

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

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**Supplementary Table 2. Forty-five differentially expressed genes between patients with early- and advanced-stage cancer**

Probe Set	GenBank	Symbol	Description	Gene ontology	p-value	Fold change (advanced / early)	Cut-off value	AUC
A_24_P316965	NM_080657	RSAD2	Radical S-adenosyl methionine domain containing 2	Catalytic activity	2.0E-02	3.65	1.68	0.81
A_23_P420431	NM_175878	XKR3	XK, Kell blood group complex subunit-related family, member 3	Membrane	2.9E-02	3.52	1.02	0.82
A_23_P17481	NM_023068	SIGLEC1	Sialic acid binding Ig-like lectin 1	Inflammatory response	4.9E-02	3.41	1.21	0.77
A_23_P161428	NM_144590	ANKRD22	Ankyrin repeat domain 22		2.9E-02	3.33	2.07	0.83
A_23_P45871	NM_006820	IFI44L	Interferon-induced protein 44-like		2.6E-02	3.13	1.47	0.79
A_23_P137366	NM_000491	C1QB	Complement component 1, q subcomponent, B chain	Innate immune response	3.7E-02	2.81	1.62	0.84
A_23_P52266	NM_001548	IFIT1	Interferon-induced protein with tetratricopeptide repeats 1	Immune response	2.9E-02	2.78	1.91	0.77
A_32_P108254	NM_017565	FAM20A	Family with sequence similarity 20, member A		2.6E-02	2.68	0.69	0.86
A_23_P35412	NM_001549	IFIT3	Interferon-induced protein with tetratricopeptide repeats 3	Immune response	1.6E-02	2.51	1.19	0.83
A_24_P868905	XR_018907	LOC391020	Similar to Interferon-induced transmembrane protein 3		1.8E-02	2.48	1.29	0.82
A_24_P179107	AF267875	AF267875	Amyloid lambda 6 light chain variable region SAR		1.6E-02	2.46	2.19	0.76
A_23_P384355	BG547557	BG547557	cDNA clone IMAGE:4703546		2.9E-02	2.38	1.51	0.75
A_23_P819	NM_005101	ISG15	ISG15 ubiquitin-like modifier	Immune response	1.5E-02	2.34	1.26	0.80
A_32_P162183	NM_000063	C2	Complement component 2	Innate immune response	2.2E-02	2.31	1.29	0.86
A_23_P23074	NM_006417	IFI44	Interferon-induced protein 44	Response to virus	4.5E-02	2.31	1.11	0.75
A_23_P370682	NM_138456	BATF2	Basic leucine zipper transcription factor, ATF-like 2	Regulation of transcription	3.3E-02	2.26	2.20	0.77
A_23_P201459	NM_022873	IFI6	Interferon, alpha-inducible protein 6	Immune response	2.6E-02	2.25	1.08	0.79
A_24_P304071	NM_001547	IFIT2	Interferon-induced protein with tetratricopeptide repeats 2	Immune response	2.2E-02	2.19	1.74	0.82
A_32_P99533	AI423557	AI423557	Similar to INTERFERON-INDUCED 17 KD PROTEIN		1.5E-02	2.16	1.34	0.80
A_23_P105794	NM_033255	EPST11	Epithelial stromal interaction 1		2.8E-02	2.16	1.20	0.80
A_23_P110196	NM_016323	HERC5	Hect domain and RLD 5	Regulation of cyclin-dependent protein kinase activity	3.2E-02	2.15	1.04	0.76
A_23_P69171	NM_033050	SUCNR1	Succinate receptor 1	G protein-coupled receptor protein signaling pathway	2.3E-02	2.10	1.01	0.84
A_23_P64828	NM_002534	OAS1	2'-5'-oligoadenylate synthetase 1	Immune response	1.6E-02	2.10	1.54	0.81
A_23_P165624	NM_007115	TNFAIP6	Tumor necrosis factor, alpha-induced protein 6	Inflammatory response	4.3E-02	2.09	1.40	0.81
A_23_P47955	NM_006187	OAS3	2'-5'-oligoadenylate synthetase 3	Immune response	4.0E-02	2.09	1.36	0.75
A_24_P235429	NM_005502	ABCA1	ATP-binding cassette, sub-family A, member 1	Transport	1.8E-02	2.07	1.44	0.85
A_23_P75769	NM_024021	MS4A4A	Membrane-spanning 4-domains, subfamily A, member 4	Signal transduction	3.8E-02	2.01	1.56	0.77
A_32_P164593	NM_024645	ZMAT4	Zinc finger, matrin type 4	Nucleic acid binding	1.1E-02	0.28	0.45	0.82
A_23_P157926	NM_152570	LINGO2	Leucine rich repeat and Ig domain containing 2	Protein binding	4.1E-02	0.40	0.48	0.79
A_23_P320242	NM_152748	KIAA1324L	KIAA1324-like		1.6E-02	0.41	0.62	0.82
A_23_P210581	NM_002237	KCNG1	Potassium voltage-gated channel, subfamily G, member 1	Ion transport	3.7E-02	0.42	0.41	0.77
A_24_P129632	NM_004747	DLG5	Discs, large homolog 5	Intracellular signaling cascade	1.1E-02	0.45	0.70	0.87
A_32_P324533	NM_053282	SH2D1B	SH2 domain containing 1B	Intracellular signaling cascade	2.2E-02	0.45	0.65	0.80
A_32_P113322	BC033331	BC033331	cDNA clone IMAGE:4827941		1.4E-02	0.46	0.60	0.81
A_32_P235358	AK124173	AK124173	cDNA FLJ42179 fis		9.0E-03	0.46	0.71	0.86
A_32_P225472	XM_926013	LOC642398	Hypothetical LOC642398		4.0E-02	0.46	0.94	0.75
A_32_P91743	THC2724906	Q96HL9_HUMAN	Q96HL9_HUMAN CHP protein		3.1E-02	0.47	1.29	0.80
A_23_P159255	NM_002845	PTPRM	Protein tyrosine phosphatase, receptor type, M	Protein amino acid dephosphorylation	1.1E-02	0.47	0.61	0.87
A_24_P354715	NM_002526	NT5E	5'-nucleotidase	DNA metabolic process	3.3E-02	0.47	0.41	0.79
A_23_P103756	NM_002557	OVGP1	Oviductal glycoprotein 1	Carbohydrate metabolic process	2.1E-02	0.48	0.75	0.79
A_24_P160413	ENST0000036051	cDNA FLJ38790	cDNA FLJ38790 fis		3.3E-02	0.48	0.44	0.79
A_32_P179998	NM_033053	DMRTC1	DMRT-like family C1	Transcription	1.1E-02	0.48	0.75	0.85
A_24_P276576	NM_032738	FCRLA	Fc receptor-like A	Cell differentiation	4.2E-02	0.49	0.44	0.75
A_32_P47643	AL137761	FAM110C	cDNA DKFZp586L2424		4.9E-02	0.49	0.49	0.75
A_23_P151046	NM_002259	KLRC1	Killer cell lectin-like receptor subfamily C, member 1	Cell surface receptor linked signal transduction	3.2E-02	0.50	0.56	0.76

AUC: Area under the curve