

doi: 10.1387/ijdb.140106ja

THE INTERNATIONAL JOURNAL OF
DEVELOPMENTAL
BIOLOGY
www.intjdevbiol.com

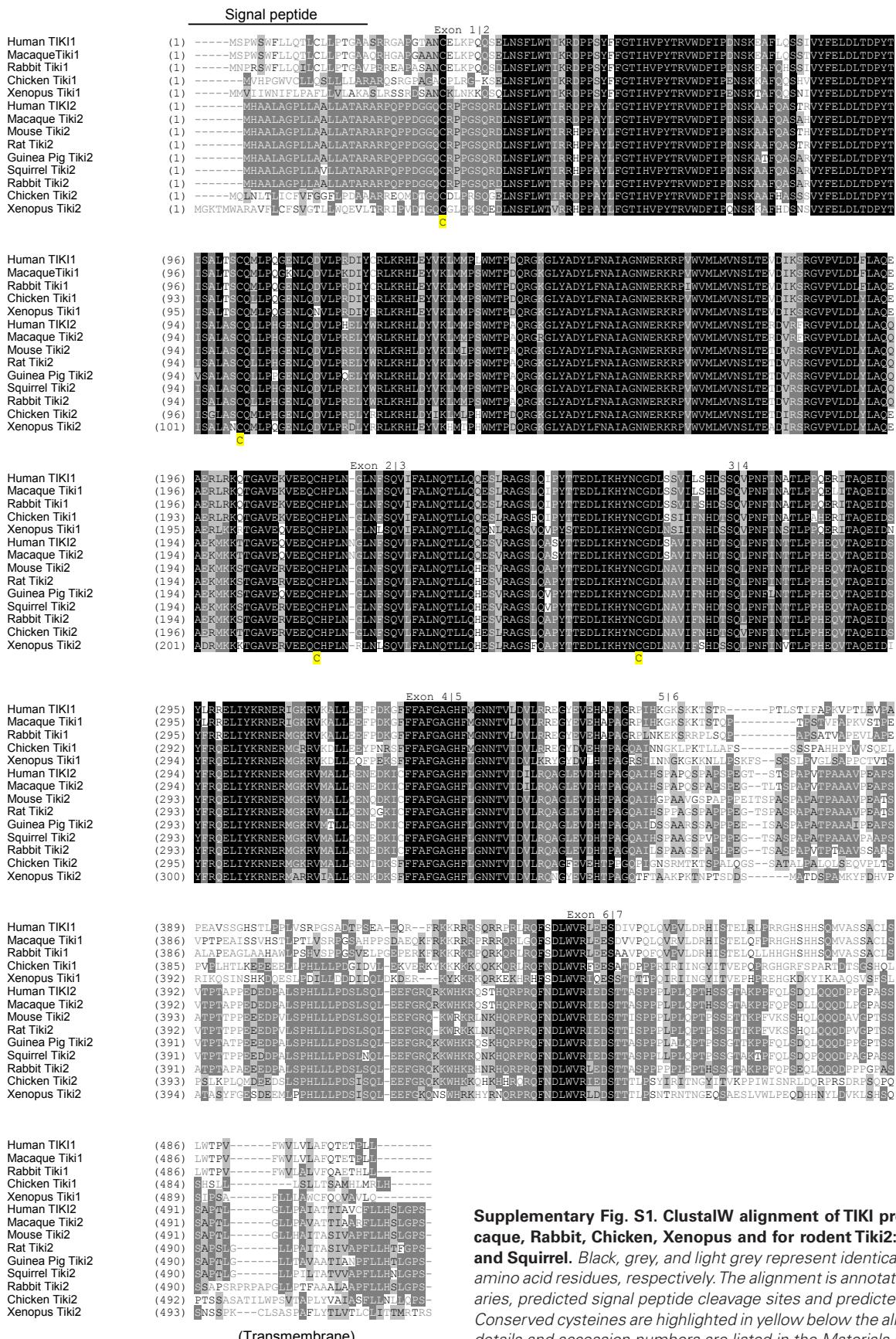
SUPPLEMENTARY MATERIAL

corresponding to:

