**Table 1. The significance of the difference in mRNA expression of the studied genes with paired comparisons of embryonic-anatomic parts of the colon in the samples from healthy donors (normal) and tumor samples (CRC)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Genes** | **Normal** | **CRC** | **RC** | **LC** | **R** |
| **RC/LC** | **RC/R** | **LC/R** |  | **RC/LC** | **RC/R** | **LC/R** |  | **Normal/CRC** |  | **Normal/CRC** |  | **Normal/CRC** |
| *CTSL2* | – | – | 0.005 | – | – | – | 0.022 | < 0.001 | < 0.001 |
| *BCL2* | – | – | – | 0.043 | – | – | < 0.001 | < 0.001 | < 0.001 |
| *MYC* | – | < 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *BIRC5* | – | – | – | – | – | – | < 0.001 | < 0.001 | 0.023 |
| *CCND1* | 0.007 | < 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *NDRG1* | 0.005 | 0.003 | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *CD68* | 0.004 | – | 0.001 | – | – | – | – | – | – |
| *KI67* | – | – | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *TERT* | < 0.001 | – | < 0.001 | 0.007 | – | – | – | < 0.001 | – |
| *HER2* | 0.026 | – | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *PTEN* | – | – | 0.046 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *BAG1* | – | < 0.001 | 0.002 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *PGR* | – | 0.005 | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *CCNB1* | – | – | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *ESR1* | – | < 0.001 | < 0.001 | – | – | – | 0.027 | < 0.001 | < 0.001 |
| *GRB7* | – | – | – | – | – | – | 0.016 | < 0.001 | < 0.001 |
| *MMP11* | – | 0.029 | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *STK15* | – | – | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *MYBL2* | – | – | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *P16INK4A* | – | < 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *SCUBE2* | – | < 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | 0.001 |
| *MMP9* | – | – | 0.013 | – | – | – | 0.003 | 0.036 | – |
| *GNLY* | – | – | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *P14ARF* | – | < 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | 0.001 |
| *IGF1* | 0.029 | – | 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *COX-2* | – | < 0.001 | < 0.001 | – | – | – | 0.018 | 0.014 | – |
| *IGF2* | – | < 0.001 | < 0.001 | – | – | – | – | – | – |
| *CYP19A* | – | 0.001 | 0.007 | – | – | – | 0.007 | – | – |
| *GREM1* | – | < 0.001 | 0.000 | – | – | – | 0.017 | 0.001 | – |
| *MMP2* | – | 0.003 | 0.014 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *PAPPA* | 0.049 | 0.003 | – | – | – | – | 0.015 | – | – |
| *MMP7* | – | < 0.001 | < 0.001 | – | 0.041 | – | < 0.001 | < 0.001 | < 0.001 |
| *IL2* | – | < 0.001 | < 0.001 | 0.041 | – | – | < 0.001 | < 0.001 | < 0.001 |
| *MMP8* | – | – | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *IL2Ra* | < 0.001 | 0.008 | – | – | – | – | – | – | – |
| *IL6* | – | 0.002 | < 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *IL12a* | 0.006 | 0.001 | < 0.001 | – | – | – | < 0.001 | – | < 0.001 |
| *IL7* | 0.010 | – | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *IL15* | – | 0.029 | 0.008 | – | – | – | – | < 0.001 | – |
| *IL8* | – | < 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *IL1b* | – | < 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *IL10* | 0.021 | 0.007 | < 0.001 | – | – | – | – | – | 0.002 |
| *TPA* | – | – | – | – | – | – | – | – | – |
| *IFNg* | – | – | – | 0.013 | – | 0.030 | < 0.001 | 0.042 | 0.001 |
| *CD45* | 0.033 | 0.042 | 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *TNFa* | 0.010 | – | 0.000 | – | – | – | 0.010 | < 0.001 | < 0.001 |
| *CD56* |  | – | – | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *TGFb* | 0.018 | 0.011 | 0.000 | – | – | – | 0.040 | – | 0.001 |
| *CD69* | 0.025 | – | – | 0.002 | – | – | – | 0.001 | – |
| *VEGFA121* | – | < 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *BAX* | – | – | 0.011 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *VEGFA165* | 0.024 | < 0.001 | – | – | – | – | – | – | 0.041 |
| *TLR2* | – | – | 0.012 | – | – | – | – | – | – |
| *VEGFA189* | 0.000 | 0.014 | – | – | – | – | 0.025 | – | 0.035 |
| *TLR4* | 0.003 | 0.014 | – | – | – | – | < 0.001 | 0.005 | 0.024 |
| *TLR7* | – | 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |
| *HLA-G5* | – | 0.005 | 0.006 | – | – | – | 0.001 | 0.001 | < 0.001 |
| *GATA3* | – | 0.001 | < 0.001 | – | – | – | – | 0.008 | < 0.001 |
| *LGALS1* | – | < 0.001 | < 0.001 | – | – | – | – | – | – |
| *LIF* | – | < 0.001 | < 0.001 | – | – | – | – | – | 0.003 |
| *LIFR* | – | < 0.001 | < 0.001 | – | – | – | < 0.001 | < 0.001 | < 0.001 |

