

Suppl Table 1. The altered functional groups associated with the top three networks using 115 differentially expressed genes ($p < 0.001$) between sensitive and resistant cells. IPA tool was used to elucidate the significantly altered pathways between sensitive and resistant cells.

Suppl Table 2. Genes with significant difference between sensitive and resistant cells ($p < 0.001$).

Suppl Table 3. Correlation analysis between GI50s of therapeutic reagents and gene expression.

Suppl Figure 1. Cluster analysis of pancreatic cancer cells. Unsupervised cluster analysis of the 6127 genes that were differentially expressed in at least two arrays with at least a two- fold change (average linkage clustering).

Suppl Figure 2. Migratory potential of pancreatic cancer cells. 1.0×10^5 cells were added to chamber and allowed to migrate in matrigel for 6 hours at 37 °C in a 5% CO₂ atmosphere. The non-migrated cells on the upper surface of the membrane were removed and the migrated cells on the lower surface of the membrane were counted. Data shown are mean \pm SEM for three experiments.

Suppl Figure 3. Expression profiling of four additional cell lines (T3M4, Colo357, Capan1, Suit2) showed clustering with sensitive or resistant sub-types in Fig 2A

according to their drug sensitivity. Unsupervised cluster analysis of the 4809 genes that were differentially expressed in at least two arrays with at least a two- fold change (average linkage clustering).

Suppl Figure 4. The expression patterns of E-cadherin transcriptional factors. Heat map includes the expression of Snail, Slug, Twist and Sip1 and demonstrated no correlation of those transcriptional factors and E-cadherin expression / drug sensitivity.

Suppl Figure 5. Log₁₀(GI₅₀) values of Taxol were plotted. If log₁₀(GI₅₀) of the cell lines were below the mean of log₁₀(GI₅₀) across the panel of cells, the cell lines were defined as sensitive, whereas resistant cell lines had log₁₀(GI₅₀) values above the mean.

Suppl Figure 6. Cluster analysis of ABC transporter pathway genes in the array. The average number of duplicates was used for clustering analysis. High expressed genes are in red and low expressed genes are in green.

Suppl. Table 1

	Score	Associated Network functions	Focus molecules
1	46	Cellular Comprise, Cellular movement, Cancer	22
2	32	Cellular Development, lipid metabolism, Molecular Transport	16
3	22	Developmental disorder, Reproductive system disease, Cellular Growth and proliferation	12

Suppl. Table 2

Ranking	p-value	Accession	Symbol	Fold-change (S/R)*
1	< 1e-07	NM_000064.1	C3	13.88
2	< 1e-07	NM_024572.2	GALNT14	5.11
3	0.0000013	XM_936226.1	LOC653879	6.34
4	0.0000016	NM_173853.2	KRTCAP3	10.17
5	0.0000021	NM_004105.2	EFEMP1	13.33
6	0.0000022	NM_025079.1	ZC3H12A	6.29
7	0.0000066	NM_001017970.1	TMEM30B	22.11
8	0.0000079	NM_052886.1	MAL2	40.21
9	0.000014	NM_033294.2	CASP1	9.89
10	0.0000321	NM_002773.2	PRSS8	16.17
11	0.0000407	NM_002754.3	MAPK13	15.16
12	0.0000455	NM_181054.1	HIF1A	3.42
13	0.0000475	NM_002961.2	S100A4	-35.16
14	0.0000479	NM_004208.2	PDCD8	-1.78
15	0.0000544	NM_001530.2	HIF1A	3.81
16	0.0000568	NM_015054.1	KIAA0701	-1.76
17	0.0000593	NM_003588.2	CUL4B	-1.81
18	0.0000642	NM_178564.2	NRBP2	-3.80
19	0.0000643	NM_203304.1	RKHD1	-1.94
20	0.0000659	NM_030941.1	LOC81691	-2.09
21	0.0000684	AK056642		1.51
22	0.0000806	NM_001002860.2	BTBD7	1.71
23	0.0000807	NM_145168.1	HSPC105	2.15
24	0.000091	NM_001010877.2	ZNF311	2.05
25	0.0000923	XM_941913.1	LOC652461	1.53
26	0.0000994	NM_012395.2	PFTK1	2.83
27	0.0001005	NM_014725.2	STARD8	-2.47
28	0.0001107	NM_000391.2	TPP1	-2.13
29	0.0001109	NM_201525.1	GPR56	15.71
30	0.0001142	XM_498810.2	LOC440667	1.85
31	0.0001171	XR_001113.1	LOC554223	2.77
32	0.0001379	XR_001114.1	LOC554223	1.59
33	0.0001429	NM_032415.2	CARD11	7.71
34	0.0001454	NM_001013622.1	FAM53A	-2.41
35	0.0001514	NM_020877.2	DNHD3	3.89
36	0.0001632	NM_002638.2	PI3	26.58
37	0.0001654	NM_033008.1	PCBP4	-2.19
38	0.0001677	NM_032316.2	NICN1	-2.36
39	0.0001731	NM_022337.1	RAB38	19.97