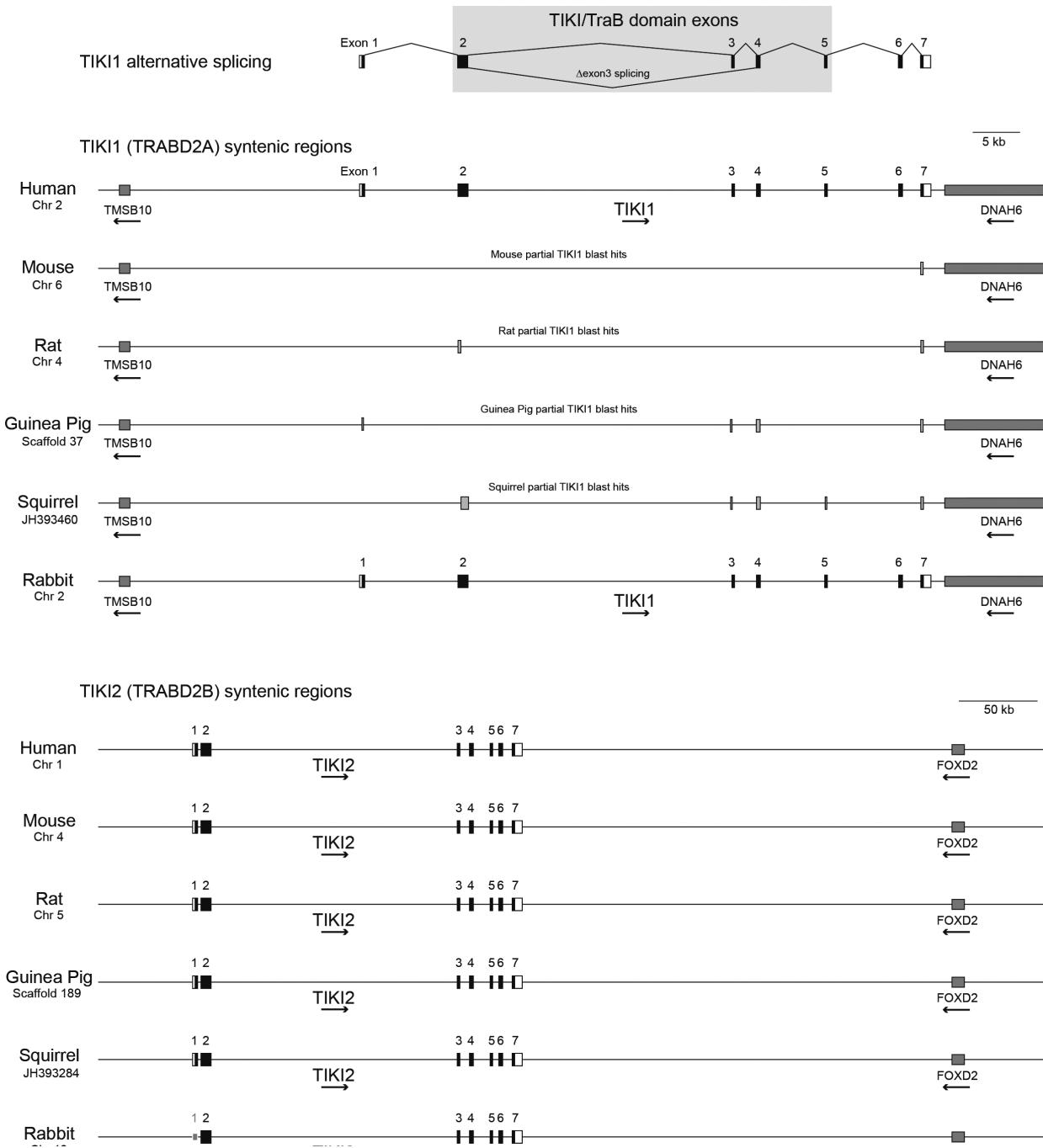
Expression and evolution of *Tiki1* and *Tiki2* genes in vertebrates

ALICE H. REIS, BRYAN T. MACDONALD, KERSTIN FEISTEL, JOSE M. BRITO,
NATHALIA G. AMADO, CHIWEI XU, JOSE G. ABREU and XI HE

***Address correspondence to:** Jose G Abreu. Instituto de Ciências Biomédicas, Universidade Federal do Rio de Janeiro, Rio de Janeiro, 21949-590, Brazil.
e-mail: garciajr@icb.ufrj.br or Xi He. F. M. Kirby Center, Boston Children's Hospital, Harvard Medical School, Boston, MA 02115, USA. e-mail: xi.he@childrens.harvard.edu



Supplementary Fig. S1. ClustalW alignment of TIK1 proteins from Human, Macaque, Rabbit, Chicken, Xenopus and for rodent Tiki2: Mouse, Rat, Guinea Pig and Squirrel. Black, grey, and light grey represent identical, conservative, and similar amino acid residues, respectively. The alignment is annotated with exon/intron boundaries, predicted signal peptide cleavage sites and predicted transmembrane regions. Conserved cysteines are highlighted in yellow below the alignment. Protein sequence details and accession numbers are listed in the Materials and Methods section.



