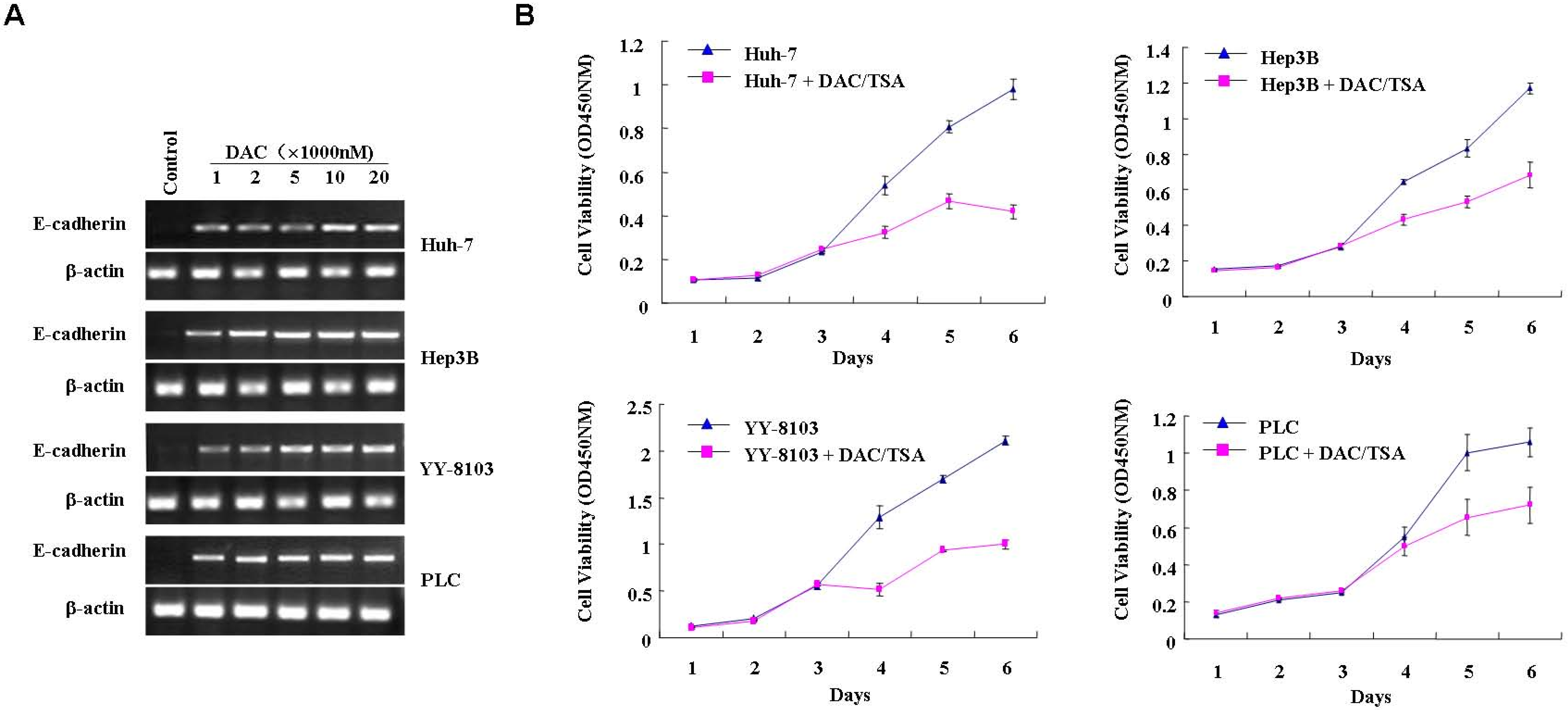
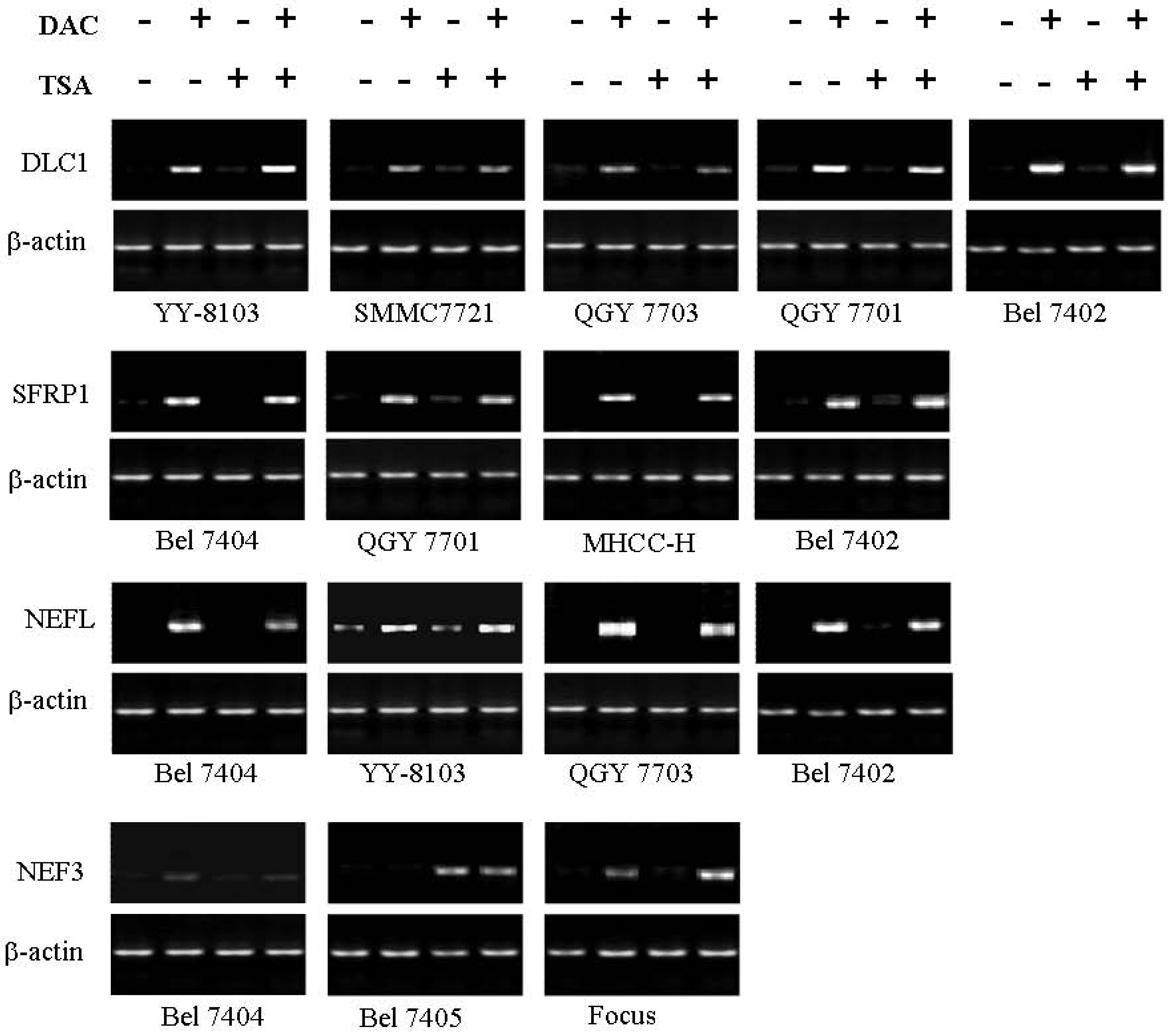
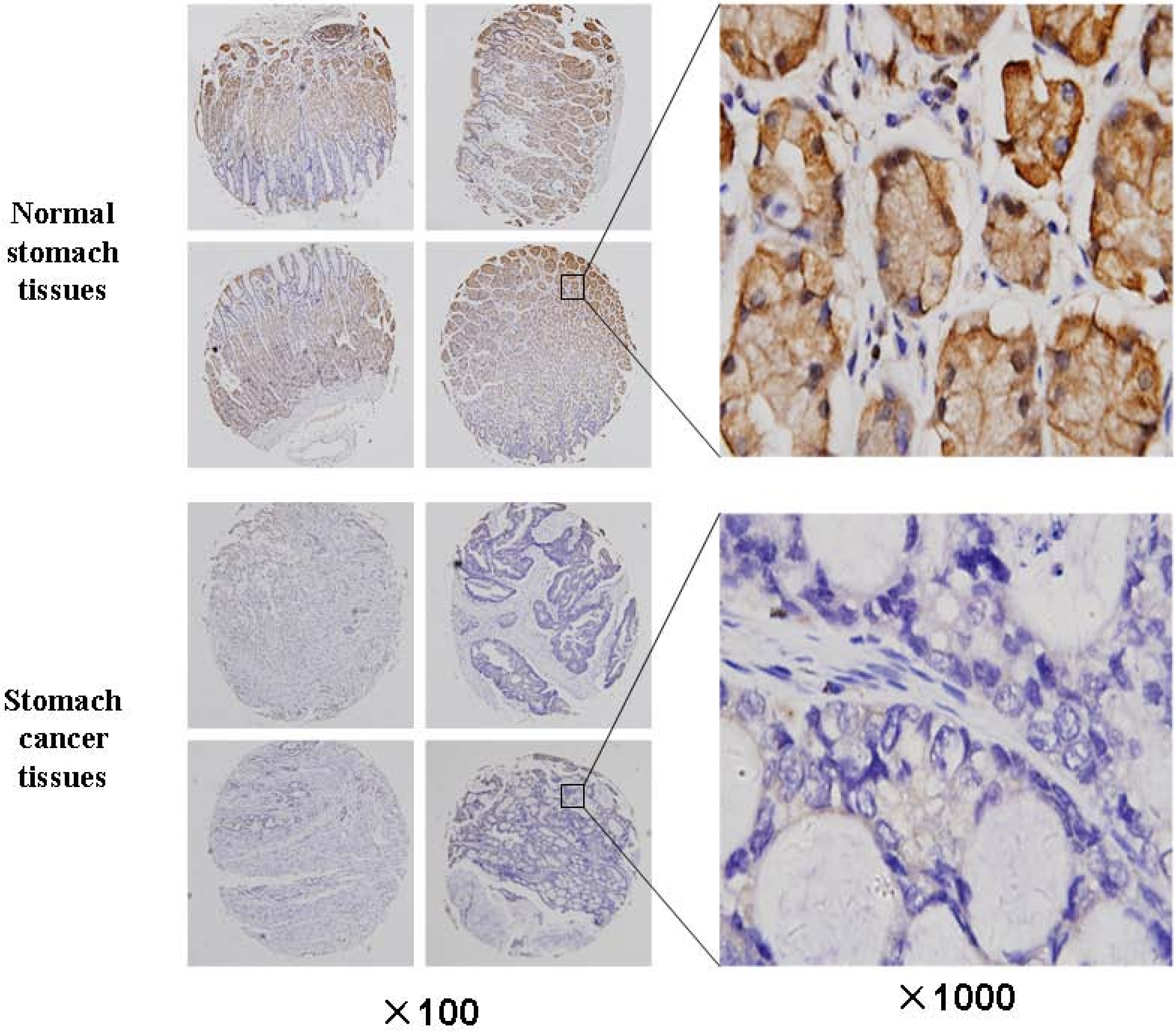


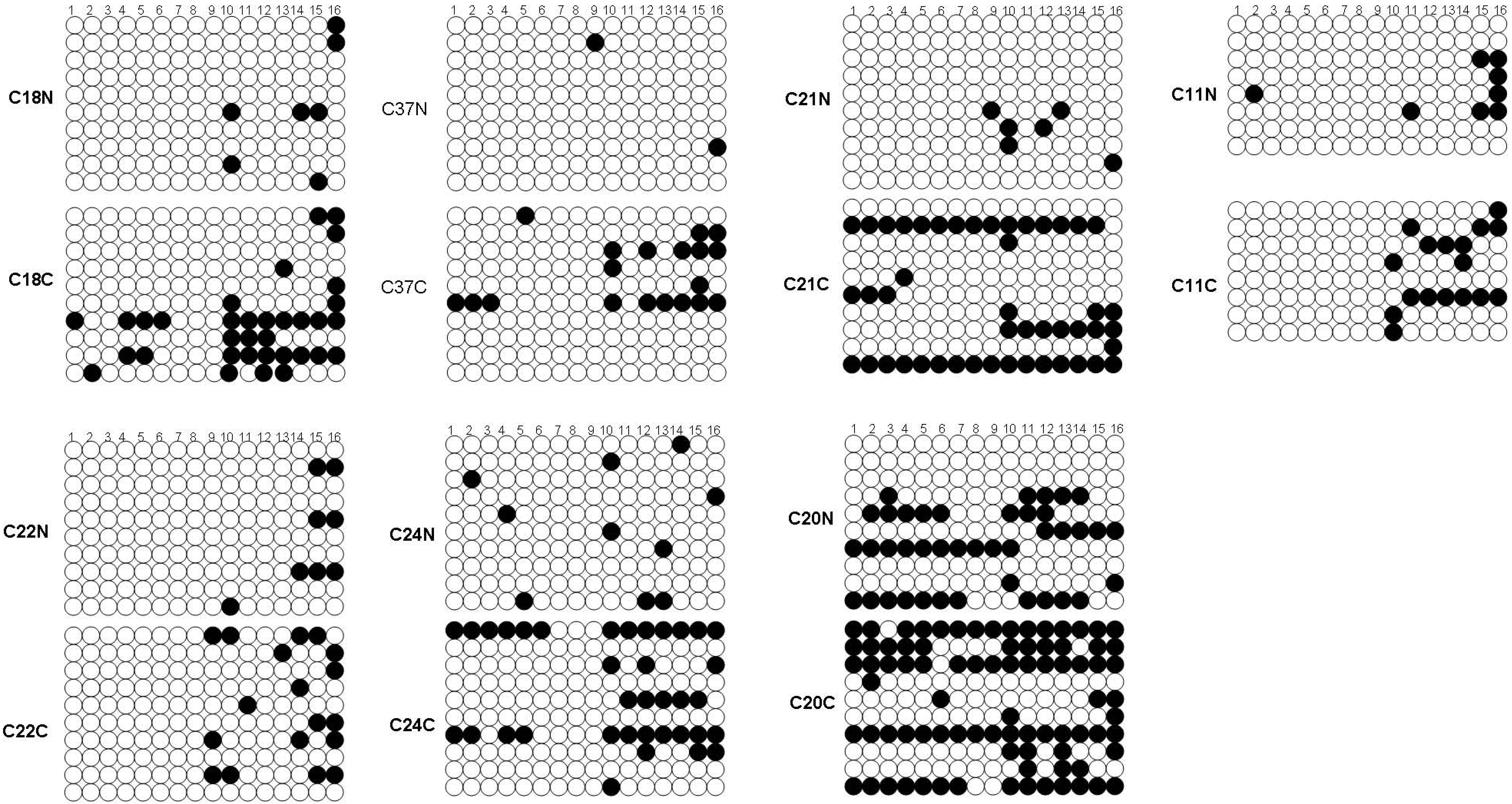
Supplemental Figure 1. Optimization of 5-Aza-dC treatment. (**A**) Four cell lines were randomly selected from the 15 cell lines used in this study and were treated with increasing concentrations of 5-Aza-dC (DAC). The effect of 5-Aza-dC treatment on reactivation of one known methylated tumor suppressor gene, E-cadherin, was evaluated by RT-PCR. (**B**) The cell growth curves of four cell lines treated with a combination of DAC (1000 nM) and TSA (300 nM) or without drugs. Drug treatment had only a minor effect on cell proliferation from day 1 to day 4; however, massive cell death was observed after prolonged treatment (days 5 to 7).



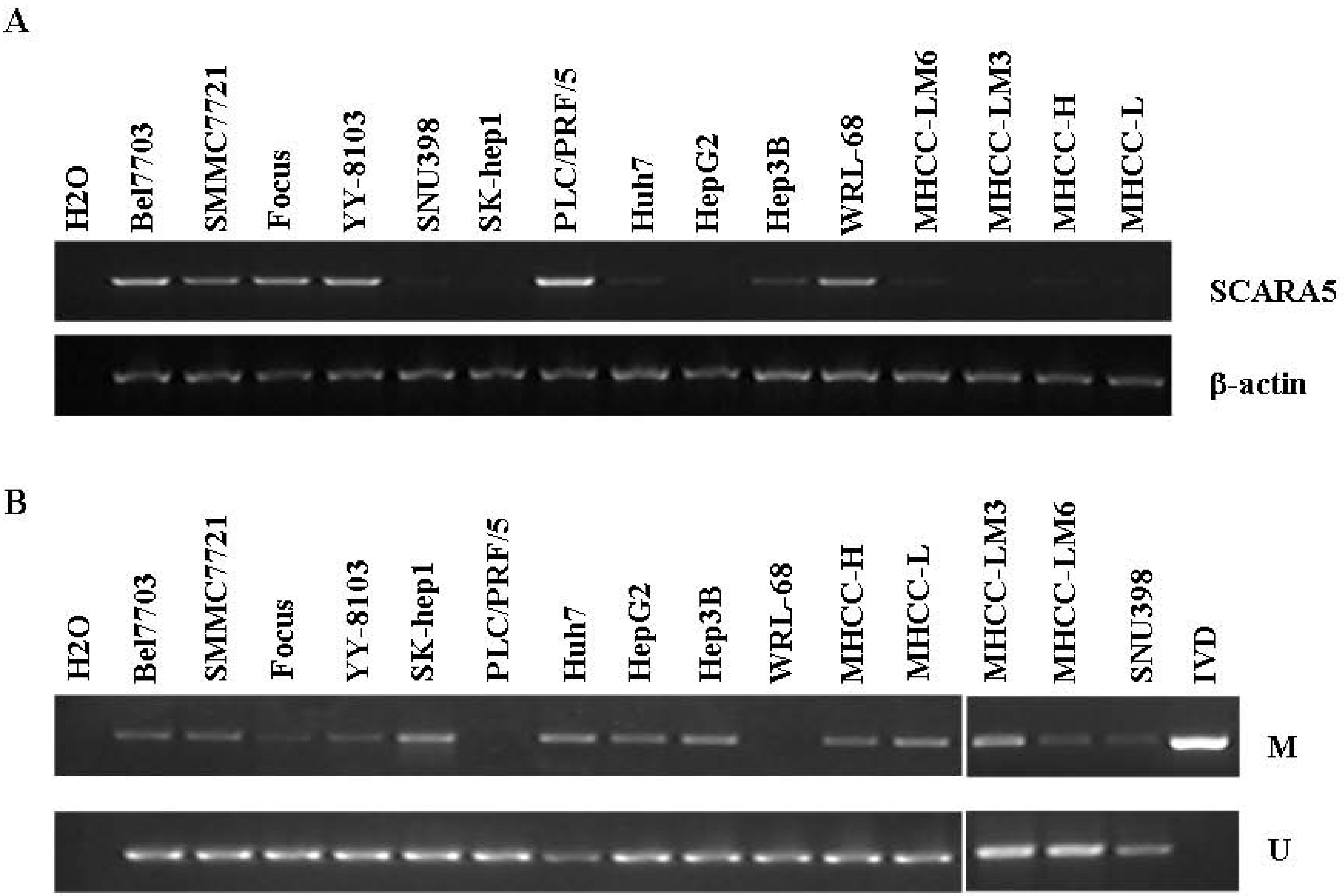
Supplemental Figure 2. The re-expression of *DLC1*, *SFRP1*, *NEFL* and *NEF3*, which all map to chromosome 8p, was evaluated by RT-PCR in the HCC cell lines treated with no drug (lane 1), DAC (lane 2), TSA (lane 3), or DAC+TSA (lane 4). β -actin was used as a loading control.