40	0.0001737	NM_024938.2	PCNXL2	2.20
41	0.0002007	NM_001031699.1	MOXD1	1.88
42	0.0002141	NM_003492.1	CXorf12	-2.07
43	0.0002194	NM_172104.1	EYA4	3.02
44	0.0002223	NM_149379.1	NSUN5C	-1.57
45	0.0002336	BG434785		2.27
46	0.0002358	NM_018991.2	DKFZP434A0131	-2.02
47	0.0002622	NM_031904.2	FKSG44	-2.08
48	0.0002781	XM_939187.1	HSGT1	-1.86
49	0.0002805	NM_015529.1	MOXD1	2.75
50	0.0002887	XM_930884.1	LOC653080	-1.67
51	0.0002956	NM_199161.1	SAA1	11.55
52	0.0003115	NM_182620.1	FAM33A	2.02
53	0.0003432	AL049435		10.50
54	0.0003509	NM_002845.2	PTPRM	3.98
55	0.0003526	NM_015888.3	HOOK1	7.46
56	0.0003606	NM_138376.1	TTC5	1.89
57	0.0003643	NM_002577.3	PAK2	-1.94
58	0.000371	NM_024930.1	ELOVL7	2.84
59	0.0003793	NM_023915.2	GPR87	10.33
60	0.0003939	NM_175924.2	ILDR1	4.99
61	0.0004018	NM_016069.8	Magmas	-1.62
62	0.0004074	NM_006674.2	HCP5	12.47
63	0.0004337	NM_024420.1	PLA2G4A	11.13
64	0.0004363	NM_144975.2	MGC19764	2.43
65	0.0004428	NM_001392.3	DTNA	2.84
66	0.0004707	NM_020335.1	VANGL2	4.04
67	0.0004811	CN362099		1.84
68	0.0004947	NM_033317.2	ZD52F10	9.32
69	0.0004976	NM_181642.2	SPINT1	3.69
70	0.0005117	NM_001005474.1	NFKBIZ	5.07
71	0.000539	NM_014824.1	FCHSD2	-1.58
72	0.0005453	NM_003363.2	USP4	-1.60
73	0.0005732	NM_015065.1	EXPH5	3.01
74	0.0005739	NM_007131.2	ZNF75	-1.58
75	0.0005884	NM_005449.3	FAIM3	2.53
76	0.0005934	NM_181501.1	ITGA1	2.78
77	0.0005978	NM_013230.2	CD24	4.29
78	0.0005981	NM_003384.2	VRK1	1.67
79	0.0006003	NM_001560.2	IL13RA1	-2.86
80	0.0006005	NM_006927.2	ST3GAL2	-1.90
81	0.0006041	NM_138446.1	C7orf30	-1.53
82	0.0006165	NM_030754.2	SAA2	10.94

83	0.0006407	NM_001025202.1	LOC442582	-1.84
84	0.0006433	NM_015262.1	FAM21C	-1.52
85	0.0006545	NM_019045.3	WDR44	-1.64
86	0.0006554	NM_000998.3	RPL37A	-1.95
87	0.0006571	AK128481		-2.40
88	0.0006584	NM_002531.1	NTSR1	-21.96
89	0.0006604	NM_004580.3	RAB27A	1.62
90	0.0006689	NM_001009944.1	PKD1	-2.12
91	0.0006891	BC034319		7.58
92	0.0006951	NM_015020.2	PHLPPL	-2.53
93	0.0007028	NM_148980.1	NSUN5C	-1.63
94	0.0007044	NM_003253.1	TIAM1	1.69
95	0.0007079	NM_006458.2	TRIM3	-1.75
96	0.0007176	XM_942130.1	KCMF1	-1.54
97	0.0007225	NM_018719.2	CDCA7L	2.21
98	0.0007575	NM_144590.1	ANKRD22	5.74
99	0.0007596	NM_002067.1	GNA11	-1.55
100	0.0007649	XM_930678.1	LOC642441	2.66
101	0.000787	NM_003082.2	SNAPC1	1.99
102	0.000793	NM_138786.1	TM4SF18	-18.79
103	0.0008124	NM_006405.5	TM9SF1	2.19
104	0.0008266	NM_024826.1	FLJ21159	4.64
105	0.000828	NM_014504.1	RABGEF1	-2.33
106	0.0008297	NM_018650.2	MARK1	2.36
107	0.0008562	NM_001017430.1	RBM3	-1.93
108	0.0008582	XM_943927.1	LOC653977	-1.55
109	0.0008863	NM_148956.1	NSUN5	-1.69
110	0.0008915	CF454867		2.34
111	0.0009018	NM_001031740.1	MANEAL	-2.09
112	0.0009073	NM_032630.2	CINP	1.53
113	0.0009086	NM_021008.2	DEAF1	-1.55
114	0.0009646	NM_005102.1	FEZ2	-2.27
115	0.0009943	NM_007257.4	PNMA2	-9.72

*S/R: Sensitive cells/Resistant cells