Supplementary Fig. S2. Genomic structures of TIKI genes and syntenic regions. (A) Vertebrate TIKI genes are encoded by seven exons, with the conserved TIKI/TraB domain mainly contained within exons 2-5. Exon coding regions are displayed in black and non-coding regions in white. Exon 3 is 147 base pairs and encodes 49 amino acids within the TIKI/TraB domain and contains one of four conserved cysteine residues (see Fig S1). Human TIKI1 has an alternative spliced transcript that lacks exon 3 (NM_001080824.2, NP_001074293.1) without altering the reading frame of the remaining 3' exons. We have independently cloned this form of Tiki1 cDNA lacking exon3 from Human, Rabbit and Chicken. (B) Syntenic genomic regions annotated and scaled to the Human TIKI1 locus based on the current genomic assemblies. For simplicity, genomic regions are presented with the TIKI genes 5' to 3'. Flanking genes TMSB10 (Thymosin beta-10) and DNAH6 (Dynenin heavy chain 6, axonemal) were identified in the "Tiki1" genomic region of all rodents. Genomic distances between TMSB10 and DNAH6 (Human 96kb, Mouse 59kb, Rat 51kb, Guinea Pig 119kb, Squirrel 106kb, Rabbit 113kb) reveal a greater number of intergenic deletions in the mouse and the rat. BLASTN alignment of the Human TIKI1 cDNA with the rodent Tiki1 genomic regions unveils the remnants of the Tiki1 exons (shown with gray boxes and positioned relative to Human TIKI1) although many coding changes are observed and the reading frame is not maintained in the rodent exon fragments. (C) The syntenic TIKI2 genomic region annotated and scaled to Human TIKI2. The neighboring gene FOXD2 (Forkhead box D2) is shown to verify the TIKI2 genomic region. The mouse, rat, guinea pig and squirrel contain a full-length Tiki2 genes in the current genomic assemblies. A gap in the genomic Rabbit Tiki2 exon1 region is shaded gray. This region is GC rich and frequently absent in other mammalian genome assemblies.

SUPPLEMENTARY TABLE S1

ALTERED EXPRESSION OF TIKI1 AND TIKI2 IN CANCERS AND OTHER DISEASES

Human TIKI1 (TRABD2A)