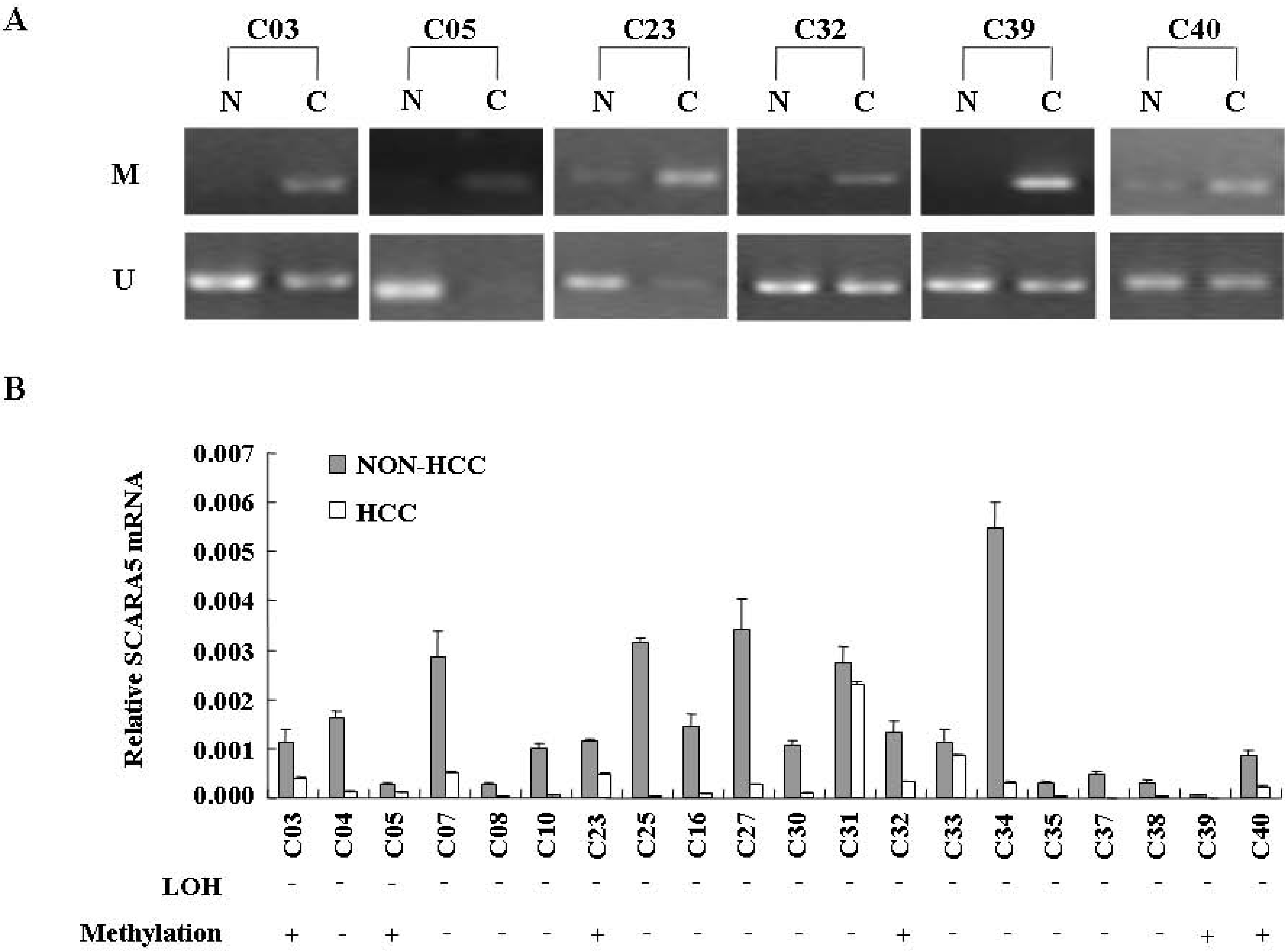
Supplemental Figure 3. Representative immunohistochemical staining of stomach cancer specimens and normal stomach tissue samples using an anti-SCARA5 antibody (homemade) on a tissue array containing 81 cancerous specimens and eight stomach tissues. Nuclei were counterstained with hematoxylin.



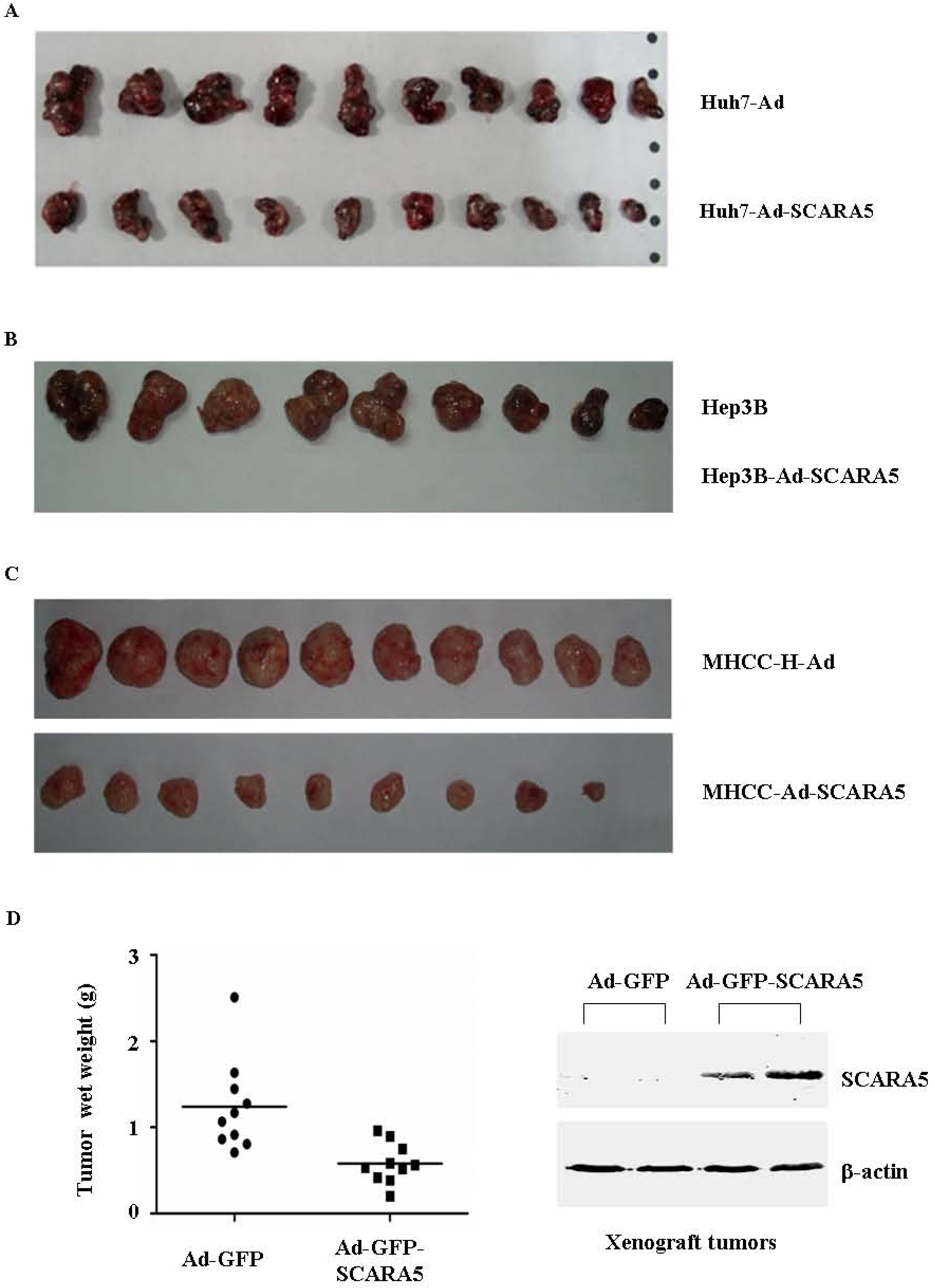
Supplemental Figure 4. Determination of the methylation status of CG1 in seven HCC specimens (C18C, C37C, C21C, C11C, C22C, C24C and C20C) and corresponding non-cancerous tissue (C18N, C37N, C21N, C11N, C22N C24N and C20N) were carried out by sequencing of bisulfite-treated genomic DNA. Each line represents the DNA sequence of a random clone, with open and filled circles indicating unmethylated and methylated CpG sites, respectively (*P* < 0.01).



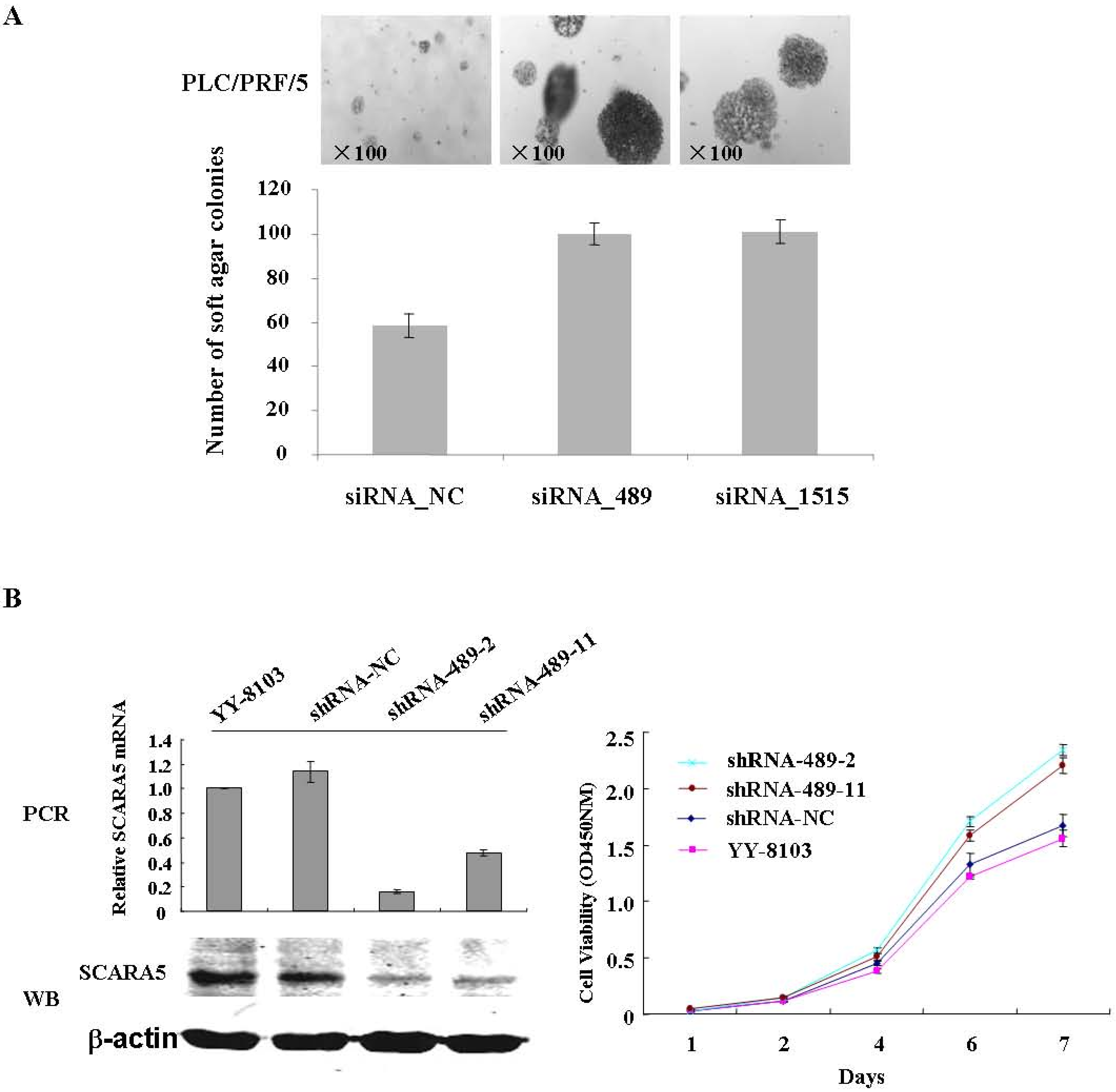
Supplemental Figure 5. Expression pattern of SCARA5 in HCC cell lines. (A) The results of semi-quantitative RT-PCR for the expression profile of SCARA5 in 15 cell lines. β -actin was used as a loading control. (B) DNA methylation status of SCARA5 promoter (CpG island I) was assessed in 15 HCC cell lines with or without the expression of endogenetic SCARA5, through methylation-specific PCR (MSP) assay with specific primers. The peripheral blood lymphocyte (PBL) DNA treated with SssI Methylase (New England Biolabs, Beverly, MA) was used as a positive control for methylation (IVD), and water was used as a negative control (H2O).



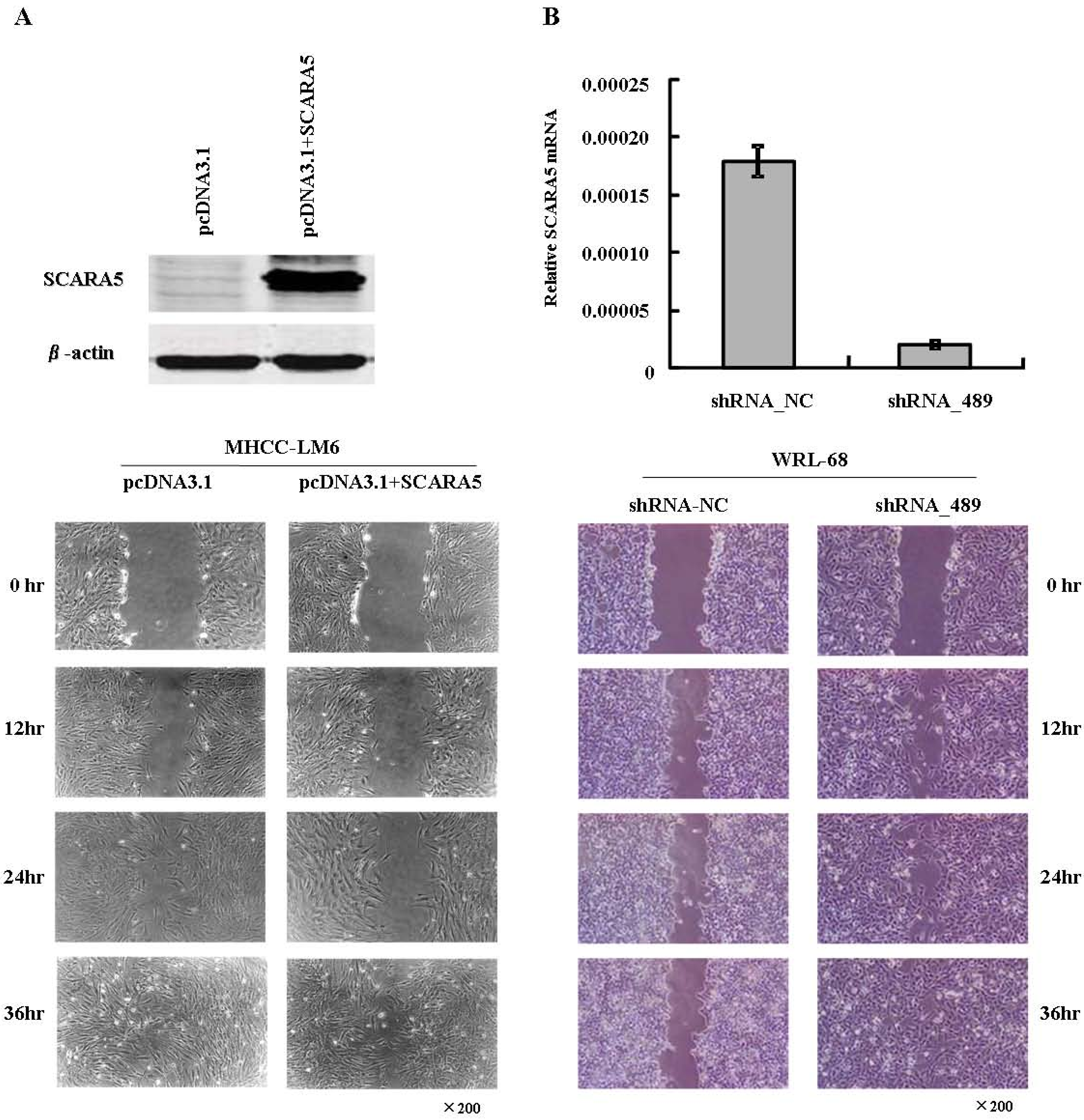
Supplemental Figure 6. DNA methylation status of SCARA5 promoter in primary HCC specimens without LOH. (**A**) DNA methylation status of SCARA5 promoter (CG1) was assessed in 20 HCCs (C) and their adjacent non-cancerous livers (N) without LOH using methylation-specific PCR. M and U represented methylated and unmethylated island, respectively. (**B**) Correlation between mRNA levels and corresponding methylation level of SCARA5 promoter in 20 primary HCCs without LOH. + indicates the increased methylation level of SCARA5 promoter.



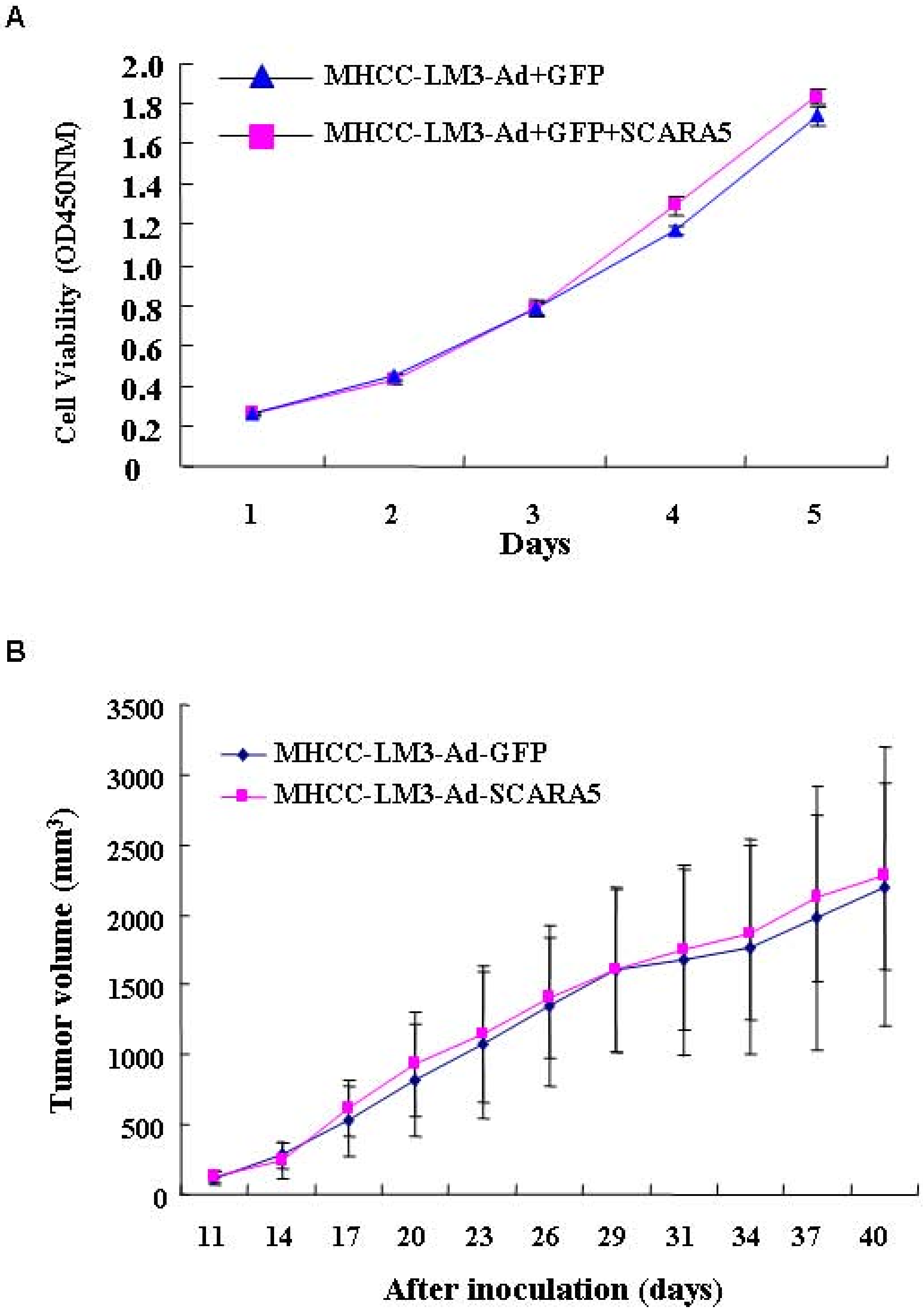
Supplemental Figure 7. Decreased tumorigenicity of some HCC cell lines in athymic nude mice by SCARA5 overexpression. Huh7 (A), Hep3B (B) and MHCC-H (C) cells, which were transfected with a recombinant adenovirus carrying either the SCARA5 ORF or an empty control vector, were injected subcutaneously into mice (n = 8). Xenografts were removed from these experimental mice after 8 weeks. (D) Tumors from two independent Huh7 cell xenograft experiments were weighed immediately after removal (left), where horizontal lines indicate mean xenograft tumor weight. Immunoblotting analysis of SCARA5 in two representative xenograft tumors at the time of sacrifice (right).



