

Differential gene expression profiling in blood from patients with digestive system cancers

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Supplementary Table 3. Forty-four differentially regulated genes between the patients with gastric or colon cancer and pancreatic cancer

Probe Set	GenBank	Symbol	Description	Gene ontology	p-value	Fold change (gastric or colon / pancreatic)	Cut-off value	AUC
A_23_P11984	NM_201649	SLC6A9	Solute carrier family 6, member 9	Amino acid transport	4.14E-02	3.41	2.23	0.56
A_23_P67708	NM_003200	TCF3	Transcription factor 3	Regulation of transcription	4.14E-02	2.40	1.70	0.65
A_23_P363426	NM_032102	SFRS2B	Splicing factor, arginine/serine-rich 2B	Nucleic acid binding	4.14E-02	1.92	1.43	0.73
A_23_P101208	NM_001914	CYB5A	Cytochrome b5 type A	Electron transport	4.14E-02	1.60	1.17	0.80
A_24_P360499	NR_002765	DDEF1IT1	DDEF1 intronic transcript 1		4.14E-02	0.47	0.81	0.82
A_32_P147063	AL355688	AL355688	EST from clone 208499		2.69E-02	0.49	0.94	0.61
A_23_P89762	NM_194449	PHLPP	PH domain and leucine rich repeat protein phosphatase	Apoptosis	4.14E-02	0.49	0.56	0.56
A_24_P7121	NM_024677	NSUN7	NOL1/NOP2/Sun domain family, member 7		4.40E-02	0.50	0.78	0.60
A_32_P175077	BC033052	BC033052	cDNA clone IMAGE:5259731		4.14E-02	0.52	0.63	0.64
A_32_P163739	BC031632	KIAA1257	KIAA1257		4.14E-02	0.52	0.59	0.70
A_23_P166297	NM_207630	ABCG1	ATP-binding cassette, sub-family G, member 1	Lipid transport	4.14E-02	0.53	0.56	0.56
A_32_P203749	AF086547	AF086547	Full length insert cDNA clone ZE12B03		4.40E-02	0.53	0.53	0.50
A_24_P717586		A_24_P717586			4.14E-02	0.54	0.59	0.77
A_24_P456452	AK074562	AK074562	cDNA FLJ90081 fis		4.35E-02	0.54	0.72	0.73
A_23_P166993	NM_004441	EPHB1	EPH receptor B1	Signal transduction	4.14E-02	0.54	0.64	0.66
A_24_P582763	AK096401	AK096401	cDNA FLJ39082		4.14E-02	0.55	0.75	0.74
A_23_P413952	AK098579	AK098579	cDNA FLJ25713		4.14E-02	0.55	0.87	0.62
A_23_P40010	BC010491	MGC4677	Hypothetical protein MGC4677		4.14E-02	0.56	0.76	0.81
A_23_P383764	AF143328	OR52K3P	clone IMAGE:110749	G protein-coupled receptor protein signaling pathway	4.96E-02	0.57	0.76	0.57
A_32_P94176		THC2713710			4.35E-02	0.58	0.63	0.78
A_23_P41227	NM_001627	ALCAM	Activated leukocyte cell adhesion molecule	Cell adhesion	4.14E-02	0.58	0.67	0.53
A_32_P114739	DB518505	DB518505	cDNA clone H013059P17		4.96E-02	0.59	0.74	0.62
A_24_P400997		ENST0000032087	clone IMAGE:4285740		2.69E-02	0.59	0.73	0.63
A_32_P27991	AK226060	BUB3	BUB3 budding uninhibited by benzimidazoles 3	Mitosis	4.14E-02	0.60	0.66	0.75
A_24_P634530	BE535679	BE535679	cDNA clone IMAGE:3446983		4.14E-02	0.60	0.69	0.55
A_24_P941946	AK022881	C20orf74	cDNA FLJ12819	Regulation of small GTPase mediated signal transduction	4.40E-02	0.61	0.72	0.65
A_32_P32585	NM_025180	CEP63	Centrosomal protein 63kDa	Protein binding	4.14E-02	0.61	0.68	0.63
A_32_P325710	BC009340	BC009340	cDNA clone IMAGE:4128659		4.14E-02	0.62	0.79	0.73
A_24_P573224	AK025388	AK025388	cDNA: FLJ21735		4.14E-02	0.63	0.71	0.70
A_32_P185361	AL109784	AL109784	Full length insert cDNA clone EUROIMAGE 122871		4.14E-02	0.63	0.97	0.69
A_24_P100605	NM_020343	C20orf74	Chromosome 20 open reading frame 74	Regulation of small GTPase mediated signal transduction	4.14E-02	0.63	0.72	0.69
A_24_P453901		THC2698150	Unnamed portein product		4.14E-02	0.64	0.94	0.71
A_32_P51707		THC2662514			4.83E-02	0.64	0.84	0.82
A_23_P140591	NM_007011	ABHD2	Abhydrolase domain containing 2	Negative regulation of cell migration	4.14E-02	0.64	0.75	0.59
A_32_P361915	NM_015079	TBC1D2B	TBC1 domain family, member 2B	Rab GTPase activator activity	4.14E-02	0.64	0.93	0.48
A_24_P342086	NM_199423	WWP2	WW domain containing E3 ubiquitin protein ligase 2	Protein modification process	4.14E-02	0.64	0.72	0.82
A_24_P22163	NM_177438	DICER1	Dicer1, Dcr-1 homolog	RNA processing	4.14E-02	0.65	0.84	0.66
A_24_P757154		THC2661968	RRN3 protein		4.14E-02	0.65	0.75	0.77
A_32_P26144		THC2660562			4.56E-02	0.65	0.91	0.74
A_32_P87631	BC017507	BC017507	clone IMAGE:4850148		4.14E-02	0.65	0.75	0.77
A_23_P37375	NM_004755	RPS6KA5	Ribosomal protein S6 kinase	Regulation of transcription	4.14E-02	0.63	0.79	0.61
A_24_P111019	BC028243	BC028243	clone IMAGE:5415705		4.96E-02	0.65	0.79	0.67
A_23_P353888	NM_203447	DOCK8	Dedicator of cytokinesis 8	GTP binding	4.14E-02	0.65	0.76	0.70
A_23_P163428	NM_021823	PPCDC	Phosphopantothenoylecysteine decarboxylase	Coenzyme A biosynthetic process	4.94E-02	0.66	0.92	0.67

AUC: Area under the curve