospondin-1	3.95	2.47	2.21
P62988	RPS27A	Ubiquitin	3.79	2.7	4.11
P17301	ITGA2	Integrin alpha-2	2.39	4.52	3.04
P68363	TUBA1B	Tubulin alpha-1B chain	2.88	2.15	4.59
P54136	RARS	Arginyl-tRNA synthetase, cytoplasmic	4.9	4.94	4.33
P12111	COL6A3	Collagen alpha-3(VI) chain	4.95	4	3.33
P02792	FTL	Ferritin light chain	3.09	2.29	5.53
Q9BUT1	BDH2	3-hydroxybutyrate dehydrogenase type 2	4.27	5.62	5.51
Q14254	FLOT2	Flotillin-2	5.07	2.81	5.73
	SERPINE				
P05121	1	Plasminogen activator inhibitor 1	2.57	2.42	5.83
Q9NZ01	GPSN2	Synaptic glycoprotein SC2	3	3	5.95
Q9NQW7	XPNPEP1	Xaa-Pro aminopeptidase 1	5.76	6.58	5.59
P46782	RPS5	40S ribosomal protein S5	5.43	6.02	6.88
P14174	MIF	Macrophage migration inhibitory factor	7.19	2.31	2.75

Q08431	MFGE8	Lactadherin	7.54	3.3	4.75
P01023	A2M	Alpha-2-macroglobulin	7.57	5.69	5.23
Q9BWD1	ACAT2	Acetyl-CoA acetyltransferase, cytosolic	7.78	2.38	3.08
	KIAA119				
Q8WUJ3	9	Protein KIAA1199	4.49	8.08	2.06
P62304	SNRPE	Small nuclear ribonucleoprotein E	8.28	2.27	7.93
P0C0L4	C4B	Complement C4-B	8.57	2.42	4.36
Q9Y617	PSAT1	Phosphoserine aminotransferase	4.54	3.09	9.81
P50502	ST13	Hsc70-interacting protein	2.54	9.95	8.39
P61513	RPL37A	60S ribosomal protein L37a	2.11	7.63	10.38
P22102	GART	Trifunctional purine biosynthetic protein adenosine-3	2.05	3.61	11.6
Q9UMS6	SYNPO2	Synaptopodin-2	11.92	2.47	3.31
P07585	DCN	Decorin	12.15	3.16	2.03
Q9UKX3	MYH13	Myosin-13	13.36	4.96	8.5
P00325	ADH1B	Alcohol dehydrogenase 1B	9.63	57.67	71.88

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Supplementary Table S5 Enrichment Analysis of GO terms and KEGG Pathways for Subnetwork Proteins

Enriched function	P-value	Bayes factor	Genes
Gene Ontology (GO)			
Cell adhesion	< 0.0001	10	APP, CD4, CD44, COL14A1, COL4A6, FLOT2, HSPG2, ILK, ITGA2, ITGB1, LAMA1, LAMA3, PARVA, THBS1
Regulation of cell migration	0.0001	6	LAMA1, LAMA3, SERPINE2
Regulation of cell motility	0.0001	6	LAMA1, LAMA3, SERPINE2
KEGG Pathway			
ECM-receptor interaction	< 0.0001	16	CD44, COL1A1, COL1A2, COL4A6, HSPG2, ITGA2, ITGB1, LAMA1, LAMA3, SDC2, THBS1
Focal adhesion	< 0.0001	15	CAV1, COL1A1, COL1A2, COL4A6, ILK, ITGA2, ITGB1, LAMA1, LAMA3, MAPK1, PARVA, PDGFB, PDGFRB, PPP1R12A, ROCK2, THBS1

Supplementary Table S6. Correlations between Cav-1 Expression and Clinical Features of GC patients

Parameters	Cav-1 expression in GCAFs			Cav-1 expression in GIAFs		
	+	-	<i>P</i>	+	-	<i>P</i>
Age (y)			.825			.577
<60	24	14		32	6	
≥60	36	18		43	11	
Sex			.161			.793
Male	37	25		51	11	
Female	23	7		24	6	
H <i>pylori</i> infection			.511			.057
Negative	30	13		39	4	
Positive	30	19		36	13	
Location			.742			<b>.041</b>
GEJ	8	3		6	5	
Stomach	52	29		69	12	
Size(cm)			<b>.048</b>			<b>.030</b>
<5	35	11		42	4	
≥5	25	21		33	13	
Histologic type			<b>.007</b>			.475
Well and moderately	44	14		46	12	
Poorly and others*	16	18		29	5	
Lauren classification			.370			.848
Intestinal	39	17		46	10	
Diffuse+Mixed	21	15		29	7	
Lymphatic invasion			<b>.000</b>			<b>.002</b>
Negative	52	16		60	7	
Positive	8	26		15	10	
Depth of tumor (T)			<b>.008</b>			.341
T1+T2	19	2		19	2	
T3+T4	41	30		56	15	
Lymph node metastasis (N)			<b>.015</b>			<b>.006</b>
N0+N1	32	8		38	2	
N2+N3	28	24		37	15	
Distant metastasis (M)			.734			.386
M0	53	29		68	14	
M1	7	3		7	3	
TNM stage			<b>.002</b>			<b>.007</b>

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I+II	36	8	41	3
III+VI	24	24	34	14

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Note: \**H. pylori* status was determined histologically and/or serologically. GEJ: gastroesophageal junction. The TNM stage of GC was determined according to the classification system of the International Union Against Cancer (7th edition). \*Other histologic types of gastric cancer mainly included mucinous adenocarcinomas and signet-ring cell carcinomas, according to the World Health Organization (WHO) classifications.