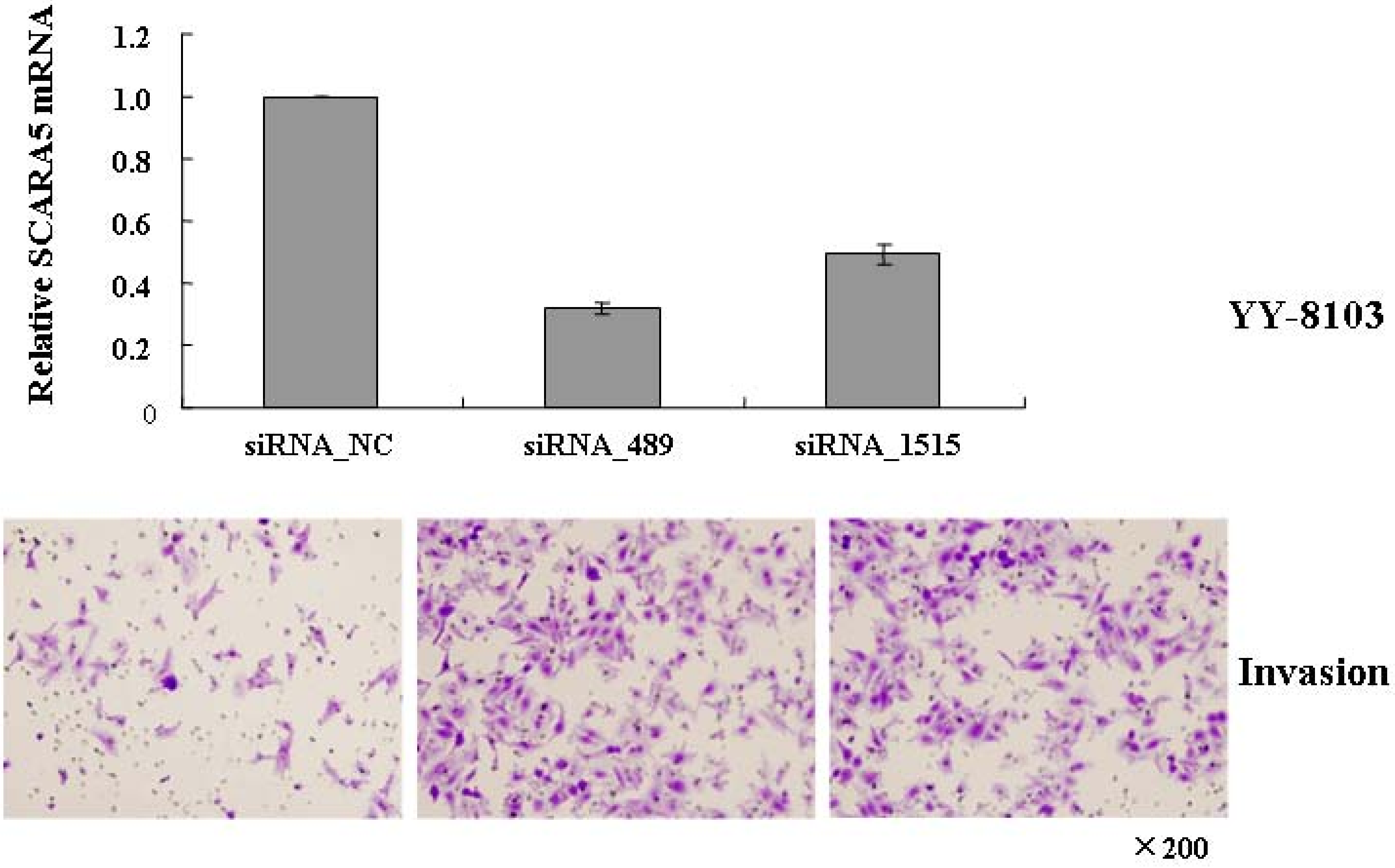
Supplemental Figure 8. Effect of silencing SCARA5 expression on cell growth, colony formation and growth of HCC cells**.** (**A**) To observe the effect of silencing SCARA5 on colony formation in soft agar, pSUPER containing shRNA_489 and shRNA_1515 was transfected into PLC/PRF/5 cells, while transfection of shRNA_NC was used as a negative control. Representative results show the increase of anchorage-independent colony formation of PLC/PRF/5 cells in soft agar, as compared to the negative controls (upper). The lower histogram shows the colony formation was significantly increased by silencing SCARA5, where the numbers represent the average value of three independent experiments, shown with standard deviation ($P < 0.01$, compared with control). (**B**) The YY-8103 cell subclones shRNA-489-2 and shRAN-489-11 with the stable silencing of endogenous *SCARA5* was established using a shRNA strategy (pSUPER vector). The real time PCR (upper) and immunoblotting (lower) show that SCARA5 was significantly lower in the two subclones than in the subclones shRNA-489-NC and YY-8103, which contained the empty vector. The growth of YY-8103 cells and those transfected by shRNAs were then measured using the Cell Counting Kit-8 (right). The results represent the average value of triplicate wells, shown with standard deviation.



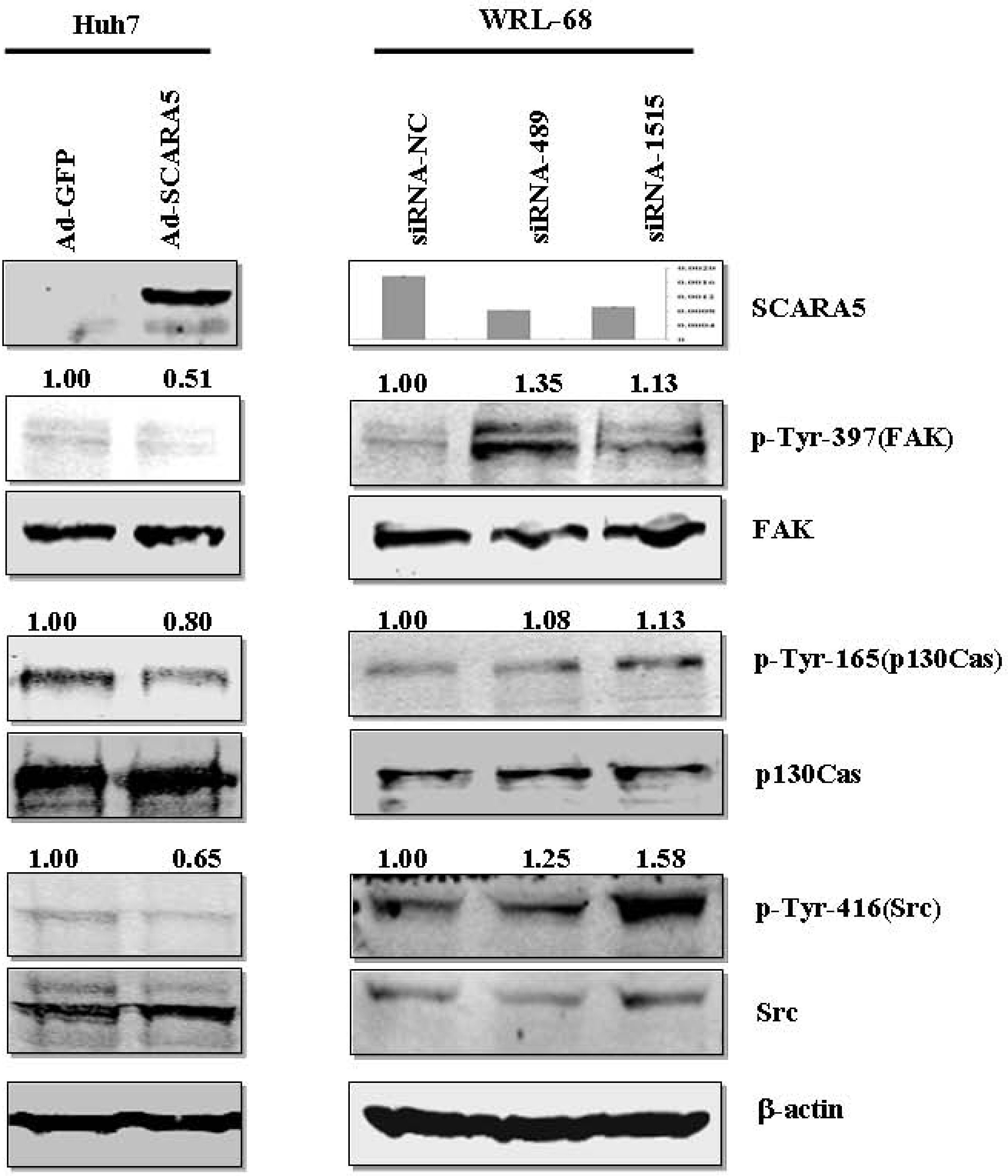
Supplemental Figure 9. The effect of SCARA5 on the migration of HCC cells. (**A**) Exogenous SCARA5 was expressed in MHCC-LM6 cells by transient transfection with the pcDNA3.1 vectors; expression was confirmed by immunoblotting assay (upper). Parental cells with empty vector were used as a control. Photomicrographs (×200 magnification) show the migration of MHCC-LM6 transfected with vectors containing SCARA5, through wound-healing experiment (lower). (**B**) WRL-68 cells were transfected by shRNA_489 and then RNA interference on endogenetic SCARA5 was evaluated by real-time RT-PCR (upper). Photomicrographs (×200 magnification) show the migration of WRL-68 cells transfected by shRNA_489 into the scraped area at 0, 12, 24, or 36 hours in the wound-healing experiment, where those cells transfected by shRNA_NC were employed as control.



Supplemental Figure 10. Overexpression of *SCARA5* did not affect cell growth of MHCC-LM3 cells. MHCC-LM3 cells were transfected with a recombinant adenovirus carrying the *SCARA5* cDNA, while MHCC-LM3 cells transfected with an empty adenovirus vector served as a control. (**A**) The growth curve was measured by CCK-8. The experiments were repeated at least three times and the spots indicate the average values of triplicate wells. Standard deviations are included for each spot ($P > 0.05$, compared with control). (B) Increased exogenous SCARA5 expression does not inhibit xenograft tumor growth of MHCC-LM3. MHCC-LM3 cells infected with recombinant adenovirus carrying SCARA5 were injected subcutaneously into nude mice, while MHCC-LM3 cells carrying the empty vector was used as control, respectively. Tumor growth was monitored for per 3 days by measuring diameter (error bars, mean ± SD).



Supplemental Figure 11. Depletion of *SCARA5* using siRNAs promotes YY-8103 cell invasion. **Upper panel**, expression of endogenous *SCARA5* was silenced in YY-8103 cells using siRNAs targeting *SCARA5* (siRNA-489 and siRNA-1515), while the siRNA-NC served as a control. The real-time PCR results show that *SCARA5* was significantly down-regulated in the cells transfected with siRNA-489 and siRNA-1515 compared to the cells transfected with siRNA-NC. **Lower panel,** cell invasion through transwells with Matrigel was measured by counting trespassed cells. Representative photomicrographs are shown.



Supplemental Figure 12. SCARA5 modulates the tyrosine phosphorylation of FAK, Src and p130Cas in Huh7 and WRL-68 cells. SCARA5 overexpression inhibits the phosphorylation of FAK (Tyr-397), Src (Tyr-416), and p130Cas (Tyr-165) in Huh7 cells (**left**), SCARA5 knockdown by shRNA promotes the phosphorylation of those proteins at same position in WRL-68 cells (**right**). Total levels of these proteins were assessed by western blot analysis with the corresponding antibodies, respectively, while phosphorylation levels at specific position of these proteins were evaluated by the corresponding antibodies. Quantifications of phosphorylation levels of FAK, Src and p130Cas, as indicated on the corresponding panels, was performed by normalizing the total FAK, Src and p130Cas, respectively, according to β -actin as loading control. SCARA5 expression was assessed by Western blot analysis in Huh-7 cells or real-time PCR in WRL-68 cells. β -actin was used as a loading control.

Supplemental Table 1. Gene list of 524 upregulated genes after drugs treatment*

Symbol	Numbers**	YY_8301	HepG2	Sk_hep	MHCC_H	Hep3B	Bel7404	Bel7405	Focus	QGY7703	SMMC7721	Bel7402	Huh7	QGY7701	PLC	MHCC_L	Chromosome	Description
ATP6V1C2	5	1.32	5.35	0.99	1.50	1.59	3.79	3.50	1.67	1.91	1.00	8.34	2.39	2.97	3.13	0.97	2	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C isoform 2
TRIM15	4	1.00	2.22	1.00	3.91	3.10	1.36	1.47	4.68	3.56	1.00	1.35	2.92	1.00	1.06	1.26	6	Tripartite motif-containing 15
NRP1	9	2.98	5.95	9.90	3.14	4.70	3.82	4.02	1.28	2.43	1.00	2.39	3.15	2.26	4.79	4.97	10p12	Neuropilin 1
APBB1IP	4	2.57	1.35	1.11	10.16	5.28	3.83	2.28	0.56	1.09	2.61	13.57	1.67	1.52	1.43	2.24	10p12.1	Amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein
VIM	4	0.81	5.98	1.50	32.71	1.79	0.93	0.87	1.18	1.23	1.06	0.92	2.33	1.12	3.34	5.98	10p13	Vimentin_Vimentin
LOC219731	3	1.00	4.29	0.75	2.16	1.21	1.05	1.13	5.61	0.92	0.76	0.86	2.65	1.85	3.09	0.58	10p14	Hypothetical protein LOC219731
SPOCK2	4	1.83	2.30	0.92	1.57	1.57	7.89	3.30	1.51	2.06	2.01	9.81	1.48	3.02	1.93	1.04	10pter-q25.3	Sparc
ZNF22	6	0.79	3.36	0.73	0.88	3.53	0.92	5.68	7.62	1.82	2.38	1.06	0.64	5.53	4.56	1.02	10q11	Zinc finger protein 22 (KOX 15)
ANXA8	3	1.02	0.91	4.20	3.13	1.38	0.95	0.94	0.49	0.99	0.67	1.44	5.02	1.23	2.27	0.95	10q11.2	Annexin A8
DKK1	3	1.75	2.21	1.06	1.15	0.43	2.64	3.03	4.80	2.25	1.58	3.85	1.00	2.93	0.56	1.25	10q11.2	Dickkopf homolog 1 (Xenopus laevis)
RASGEF1A	9	1.85	1.77	2.40	3.97	1.57	26.97	11.12	3.00	4.20	10.37	9.25	2.39	10.95	3.05	1.21	10q11.21	RasGEF domain family, member 1A_RasGEF domain family, member 1A
FLJ22761	3	0.80	0.96	1.44	1.18	0.49	1.46	6.11	1.11	3.97	2.05	1.38	1.54	11.32	1.31	1.12	10q22.1	Hypothetical protein FLJ22761
PRG1	7	1.12	5.13	1.09	4.82	4.83	13.72	0.98	8.68	1.01	0.76	20.10	1.05	2.80	4.28	1.79	10q22.1	Proteoglycan 1, secretory granule
UNC5B	5	1.10	3.00	3.22	1.87	5.85	1.67	4.42	5.92	1.14	0.96	0.83	1.45	1.02	2.04	1.15	10q22.1	Unc-5 homolog B (C. elegans)
SYNPO2L	4	1.94	11.01	2.64	1.21	8.26	1.50	1.35	20.02	1.03	1.00	1.00	12.40	1.71	2.47	0.72	10q22.2	Synaptopodin 2-like
MGC16186	4	1.00	3.92	0.86	1.00	1.00	4.57	0.66	0.84	1.00	3.68	0.60	2.64	3.34	1.00	1.00	10q22.3	Hypothetical protein MGC16186
LRRC22	3	1.37	1.63	1.00	1.74	0.62	12.45	1.69	1.64	1.00	2.00	0.67	4.51	4.58	0.66	1.09	10q23.1	Leucine rich repeat containing 22
C10orf116	9	3.65	3.46	1.20	1.11	0.87	13.67	11.79	3.32	4.39	21.27	12.22	2.07	16.58	1.91	0.99	10q23.2	Chromosome 10 open reading frame 116
KIAA1975	5	1.14	1.77	1.82	2.87	4.05	1.88	3.91	8.36	2.14	2.57	1.99	3.67	4.95	2.08	1.06	10q23.2	KIAA1975 protein similar to MRIP2
ANKRD1	5	1.97	5.50	2.66	1.11	6.60	1.00	1.37	9.27	1.18	0.48	2.06	3.73	1.37	3.17	1.35	10q23.31	Ankyrin repeat domain 1 (cardiac muscle)
RBP4	3	2.56	0.60	1.92	1.62	0.61	4.66	5.83	0.93	2.74	2.45	2.24	1.11	3.66	1.78	1.11	10q23-q24	Retinol binding protein 4, plasma
PLAU	3	1.16	2.15	1.26	1.43	0.99	1.05	2.50	1.27	1.62	1.64	3.12	1.11	3.88	3.17	1.09	10q24	Plasminogen activator, urokinase
PKD2L1	4	2.13	2.16	1.16	1.80	5.41	3.39	1.11	1.67	1.35	2.02	3.99	2.17	1.46	10.33	1.19	10q24	Polycystic kidney disease 2-like 1
DUSP5	4	1.59	3.35	2.26	1.29	4.25	1.51	3.97	3.32	1.89	1.11	2.43	2.14	2.46	2.22	1.06	10q25	Dual specificity phosphatase 5
LOC387763	4	1.73	1.35	1.13	6.09	1.79	4.42	1.88	4.31	1.91	1.56	6.53	0.49	1.66	0.63	1.15	11p11.2	Hypothetical LOC387763
MDK	3	1.08	1.04	1.45	0.89	1.00	3.07	4.52	2.73	2.31	1.03	3.97	1.08	1.36	1.31	1.06	11p11.2	Midkine (neurite growth-promoting factor 2)
F2	3	1.99	0.77	1.51	3.06	0.38	3.61	2.74	2.13	1.49	1.86	4.57	1.42	1.81	1.45	1.06	11p11-q12	Coagulation factor II (thrombin)
PTDSS2	3	1.32	0.52	0.94	0.74	0.68	2.09	3.52	0.48	4.27	2.99	1.56	0.95	4.50	0.91	0.92	11p15	Phosphatidylserine synthase 2
HNRNPG-T	3	0.90	1.27	4.42	2.08	2.70	1.68	1.23	2.09	1.50	1.88	0.53	4.77	1.20	3.05	0.93	11p15	Testes-specific heterogenous nuclear ribonucleoprotein G-T
FLJ90119	4	1.33	0.99	1.78	2.93	1.07	2.73	1.00	0.48	1.00	3.81	0.47	3.69	4.28	3.74	2.55	11p15.1	Hypothetical protein FLJ90119
SAA1	11	4.65	5.07	17.27	1.70	4.01	7.82	4.84	0.87	2.44	3.17	7.20	9.05	5.82	4.10	1.58	11p15.1	Serum amyloid A1
SAA2	5	1.06	1.59	10.15	1.07	1.44	3.17	2.20	0.76	1.94	2.41	3.17	7.66	4.61	1.76	1.04	11p15.1-p14	Serum amyloid A2
FLJ14966	3	1.00	5.29	1.46	9.86	4.08	1.44	1.01	1.00	0.43	0.64	0.26	1.66	1.77	1.00	1.20	11p15.3	Hypothetical protein FLJ14966
ART5	4	3.19	1.55	1.26	1.34	1.79	5.88	3.68	1.14	1.73	1.97	2.01	2.07	5.56	1.71	1.25	11p15.4	ADP-ribosyltransferase 5
H19	4	1.88	5.37	1.43	0.98	0.09	1.79	9.87	1.28	1.17	4.42	2.61	3.13	0.90	0.99	0.86	11p15.5	H19, imprinted maternally expressed untranslated mRNA
IFITM1	4	3.62	0.94	3.15	0.85	1.76	4.89	1.64	0.95	0.99	2.69	4.15	1.06	0.71	1.31	1.07	11p15.5	Interferon induced transmembrane protein 1 (9-27)
IRF7	6	1.95	3.34	3.51	1.75	3.23	4.40	1.36	1.41	1.83	2.69	3.22	2.15	0.90	3.73	1.19	11p15.5	Interferon regulatory factor 7
HRASLS2	3	1.21	1.07	1.48	1.28	2.10	1.35	4.13	2.26	1.94	1.64	4.33	1.41	4.13	1.03	1.12	11q12.3	HRAS-like suppressor 2

