

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