| Tissue/cell type | Comparison groups (a vs b) | log2foldchange (a/b) | p-value | Sample size (a vs b) | DataSet accession | Design Element/reporter |
|-------------------------------------------------|----------------------------------------------------------------|-------------------------|----------|-------------------------|--------------------|-------------------------|
| gastric tissue | Gastric Cancer vs. Normal | 1,95 | 1,00E-03 | 12 vs 3 | GSE19826 | 227867_at |
| endometrial tissues | disease state: 'ovarian endometriosis' vs 'normal' | 1,83 | 7,19E-05 | 10 vs 10 | GDS2835 | 227867_at |
| testicular parenchyma | Testicular Seminoma vs. Normal | 1,81 | 2,90E-02 | 3 vs 3 | GSE1818 | BC051789 |
| gastric vs. mucosa | Gastric Mixed Adenocarcinoma vs. Normal mucosa | 1,28 | 4,10E-02 | 4 vs 31 | GSE13911 | 227867_at |
| kidney | Papillary Renal Cell Carcinoma vs. Normal | 1,18 | 9,00E-03 | 19 vs 3 | GSE11151 | 227867_at |
| prostate gland | Prostate Carcinoma vs. Normal | 1,04 | 4,80E-02 | 7 vs 6 | GSE3325 | 227867_at |
| B-lymphocytes | Follicular Lymphoma vs. Normal | 1,03 | 9,57E-15 | 38 vs 20 | GSE12195 | 227867_at |
| gastric vs. mucosa | Gastric Intestinal Type Adenocarcinoma vs. Normal mucosa | 1,02 | 3,00E-03 | 26 vs 31 | GSE13911 | 227867_at |
| B-lymphocytes | Activated B-Cell-Like Diffuse Large B-Cell Lymphoma vs. Normal | 0,88 | 1,25E-05 | 17 vs 20 | GSE12195 | 227867_at |
| colon vs. mucosa | Colon Adenoma vs. Normal mucosa | 0,76 | 1,14E-04 | 5 vs 10 | GSE20916 | 227867_at |
| colon vs. mucosa | Colon Carcinoma vs. Normal mucosa | 0,65 | 7,00E-05 | 5 vs 10 | GSE20916 | 227867_at |
| bone marrow | Monoclonal Gammopathy of Undetermined Significance vs. Normal | 0,64 | 2,57E-04 | 44 vs 22 | GSE5900 | 227867_at |
| thyroid gland | Thyroid Gland Papillary Carcinoma vs. Normal | 0,61 | 2,70E-02 | 14 vs 4 | GSE6004 | 227867_at |
| B-lymphocytes | Diffuse Large B-Cell Lymphoma vs. Normal | 0,61 | 1,66E-08 | 44 vs 20 | GSE12195 | 227867_at |
| umbilical cord tissues (higher gestational age) | disease state: 'bronchopulmonary dysplasia' vs 'control' | 0,61 | 3,63E-02 | 5 vs 21 | GDS3356 | 227867_at |
| T-lymphocyte | Angioimmunoblastic T-Cell Lymphoma vs. Normal | -0,60 | 3,60E-02 | 6 vs 20 | GSE6338 | 227867_at |
| colon | Cecum Adenocarcinoma vs. Normal | -0,62 | 7,11E-04 | 17 vs 5 | GSE5206 | 227867_at |
| colon | Rectal Adenocarcinoma vs. Normal | -0,63 | 1,20E-02 | 8 vs 5 | GSE5206 | 227867_at |
| bone marrow | Acute Myeloid Leukemia vs. Normal | -0,66 | 1,50E-13 | 542 vs 74 | GSE13159 | 227867_at |
| brain | Anaplastic Astrocytoma vs. Normal | -0,69 | 3,88E-06 | 19 vs 23 | GSE4290 | 227867_at |
| lung | Large Cell Lung Carcinoma vs. Normal | -0,69 | 2,04E-08 | 19 vs 65 | GSE19188 | 227867_at |
| brain | Glioblastoma vs. Normal | -0,70 | 2,67E-07 | 81 vs 23 | GSE4290 | 227867_at |
| colon | Rectosigmoid Adenocarcinoma vs. Normal | -0,70 | 1,00E-03 | 10 vs 5 | GSE5206 | 227867_at |
| breast | Invasive Breast Carcinoma vs. Normal | -0,70 | 1,00E-05 | 76 vs 61 | TCGA RNA-seq | A_24_P268487 |
| bone marrow | Pro-B Acute Lymphoblastic Leukemia vs. Normal | -0,75 | 2,64E-15 | 70 vs 74 | GSE13159 | 227867_at |
| bone marrow | T-Cell Acute Lymphoblastic Leukemia vs. Normal | -0,76 | 9,68E-16 | 174 vs 74 | GSE13159 | 227867_at |
| brain | Oligodendroglioma vs. Normal | -0,76 | 8,02E-07 | 50 vs 23 | GSE4290 | 227867_at |
| bone marrow | Chronic Myelogenous Leukemia vs. Normal | -0,77 | 5,22E-14 | 76 vs 74 | GSE13159 | 227867_at |
| ovarian surface epithelium | Ovarian Mucinous Adenocarcinoma vs. Normal | -0,91 | 1,30E-02 | 9 vs 5 | Lu KH et al., 2004 | 51270_at |
| brain | Diffuse Astrocytoma vs. Normal | -0,91 | 2,60E-02 | 7 vs 23 | GSE4290 | 227867_at |
| breast | Invasive Ductal Breast Carcinoma vs. Normal | -0,96 | 3,00E-03 | 23 vs 2 | GSE1477 | AA399461 |
| colon | Colon Mucinous Adenocarcinoma vs. Normal | -0,96 | 6,86E-05 | 13 vs 5 | GSE5206 | 227867_at |
| ovarian surface epithelium | Ovarian Clear Cell Adenocarcinoma vs. Normal | -1,02 | 8,00E-03 | 7 vs 5 | Lu KH et al., 2004 | 51270_at |
| rectum and colon | Rectosigmoid Adenocarcinoma vs. Normal | -1,14 | 2,60E-02 | 3 vs 22 | TCGA RNA-seq | A_23_P255897 |
| breast | Invasive Ductal Breast Carcinoma vs. Normal | -1,14 | 6,76E-13 | 389 vs 61 | TCGA RNA-seq | A_23_P56703 |
| ovarian surface epithelium | Ovarian Endometrioid Adenocarcinoma vs. Normal | -1,28 | 4,00E-03 | 9 vs 5 | Lu KH et al., 2004 | 51270_at |
| ovarian surface epithelium | Ovarian Serous Adenocarcinoma vs. Normal | -1,34 | 4,00E-03 | 20 vs 5 | Lu KH et al., 2004 | 51270_at |
| breast | Male Breast Carcinoma vs. Normal | -1,46 | 2,00E-03 | 3 vs 61 | TCGA RNA-seq | A_24_P268487 |
| breast | Mucinous Breast Carcinoma vs. Normal | -1,55 | 5,80E-15 | 4 vs 61 | TCGA RNA-seq | A_24_P268487 |
| breast | Invasive Mixed Breast Carcinoma vs. Normal | -1,63 | 3,60E-02 | 3 vs 8 | GSE1477 | H53191 |
| bone | disease:'osteosarcoma' vs 'normal' on A-AFFY-44 | -1,85 | 1,43E-06 | 14 vs 4 | E-MEXP-3628 | 227867_at |