CST6	12	0.90	6.68	8.62	11.70	8.97	4.48	7.33	16.99	6.25	2.37	6.36	5.98	8.54	5.95	1.00	11q13	Cystatin E
GSTP1	7	1.04	54.51	1.32	1.03	95.98	1.22	40.60	83.21	14.00	7.12	1.46	1.76	15.28	2.06	1.11	11q13	Glutathione S-transferase pi
KCNE3	3	1.21	4.07	1.00	3.98	0.63	1.77	1.61	0.80	1.20	1.00	2.38	3.79	0.83	1.00	1.15	11q13-q14	Potassium voltage-gated channel, Isk-related family, member 3
CHRDL2	4	1.00	1.04	1.00	2.44	2.71	3.89	0.53	3.43	0.92	5.87	0.77	3.22	1.29	2.16	1.00	11q14	Chordin-like 2
MMP1	4	0.43	1.28	1.93	2.52	1.03	1.00	6.13	4.76	1.95	0.62	1.17	6.15	3.20	0.79	1.45	11q22.3	Matrix metalloproteinase 1 (interstitial collagenase)
HSPB2	4	1.50	2.91	0.88	1.26	6.04	2.63	1.34	3.29	1.08	0.72	3.77	1.23	1.85	9.18	0.74	11q22-q23	Heat shock 27kDa protein 2
CD3D	5	1.74	13.76	2.20	3.55	12.47	1.00	0.64	7.37	2.11	1.27	1.00	4.22	1.30	2.69	1.83	11q23	CD3D antigen, delta polypeptide (TiT3 complex)
POU2AF1	4	1.00	7.51	0.80	0.67	5.08	1.07	0.80	1.78	1.14	1.00	2.64	3.23	0.38	5.00	1.00	11q23.1	POU domain, class 2, associating factor 1
LOC283152	3	1.55	6.17	2.01	3.06	3.51	0.71	1.47	2.73	0.76	1.24	1.17	2.44	2.19	2.04	1.54	11q23.3	Hypothetical protein LOC283152
MCAM	3	1.09	2.61	1.78	3.36	2.19	1.07	1.04	0.94	1.00	1.05	0.96	3.18	1.26	6.39	1.45	11q23.3	Melanoma cell adhesion molecule
TMEM25	4	0.57	1.29	1.11	4.07	1.40	1.65	3.73	3.85	1.11	1.48	1.96	1.24	2.15	4.73	0.99	11q23.3	Transmembrane protein 25
ESAM	5	0.54	3.74	2.78	2.35	4.78	1.11	2.06	4.00	1.01	0.31	1.08	5.80	1.94	6.14	1.33	11q24.2	Endothelial cell adhesion molecule
FLJ32915	3	1.00	1.44	0.87	0.93	3.24	3.69	2.93	2.88	1.74	3.84	2.91	0.61	1.89	1.57	1.18	11q24.2	Hypothetical protein FLJ32915
MGC10946	5	1.83	2.00	2.54	3.09	4.01	8.24	1.53	1.90	1.72	1.13	4.26	3.54	1.64	0.61	1.48	12p12.1	Hypothetical protein MGC10946
ARHGDIB	3	1.16	0.93	1.12	1.04	3.76	3.15	1.51	2.84	1.38	2.95	1.96	0.65	3.48	2.41	1.05	12p12.3	Rho GDP dissociation inhibitor (GDI) beta
KLRC1	3	0.84	3.03	1.71	1.50	1.00	1.00	0.80	3.84	0.60	1.46	1.00	4.57	0.72	1.31	1.31	12p13	Killer cell lectin-like receptor subfamily C, member 1
KLRC3	3	1.11	5.00	1.63	1.86	1.00	1.00	0.76	3.79	0.62	1.46	0.67	4.64	0.70	1.43	1.09	12p13	Killer cell lectin-like receptor subfamily C, member 2
GSG1	3	1.24	1.36	3.11	1.88	1.19	1.02	1.41	2.33	1.65	1.73	1.70	4.43	3.37	1.15	1.14	12p13.1	Germ cell associated 1
FLJ22662	4	1.54	1.17	1.07	2.05	1.39	3.16	2.29	2.71	3.80	1.46	4.41	1.04	13.15	0.95	0.95	12p13.1	Hypothetical protein FLJ22662
GABARAPL1	5	1.35	3.35	3.34	2.33	3.72	1.77	2.03	4.30	1.38	1.91	1.54	3.19	1.46	2.81	1.05	12p13.2	GABA(A) receptor-associated protein like 1
STYK1	3	1.00	1.21	0.97	3.33	4.03	1.00	1.23	1.23	1.70	1.76	1.87	1.41	1.44	4.00	0.17	12p13.2	Protein kinase STYK1
OLR1	4	1.00	0.85	7.63	1.00	1.29	0.62	1.19	12.79	1.25	1.37	2.51	4.61	1.65	3.04	0.99	12p13.2-p12.3	Oxidised low density lipoprotein (lectin-like) receptor 1
BCAT1	6	1.55	1.82	1.18	1.33	4.65	3.76	1.74	3.25	11.53	1.00	4.40	1.49	8.56	1.51	1.00	12pter-q12	Branched chain aminotransferase 1, cytosolic_Branched chain aminotransferase 1, cytosolic
SYCP3	13	2.71	8.57	3.14	7.92	30.71	6.72	8.41	32.84	4.20	12.73	11.49	8.34	7.69	15.07	1.10	12q	Synaptonemal complex protein 3
FLJ40126	3	1.00	1.00	1.00	1.77	1.99	2.52	1.00	1.67	3.17	1.57	1.00	3.07	4.01	2.62	1.38	12q12	Hypothetical protein FLJ40126
HOXC12	4	1.14	1.37	1.63	2.30	1.03	7.31	2.85	2.15	4.74	3.19	8.04	2.40	2.18	1.84	1.57	12q12-q13	Homeo box C12
KRT7	3	1.03	1.25	1.47	9.07	1.52	1.24	1.04	7.78	1.65	1.41	1.44	8.16	1.66	1.09	1.10	12q12-q13	Keratin 7
KRT18	3	1.24	3.50	1.50	1.39	0.82	1.25	2.53	4.38	1.66	1.32	1.49	1.85	3.07	1.41	1.08	12q13	Keratin 18
LOC144501	3	1.11	2.14	1.06	6.34	4.28	1.03	1.16	1.35	1.14	1.08	1.81	1.34	1.24	4.16	1.10	12q13.13	Hypothetical protein LOC144501
FLJ32942	11	0.97	4.68	10.60	26.72	20.96	18.10	18.77	1.71	14.45	27.90	11.55	1.19	15.42	1.06	6.68	12q13.2	Hypothetical protein FLJ32942
IL23A	3	1.40	3.57	2.27	2.59	1.14	1.54	0.96	8.66	1.48	0.97	0.59	3.61	1.79	2.69	1.13	12q13.3	Interleukin 23, alpha subunit p19
SILV	3	0.79	5.49	0.98	1.10	7.92	2.20	1.33	2.29	1.10	1.05	1.16	1.67	3.63	1.69	0.91	12q13-q14	Silver homolog (mouse)
TAC3	3	1.24	6.09	1.23	1.86	5.97	1.73	0.95	1.02	1.06	1.18	1.68	3.76	1.20	1.46	0.89	12q13-q21	Tachykinin 3 (neuromedin K, neurokinin beta)
LUM	3	1.20	2.52	2.11	3.46	7.93	1.93	0.58	0.31	0.56	2.29	4.63	2.68	0.88	1.16	1.00	12q21.3-q22	Lumican
KITLG	5	2.23	1.51	4.93	2.64	1.30	1.36	1.00	1.43	3.31	2.05	1.00	3.96	3.73	3.26	1.90	12q22	KIT ligand
DUSP6	3	0.99	3.47	3.22	1.27	2.62	1.51	3.97	0.86	2.19	0.89	2.29	2.94	2.00	1.22	1.41	12q22-q23	Dual specificity phosphatase 6
IQCD	4	1.19	8.78	1.98	2.35	6.35	2.07	1.69	2.25	1.43	0.99	3.21	2.12	2.12	3.17	1.36	12q24.13	IQ motif containing D
OAS2	3	1.00	1.00	4.32	1.83	1.00	2.13	0.79	4.21	1.00	1.00	1.00	4.48	0.53	1.00	1.24	12q24.2	2’-5’-oligoadenylate synthetase 2, 69
MGC33630	13	2.59	5.00	8.37	11.84	4.25	14.14	21.20	4.37	3.16	3.35	16.83	6.47	7.75	7.30	1.03	12q24.31	Hypothetical protein MGC33630_Hypothetical protein MGC33630
EP400	5	4.41	3.75	3.71	2.39	1.38	2.18	3.13	1.42	2.11	1.39	1.50	2.51	2.99	4.42	1.15	12q24.33	E1A binding protein p400
GPR133	5	1.00	22.58	1.00	1.00	3.63	1.81	1.00	1.22	1.19	2.84	4.38	3.90	3.17	1.84	1.93	12q24.33	G protein-coupled receptor 133
CCNA1	7	1.87	13.79	1.71	1.00	2.71	11.39	26.73	10.79	23.07	1.00	44.70	1.00	14.74	1.00	1.00	13q12.3-q13	Cyclin A1
EPSTI1	3	1.00	1.23	1.87	1.00	1.00	1.00	1.00	1.06	2.44	1.00	3.65	2.99	1.00	3.99	4.12	13q13.3	Epithelial stromal interaction 1 (breast)
DNAJD1	3	1.18	0.99	2.97	1.31	4.30	1.09	1.91	1.49	2.04	5.14	0.96	1.68	14.92	1.28	1.01	13q14.1	DnaJ (Hsp40) homolog, subfamily D, member 1
RGC32	4	1.92	7.31	1.46	1.38	4.24	4.31	2.37	0.97	1.59	1.18	5.89	2.05	0.91	2.27	1.20	13q14.11	Response gene to complement 32_Response gene to complement 32

SLC7A7	3	1.40	5.14	1.72	1.39	4.04	1.32	1.71	0.38	0.91	1.00	1.25	5.15	1.33	1.45	1.00	14q11.2	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 7
DHRS2	3	2.27	1.26	2.43	1.07	17.99	15.19	2.70	14.42	1.08	1.59	2.04	2.26	1.68	1.35	0.90	14q11.2	Dehydrogenase
EGLN3	3	0.88	1.47	1.08	6.26	1.56	6.50	1.17	6.12	0.85	1.11	0.80	1.55	1.62	1.11	1.07	14q13.1	Egl nine homolog 3 (C. elegans)
NID2	8	2.46	3.93	1.61	3.99	9.34	3.65	2.90	1.73	4.90	6.41	5.01	2.60	3.74	2.15	1.29	14q21-q22	Nidogen 2 (osteonidogen)
C14orf29	6	1.00	3.03	1.46	1.00	1.00	2.26	3.23	12.01	4.45	1.00	7.51	2.00	11.53	0.75	1.00	14q22.1	Chromosome 14 open reading frame 29
TGFB3	4	1.03	1.68	1.00	1.00	1.00	3.15	1.00	1.14	1.00	1.15	0.33	3.08	3.02	4.16	1.19	14q24	Transforming growth factor, beta 3
HSPA2	6	5.32	2.03	1.55	1.37	4.22	5.58	4.05	0.99	2.07	2.27	4.02	1.23	4.04	1.79	0.91	14q24.1	Heat shock 70kDa protein 2
BATF	5	1.60	3.38	1.20	1.97	9.15	1.63	6.86	0.99	2.09	5.19	2.61	2.58	3.98	1.27	0.99	14q24.3	Basic leucine zipper transcription factor, ATF-like
DIO3	4	1.71	0.83	1.00	3.33	3.01	7.50	1.46	1.16	1.23	1.29	4.46	1.19	2.20	0.85	1.15	14q32	Deiodinase, iodothyronine, type III
IFI27	9	1.51	2.38	13.84	3.82	11.87	4.58	3.17	1.39	2.09	3.35	5.36	4.23	0.76	4.15	1.78	14q32	Interferon, alpha-inducible protein 27
MEG3	4	1.63	8.17	0.88	1.57	8.88	50.83	1.50	0.94	1.67	1.13	2.09	1.29	4.55	2.07	1.00	14q32	Maternally expressed 3
FAM14A	3	1.15	3.29	0.97	0.85	3.42	1.13	0.54	0.55	0.81	0.85	1.01	1.10	1.35	4.64	0.93	14q32.13	Family with sequence similarity 14, member A
TDRD9	6	1.43	3.12	1.66	5.94	7.30	14.63	1.05	2.60	0.92	0.93	7.81	1.57	1.16	4.52	1.02	14q32.33	Tudor domain containing 9
NDN	3	1.98	3.82	1.03	1.28	4.35	2.88	1.34	1.24	1.10	1.27	1.08	10.82	1.13	1.67	1.12	15q11.2-q12	Necdin homolog (mouse)
GREM1	3	1.04	1.10	1.87	6.82	2.99	1.68	2.78	5.17	1.66	1.00	0.63	1.41	3.71	1.00	0.77	15q13-q15	Gremlin 1 homolog, cysteine knot superfamily (Xenopus laevis)
CKMT1	5	1.08	9.13	1.83	8.09	3.76	0.98	2.45	2.55	2.27	2.59	1.83	2.79	3.80	5.15	2.27	15q15	Creatine kinase, mitochondrial 1 (ubiquitous)
SPINT1	8	1.24	5.41	1.68	4.13	1.18	1.34	3.31	7.36	3.89	2.39	3.17	3.21	2.52	3.24	1.35	15q15.1	Serine protease inhibitor, Kunitz type 1
NIP	3	1.00	3.46	1.35	5.59	2.86	3.25	2.12	1.94	1.42	1.01	1.19	2.80	2.37	1.59	2.35	15q21.1	Homolog of Drosophila Numb-interacting protein
NMES1	10	2.02	2.48	9.00	16.08	7.28	9.84	2.68	1.32	4.26	5.58	8.10	9.06	3.07	7.60	1.90	15q21.1	Normal mucosa of esophagus specific 1
JACOP	3	1.93	0.49	0.66	0.29	0.27	5.52	1.35	0.41	0.96	0.76	3.13	0.93	4.17	0.80	0.92	15q21.3	Likely ortholog of mouse junction-associated coiled-coil protein
LIPC	3	1.00	0.77	2.51	0.97	0.23	4.23	7.41	5.20	1.00	1.79	1.88	0.72	2.21	0.70	1.10	15q21-q23	Lipase, hepatic
CILP	3	1.00	3.41	0.74	3.67	1.64	1.00	1.00	8.45	0.92	1.00	2.58	1.50	1.92	0.70	1.27	15q22	Cartilage intermediate layer protein, nucleotide pyrophosphohydrolase
NMB	9	4.33	2.62	2.29	1.40	2.76	44.40	22.81	22.80	5.67	7.61	13.45	3.26	13.70	2.36	1.01	15q22-qter	Neuromedin B
BCL2A1	3	1.00	10.18	3.32	19.81	1.88	1.00	1.00	2.04	1.29	1.00	1.00	2.87	1.00	2.90	1.64	15q24.3	BCL2-related protein A1
LOC440312	3	1.42	1.91	1.28	1.51	0.72	4.47	1.33	3.28	2.33	3.08	0.82	1.22	1.79	1.32	1.24	15q26.2	LOC440312
ARRDC4	3	0.70	9.70	1.59	1.63	32.53	0.58	1.80	3.89	1.30	1.42	1.07	0.75	1.08	1.60	0.88	15q26.3	Arrestin domain containing 4
QPRT	3	5.20	0.77	1.51	2.74	0.69	11.77	1.00	0.56	0.99	1.07	6.99	1.35	2.17	1.18	1.40	16p11.2	Quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))
PYCARD	3	1.44	1.01	1.23	1.05	1.04	4.01	2.88	1.94	1.86	3.18	3.37	2.37	2.68	2.60	0.96	16p12-p11.2	PYD and CARD domain containing
C16orf30	4	1.00	3.71	1.75	1.32	1.23	6.17	0.63	2.89	1.03	3.44	5.12	2.22	0.72	1.40	0.72	16p13.3	Chromosome 16 open reading frame 30
MGC35212	3	2.12	1.58	0.83	2.13	1.00	5.78	2.30	8.81	2.33	1.30	8.73	0.67	2.72	0.80	1.03	16p13.3	Hypothetical protein MGC35212
MGC52282	4	1.74	3.43	1.55	5.18	1.22	2.16	1.17	4.22	1.77	3.01	1.88	1.21	2.64	1.75	1.28	16p13.3	Hypothetical protein MGC52282
PPL8	3	2.41	2.49	1.18	2.55	0.70	6.63	2.26	1.16	1.69	4.23	4.36	2.12	2.46	2.70	1.33	16p13.3	Similar to prepro-Neuropeptide W polypeptide
GPR56	3	1.68	2.41	0.82	3.98	1.23	1.63	0.75	0.52	0.95	1.40	1.33	4.55	1.34	4.24	1.33	16q13	G protein-coupled receptor 56
MT1E	4	1.31	6.39	1.30	4.16	7.77	0.94	0.95	1.42	0.99	0.90	1.08	1.32	1.24	3.04	1.56	16q13	Metallothionein 1E (functional)
MT1K	5	1.29	6.26	1.28	5.63	9.46	0.97	0.84	15.66	1.03	1.35	1.10	1.73	0.98	7.12	0.78	16q13	Metallothionein 1K
MT1L	3	1.23	5.94	1.17	3.77	5.30	0.87	0.98	1.35	1.01	0.80	1.09	1.17	1.31	2.49	1.51	16q13	Metallothionein 1L
MT1J	3	1.29	5.37	1.12	3.71	5.40	0.91	0.93	1.34	0.91	0.79	1.05	1.10	1.22	2.02	1.55	16q13	MTB (MTB)
MT1X	3	1.32	6.45	1.21	5.06	5.69	0.89	0.97	1.37	0.95	0.79	1.06	1.19	1.30	2.16	1.61	16q13	Metallothionein 1X_Metallothionein 1X
MT2A	3	1.17	6.66	1.42	4.70	6.65	0.85	0.94	1.30	0.97	0.78	1.09	1.50	1.42	2.36	1.88	16q13	Metallothionein 2A_Metallothionein 2A
CDH1	9	1.36	3.08	2.68	5.27	1.84	5.41	27.06	6.80	4.46	4.50	9.04	1.87	20.03	2.74	0.93	16q22.1	Cadherin 1, type 1, E-cadherin (epithelial)
RRAD	4	2.16	2.81	1.53	5.47	3.71	1.47	3.03	1.24	1.60	1.32	2.43	3.45	1.34	1.19	1.03	16q22	Ras-related associated with diabetes_Ras-related associated with diabetes

COTL1	5	1.23	4.35	1.11	21.58	3.72	1.44	1.12	7.47	1.54	1.06	1.78	1.24	1.66	1.95	3.05	16q24.1	Coactosin-like 1 (Dictyostelium)_Coactosin-like 1 (Dictyostelium)
TRPV2	7	1.47	3.23	6.12	1.91	6.58	3.50	3.04	1.20	1.78	1.42	2.72	6.18	3.08	1.57	1.43	17p11.2	Transient receptor potential cation channel, subfamily V, member 2
CLDN7	3	0.94	2.58	1.54	4.26	4.08	1.10	1.35	3.02	1.57	2.39	1.06	1.98	1.95	1.47	1.18	17p13	Claudin 7
NALP1	3	0.91	4.90	1.48	2.06	6.06	1.20	1.20	0.77	1.06	0.76	1.02	2.37	1.57	3.36	0.81	17p13	NACHT, leucine rich repeat and PYD containing 1
FLJ34790	3	1.35	0.95	0.99	1.18	3.72	1.13	0.76	0.91	0.73	0.73	2.00	3.41	2.35	4.87	0.90	17p13.1	Hypothetical protein FLJ34790
LOC388335	3	1.07	1.34	1.34	0.99	0.64	4.66	3.96	2.07	2.07	1.60	4.82	0.96	1.67	1.24	0.84	17p13.1	Similar to RIKEN cDNA A730055C05 gene
LOC284013	3	1.73	6.71	0.86	1.22	4.13	1.95	2.16	1.11	3.21	1.91	2.14	1.60	2.01	1.90	1.00	17p13.2	Secretory protein LOC284013
ENO3	3	1.09	0.71	2.31	1.42	1.17	1.67	3.71	4.16	1.06	2.02	1.38	2.75	3.29	1.59	1.38	17pter-p11	Enolase 3, (beta, muscle)
CCL15	3	2.72	1.75	3.08	1.71	0.97	2.89	2.26	2.22	1.00	3.13	1.23	1.86	4.33	1.62	1.86	17q11.2	Chemokine (C-C motif) ligand 14
RNF135	3	0.56	0.58	0.83	9.60	2.56	0.70	0.91	3.88	0.98	0.84	0.74	0.86	0.92	3.09	0.92	17q11.2	Ring finger protein 135
CCL5	3	1.34	0.96	7.58	1.48	3.72	0.92	0.71	1.00	1.39	0.76	1.09	4.32	0.91	1.14	1.07	17q11.2-q12	Chemokine (C-C motif) ligand 5
HSD17B1	5	1.77	4.59	2.06	1.61	2.00	7.04	4.91	2.72	2.47	2.59	5.50	1.45	3.36	1.78	1.04	17q11-q21	Hydroxysteroid (17-beta) dehydrogenase 1
KRT12	9	1.30	8.99	2.57	2.96	12.09	4.75	2.73	6.30	3.09	3.71	7.25	5.49	3.77	2.49	1.18	17q12	Keratin 12 (Meesmann corneal dystrophy)
KRT17	5	3.40	3.21	1.82	2.33	1.53	3.45	1.37	1.42	1.65	3.04	2.41	3.90	1.60	1.92	0.91	17q12-q21	Keratin 17
SOST	3	0.52	0.97	1.57	0.45	1.19	3.33	2.36	6.72	1.12	2.23	0.80	1.31	2.02	9.04	1.13	17q12-q21	Sclerosteosis
GAS	3	1.49	3.57	1.25	2.35	1.91	1.81	3.41	2.03	1.70	1.21	1.46	1.14	4.17	1.43	1.29	17q21	Gastrin
CTEN	5	1.40	5.65	1.36	6.01	4.05	1.05	1.41	3.95	1.34	0.81	2.16	0.77	1.24	0.96	3.52	17q21.2	C-terminal tensin-like
KRT19	9	9.41	2.93	1.22	1.82	2.08	11.27	9.97	12.92	5.91	9.89	12.48	2.86	7.20	3.96	1.06	17q21.2	Keratin 19
FLJ35848	3	1.00	1.00	1.19	1.00	3.68	1.40	1.29	23.67	4.33	1.00	2.87	1.28	1.00	1.38	1.00	17q21.31	Hypothetical protein FLJ35848
TCAM1	5	1.00	3.00	2.42	1.17	3.27	4.06	1.82	1.70	2.44	1.80	0.96	0.92	5.88	4.34	0.51	17q22	Testicular cell adhesion molecule 1
FOXJ1	3	1.25	3.03	1.30	4.45	0.67	2.90	3.12	2.27	1.78	2.60	2.09	1.64	1.82	2.55	1.42	17q22-17q25	Forkhead box J1
PECAM1	6	1.00	0.88	2.09	1.22	6.87	3.29	2.28	0.49	2.60	1.94	4.06	3.21	3.51	3.71	0.84	17q23	Platelet
TEX14	6	2.45	1.22	1.79	1.39	7.31	3.53	4.41	6.57	1.53	1.50	2.06	2.28	3.43	3.44	2.20	17q23.2	Testis expressed sequence 14
RGS9	7	1.62	3.93	2.27	3.97	3.35	2.23	1.92	7.88	2.88	0.94	1.97	5.13	4.46	3.23	1.03	17q23-q24	Regulator of G-protein signalling 9
ICAM2	8	1.23	2.47	3.78	2.45	8.64	4.91	3.26	4.52	2.78	3.73	5.70	1.59	5.96	2.61	1.37	17q23-q25	Intercellular adhesion molecule 2
NPTX1	4	0.74	5.72	1.53	8.98	6.44	0.59	1.67	1.38	1.13	1.10	0.49	8.47	0.80	0.89	2.10	17q25.1-q25.2	Neuronal pentraxin I
FLJ35767	3	1.37	6.07	0.99	1.60	6.44	3.86	1.39	2.94	0.52	1.11	2.61	1.04	1.22	2.05	1.45	17q25.3	FLJ35767 protein
DKFZp779B1634	4	1.05	1.14	3.56	2.12	1.00	1.00	2.48	6.91	1.57	1.51	1.69	3.58	2.34	1.80	3.75	18p11.21	Similar to POTE8A
MGC4083	3	1.06	3.95	0.82	23.31	4.34	1.23	1.74	1.09	1.36	1.35	1.29	1.35	1.49	2.59	1.89	18p11.21	Tubulin beta MGC4083
EMILIN2	7	1.24	1.09	1.14	11.08	2.32	4.33	9.30	0.71	5.26	5.35	7.24	1.44	3.63	1.40	1.06	18p11.3	Elastin microfibril interfacer 2
CABYR	7	1.28	2.48	0.69	0.96	2.45	8.40	10.25	3.92	3.36	3.85	12.32	0.77	12.70	1.99	0.90	18q11.2	Calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)
CRLF1	5	1.78	1.09	1.71	1.50	1.26	2.32	3.88	6.92	2.87	2.54	2.15	3.93	5.57	3.01	1.23	19p12	Cytokine receptor-like factor 1
COMP	4	5.20	8.41	1.21	1.01	2.58	10.69	1.58	0.86	1.41	1.48	4.49	1.74	1.32	2.00	1.27	19p13.1	Cartilage oligomeric matrix protein
JAK3	4	0.85	1.58	3.80	1.32	3.39	0.94	0.82	7.66	1.12	0.97	1.18	3.27	1.29	1.36	1.26	19p13.1	Janus kinase 3 (a protein tyrosine kinase, leukocyte)
GDF15	4	1.08	3.02	4.03	0.77	5.53	1.73	1.52	0.78	2.84	1.26	2.51	2.79	9.15	0.53	1.07	19p13.1-13.2	Growth differentiation factor 15
CNN1	8	1.74	4.67	5.85	3.22	21.90	1.50	1.84	6.67	2.08	1.90	2.30	3.40	3.00	7.17	1.37	19p13.2-p13.1	Calponin 1, basic, smooth muscle
ANGPTL4	4	0.61	2.43	2.06	3.76	9.11	3.07	1.43	4.69	2.25	1.34	2.27	2.32	1.89	1.74	1.24	19p13.3	Angiopoietin-like 4
ATP8B3	4	1.87	1.74	1.32	1.41	3.38	5.20	1.21	3.03	1.71	1.06	4.72	1.20	1.72	1.59	1.49	19p13.3	ATPase, Class I, type 8B, member 3
CAPS	4	2.98	3.28	1.17	1.11	2.74	4.52	2.26	0.78	1.59	1.59	6.73	1.81	4.07	1.20	0.98	19p13.3	Calcyphosine
C19orf21	4	1.42	3.48	1.48	2.27	3.50	1.48	1.71	3.41	2.05	1.55	1.70	6.44	2.11	1.68	1.37	19p13.3	Chromosome 19 open reading frame 21
FGF22	3	0.88	1.00	1.00	0.76	0.60	0.66	1.18	1.32	2.60	2.41	4.01	4.08	5.62	1.72	1.18	19p13.3	Fibroblast growth factor 22
FUT3	4	1.09	3.74	0.77	1.92	3.28	3.20	1.47	1.57	2.22	1.02	2.67	1.50	1.42	4.68	1.07	19p13.3	Fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included)

