

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

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Supplementary Table 1. Representative differentially regulated genes between cancer patients and normal subjects

Probe Set	GenBank	Symbol	Description	Gene Ontology	p-value	Fold Change (cancer/normal)	Cut-off Value	AUC	25 probes
A_24_P126741		ENST00000309178			3.61E-09	3.57	1.62	0.98	✓
A_24_P276583	NM_019026	TMCO1	Tansmembrane and coiled-coil domains 1	Endoplasmic reticulum	1.44E-08	2.94	1.74	0.97	✓
A_23_P78092	NM_001003927	EVI2A	Ecotropic viral integration site 2A	Transmembrane receptor activity	1.59E-08	3.94	1.60	0.95	✓
A_24_P333112		A_24_P333112			3.60E-07	3.20	1.55	0.93	✓
A_23_P70007	NM_012484	HMMR	Hyaluronan-mediated motility receptor	Cell motility	6.08E-07	4.99	1.99	0.98	✓
A_23_P70328	NM_018132	CENPQ	Centromere protein Q	Chromosome	7.68E-07	3.26	1.84	0.94	✓
A_23_P65768	NM_016304	C15orf15	Chromosome 15 open reading frame 15	Translation	8.13E-07	3.45	1.87	0.93	✓
A_24_P169378	NM_001011	RPS7	Ribosomal protein S7	Translation	9.74E-07	2.95	1.67	0.93	✓
A_24_P201702	NM_005127	CLEC2B	C-type lectin domain family 2, member B	Sugar binding	1.18E-06	3.01	1.55	0.91	✓
A_24_P11045		THC2785765	Cytochrome c oxidase polypeptide VIIb	Electron transport	1.65E-06	3.48	1.37	0.92	✓
A_23_P41664		ENST0000033499	Synleurin		2.12E-06	4.04	1.90	0.95	✓
A_24_P287756	NM_007006	NUDT21	Nudix-type motif 21	mRNA processing	2.86E-06	2.96		0.86	
A_24_P56317	NM_144778	MBNL2	Muscleblind-like 2	Nucleic acid binding	3.45E-06	2.68		0.84	
A_23_P302550	NM_130782	RGS18	Regulator of G-protein signalling 18	Regulation of G protein-coupled receptor protein signaling pathway	3.80E-06	2.77		0.86	
A_23_P159650	NM_001866	COX7B	Cytochrome c oxidase subunit VIIb	Electron transport	5.22E-06	2.97		0.83	
A_24_P119141	NM_000313	PROS1	Protein S	Blood coagulation	6.26E-06	4.01		0.71	
A_24_P286054		ZFYVE16	Zinc finger FYVE domain-containing protein 16	Regulation of endocytosis	7.20E-06	2.82		0.98	
A_23_P50907	NM_002210	ITGAV	Integrin, alpha V	Cell adhesion	1.06E-05	2.83		0.92	
A_23_P75769	NM_024021	MS4A4A	Membrane-spanning 4-domains, subfamily A, member 4	Signal transduction	1.09E-05	2.69		0.95	
A_23_P218928	NM_016613	C4orf18	Chromosome 4 open reading frame 18	Golgi apparatus	1.38E-05	2.82		0.96	
A_23_P87879	NM_001781	CD69	CD69 molecule	Defense response	1.91E-05	2.61		0.81	
A_32_P178945	NM_018566	YOD1	YOD1 OTU deubiquinating enzyme 1 homolog	Ubiquitin cycle	2.34E-05	2.72		0.75	
A_23_P115872	NM_018131	CEP55	Centrosomal protein 55kDa	Cell cycle	3.93E-05	2.67		0.82	
A_24_P320880	NM_022133	SNX16	Sorting nexin 16	Cell communication	4.34E-05	2.63		0.88	
A_24_P941643	NM_182734	PLCB1	Phospholipase C, beta 1	Regulation of progression through cell cycle	4.79E-05	3.14		0.93	
A_24_P931364	AK022062	AK022062	cDNA FLJ12000 fis		1.47E-08	0.33	0.58	0.97	✓
A_32_P98940		THC2745859			1.51E-07	0.31	0.64	0.96	✓
A_32_P209582		THC2663167	ALU1_HUMAN Alu subfamily J		2.33E-07	0.32	0.54	0.97	✓
A_32_P71171		A_32_P71171			5.02E-07	0.26	0.47	0.97	✓
A_32_P111394		THC2643957			5.34E-07	0.23	0.43	0.94	✓
A_32_P125589		THC2649341			6.40E-07	0.28	0.53	0.91	✓
A_24_P930391	AK022351	AK022351	cDNA FLJ12289 fis		7.15E-07	0.27	0.59	0.97	✓
A_23_P359174	BC069659	BC069659	cDNA clone IMAGE:7262526		1.31E-06	0.27	0.43	0.96	✓
A_32_P19561		THC2728305			1.54E-06	0.18	0.31	0.96	✓
A_23_P341938	NM_005450	NOG	Noggin	Cell differentiation	1.73E-06	0.29	0.45	0.93	✓
A_32_P33304	AK126851	ANK3	cDNA FLJ44903 fis	Signal transduction	2.14E-06	0.26	0.45	0.94	✓
A_32_P226941		THC2689491			3.20E-06	0.32	0.47	0.92	✓
A_32_P142802		THC2699446			3.80E-06	0.31	0.56	0.85	✓
A_24_P15797	AK091796	NUDT22	cDNA FLJ34477 fis	Biological process	4.14E-06	0.19	0.30	0.92	✓
A_24_P366122	NM_024722	ACBD4	Acyl-Coenzyme A binding domain containing 4	Binding	6.23E-06	0.22		0.69	
A_24_P363315	NM_021959	PPP1R11	Protein phosphatase 1, regulatory subunit 11	Protein binding	6.36E-06	0.24		0.66	
A_23_P358370	X94553	FOXE1	HFKH4 mRNA for fork head like protein	Transcription	7.10E-06	0.24		0.74	
A_32_P74615	NM_001003845	SP5	Sp5 transcription factor	Transcription	8.86E-06	0.31		0.73	
A_24_P419028	AB014771	MOP-1	MOP-1	Signal transduction	1.08E-05	0.28		0.74	
A_23_P433063	NM_033064	ATCAY	Ataxia, cerebellar	Transport	1.25E-05	0.33		0.62	
A_24_P345837	NM_002448	MSX1	Msh homeobox 1	Organ morphogenesis	1.69E-05	0.29		0.48	
A_23_P84399	NM_014141	CNTNAP2	Contactin associated protein-like 2	Cell adhesion	2.48E-05	0.30		0.82	
A_24_P168495	NM_001082	CYP4F2	Cytochrome P450, family 4, subfamily F, polypeptide 2	Electron transport	2.70E-05	0.29		0.71	
A_24_P106542	NM_032784	RSPO3	R-spondin 3 homolog	Electron transport	3.21E-05	0.30		0.54	
A_23_P119143	NM_003259	ICAM5	Intercellular adhesion molecule 5	Cell-cell adhesion	3.57E-05	0.31		0.52	
A_24_P207195	NM_024336	IRX3	Iroquois homeobox protein 3	Regulation of transcription, DNA-dependent	3.90E-05	0.30		0.69	
A_24_P272845	NM_004947	DOCK3	Dedicator of cytokinesis 3	Protein binding	4.87E-05	0.19		0.67	

AUC: Area under the curve