CRC, colorectal cancer; LC, left colon; R, rectum; RC, right colon

The table gives P values of < 0.05, non-significant difference marked by “–”

**Table 2. Summary of discriminant analysis for determination of belonging of healthy colonic mucosa samples to the sections of the colon**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene** | **Wilks' lambda** | **Case lambda** | **F criterion** | **Significance of F criterion (p)** | **Tolerance** |
| *SCUBE2* | 0.038 | 0.775 | 12.903 | 0.000\* | 0.245 |
| *IL2Ra* | 0.035 | 0.83 | 9.088 | 0.000\*\* | 0.182 |
| *CCND1* | 0.035 | 0.831 | 9.021 | 0.000\*\* | 0.577 |
| *TERT* | 0.035 | 0.849 | 7.896 | 0.001 | 0.328 |
| *IGF1* | 0.034 | 0.866 | 6.856 | 0.002 | 0.101 |
| *LIFR* | 0.034 | 0.869 | 6.681 | 0.002 | 0.263 |
| *NDRG1* | 0.034 | 0.875 | 6.358 | 0.003 | 0.119 |
| *CD45* | 0.033 | 0.883 | 5.883 | 0.004 | 0.043 |
| *CD69* | 0.033 | 0.884 | 5.84 | 0.004 | 0.104 |
| *IL1b* | 0.033 | 0.895 | 5.247 | 0.007 | 0.197 |
| *MMP11* | 0.033 | 0.895 | 5.223 | 0.007 | 0.096 |
| *TLR2* | 0.032 | 0.91 | 4.381 | 0.015 | 0.112 |
| *IL7* | 0.032 | 0.911 | 4.349 | 0.016 | 0.197 |
| *ESR1* | 0.032 | 0.912 | 4.287 | 0.017 | 0.18 |
| *TGFb* | 0.032 | 0.914 | 4.167 | 0.019 | 0.047 |
| *TLR4* | 0.032 | 0.92 | 3.883 | 0.024 | 0.13 |
| *BAG1* | 0.032 | 0.927 | 3.495 | 0.035 | 0.473 |
| *MMP9* | 0.031 | 0.932 | 3.251 | 0.043 | 0.155 |
| *PAPPA* | 0.031 | 0.934 | 3.142 | 0.048 | 0.208 |

The significant of the difference: \* р < 0.0001; \*\* р < 0.001. The genes with the biggest contribution to the classification accuracy are given in bold

**Table 3. Concordance of the observed and predicted sample classification by molecular phenotype for the three parts of the colon in the normal group**

|  |  |  |
| --- | --- | --- |
| **Colon part** | **Concordance of the classification, %** | **Sample distribution throughout the colon parts according to the discriminant model, n** |
| RC (normal) | LC (normal) | R (normal) |
| RC (normal) | 95.7 | 45 | 2 | 0 |
| LC (normal) | 96.8 | 2 | 60 | 0 |
| R (normal) | 93.0 | 0 | 2 | 31 |
| Total | 95.8 | 47 | 64 | 31 |

LC, left colon; R, rectum; RC, right colon

The diagonal in the table (in grey): the numbers of samples correctly classified as originating from specific colon parts. Other cells: the numbers of samples with incorrect classification

**Table 4. Concordance of the observed and predicted sample classification by molecular phenotype for the three parts of the colon in the CRC group. The classification matrix for the discriminant analysis included 27 genes**

|  |  |  |
| --- | --- | --- |
| **Colon part** | **Concordance of the classification, %** | **Sample distribution throughout the colon parts according to the discriminant model, n** |
| **RC (CRC)** | **LC (CRC)** | **R (CRC)** |
| RC (CRC) | 76.0 | 19 | 0 | 6 |
| LC (CRC) | 71.4 | 4 | 25 | 6 |
| R (CRC) | 78.0 | 3 | 6 | 32 |
| Total | 75.2 | 26 | 31 | 44 |

CRC, colorectal cancer; LC, left colon; R, rectum; RC, right colon

The diagonal in the table (in grey): the numbers of samples correctly classified as originating from specific colon parts. Other cells: the numbers of samples with incorrect classification