FLJ32416	9	3.57	2.14	1.76	1.59	1.71	9.02	5.89	4.60	7.60	5.44	10.49	3.45	3.89	2.38	1.44	19p13.3	Homolog of mouse skeletal muscle sarcoplasmic reticulum protein JP-45
ACP5	5	2.24	0.82	1.77	3.13	0.72	1.77	4.35	0.41	1.95	3.28	1.67	1.59	4.04	3.91	1.35	19p13.3-p13.2	Acid phosphatase 5, tartrate resistant
COX7A1	12	4.31	2.44	3.52	1.81	11.14	18.06	4.85	5.27	4.82	4.97	10.42	5.53	9.13	7.86	1.06	19q13.1	Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
PPP1R14A	7	2.30	0.91	1.83	6.99	3.73	9.20	11.77	2.90	2.66	2.74	8.60	3.12	6.12	1.65	1.22	19q13.1	Protein phosphatase 1, regulatory (inhibitor) subunit 14A
SPINT2	12	3.84	6.48	4.47	11.49	16.23	10.00	6.47	4.83	3.00	2.20	6.66	8.09	5.51	1.59	1.34	19q13.1	Serine protease inhibitor, Kunitz type, 2
TZFP	4	0.93	3.90	1.46	2.69	1.81	1.00	1.00	1.96	4.00	1.21	1.00	2.57	5.14	3.35	2.26	19q13.1	Testis zinc finger protein
FLJ13072	9	1.62	2.12	3.57	3.74	5.69	33.42	2.60	9.57	2.24	4.87	15.20	2.10	3.41	5.71	0.91	19q13.11	Hypothetical gene FLJ13072
ZNF302	4	0.83	4.31	1.09	1.34	1.01	0.80	3.10	3.20	2.21	2.16	1.22	1.21	2.06	6.80	1.08	19q13.11	Zinc finger protein 302
KIRREL2	3	1.14	1.16	1.07	1.94	9.87	1.61	1.64	3.10	1.15	1.12	1.92	0.76	2.07	7.92	1.64	19q13.12	Kin of IRRE like 2 (Drosophila)
C19orf33	4	1.11	3.99	1.20	1.13	8.11	1.00	1.01	0.95	1.25	0.97	1.13	4.19	1.20	3.77	0.94	19q13.2	Chromosome 19 open reading frame 33
GMFG	4	1.27	5.49	1.92	3.22	3.54	0.93	1.22	0.55	1.12	0.96	1.19	2.10	1.35	3.37	1.16	19q13.2	Glia maturation factor, gamma
LGALS7	3	3.70	4.04	1.51	3.25	1.79	2.65	2.00	1.56	1.82	1.47	2.58	1.57	2.37	1.97	1.30	19q13.2	Lectin, galactoside-binding, soluble, 7 (galectin 7)
PSG1	3	1.34	1.16	2.30	1.22	3.13	2.03	1.29	3.79	1.20	1.76	1.26	2.56	3.64	1.07	1.04	19q13.2	Pregnancy specific beta-1-glycoprotein 1
PSG11	4	1.00	1.64	1.75	1.00	14.90	1.00	6.02	11.05	2.93	2.69	1.63	2.25	20.82	1.00	1.29	19q13.2	Pregnancy specific beta-1-glycoprotein 11
PSG3	3	0.51	1.40	1.74	2.14	5.00	1.00	2.98	5.41	1.36	2.23	1.52	1.98	8.53	1.23	0.92	19q13.2	Pregnancy specific beta-1-glycoprotein 3
PSG6	3	0.65	1.25	1.78	1.15	4.42	0.85	2.28	5.42	1.23	1.94	1.09	2.18	6.05	1.03	0.87	19q13.2	Pregnancy specific beta-1-glycoprotein 6
PSG9	5	1.00	1.00	11.74	1.00	3.30	1.00	1.48	8.19	1.00	1.21	2.14	5.32	3.61	1.00	1.00	19q13.2	Pregnancy specific beta-1-glycoprotein 9
APOC1	3	1.99	1.07	2.89	2.00	0.65	9.36	2.00	0.43	2.24	4.48	11.03	1.02	2.76	1.42	1.23	19q13.2	Apolipoprotein C-I_Apolipoprotein C-I
CKM	12	1.00	9.26	2.50	3.89	7.41	4.27	4.81	5.72	3.09	5.83	7.23	5.36	7.97	11.75	1.25	19q13.2-q13.3	Creatine kinase, muscle
FUT1	4	1.89	3.40	1.49	1.33	1.28	4.05	6.25	2.82	2.21	1.81	4.31	0.89	2.45	2.37	1.58	19q13.3	Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase)
NTF5	4	3.70	2.45	3.09	1.77	2.17	1.27	1.72	1.32	1.99	3.81	1.73	2.89	2.14	3.69	1.48	19q13.3	Neurotrophin 5 (neurotrophin 4
LOC284344	3	0.71	0.77	3.59	1.42	7.21	1.21	2.59	2.01	1.87	1.81	1.50	2.93	4.77	1.69	0.89	19q13.32	Hypothetical protein LOC284344
IGFL2	3	0.78	1.57	1.05	2.35	4.30	1.20	3.38	3.10	2.03	1.36	1.00	1.34	1.25	1.61	0.88	19q13.32	Insulin growth factor-like family member 2
MIA	7	1.56	4.56	3.30	5.75	8.20	1.53	1.45	7.36	1.40	2.16	3.24	3.14	1.97	2.46	1.50	19q13.32-q13.33	Melanoma inhibitory activity
LOC112703	3	1.20	2.28	2.85	1.91	7.88	2.08	1.31	1.64	1.31	0.88	1.89	3.48	2.52	3.00	1.04	19q13.33	Hypothetical protein BC004941
NUP62	4	0.82	1.49	3.36	5.67	3.12	4.24	2.50	1.17	1.27	1.18	2.21	2.26	1.73	1.70	1.72	19q13.33	Nucleoporin 62kDa
RASIP1	5	0.91	8.58	2.63	3.10	2.15	0.92	1.25	9.80	1.41	1.35	5.44	1.79	1.02	4.64	1.13	19q13.33	Ras interacting protein 1
TRPM4	3	1.42	2.41	1.61	1.62	1.68	1.63	2.66	2.44	1.67	4.02	4.59	1.66	3.30	2.02	1.07	19q13.33	Transient receptor potential cation channel, subfamily M, member 4
OSCAR	4	1.12	5.52	1.85	1.65	10.01	7.06	2.91	2.74	1.22	2.34	3.27	2.23	2.49	1.76	1.19	19q13.42	Osteoclast-associated receptor
FLJ23506	6	1.00	1.80	1.00	2.00	9.33	5.55	2.96	4.64	2.61	3.17	4.83	1.02	6.16	1.63	1.79	19q13.43	Hypothetical protein FLJ23506
CHI3L2	3	2.17	3.98	3.28	1.10	3.16	1.00	1.48	0.98	0.92	1.67	1.51	1.68	1.59	2.25	1.44	1p13.3	Chitinase 3-like 2
FLJ22457	5	0.58	4.29	1.56	1.20	10.84	2.99	3.48	0.80	1.34	1.86	4.42	1.82	1.65	3.67	0.88	1p13.3	Hypothetical protein FLJ22457
BRDT	3	0.94	2.32	1.41	1.05	6.36	1.14	2.64	7.25	1.51	1.00	1.03	0.96	2.54	9.21	1.01	1p22.1	Bromodomain, testis-specific
PARG1	3	2.47	2.40	2.64	2.64	2.78	3.11	3.43	1.42	1.39	1.12	2.16	2.04	3.14	1.68	2.66	1p22.1	PTPL1-associated RhoGAP 1
CNN3	4	0.91	1.03	0.87	1.49	1.25	1.17	5.86	1.03	3.91	4.25	0.88	0.95	9.51	1.26	1.10	1p22-p21	Calponin 3, acidic
AK5	12	3.52	4.73	1.52	6.40	9.54	16.26	14.36	6.99	5.93	10.05	9.73	1.43	13.15	5.10	0.79	1p31	Adenylate kinase 5
FLJ10884	12	2.43	12.87	12.47	1.29	35.75	5.36	15.00	30.70	5.35	7.41	3.28	11.84	21.59	17.27	0.78	1p31.3	Hypothetical protein FLJ10884
GPX7	3	1.11	0.55	1.63	1.46	0.66	1.01	10.99	2.35	2.78	1.23	4.80	1.40	2.52	7.75	0.84	1p32	Glutathione peroxidase 7
C1orf34	5	1.16	2.89	3.31	0.95	1.34	3.40	1.94	1.01	2.11	3.48	3.96	1.48	5.69	1.86	1.02	1p32.3	Chromosome 1 open reading frame 34
DMRTB1	12	7.74	1.02	2.40	10.56	3.60	33.89	25.67	14.72	10.11	13.94	98.09	7.45	46.05	43.08	0.83	1p32.3	DMRT-like family B with proline-rich C-terminal, 1

SLC1A7	3	0.99	1.91	1.67	1.31	3.05	1.72	1.37	0.62	1.70	1.43	3.37	3.46	2.01	1.80	1.09	1p32.3	Solute carrier family 1 (glutamate transporter), member 7
TACSTD2	4	0.98	2.52	2.51	1.70	3.34	1.09	3.64	0.65	1.10	4.10	1.15	6.65	1.82	1.22	0.94	1p32-p31	Tumor-associated calcium signal transducer 2
FABP3	4	1.90	1.92	1.60	4.44	3.05	1.53	1.65	6.83	1.75	1.06	1.35	2.44	4.02	2.41	1.22	1p33-p32	Fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)
COL8A2	7	1.00	6.62	5.16	2.44	0.91	1.49	2.19	3.46	3.49	1.42	1.71	10.63	9.20	7.98	1.49	1p34.2	Collagen, type VIII, alpha 2
DNALI1	10	2.11	5.81	3.43	0.94	12.48	12.56	5.64	7.27	2.48	4.94	13.30	1.95	6.65	5.62	1.07	1p35.1	Dynein, axonemal, light intermediate polypeptide 1
LCN7	3	1.25	1.76	1.63	1.18	1.13	2.34	3.16	1.91	1.93	2.14	3.59	3.08	2.97	1.49	1.40	1p35.2	Lipocalin 7
COL16A1	3	1.42	0.83	2.43	6.01	9.55	1.62	1.16	1.01	1.73	1.17	1.47	1.99	1.50	5.60	1.14	1p35-p34	Collagen, type XVI, alpha 1
CDW52	5	2.15	5.28	1.48	8.27	2.05	1.73	2.19	1.52	1.42	6.68	0.93	3.05	3.82	1.63	2.14	1p36	CDW52 antigen (CAMPATH-1 antigen)
AIM1L	4	1.61	3.25	4.07	4.77	2.22	2.05	1.94	1.50	1.49	2.18	1.94	4.25	1.77	1.52	1.21	1p36.11	Absent in melanoma 1-like
MYOM3	4	1.81	1.56	3.14	2.33	1.98	0.84	2.82	1.36	1.44	1.87	3.10	3.75	1.95	4.11	1.67	1p36.11	Myomesin family, member 3
ELA3B	4	1.90	6.74	1.52	2.08	0.78	4.64	1.54	1.45	0.26	3.21	1.47	2.39	3.46	2.63	1.49	1p36.12	Elastase 3B, pancreatic
MGC24047	3	0.83	3.03	1.01	0.94	1.36	5.60	0.95	2.06	0.78	0.74	1.60	1.59	0.87	3.15	1.05	1p36.13	Hypothetical protein MGC24047
FBXO2	4	2.88	1.29	2.38	8.77	2.03	6.75	1.83	5.00	1.26	5.72	1.91	1.95	2.88	1.58	1.58	1p36.22	F-box protein 2
RBP7	6	0.85	2.06	0.86	1.92	3.88	1.00	5.83	6.69	1.86	2.08	3.36	1.54	3.29	4.29	0.97	1p36.22	Retinol binding protein 7, cellular
HSPB7	3	0.82	0.89	0.86	1.00	1.64	1.52	2.82	0.98	3.31	4.97	1.20	3.60	2.41	2.28	1.06	1p36.23-p34.3	Heat shock 27kDa protein family, member 7 (cardiovascular)
LOC81569	3	3.85	1.27	1.70	0.75	1.07	5.65	1.54	1.52	1.54	1.72	3.96	1.99	1.33	1.56	0.93	1p36.2-p35	Actin like protein
FLJ32096	3	2.26	1.25	1.74	0.66	1.01	1.17	1.40	1.89	1.65	2.21	3.60	2.14	4.39	3.36	2.24	1p36.31	Hypothetical protein FLJ32096
MGC3047	3	1.62	1.12	0.80	1.00	2.38	3.47	1.54	6.69	1.87	1.14	2.49	2.34	4.38	2.51	1.02	1p36.33	Hypothetical protein MGC3047
CDT6	3	0.95	1.92	2.24	0.67	18.94	1.00	1.12	1.00	0.81	1.17	1.00	4.05	1.25	8.01	0.96	1p36.3-p36.2	Angiopoietin-like factor
C1orf42	3	0.79	1.62	0.88	18.30	1.18	1.13	0.87	8.44	0.97	0.80	1.29	3.21	1.41	2.03	0.91	1q21	Chromosome 1 open reading frame 42
PDZK1	5	3.27	0.54	2.70	5.74	0.18	1.99	2.09	0.90	1.89	4.69	4.07	0.74	3.66	0.86	1.11	1q21	PDZ domain containing 1
S100A2	4	2.01	21.54	1.85	8.63	6.24	2.37	1.83	1.35	2.38	1.68	3.10	2.35	2.28	2.60	1.60	1q21	S100 calcium binding protein A2
S100A4	4	1.33	5.57	3.80	0.78	5.01	1.05	0.52	0.30	0.67	1.59	0.76	4.76	0.75	2.52	1.36	1q21	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)
LOC440679	3	0.47	12.06	1.00	1.00	18.95	0.15	1.00	1.00	1.05	0.28	1.37	4.70	0.25	0.68	1.00	1q21.1	LOC440679
HIST2H2AA	4	1.34	5.86	4.36	3.70	6.41	1.93	1.15	2.45	0.91	0.98	1.75	2.34	1.00	2.28	1.08	1q21.2	Histone 2, H2aa
NOHMA	4	1.24	1.42	1.19	3.90	2.27	2.71	3.96	9.51	2.71	2.31	1.82	1.29	7.51	1.05	0.76	1q21.2	HORMA domain containing protein
SYT11	6	1.73	4.27	1.68	8.86	6.35	1.00	1.80	4.64	1.21	2.66	2.24	2.93	3.50	6.74	1.53	1q21.2	Synaptotagmin XI_Synaptotagmin XI
F11R	10	1.49	12.99	1.87	0.88	1.79	8.98	8.09	7.26	12.07	9.56	4.75	6.08	12.09	14.77	1.08	1q21.2-q21.3	F11 receptor
FLJ14904	5	0.74	1.95	1.36	3.84	10.24	7.58	2.20	5.58	1.28	2.05	5.58	1.48	2.14	1.66	1.04	1q24.1	Hypothetical protein FLJ14904
NCF2	3	0.75	3.41	4.02	4.66	0.64	0.44	1.76	0.88	1.30	1.02	1.18	1.00	1.16	1.00	1.14	1q25	Neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)
LAD1	4	1.00	1.37	1.38	2.09	0.75	4.09	1.67	3.88	0.89	1.00	7.61	1.83	1.07	9.00	1.02	1q25.1-q32.3	Ladinin 1
PTGS2	3	1.80	0.68	0.88	2.12	5.25	0.52	0.99	1.52	3.33	1.00	0.78	1.34	3.63	0.64	1.20	1q25.2-q25.3	Prostaglandin-endoperoxide synthase 2 (prostaglandin G
LAMB3	3	0.89	7.65	1.69	6.51	9.41	0.93	0.80	2.75	0.97	0.75	1.15	1.84	1.56	1.94	1.43	1q32	Laminin, beta 3
GOS2	4	0.91	1.55	2.80	3.34	10.02	2.03	1.13	1.18	9.70	1.04	4.49	1.21	2.53	1.12	1.12	1q32.2-q41	Putative lymphocyte G0
MIA3	3	3.28	2.11	3.35	3.25	1.93	1.18	1.00	1.07	1.16	1.21	0.88	1.39	1.05	1.33	1.04	1q41	C219-reactive peptide
LEFTB	3	2.94	2.65	0.86	3.41	1.85	3.02	0.93	0.81	0.81	1.16	2.72	3.17	0.93	2.08	0.91	1q42.1	Left-right determination, factor B
ACTN2	9	1.00	3.89	12.33	5.30	7.41	3.44	2.87	13.16	1.42	2.80	1.12	9.53	8.54	9.77	1.37	1q42-q43	Actinin, alpha 2
FMN2	4	2.02	0.94	1.17	0.96	1.00	2.17	5.65	1.06	5.17	2.39	3.38	0.80	13.68	0.84	0.93	1q43	Formin 2
GREM2	3	1.00	0.56	0.82	1.00	0.83	2.16	1.18	0.32	3.24	2.60	5.81	0.69	4.90	0.86	1.07	1q43	Gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)
BMP2	4	3.48	1.50	1.44	1.74	3.53	3.37	1.60	6.18	1.17	1.24	2.08	2.81	1.91	1.78	1.10	20p12	Bone morphogenetic protein 2
THBD	3	1.09	1.58	2.59	4.85	3.10	1.60	2.07	4.78	1.11	0.91	1.53	2.40	0.91	1.09	1.09	20p12-cen	Thrombomodulin

SDCBP2	3	1.54	3.47	1.31	5.93	0.91	1.74	1.24	1.10	1.06	1.29	1.14	3.52	0.99	1.47	1.43	20p13	Syndecan binding protein (syntenin) 2
RASSF2	3	1.03	0.84	0.52	6.47	4.84	1.66	1.45	0.49	1.37	1.00	1.47	1.42	2.71	3.17	1.17	20pter-p12.1	Ras association (RalGDS
PROCR	3	1.13	5.51	1.16	2.07	11.01	1.67	2.04	1.03	1.09	1.26	1.50	1.28	2.50	9.44	1.21	20q11.2	Protein C receptor, endothelial (EPCR)
NNAT	5	1.99	3.76	1.26	1.18	3.42	6.80	2.50	1.67	2.45	3.00	1.70	2.07	5.33	2.08	1.41	20q11.2-q12	Neuronatin
TNNC2	9	1.69	2.88	2.49	4.37	9.10	3.63	7.00	4.91	2.42	2.89	3.87	3.29	5.43	4.21	1.21	20q12-q13.11	Troponin C2, fast
BMP7	4	1.00	2.32	1.38	7.95	7.79	2.51	3.28	2.92	0.74	1.00	1.00	3.22	2.49	1.18	1.43	20q13	Bone morphogenetic protein 7 (osteogenic protein 1)
FLJ20825	4	2.37	1.75	0.77	2.98	1.24	5.94	3.31	2.28	1.01	4.29	2.96	2.01	3.05	1.51	2.03	20q13	CDNA FLJ20825 fis, clone ADSE00160
PTGIS	3	1.00	1.25	0.66	3.09	1.00	1.00	1.00	5.10	0.83	1.00	1.00	0.96	4.36	0.55	0.97	20q13.11-q13.13	Prostaglandin I2 (prostacyclin) synthase
PREX1	3	0.74	4.81	1.07	1.46	5.89	1.06	0.70	1.13	0.75	0.72	0.79	1.41	1.00	3.65	1.02	20q13.13	Phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1
SALL4	3	2.31	1.39	1.67	1.66	1.52	1.96	2.88	5.96	3.33	2.71	2.29	1.93	5.29	1.21	1.09	20q13.13-q13.2	Sal-like 4 (Drosophila)
COL9A3	3	0.91	0.82	1.91	1.56	0.69	1.20	2.03	3.40	0.75	1.20	1.55	3.70	1.84	3.92	0.96	20q13.3	Collagen, type IX, alpha 3
STMN3	5	0.62	0.62	0.87	1.72	5.08	4.62	5.80	5.30	2.31	2.80	1.39	0.67	3.86	1.87	1.36	20q13.3	Stathmin-like 3
CTCFL	5	2.13	0.88	1.85	1.11	0.87	12.38	2.93	4.40	1.09	1.08	12.26	3.73	2.41	4.19	0.91	20q13.31	CCCTC-binding factor (zinc finger protein)-like
DSCR8	5	1.65	1.25	1.80	3.34	1.58	6.07	2.00	0.47	2.95	3.01	5.91	0.72	6.21	0.90	1.32	21q22.2	Down syndrome critical region gene 8
C21orf105	3	1.20	2.32	1.07	1.56	3.57	2.79	3.08	1.51	2.32	1.78	4.68	1.42	1.71	2.53	1.02	21q22.3	Chromosome 21 open reading frame 105
C21orf129	4	1.57	1.72	1.05	1.02	2.32	3.93	1.75	11.93	2.00	1.01	2.98	2.27	11.08	4.61	0.77	21q22.3	Chromosome 21 open reading frame 129
TFF1	4	0.79	2.76	0.93	2.74	3.32	3.39	1.84	1.94	1.90	2.07	3.09	4.72	2.89	0.93	1.24	21q22.3	Trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in)
PRAME	4	2.84	13.86	1.50	7.91	7.64	28.24	1.38	0.95	1.67	2.13	2.05	1.30	1.83	2.60	1.38	22q11.22	Preferentially expressed antigen in melanoma
SUSD2	4	1.63	3.43	4.19	2.53	5.05	1.65	2.04	1.82	1.40	0.80	1.83	6.30	1.79	1.43	1.18	22q11-q12	Sushi domain containing 2
GAL3ST1	3	0.75	2.09	4.86	0.96	1.42	6.83	2.99	2.59	1.79	1.06	1.55	1.63	5.16	1.25	1.00	22q12.2	Galactose-3-O-sulfotransferase 1
NEFH	14	5.16	5.09	3.87	9.40	10.49	57.05	38.26	9.46	9.12	10.77	30.09	3.60	18.62	11.09	0.85	22q12.2	Neurofilament, heavy polypeptide 200kDa
LGALS2	5	1.12	0.89	0.92	0.84	3.76	4.54	1.78	1.84	0.83	1.59	3.46	3.48	1.76	5.88	0.68	22q12-q13	Lectin, galactoside-binding, soluble, 2 (galectin 2)
MGAT3	4	0.74	1.64	1.84	5.96	6.85	1.45	2.26	0.76	2.39	1.00	3.80	1.46	2.14	5.73	0.90	22q13.1	Mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase
RAC2	7	2.07	4.46	1.30	1.21	10.48	10.59	1.42	0.64	6.53	23.88	6.19	0.98	11.77	2.21	1.20	22q13.1	Ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
MEI1	11	1.05	4.94	4.78	9.85	7.65	12.29	5.86	2.13	1.44	4.43	10.67	5.26	6.23	5.54	1.14	22q13.2	Similar to mouse meiosis defective 1 gene
BIK	5	1.45	3.08	2.29	4.16	1.44	2.07	2.24	1.24	2.05	3.01	2.22	1.63	3.09	3.86	1.73	22q13.31	BCL2-interacting killer (apoptosis-inducing)
MOV10L1	4	1.00	0.70	0.95	2.04	1.11	10.03	2.79	4.68	2.58	1.02	9.50	1.00	7.66	1.78	0.80	22q13.33	Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse)
RGPD1	3	1.30	3.01	1.32	2.45	4.11	2.00	3.02	1.33	1.80	1.81	2.02	1.49	1.95	1.28	1.19	2p11.2	RAN-binding protein 2-like 1 short isoform
EFEMP1	3	0.87	2.44	1.78	3.54	7.68	0.85	1.02	2.32	1.08	0.97	1.96	3.40	1.16	0.94	1.49	2p16	EGF-containing fibulin-like extracellular matrix protein 1
TSPYL6	12	1.00	23.20	6.44	9.25	51.46	16.67	11.30	25.54	2.05	3.89	11.73	23.19	15.21	13.08	0.98	2p16.3	TSPY-like 6
TACSTD1	6	1.03	1.60	0.94	43.89	1.03	1.26	4.56	11.99	6.50	1.00	1.04	1.65	10.27	45.58	1.49	2p21	Tumor-associated calcium signal transducer 1
QPCT	4	1.95	1.66	1.68	1.34	2.19	6.40	4.09	0.46	2.54	2.15	9.63	1.98	9.96	2.01	1.03	2p22.2	Glutaminyl-peptide cyclotransferase (glutaminyl cyclase)
CGREF1	4	1.27	1.85	1.32	1.35	3.72	21.87	1.25	9.23	0.80	2.68	1.23	2.75	3.81	1.54	1.10	2p23.3	Cell growth regulator with EF hand domain 1
KRTCAP3	6	2.35	4.93	1.39	1.98	2.30	3.76	7.65	4.47	2.78	1.48	3.05	1.72	2.70	4.52	1.10	2p23.3	Keratinocyte associated protein 3
POMC	7	1.68	3.79	1.23	2.40	3.23	8.07	2.74	4.25	1.54	1.88	4.13	1.92	4.17	4.56	1.23	2p23.3	Proopiomelanocortin (adrenocorticotropin
LOC285016	3	1.00	3.09	1.00	1.00	4.12	2.73	3.43	1.00	1.01	1.00	1.64	1.00	1.27	1.83	1.00	2p25.3	Hypothetical protein LOC285016
PAX8	7	3.10	3.47	5.69	1.79	1.55	1.92	5.10	2.28	2.32	1.00	2.49	3.62	3.15	4.25	1.91	2q12-q14	Paired box gene 8
IL1R2	3	1.12	3.18	1.26	1.50	3.59	2.13	1.52	2.96	0.83	0.88	3.49	2.57	2.76	0.86	1.11	2q12-q22	Interleukin 1 receptor, type II

BENE	3	1.12	1.94	1.21	0.74	3.21	1.49	1.75	12.56	1.42	1.20	3.54	2.08	2.34	1.11	1.06	2q13	BENE protein
LIMS3	6	1.64	3.20	2.52	1.53	4.01	5.72	3.41	4.00	1.09	1.66	2.72	3.50	2.20	1.13	0.89	2q14-q21	LIM and senescent cell antigen-like domains 3
LOC90557	6	1.00	6.32	0.81	1.16	4.59	1.52	2.17	3.27	1.51	4.23	3.75	0.75	7.35	1.08	1.07	2q21.1	Hypothetical protein BC016861
DKFZp434E2321	6	0.94	5.93	0.80	1.17	4.27	1.66	2.87	3.66	3.42	4.07	2.22	0.78	4.29	1.05	1.13	2q21.1	Hypothetical protein DKFZp434E2321
H2-ALPHA	5	1.21	4.48	1.86	3.81	9.83	2.71	2.12	5.75	1.79	1.41	1.90	1.98	2.64	4.22	1.11	2q21.1	Tubulin, alpha 2
KIF5C	5	1.00	5.46	0.90	1.00	11.67	3.16	1.27	2.49	2.60	1.46	1.00	1.49	6.71	3.37	1.00	2q23.1	Kinesin family member 5C
BBS5	5	1.67	3.42	2.84	1.97	3.50	3.79	5.05	5.31	1.62	1.54	2.90	2.99	2.30	2.07	1.12	2q31.1	Bardet-Biedl syndrome 5
LOC375295	5	1.56	1.00	1.10	1.37	1.26	1.38	6.90	3.04	5.06	1.82	5.12	1.54	34.70	1.00	1.12	2q31.1	Hypothetical gene supported by BC013438
TMEFF2	4	1.00	0.89	2.04	1.00	4.43	1.35	0.81	3.65	1.00	1.00	1.00	3.93	3.39	1.39	0.70	2q32.3	Transmembrane protein with EGF-like and two follistatin-like domains 2
IGFBP2	4	1.15	6.34	1.08	1.40	9.28	5.69	1.88	1.39	1.13	1.04	3.04	2.77	1.69	1.57	0.99	2q33-q34	Insulin-like growth factor binding protein 2, 36kDa
CRYGC	5	0.66	2.45	1.22	1.00	5.74	1.00	3.25	3.93	1.64	1.44	0.53	4.84	5.12	1.02	0.89	2q33-q35	Crystallin, gamma C
MARCH-IV	3	1.00	0.42	1.02	2.29	1.00	6.15	1.60	5.57	2.00	1.00	6.85	0.97	1.28	0.71	1.50	2q35	Membrane-associated RING-CH protein IV
TUBA1	4	0.90	6.23	3.25	1.32	8.09	1.15	1.26	1.28	1.36	1.37	1.11	4.31	1.31	0.98	1.02	2q35	Tubulin, alpha 1 (testis specific)
FLJ25955	7	1.41	1.51	2.22	2.27	5.40	1.74	4.65	9.84	3.70	1.46	3.45	1.94	4.10	3.65	1.35	2q36.3	Hypothetical protein FLJ25955
ECEL1	4	2.59	1.12	1.06	1.11	5.26	7.30	7.14	1.29	2.94	2.05	17.48	1.08	2.67	1.17	1.14	2q36-q37	Endothelin converting enzyme-like 1
INPP5D	3	0.98	1.32	1.54	1.77	1.31	3.45	1.01	1.78	1.05	1.01	3.09	0.83	3.32	1.90	0.91	2q36-q37	Inositol polyphosphate-5-phosphatase, 145kDa
RAMP1	3	2.52	1.25	1.70	0.97	2.88	24.06	1.65	0.37	1.72	1.24	12.48	2.34	3.99	1.62	1.00	2q36-q37.1	Receptor (calcitonin) activity modifying protein 1
LOC339766	6	1.86	1.48	1.55	2.04	6.07	3.13	5.38	1.17	2.83	3.58	7.04	1.25	9.39	1.13	1.04	2q37.1	Hypothetical protein LOC339766
C3orf14	4	1.00	11.11	0.75	1.24	1.10	1.30	5.96	6.85	1.66	1.20	2.98	0.60	4.07	0.92	0.98	3p14.2	Chromosome 3 open reading frame 14
FLJ40427	3	1.00	2.20	6.57	3.07	1.15	1.00	1.00	1.77	0.45	1.00	1.00	3.70	0.56	1.31	1.07	3p14.3	Hypothetical protein FLJ40427
TSP50	3	1.33	1.70	1.02	2.81	13.21	1.12	1.66	3.98	0.86	1.10	2.27	2.19	1.29	3.36	1.21	3p14-p12	Testes-specific protease 50
CAMP	8	1.00	8.20	4.59	1.01	1.90	6.40	7.97	0.56	1.97	1.00	3.44	3.17	4.36	6.20	1.03	3p21.3	Cathelicidin antimicrobial peptide
TMEM7	7	1.26	1.00	8.20	1.46	2.75	3.83	6.30	4.00	2.14	1.81	3.85	10.11	6.46	1.22	0.97	3p21.3	Transmembrane protein 7
XLHSRF-1	4	3.21	2.40	2.47	2.60	0.83	3.70	3.71	1.30	1.73	2.48	1.78	3.30	2.25	2.33	2.49	3p21.31	Heat shock regulated 1
TNNC1	6	1.57	4.12	4.70	1.99	0.93	4.19	2.50	3.74	2.17	2.14	2.24	3.02	3.78	1.20	1.12	3p21.3-p14.3	Troponin C, slow
HYAL1	3	0.98	1.96	1.01	3.12	1.13	1.00	2.75	1.63	1.31	4.71	1.05	1.62	3.06	0.90	1.24	3p21.3-p21.2	Hyaluronoglucosaminidase 1
LOC339903	11	1.00	4.89	8.50	4.94	27.48	36.32	22.60	73.17	5.59	3.35	19.69	1.08	41.13	1.44	0.97	3p22.1	Hypothetical protein LOC339903
CCK	10	2.02	6.63	2.37	13.86	34.25	18.05	12.47	5.66	4.52	2.51	6.22	1.58	69.73	4.28	1.53	3p22-p21.3	Cholecystokinin
TGM4	4	2.09	1.09	1.03	1.82	1.11	3.81	2.40	2.60	2.57	2.68	1.00	3.78	5.04	3.88	2.16	3p22-p21.33	Transglutaminase 4 (prostate)
DAZL	14	11.37	3.93	9.96	10.05	55.49	87.62	43.67	22.32	19.71	20.81	78.85	15.43	54.36	36.46	0.86	3p24.3	Deleted in azoospermia-like
OXTR	4	1.05	3.05	0.97	4.99	4.23	1.24	0.74	1.49	0.68	0.75	0.75	1.01	0.74	3.48	1.51	3p25	Oxytocin receptor
FBLN2	6	1.50	1.83	1.89	1.15	1.79	3.60	4.80	2.82	3.37	4.90	4.31	2.02	6.29	1.53	0.87	3p25.1	Fibulin 2
TIP120B	6	1.95	1.19	1.05	2.05	1.81	14.36	7.44	19.94	2.69	2.33	6.59	0.92	6.17	6.45	0.84	3p25.2	TBP-interacting protein
DPPA4	5	1.00	1.00	1.00	4.32	5.94	1.64	1.00	4.27	4.14	1.00	1.00	2.08	3.09	1.00	1.00	3q13.13	Developmental pluripotency associated 4
LOC151871	5	2.41	1.24	1.38	3.70	7.49	2.58	1.97	2.61	1.44	3.84	2.35	2.58	4.36	3.61	1.05	3q13.13	Hypothetical protein BC018070
UPK1B	4	1.20	1.09	2.15	3.02	3.10	1.95	2.39	0.93	1.55	1.00	2.66	3.19	5.08	1.45	0.99	3q13.3-q21	Uroplakin 1B
CSTA	3	0.57	4.86	1.46	2.38	12.06	0.65	1.61	1.96	1.03	0.87	0.58	3.63	2.33	1.19	1.37	3q21	Cystatin A (stefin A)
MGC34923	3	14.72	3.23	2.16	1.25	5.57	1.21	1.11	1.12	1.07	0.82	2.52	1.99	2.05	1.70	0.91	3q22.3	Hypothetical protein MGC34923
TM4SF4	3	1.21	1.07	1.57	0.49	0.14	11.21	0.81	0.03	1.48	3.01	6.75	0.87	2.55	1.29	1.04	3q25	Transmembrane 4 superfamily member 4
MLF1	3	1.36	6.15	1.19	1.77	3.81	1.61	1.50	15.53	0.96	1.72	1.32	1.15	1.21	1.35	1.08	3q25.1	Myeloid leukemia factor 1
LXN	6	1.25	2.23	1.67	8.91	2.29	10.90	1.61	7.72	24.82	2.34	39.67	4.20	1.70	2.82	1.25	3q25.32	Latexin
RARRES1	4	1.40	1.18	1.24	1.24	0.37	0.92	5.91	1.39	3.09	13.39	2.52	0.72	14.62	1.19	0.88	3q25.32	Retinoic acid receptor responder (tazarotene induced) 1
TRIM59	3	1.56	1.92	0.78	1.25	13.53	2.10	3.32	21.12	1.34	1.93	2.05	0.68	2.11	1.70	0.92	3q25.33	Tripartite motif-containing 59
PHC3	3	1.24	1.60	1.20	1.10	0.52	5.70	4.47	1.02	0.83	3.63	1.00	1.94	2.23	1.40	0.73	3q26.2	Polyhomeotic like 3 (Drosophila)

DKFZp434A128	3	0.87	1.00	0.62	1.00	1.00	1.00	0.53	1.00	1.25	2.61	1.00	1.00	4.45	3.85	3.46	3q26.33	Hypothetical protein DKFZp434A128
TP73L	6	1.60	1.09	1.68	3.27	14.03	11.91	3.96	3.36	1.19	2.20	5.45	1.85	2.89	1.56	1.04	3q27-q29	Tumor protein p73-like
SST	3	2.18	1.17	1.48	0.91	0.98	4.20	1.95	0.91	1.26	3.95	4.94	1.63	1.80	2.16	0.89	3q28	Somatostatin
CLDN1	3	0.90	0.92	4.18	2.76	1.05	0.38	2.64	0.36	3.34	0.88	1.26	1.17	5.41	0.68	1.40	3q28-q29	Claudin 1
COX7B2	7	1.00	7.14	6.75	0.93	100.00	1.57	6.91	1.35	4.55	2.48	2.14	27.80	41.80	1.01	0.92	4p12	Cytochrome c oxidase subunit VIIb2
OCIAD2	3	1.02	3.49	1.06	0.94	26.53	1.13	0.90	0.66	1.05	0.98	1.17	1.41	1.07	13.79	0.94	4p12	OCIA domain containing 2
UCHL1	11	5.28	19.69	1.08	1.44	3.19	38.30	38.48	18.67	8.85	14.37	36.99	1.10	31.56	7.22	1.15	4p14	Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
ART3	5	1.00	1.00	4.73	1.00	9.54	1.00	1.59	2.16	1.00	1.00	2.98	4.64	6.15	3.83	1.14	4p15.1-p14	ADP-ribosyltransferase 3
AFAP	3	1.18	6.97	1.16	1.26	4.73	1.46	2.05	2.11	1.14	1.66	3.46	1.33	1.00	1.18	1.06	4p16	Hypothetical protein LOC254848
KSP37	5	1.46	1.62	1.39	4.51	22.15	3.13	1.95	1.58	1.33	1.13	8.41	1.64	4.13	2.77	1.61	4p16	Ksp37 protein
S100P	3	1.29	1.55	1.24	0.96	17.59	0.90	2.13	4.01	1.29	1.70	1.89	4.87	1.96	2.84	1.20	4p16	S100 calcium binding protein P
SPON2	4	1.12	0.80	2.06	0.68	0.37	1.43	11.32	1.70	6.03	4.16	1.21	0.91	1.31	7.18	0.98	4p16.3	Spondin 2, extracellular matrix protein
PDCL2	4	1.00	1.86	1.50	1.72	3.77	1.00	1.93	9.33	1.49	1.65	2.30	3.60	5.55	2.23	1.52	4q12	Phosducin-like 2
SPINK2	6	1.00	5.81	1.78	2.95	25.93	2.29	2.03	47.11	2.28	1.00	1.00	3.26	3.67	4.33	0.74	4q12	Serine protease inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)
AREG	4	1.64	4.60	1.72	4.21	2.86	1.34	3.20	1.69	1.96	1.05	2.98	3.45	2.75	2.04	1.55	4q13-q21	Amphiregulin (schwannoma-derived growth factor)
ANXA3	3	1.48	4.05	2.13	5.17	1.72	0.88	1.01	44.49	1.28	0.84	2.06	2.58	2.12	2.19	1.31	4q13-q22	Annexin A3
SNCA	3	0.82	0.92	1.22	1.50	7.65	3.44	1.44	0.99	1.04	1.65	2.54	1.50	4.62	1.28	0.93	4q21	Synuclein, alpha (non A4 component of amyloid precursor)
SPP1	3	1.83	0.99	0.99	1.37	70.50	2.93	13.71	0.37	1.68	1.81	1.17	1.30	8.16	0.46	1.08	4q21-q25	Secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)
ATOH1	7	3.67	4.32	6.58	2.06	1.84	2.68	3.15	2.01	1.63	1.01	1.69	4.08	2.39	4.02	3.62	4q22	Atonal homolog 1 (Drosophila)
SYNPO2	3	1.00	0.82	1.63	2.00	2.53	3.95	0.84	1.25	0.93	0.49	4.77	2.20	3.52	0.92	1.85	4q26	Synaptopodin 2
DKFZP434N1235	4	1.00	1.18	0.57	3.63	2.98	3.85	1.03	6.41	1.14	1.35	1.00	2.34	3.24	1.95	1.00	4q28.1	Hypothetical protein DKFZp434N1235
CLTB	12	5.46	6.52	7.56	3.47	5.88	3.65	3.94	3.62	1.75	2.65	2.92	5.43	4.24	8.26	4.35	4q2-q3	Clathrin, light polypeptide (Lcb)
DKFZp434L142	3	1.00	0.68	1.57	0.68	4.88	7.74	1.40	0.61	1.15	0.74	1.00	2.52	3.47	1.01	0.96	4q32.1	Hypothetical protein DKFZp434L142
RNF129	3	1.35	1.11	1.69	1.41	3.50	1.00	2.15	7.17	2.61	1.10	1.17	1.97	3.20	1.83	0.99	4q32.3	Ring finger protein 129
ASB5	3	0.62	0.98	1.88	3.23	1.21	1.59	0.95	3.79	0.93	1.86	1.73	6.17	0.80	0.87	0.95	4q34.2	Ankyrin repeat and SOCS box-containing 5
PDLIM3	3	1.00	1.24	0.84	0.89	5.44	4.79	3.19	0.31	1.44	1.00	1.32	1.31	1.55	0.96	0.92	4q35	PDZ and LIM domain 3
Lrp2bp	4	1.56	0.87	3.99	1.42	2.13	2.51	1.99	0.29	2.03	3.40	2.83	3.12	3.73	1.96	1.12	4q35.1	Low density lipoprotein receptor-related protein binding protein
ZFP42	10	1.41	0.81	1.93	5.08	1.03	8.53	28.58	9.41	24.48	16.58	31.54	12.41	45.65	3.37	0.89	4q35.2	Zinc finger protein 42
DDX4	5	1.12	2.37	1.92	3.34	10.14	2.64	1.35	14.54	2.82	1.09	4.01	2.07	2.24	8.09	1.29	5p15.2-p13.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4
IRX4	3	9.83	1.11	1.02	1.05	1.34	24.72	1.43	1.35	1.39	1.10	17.10	0.88	1.19	1.02	0.96	5p15.3	Iroquois homeobox protein 4
FST	4	0.63	3.15	1.74	8.95	5.75	0.55	1.69	1.67	1.39	1.45	0.79	1.83	1.49	1.01	3.04	5q11.2	Follistatin
HSPB3	4	2.35	0.82	1.09	4.76	2.79	10.47	1.74	1.42	1.01	1.39	9.14	1.50	1.66	11.66	1.42	5q11.2	Heat shock 27kDa protein 3
BHMT	5	3.19	1.72	1.51	1.54	4.34	1.52	0.98	1.95	1.84	3.89	2.35	2.79	3.59	4.97	2.04	5q13.1-q15	Betaine-homocysteine methyltransferase
BHMT2	5	1.00	1.16	1.86	1.71	1.47	10.67	8.47	1.28	4.16	1.05	5.22	1.27	20.00	0.73	1.23	5q13	Betaine-homocysteine methyltransferase 2
MAP1B	4	0.51	1.39	1.04	23.70	4.38	0.71	0.71	18.29	0.94	0.85	0.85	1.13	1.12	1.28	3.31	5q13	Microtubule-associated protein 1B
LOC134548	3	1.00	1.05	0.84	1.38	0.72	1.00	1.56	3.02	1.11	1.00	3.25	1.28	2.97	3.91	0.85	5q23.3	Hypothetical protein LOC134548
NRG2	9	1.00	6.81	5.47	5.80	3.64	1.67	6.06	1.48	1.65	1.00	1.93	6.15	3.60	5.08	4.21	5q23-q33	Neuregulin 2
PCDHB5	3	1.00	3.16	0.61	1.37	11.42	1.43	1.78	0.65	2.72	1.22	1.00	0.83	3.78	1.77	1.06	5q31	Protocadherin beta 5
TGFBI	3	3.28	0.97	2.51	1.40	0.57	5.15	0.51	1.22	2.73	2.00	4.80	1.04	1.86	1.31	1.11	5q31	Transforming growth factor, beta-induced, 68kDa

CSF2	3	1.51	1.24	1.88	4.04	1.24	5.73	1.35	4.90	0.66	1.17	0.80	2.74	0.88	1.49	1.34	5q31.1	Colony stimulating factor 2 (granulocyte-macrophage)
SPARC	3	1.07	1.34	0.88	1.61	7.04	1.58	2.31	0.78	1.49	1.50	3.37	1.03	3.83	1.61	0.94	5q31.3-q32	Secreted protein, acidic, cysteine-rich (osteonectin)
PDGFRB	3	0.75	5.61	2.33	5.27	0.93	1.44	1.62	2.68	1.43	0.73	0.92	2.75	2.30	3.68	1.00	5q31-q32	Platelet-derived growth factor receptor, beta polypeptide
SPINK1	3	1.85	1.86	1.08	3.08	3.70	3.38	1.15	1.95	1.12	1.65	2.25	1.04	1.44	1.05	0.97	5q32	Serine protease inhibitor, Kazal type 1
LOC134466	4	2.10	1.48	2.47	2.03	9.18	5.53	2.90	4.39	2.88	1.32	3.08	2.84	1.86	2.61	0.94	5q33.1	Hypothetical protein LOC134466
DUSP1	4	1.13	2.58	3.87	3.49	2.67	1.27	1.77	5.25	1.53	1.08	1.59	2.65	3.03	1.74	1.19	5q34	Dual specificity phosphatase 1
FGF18	4	0.70	2.81	1.23	1.53	4.78	2.54	7.11	7.50	1.37	2.91	4.12	2.44	2.40	1.14	1.08	5q34	Fibroblast growth factor 18
LOC255458	4	0.60	15.36	0.93	1.82	13.25	1.34	1.31	3.77	1.11	0.93	1.75	0.99	0.99	13.17	1.03	5q35.3	Hypothetical protein LOC255458
CAPN11	3	2.41	1.00	2.11	1.00	1.21	1.55	1.12	1.00	5.75	1.00	3.14	2.67	4.10	1.33	1.36	6p12	Calpain 11
APOBEC2	3	0.82	1.54	1.84	1.01	6.77	1.17	1.28	2.35	0.96	0.60	0.88	6.65	0.88	3.38	0.93	6p21	Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2
DEFB114	4	0.81	1.45	1.00	1.00	1.00	10.20	1.00	1.00	1.00	3.04	0.43	3.81	3.79	0.93	0.61	6p21	Defensin, beta 114
AIF1	4	0.90	3.05	1.73	1.46	4.66	0.78	1.38	2.15	0.89	0.83	1.32	3.18	1.38	4.07	1.09	6p21.3	Allograft inflammatory factor 1
CRISP1	4	1.00	1.28	0.77	1.30	1.00	2.69	1.00	1.00	3.16	1.20	1.00	4.65	3.27	3.17	2.18	6p21.3	Cysteine-rich secretory protein 1
HIST1H1A	6	1.02	7.23	0.90	0.90	2.10	1.26	1.91	2.23	3.08	20.43	10.70	0.88	26.03	38.65	1.61	6p21.3	Histone 1, H1a
HIST1H1C	4	1.27	4.93	3.72	3.10	4.17	1.98	1.05	2.08	0.78	0.88	1.31	2.11	1.23	2.51	1.10	6p21.3	Histone 1, H1c
PSMB8	3	1.41	0.87	1.43	1.19	3.44	4.45	0.64	1.57	0.93	1.13	1.07	1.23	0.86	3.25	0.94	6p21.3	Proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)
TNXB	4	3.20	3.26	1.48	5.46	1.80	3.54	2.41	1.04	1.55	2.49	2.71	2.09	2.56	1.68	1.66	6p21.3	Tenascin XB
B3GALT4	3	1.23	3.82	2.31	1.65	1.47	1.30	1.18	0.63	1.01	4.61	3.16	1.92	1.34	1.89	1.07	6p21.3	galactosyltransferase, polypeptide 4
C6orf194	8	1.00	4.63	5.15	5.49	6.14	2.65	4.98	7.99	2.83	1.33	2.48	16.22	2.66	5.20	0.92	6p22.1	Chromosome 6 open reading frame 194
MGC8685	6	1.80	3.24	0.89	4.49	3.11	4.25	8.14	6.48	2.01	1.00	2.13	0.95	1.89	2.75	1.64	6p25	Tubulin, beta polypeptide paralog
GLULD1	4	1.23	3.36	0.94	3.53	7.94	4.89	0.83	0.83	0.37	0.26	0.54	0.82	0.28	1.38	0.81	6pter-q22.33	Glutamate-ammonia ligase (glutamine synthase) domain containing 1
DDX43	9	2.52	3.90	7.91	1.24	2.39	17.64	21.79	23.36	7.30	11.46	30.03	2.29	17.42	1.04	1.00	6q12-q13	DEAD (Asp-Glu-Ala-Asp) box polypeptide 43
CGA	5	2.57	0.91	1.20	1.02	10.65	1.51	3.37	0.87	0.93	1.69	4.41	3.63	6.79	1.48	0.99	6q12-q21	Glycoprotein hormones, alpha polypeptide
C6orf148	4	1.32	23.19	1.57	4.61	5.09	1.83	7.82	2.77	1.23	1.40	1.53	1.03	2.65	1.00	1.53	6q13	Chromosome 6 open reading frame 148
FILIP1	9	1.00	1.50	3.83	1.00	65.17	9.80	4.39	100.00	2.37	1.11	9.04	5.17	9.83	7.64	1.00	6q14.1	Filamin A interacting protein 1
LAMA4	4	0.88	0.61	9.50	1.62	7.91	1.00	0.89	0.55	1.48	0.64	3.78	3.81	0.95	1.37	1.08	6q21	Laminin, alpha 4
GJA1	5	1.00	1.28	5.55	1.72	2.14	1.00	9.08	2.82	22.72	10.17	1.00	2.45	42.30	0.90	1.32	6q21-q23.2	Gap junction protein, alpha 1, 43kDa (connexin 43)
PKIB	3	1.00	2.62	2.19	1.80	1.22	1.89	4.18	2.69	2.92	1.19	4.84	1.32	9.19	0.60	1.01	6q22.31	Protein kinase (cAMP-dependent, catalytic) inhibitor beta
CTGF	3	1.33	2.54	2.96	1.45	2.68	2.50	3.05	3.81	2.50	2.04	2.18	2.82	2.47	3.04	1.05	6q23.1	Connective tissue growth factor
GPR126	3	1.10	1.38	1.24	1.16	3.26	3.59	1.20	6.23	1.03	0.93	1.76	1.43	1.28	1.46	0.92	6q24.1	G protein-coupled receptor 126
C6orf97	3	1.50	1.20	6.67	2.38	1.54	1.00	1.69	1.00	1.73	2.88	1.83	2.71	4.36	2.76	3.03	6q25.1	Chromosome 6 open reading frame 97
PNLDC1	4	1.41	2.40	2.96	2.86	4.66	4.83	2.75	2.23	2.25	1.90	3.66	1.52	4.13	2.84	0.94	6q25.3	Poly(A)-specific ribonuclease (PARN)-like domain containing 1
ACAT2	5	1.00	0.30	0.72	1.23	1.06	0.80	9.15	6.26	7.17	4.43	1.05	0.60	4.48	1.05	0.96	6q25.3-q26	Acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
DACT2	3	1.00	6.77	1.00	0.47	0.63	8.15	1.72	1.00	1.75	1.35	4.69	0.98	1.26	0.44	1.02	6q27	Dapper homolog 2, antagonist of beta-catenin (xenopus)
SUNC1	9	1.71	2.98	3.64	10.25	4.26	5.55	6.13	1.73	2.82	4.61	2.39	7.08	7.10	3.32	1.42	7p12.3	Sad1 and UNC84 domain containing 1
AEBP1	7	1.41	1.07	4.15	0.89	3.99	3.97	4.50	6.73	0.53	1.16	2.76	4.74	2.85	3.27	2.07	7p13	AE binding protein 1
AQP1	3	1.72	1.08	0.81	6.04	12.02	1.99	1.42	3.76	1.79	1.67	1.94	2.03	1.29	2.10	1.07	7p14	Aquaporin 1 (channel-forming integral protein, 28kDa)
GPNMB	4	1.02	2.58	3.25	2.78	3.31	1.41	0.76	0.18	1.28	0.57	1.22	3.48	3.25	1.27	1.05	7p15	Glycoprotein (transmembrane) nmb
STK31	10	5.99	2.61	2.66	4.39	33.90	66.38	2.74	37.15	2.94	4.18	100.00	7.14	13.12	26.29	1.29	7p15.3	Serine
SCIN	5	0.95	1.48	1.99	2.29	17.85	1.86	3.07	5.45	3.02	1.46	0.89	2.28	3.27	1.49	1.24	7p21.3	Scinderin

FLJ10324	8	4.10	1.89	0.62	0.84	9.74	24.41	3.13	8.75	3.08	3.30	10.33	0.33	2.58	1.14	1.00	7p22	Hypothetical protein FLJ10324
KIAA1950	6	1.00	1.55	3.87	7.21	0.28	2.92	1.53	1.32	3.10	2.16	3.96	8.63	3.48	1.00	0.89	7p22.3	KIAA1950 protein
CCL26	10	3.04	21.68	2.72	5.03	9.26	8.64	9.28	5.06	1.94	2.69	6.59	5.76	4.10	2.61	1.98	7q11.23	Chemokine (C-C motif) ligand 26
NPTX2	3	1.54	1.76	1.31	2.68	9.22	6.92	1.98	7.04	0.89	1.15	2.32	1.92	1.12	2.63	1.12	7q21.3-q22.1	Neuronal pentraxin II
TAC1	3	1.07	1.00	1.61	6.02	1.00	1.00	1.75	3.93	1.78	4.07	1.00	1.00	0.99	1.32	1.24	7q21-q22	Tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neuroki
COL1A2	7	1.43	1.11	7.83	3.14	7.54	3.75	3.33	1.29	0.98	1.17	1.95	3.03	2.09	5.81	1.08	7q22.1	Collagen, type I, alpha 2
DKFZp761L1417	3	1.30	0.89	3.08	3.93	2.27	1.37	1.09	1.90	1.18	1.40	1.01	3.82	1.26	1.58	0.94	7q22.1	Hypothetical protein DKFZp761L1417
MYLC2PL	3	1.05	1.14	2.69	1.51	1.29	1.18	1.47	3.17	1.28	1.23	2.16	4.44	2.41	3.37	1.42	7q22.1	Myosin light chain 2, precursor lymphocyte-specific
STAG3	4	1.53	1.80	1.36	2.21	3.78	4.09	1.49	3.05	1.50	1.60	3.12	1.42	1.52	2.54	1.07	7q22.1	Stromal antigen 3
TFPI2	11	7.24	13.45	8.00	9.14	44.82	61.29	5.63	5.59	4.04	2.04	4.97	3.79	2.80	1.56	1.87	7q22	Tissue factor pathway inhibitor 2
FLJ11000	3	1.33	1.29	1.81	2.34	4.40	3.22	1.42	0.90	0.97	1.53	2.80	2.56	4.89	1.83	1.11	7q33	Hypothetical protein FLJ11000
LOC346673	5	1.00	6.32	1.94	1.38	10.34	1.19	2.75	4.58	1.27	1.46	1.00	6.35	1.00	12.94	0.87	7q33	STRA8
KCNH2	4	1.00	2.36	0.49	2.49	6.13	1.00	1.00	7.96	1.79	1.00	1.00	1.36	4.70	5.95	0.90	7q35-q36	Potassium voltage-gated channel, subfamily H (eag-related), member 2
RARRES2	3	1.12	0.98	1.38	2.85	1.08	1.22	5.80	4.82	1.05	2.92	1.48	2.83	1.08	6.10	1.03	7q36.1	Retinoic acid receptor responder (tazarotene induced) 2
LOC154822	4	2.83	1.22	1.30	1.11	1.81	5.97	3.02	0.97	1.98	3.82	4.12	0.92	2.49	1.56	1.08	7q36.3	Hypothetical protein LOC154822
PLAT	6	3.00	1.74	1.17	1.80	11.69	7.35	4.04	2.29	1.18	5.54	6.73	1.18	2.80	4.05	2.28	8p12	Plasminogen activator, tissue
SFRP1	4	0.83	0.88	0.73	4.34	1.60	6.80	1.18	0.95	0.86	0.74	3.33	0.65	3.86	0.90	1.00	8p12-p11.1	Secreted frizzled-related protein 1
NEF3	3	0.84	1.32	0.85	1.10	5.53	5.98	2.64	4.45	0.79	1.00	1.02	0.97	1.09	0.87	0.97	8p21	Neurofilament 3 (150kDa medium)
NEFL	3	1.24	1.17	0.71	2.03	1.15	1.53	3.55	9.09	1.97	1.15	3.71	0.82	0.82	1.20	1.13	8p21	Neurofilament, light polypeptide 68kDa
SCARA5	6	5.01	1.02	0.92	2.03	1.22	29.41	8.59	1.49	3.93	12.72	3.50	0.68	2.85	2.98	1.24	8p21.1	Hypothetical protein MGC45780
DLC1	5	1.75	1.40	0.85	1.11	2.39	2.67	4.77	0.75	6.39	5.65	8.62	1.00	7.32	1.19	1.02	8p22	Deleted in liver cancer 1_Deleted in liver cancer 1
TUSC3	3	1.31	2.45	0.98	1.18	1.47	1.29	10.08	0.81	3.18	0.93	18.02	0.84	1.20	1.19	1.02	8p22	Tumor suppressor candidate 3
DEFB103A	3	0.43	1.50	0.93	15.98	1.41	5.26	0.97	4.99	0.66	1.23	0.57	1.60	1.06	1.23	1.26	8p23	Defensin, beta 103A
ANGPT2	3	1.00	11.74	0.77	2.57	4.26	1.00	1.05	13.47	0.44	1.00	0.14	2.30	0.38	0.38	0.86	8p23.1	Angiopoietin 2
MGC39325	3	1.55	1.84	1.16	1.00	1.36	3.34	1.36	1.76	2.18	1.81	3.62	1.07	5.46	1.05	0.93	8q12.1	Hypothetical protein MGC39325
TRPA1	3	2.55	2.84	1.35	1.40	1.53	8.58	0.96	1.42	1.00	3.05	0.52	2.84	4.21	1.89	1.02	8q13	Transient receptor potential cation channel, subfamily A, member 1
RNF29	4	1.00	1.00	9.23	9.59	1.78	2.75	1.00	10.32	1.00	1.00	1.33	11.86	1.00	1.42	1.05	8q13.1	Ring finger protein 29
CA3	3	1.00	0.95	1.00	1.00	1.35	2.71	1.61	2.92	8.60	1.00	1.00	3.21	22.39	1.00	1.00	8q13-q22	Carbonic anhydrase III, muscle specific
RDH10	3	1.72	1.32	1.26	0.87	3.07	6.38	5.55	1.26	1.19	2.09	2.87	1.62	2.88	1.49	0.92	8q21.11	Retinol dehydrogenase 10 (all-trans)
ZFHX4	3	1.68	1.26	1.01	1.11	1.31	1.67	3.17	0.79	3.78	2.15	2.77	0.78	4.52	1.00	1.04	8q21.11	Zinc finger homeodomain 4
PAG	3	1.68	0.99	1.54	1.06	1.52	5.60	3.11	0.64	1.35	1.22	3.20	1.59	2.06	1.02	1.00	8q21.13	Phosphoprotein associated with glycosphingolipid-enriched microdomains
FABP5	6	2.82	1.01	1.39	1.48	1.62	15.83	35.84	4.41	7.84	20.18	17.16	0.83	0.95	0.92	0.94	8q21.13	Fatty acid binding protein 5 (psoriasis-associated)
LOC286149	10	1.79	13.34	25.06	6.85	4.74	2.83	6.80	2.15	6.34	1.37	2.34	7.58	6.41	8.27	8.55	8q22.1	Hypothetical protein LOC286149
TSPYL5	8	2.37	4.47	1.14	2.93	13.08	15.24	8.62	20.79	2.10	2.79	13.38	0.99	6.65	3.17	0.73	8q22.1	TSPY-like 5
FLJ39553	4	1.19	2.25	0.82	4.71	1.37	1.00	5.68	1.08	3.84	1.49	1.00	1.44	3.24	1.33	1.60	8q22.2	Hypothetical protein FLJ39553
CTHRC1	5	0.83	2.37	1.05	3.13	1.19	3.30	1.98	1.09	1.45	1.00	4.00	1.53	4.14	4.85	1.42	8q22.3	Collagen triple helix repeat containing 1
LY6K	5	1.17	4.84	1.17	12.08	6.56	1.17	1.21	12.85	1.20	0.87	1.25	1.01	1.11	4.31	0.98	8q24.3	CDNA for differentially expressed CO16 gene_CDNA for differentially expressed CO16 gene
AQP3	3	1.08	3.88	0.99	5.96	1.52	1.24	1.14	1.23	1.08	1.02	1.22	1.91	1.05	3.06	1.22	9p13	Aquaporin 3
TPM2	3	0.79	6.05	1.16	0.99	8.81	1.19	0.77	3.78	1.16	1.04	1.10	1.25	0.95	0.79	0.93	9p13.2-p13.1	Tropomyosin 2 (beta)
SPINK4	9	2.09	4.73	1.71	12.60	10.17	2.30	7.81	1.72	1.25	3.97	4.39	5.06	3.41	4.15	1.65	9p13.3	Serine protease inhibitor, Kazal type 4
ADFP	3	1.14	1.07	1.14	1.36	1.05	1.05	6.60	0.54	3.83	2.59	2.09	1.36	4.58	1.08	1.13	9p22.1	Adipose differentiation-related protein

RLN2	3	1.21	1.29	1.01	1.00	3.18	1.00	1.00	3.22	1.63	3.56	1.00	1.37	0.69	1.00	0.86	9p24.1	Relaxin 2 (H2)
FBP1	3	1.00	2.63	1.52	1.08	0.74	6.79	3.21	2.96	1.18	2.19	2.87	0.81	6.01	1.49	0.88	9q22.3	Fructose-1,6-bisphosphatase 1
BSPRY	4	1.14	8.68	1.08	5.93	0.92	1.22	2.22	14.76	1.17	0.83	0.51	3.33	0.98	1.79	1.37	9q32	B-box and SPRY domain containing
PTGS1	3	1.32	1.10	1.39	2.46	4.85	1.68	2.70	1.84	1.42	1.15	13.75	1.35	6.54	1.61	0.99	9q32-q33.3	Prostaglandin-endoperoxide synthase 1 (prostaglandin G
LCN2	5	0.70	3.77	9.84	0.72	1.38	3.93	2.42	3.46	2.61	1.57	4.00	1.45	1.60	2.46	0.97	9q34	Lipocalin 2 (oncogene 24p3)
PAEP	3	0.84	3.25	1.06	1.59	1.20	3.42	0.98	2.11	1.09	1.16	3.40	1.20	0.98	1.20	1.01	9q34	Progestagen-associated endometrial protein (placental protein 14
PRRX2	5	1.42	0.89	1.02	2.49	4.25	2.33	11.66	5.11	2.42	4.00	9.26	0.76	1.57	2.88	1.14	9q34.1	Paired related homeobox 2
C9orf67	5	1.70	1.02	2.20	0.96	1.47	6.06	4.91	1.69	2.53	9.32	4.17	0.71	4.21	0.46	1.19	9q34.13	Chromosome 9 open reading frame 67
CLIC3	4	0.92	2.83	7.91	3.06	2.81	1.19	1.28	1.22	1.26	2.07	1.47	4.49	2.62	5.58	1.21	9q34.3	Chloride intracellular channel 3
C9orf157	12	1.96	4.05	4.87	7.99	12.00	31.91	18.92	29.67	2.80	10.08	12.97	5.21	11.63	9.51	1.55	9q34.3	Chromosome 9 open reading frame 157
SSX6	10	4.35	6.89	8.84	13.47	2.61	38.34	17.03	1.64	2.36	17.69	17.09	6.64	13.25	0.81	2.22	Xp11.2	Synovial sarcoma, X breakpoint 6
GAGED5	3	1.00	1.12	2.35	6.73	1.94	4.94	1.19	1.79	1.24	1.00	1.68	6.04	1.35	2.84	1.10	Xp11.22	G antigen, family D, 5
PAGE-5	13	14.01	15.10	18.94	38.31	39.57	75.90	35.75	1.80	14.12	30.81	38.24	29.97	27.25	2.06	3.46	Xp11.22	PAGE-5 protein_PAGE-5 protein
MGC62094	12	8.76	6.85	16.10	27.57	28.29	100.00	22.03	2.27	8.94	13.71	37.03	16.17	19.15	1.97	2.48	Xp11.22	Similar to PAGE-5 protein
GAGED2	13	53.25	14.74	40.91	33.09	41.02	48.41	42.17	1.50	27.29	28.15	33.05	24.85	25.81	1.52	8.87	Xp11.22-p11.21	G antigen, family D, 2
GAGED3	4	1.32	1.01	1.94	1.63	1.91	3.38	1.74	3.82	1.36	1.56	1.56	4.68	3.55	2.06	1.21	Xp11.22-p11.21	G antigen, family D, 3
GAGED4	9	0.87	0.90	10.55	10.69	5.64	9.03	3.58	9.00	1.02	0.99	2.11	14.34	4.99	6.51	1.20	Xp11.22-p11.21	G antigen, family D, 4
GAGEB1	9	0.95	9.06	3.95	7.76	4.31	1.17	8.19	5.13	1.32	4.63	1.04	6.34	8.42	2.12	1.49	Xp11.23	G antigen, family B, 1 (prostate associated)
GAGEC1	3	1.37	3.76	1.03	0.62	1.32	1.79	1.00	1.79	1.13	1.00	1.00	3.50	1.49	3.78	0.96	Xp11.23	G antigen, family C, 1
SSX4	6	2.34	1.36	2.69	3.80	1.66	47.10	3.57	1.60	1.06	8.21	19.78	2.14	4.62	1.79	1.02	Xp11.23	Synovial sarcoma, X breakpoint 4
SSX1	8	1.00	2.75	7.15	13.82	2.36	32.61	10.92	1.68	2.30	19.41	21.24	3.88	10.28	0.87	1.74	Xp11.23-p11.22	Synovial sarcoma, X breakpoint 1
RGN	8	2.87	0.67	3.46	1.12	0.36	5.63	7.31	11.92	4.29	6.08	8.24	0.80	4.99	0.91	1.03	Xp11.3	Regucalcin (senescence marker protein-30)
GAGE5	10	1.79	13.10	1.65	4.65	17.21	3.56	19.45	4.65	4.80	20.43	3.06	1.70	13.55	1.19	1.30	Xp11.4-p11.2	G antigen 7
MAGEB2	5	0.85	1.76	1.95	2.41	2.84	4.51	3.57	2.02	5.45	1.63	1.07	1.77	6.40	3.19	1.21	Xp21.3	Melanoma antigen, family B, 2
MAGEB6	3	2.11	1.45	1.28	1.06	2.38	11.76	1.49	6.11	2.53	2.75	1.90	1.07	3.93	1.28	1.02	Xp21.3	Melanoma antigen, family B, 6
FAM9B	3	1.12	1.11	1.03	1.04	3.35	4.61	2.29	1.51	1.42	1.43	3.76	1.11	2.30	2.35	0.87	Xp22.32	Family with sequence similarity 9, member B
FAM9C	12	3.20	1.54	3.81	4.46	17.64	18.61	13.18	18.75	8.56	9.04	14.46	4.53	20.49	1.31	1.50	Xp22.32	Family with sequence similarity 9, member C
XG	4	1.00	0.62	3.52	1.00	1.00	1.00	1.64	2.61	2.69	3.67	1.86	5.22	6.93	1.12	0.86	Xp22.33	Xg blood group (pseudoautosomal boundary-divided on the X chromosome)
VCX3	14	100.00	37.84	76.20	7.92	58.14	82.59	88.20	19.67	24.49	36.65	81.13	26.65	53.93	3.56	2.34	Xp22	Variable charge, X-linked_Variable charge
ACRC	14	16.43	35.61	16.60	6.61	44.04	28.54	21.63	39.10	14.94	16.58	27.08	16.96	19.39	33.61	0.97	Xq13.1	Acidic repeat containing
TEX11	12	1.10	3.07	4.57	3.15	8.02	17.04	18.19	14.84	4.66	14.40	9.21	1.00	5.32	6.08	2.01	Xq13.1	Testis expressed sequence 11
IL13RA2	5	1.00	3.14	3.10	1.96	1.63	5.76	3.94	14.41	1.50	1.43	1.24	2.81	0.82	1.32	1.57	Xq13.1-q28	Interleukin 13 receptor, alpha 2
XIST	13	3.39	3.11	3.40	30.81	63.63	100.00	29.58	13.16	18.73	43.07	33.23	1.00	16.16	18.59	1.66	Xq13.2	X (inactive)-specific transcript
FLJ37659	7	1.00	1.81	1.44	1.67	13.22	3.30	6.83	3.23	4.04	2.59	4.12	0.92	12.59	1.52	1.51	Xq21.33	Hypothetical protein FLJ37659_Hypothetical protein FLJ37659
RPA4	3	1.31	3.53	1.19	0.93	4.19	0.80	0.98	2.49	1.01	3.25	1.57	1.07	1.04	0.73	1.43	Xq21.33	Replication protein A4, 34kDa
ARMCX2	3	3.33	1.10	1.40	1.47	1.50	9.41	0.96	1.64	1.07	0.89	6.98	1.58	1.03	1.89	0.89	Xq21.33-q22.2	Armadillo repeat containing, X-linked 2
BEX1	6	1.00	1.19	2.97	2.03	4.39	3.07	9.29	7.24	11.94	1.00	2.68	1.61	31.65	1.86	0.94	Xq21-q23	Brain expressed, X-linked 1
BEX2	4	0.90	1.33	1.89	3.82	1.54	3.94	2.20	4.16	1.52	0.59	1.96	1.57	8.41	1.35	1.11	Xq22	Brain expressed X-linked 2
ARMCX4	3	1.00	1.00	1.00	1.00	1.00	7.52	4.98	4.46	1.00	1.00	1.00	2.69	2.87	1.00	1.00	Xq22.1	Armadillo repeat containing, X-linked 4
BEXL1	7	1.00	3.69	1.31	2.38	4.03	12.02	3.14	31.43	1.00	1.40	1.30	1.40	3.58	4.76	0.86	Xq22.1-q22.3	Brain expressed X-linked-like 1

TCEAL3	3	1.17	2.13	0.94	1.68	0.98	3.71	0.91	0.88	1.36	1.42	3.53	1.28	1.76	4.86	1.20	Xq22.2	Transcription elongation factor A (SII)-like 3
LOC203413	3	0.97	6.12	1.00	10.37	7.51	1.39	0.84	0.95	0.95	0.64	1.24	1.14	1.24	0.59	1.47	Xq23	Hypothetical LOC203413
FLJ40249	3	1.00	1.00	4.36	2.21	2.28	2.95	1.22	14.88	1.00	1.00	1.88	5.03	1.00	1.00	1.00	Xq23	Hypothetical protein FLJ40249
LOC255313	11	1.44	5.70	13.25	5.37	14.25	3.44	14.09	1.00	2.05	4.94	4.89	9.07	10.09	4.99	1.56	Xq24	Hypothetical protein LOC255313
OTEX	10	2.09	1.47	3.23	2.56	4.84	4.71	11.07	11.80	2.12	4.25	4.11	5.54	7.41	15.40	1.67	Xq24	Paired-like homeobox protein OTEX
PEPP-2	8	0.74	2.71	12.27	14.14	62.71	98.36	1.91	48.31	1.13	0.95	25.43	14.46	1.26	44.74	1.70	Xq24	PEPP subfamily gene 2
WDR40B	5	2.79	1.61	1.51	1.58	2.90	3.38	6.08	0.75	14.49	1.00	6.50	1.74	8.72	1.00	0.77	Xq25	WD repeat domain 40B
MAGEC1	5	1.11	1.08	1.25	2.46	9.59	5.47	2.81	1.49	1.58	4.71	4.37	1.53	4.50	1.44	1.27	Xq26	Melanoma antigen，family C，1
MGC27005	12	5.07	34.74	14.60	38.78	29.56	36.00	59.71	2.99	15.06	22.89	11.08	16.24	34.00	1.59	1.00	Xq26.3	Hypothetical protein MGC27005
MGC39606	4	3.15	2.12	2.39	2.28	2.27	3.91	2.56	1.60	1.03	1.98	3.21	1.86	3.80	2.43	1.50	Xq26.3	Hypothetical protein MGC39606
MAGEC2	6	1.32	1.08	2.23	1.54	3.90	4.24	4.12	1.20	1.98	6.88	4.18	2.34	5.19	1.78	1.13	Xq27	Melanoma antigen，family C，2
SPANXA2	12	35.24	6.37	17.73	3.17	46.92	67.93	33.94	1.35	19.02	22.33	23.23	11.63	20.14	1.64	1.44	Xq27.1	SPANX family，member A2
SPANXE	12	55.43	13.97	41.43	3.38	29.32	46.52	38.61	1.36	25.59	29.07	28.15	14.42	29.70	1.65	1.44	Xq27.1	SPANX family，member A2
SPANXB1	12	44.39	3.20	4.06	3.57	11.64	43.15	60.87	1.26	29.67	30.39	34.98	11.04	38.61	1.71	1.91	Xq27.1	SPANX family，member B1
SPANXC	12	8.01	5.62	31.79	3.14	100.00	16.32	59.62	0.99	17.22	47.32	29.49	19.33	42.22	1.57	1.32	Xq27.1	SPANX family，member C
FMR1NB	13	2.10	27.36	10.79	37.52	54.71	43.04	39.71	13.05	10.12	26.34	25.89	17.53	22.84	21.07	2.18	Xq27.3-q28	Fragile X mental retardation 1 neighbor
CTAG1B	13	12.43	8.39	12.10	5.53	7.61	48.91	22.52	13.02	18.42	22.24	27.95	11.41	16.05	1.22	1.42	Xq28	cancer/testis antigen 1B
CTAG2	3	1.26	1.87	3.82	1.80	2.53	1.23	3.15	5.04	1.82	2.48	1.24	1.84	2.28	0.90	1.10	Xq28	cancer/testis antigen 2
CSAG1	3	1.81	1.72	1.80	3.75	2.05	3.37	4.17	2.71	1.34	2.52	2.68	2.76	2.13	0.95	1.20	Xq28	Chondrosarcoma associated gene 1
CSAG2	4	0.99	1.32	1.81	3.47	1.67	3.40	4.73	2.55	1.61	2.48	2.54	3.06	1.85	0.91	1.07	Xq28	CSAG family，member 2
MAGEA1	4	0.91	39.10	70.37	2.10	2.98	1.64	1.98	2.62	1.69	1.52	1.32	17.74	96.41	1.02	0.93	Xq28	Melanoma antigen，family A
MAGEA10	8	1.39	1.05	1.10	6.53	2.09	8.49	17.43	23.33	4.04	10.56	14.02	2.17	13.99	1.02	0.83	Xq28	Melanoma antigen，family A，10
MAGEA12	3	1.33	1.27	1.00	3.32	1.75	5.09	3.15	2.80	1.14	2.42	1.79	1.69	1.74	0.92	1.16	Xq28	Melanoma antigen，family A，12
MAGEA2	7	1.08	3.31	5.95	1.35	1.98	17.94	13.31	1.59	2.46	10.58	1.38	7.52	7.41	0.92	0.98	Xq28	Melanoma antigen，family A，2
MAGEA4	9	1.25	3.60	2.65	2.53	1.23	10.85	15.28	5.69	6.62	12.82	3.68	5.95	10.29	1.08	1.07	Xq28	Melanoma antigen，family A，4
MAGEA9	12	1.23	16.72	3.14	7.12	17.93	18.24	8.64	16.54	1.90	8.70	11.93	11.38	9.81	7.43	1.13	Xq28	Melanoma antigen，family A，9
PNMA5	3	1.57	1.37	1.30	1.81	0.73	4.09	2.98	3.28	1.22	1.56	3.83	1.08	1.94	2.02	1.01	Xq28	Paraneoplastic antigen like 5
PNMA3	10	3.80	2.31	1.50	3.04	0.57	12.37	6.18	9.79	3.34	7.29	8.89	1.04	5.61	3.08	0.94	Xq28	Paraneoplastic antigen MA3
PASD1	4	1.08	7.63	0.76	1.52	0.90	1.28	11.64	1.54	1.24	2.96	1.29	1.27	4.26	3.08	0.73	Xq28	PAS domain containing 1
LOC389903	3	1.57	1.38	1.69	4.47	1.74	4.39	4.06	2.75	1.43	2.75	2.67	2.99	1.79	0.99	1.21	Xq28	Similar to Taxol resistant associated protein 3
TKTL1	7	2.46	1.17	1.72	2.71	1.46	25.78	15.80	32.64	7.33	22.70	29.70	1.50	18.36	1.36	0.99	Xq28	Transketolase-like 1
TSPY1	3	1.00	7.79	1.49	8.55	1.46	1.01	1.41	6.66	0.86	1.22	1.14	1.02	2.24	2.00	1.98	Yp11.2	Testis specific protein，Y-linked 1
VCY	6	6.30	1.65	3.98	1.25	14.09	49.36	2.84	2.06	1.43	1.32	16.53	3.38	1.71	2.58	1.10	Yq11.221	Variable charge，Y-linked
DAZ2	6	1.55	1.43	1.65	1.76	3.84	7.90	4.40	9.55	2.35	1.58	3.15	2.01	4.75	2.87	0.94	Yq11.223	Deleted in azoospermia 2
DAZ4	14	4.99	19.30	34.06	18.52	77.75	80.65	92.38	31.20	49.58	18.40	81.90	23.02	66.51	63.44	1.68	Yq11.223	Deleted in azoospermia 4

*, The numbers in columns indicate the re-expressed folds of genes in all 15 HCC cell lines treated by DAC and TSA as compared with those without drug treatment;**,numbers of HCC cell lines with upregulated genes

Supplementary Table 2. Summary of Analyses of the SCARA5 mRNA in 40 HCC Tissues

Case ID	Gender	Age	HBV	HCV	Size(cm)	Folds	LOH	Methylation*
C06	M	60	+	−	3	0.35	+	−(BSP)
C11	M	40	+	−	5	0.01	+	+(BSP)
C13	F	50	+	−	4	0.50	+	−(BSP)
C14	M	52	+	−	9	0.03	+	−(BSP)
C15	M	53	+	−	4	0.17	+	−(BSP)
C16	M	46	+	−	5	0.01	+	−(BSP)
C17	M	48	+	−	12	0.02	+	+(BSP)
C18	M	41	+	−	3	0.00	+	+(BSP)
C19	M	60	+	−	3.5	0.00	+	−(BSP)
C20	M	45	+	−	15	0.10	+	+(BSP)
C22	M	49	+	−	5	0.01	+	+(BSP)
C24	M	44	+	−	4	0.09	+	+(BSP)
C28	M	75	+	−	2.5	0.05	+	+(BSP)
C29	M	44	+	−	3.5	0.05	+	−(BSP)
C03	M	50	+	−	3.5	0.35	−	+(MSP)
C04	M	37	+	−	11	0.08	−	−(MSP)
C05	M	55	+	−	4	0.42	−	+(MSP)
C07	M	65	+	−	7	0.18	−	−(MSP)
C08	M	50	+	+	16	0.10	−	−(MSP)
C10	M	50	+	−	16	0.05	−	−(MSP)
C23	M	30	+	−	3	0.41	−	+(MSP)
C25	M	65	+	−	11	0.01	−	−(MSP)
C26	M	37	+	−	18	0.05	−	−(MSP)
C27	M	49	+	−	9	0.08	−	−(MSP)
C30	M	53	+	−	5	0.08	−	−(MSP)
C31	M	41	+	−	4.5	0.85	−	−(MSP)
C32	M	61	+	−	14	0.25	−	+(MSP)
C33	M	70	+	−	3	0.76	−	−(MSP)
C34	F	48	+	−	5	0.06	−	−(MSP)
C35	M	48	+	−	4	0.09	−	−(MSP)

C37	M	51	+	−	5	0.01	−	−(MSP)
C38	M	51	+	−	4.5	0.08	−	−(MSP)
C39	F	33	+	−	15	0.12	−	+(MSP)
C40	M	53	+	−	6	0.27	−	+(MSP)
C01	M	40	+	−	3	0.97	−	ND
C02	M	45	+	+	2	1.05	−	ND
C09	M	50	+	−	16	3.73	−	ND
C12	M	34	+	−	11	0.60	−	ND
C21	M	41	+	−	10	0.73	−	ND
C36	F	59	+	−	6	2.54	−	ND

* +, the methylation levels of the CpG island within SCARA5 promoter in HCCs is significantly higher than in corresponding adjacent non-cancerous livers using sequencing of bisulfite-treated DNA (BSP) or methylation sepecific PCR (MSP); - indicats that the methylation levels of the CpG island within SCARA5 promoter has no significantly difference between in HCCs and in non-HCCs using BSP or MSP; ND, not detected.

Supplementary Table 3. Summary of Analyses of the SCARA5 protein in 78 HCC Tissues

Case ID	Gender	Age	Differentiation grade	Portal vein tumor thrombosis	SCARA5 Score (tumor/adjacent non-tumor liver)
1	M	53	II	Yes	2/4
2	M	67	II	Yes	2/3
3	M	56	I	Yes	1/2
4	M	74	II	Yes	1/4
5	F	45	III	Yes	1/2
6	M	69	III	Yes	1/2
7	M	45	III	Yes	0/2
8	M	57	II	Yes	2/3
9	M	67	II	Yes	2/4
10	M	50	II	Yes	1/4
11	M	47	II	Yes	2/3
12	M	57	III	Yes	2/4
13	M	59	II	Yes	1/4
14	M	60	II	Yes	2/4
15	M	76	III	Yes	0/4
16	M	53	II	Yes	0/4
17	M	53	III	Yes	1/4
18	M	72	II	Yes	1/2
19	M	54	III	Yes	1/4
20	M	42	II	Yes	2/3
21	M	58	II	Yes	3/0
22	M	69	II	Yes	1/4
23	M	61	II	Yes	3/2
24	M	71	III	Yes	1/2
25	M	56	/	Yes	0/2
26	F	57	III	Yes	0/3
27	F	74	II	Yes	1/3
28	M	46	/	Yes	1/4

29	M	52	II	Yes	1/4
30	M	49	II	Yes	0/3
31	M	41	III	Yes	1/1
32	M	65	III	Yes	0/2
33	M	69	II	Yes	2/2
34	M	65	III	Yes	1/4
35	M	45	II	Yes	0/3
36	M	58	II	Yes	0/3
37	M	56	III	Yes	1/2
38	M	50	II	Yes	2/3
39	M	57	II	No	2/3
40	M	73	I	No	0/4
41	M	59	II	No	3/1
42	M	66	II	No	2/2
43	M	49	II	No	0/2
44	M	76	II	No	2/2
45	M	72	II	No	2/4
46	M	57	/	No	2/2
47	M	69	II	No	2/3
48	M	46	I	No	2/2
49	M	59	II	No	0/2
50	M	58	I	No	1/2
51	M	40	II	No	1/2
52	F	82	II	No	3/4
53	M	71	I	No	2/3
54	M	46	II	No	1/2
55	M	52	III	No	0/2
56	M	49	II	No	2/2
57	M	41	II	No	2/4
58	M	62	III	No	1/1
59	M	50	II	No	2/2
60	M	30	III	No	2/4
61	M	39	II	No	2/3

62	M	73	II	No	2/4
63	M	63	II	No	1/4
64	M	30	II	No	2/2
65	M	53	II	No	2/4
66	M	48	II	No	1/4
67	M	57	I	No	0/2
68	M	69	II	No	0/2
69	M	67	II	No	1/4
70	M	82	III	No	1/1
71	M	49	III	No	1/3
72	M	45	II	No	2/3
73	M	62	II	No	2/2
74	M	67	III	No	2/2
75	M	50	II	No	1/2
76	F	30	II	No	2/4
77	M	39	II	No	3/4
78	M	54	II	No	2/2

Tissues were scored on a scale of negative (0), low expression (1), moderate expression (2), high expression (3), or strong expression (4).