Human TIKI2 (TRABD2B)

| Tissue/cell type | Comparison groups (a vs b) | log2foldchange (a/b) | p-value | Sample size (a vs b) | DataSet accession | Design Element/reporter |
|---------------------------------------------------|---------------------------------------------------------------|-------------------------|----------|-------------------------|-------------------|-------------------------|
| peripheral blood from multiple sclerosis patients | genotype/variation: 'high serum Sema4A' vs 'low serum Sema4A' | 2,35 | 3,79E-02 | 3 vs 3 | GDS4152 | 241707_at |
| skin | Skin Basal Cell Carcinoma vs. Normal | 1,78 | 4,00E-03 | 15 vs 4 | GSE7553 | 241707_at |
| skin | Skin Squamous Cell Carcinoma vs. Normal | 1,52 | 1,00E-02 | 11 vs 4 | GSE7553 | 241707_at |
| cancer stroma vs. normal breast | Invasive Breast Carcinoma Stroma vs. Normal | 1,36 | 7,62E-05 | 53 vs 6 | GSE9014 | A_32_P232214 |
| breast | Invasive Mixed Breast Carcinoma vs. Normal | 1,30 | 1,40E-02 | 3 vs 7 | GSE1477 | AW291482 |
| vulva | Vulvar Intraepithelial Neoplasia vs. Normal | 1,25 | 1,00E-02 | 9 vs 10 | GSE5563 | 241707_at |
| kidney | Clear Cell Renal Cell Carcinoma vs. Normal | 1,10 | 7,14E-05 | 26 vs 3 | GSE11151 | 241707_at |
| gastric tissue | Gastric Cancer vs. Normal | 1,06 | 1,50E-02 | 12 vs 3 | GSE19826 | 244472_at |
| skin | Cutaneous Melanoma vs. Normal | 1,05 | 3,60E-02 | 14 vs 4 | GSE7553 | 241707_at |
| breast | Ductal Breast Carcinoma in Situ vs. Normal | 1,04 | 3,40E-02 | 3 vs 7 | GSE1477 | AW291482 |
| testis | Yolk Sac Tumor, NOS vs. Normal | 1,01 | 6,81E-09 | 9 vs 6 | GSE3218 | 241707_at |
| breast | Invasive Lobular Breast Carcinoma vs. Normal | 0,98 | 4,10E-02 | 6 vs 7 | GSE1477 | AW291482 |
| gastric vs. mucosa | Gastric Intestinal Type Adenocarcinoma vs. Normal mucosa | 0,65 | 2,00E-02 | 26 vs 31 | GSE13911 | 244472_at |
| rectum and colon | Rectal Adenocarcinoma vs. Normal | -0,59 | 1,00E-03 | 60 vs 22 | TCGA RNA-seq | A_32_P232218 |
| prostate gland | Prostate Carcinoma vs. Normal | -0,71 | 3,20E-02 | 7 vs 6 | GSE3325 | 244472_at |
| gastric tissue | Gastric Cancer vs. Normal | -0,72 | 2,70E-02 | 12 vs 3 | GSE19826 | 241707_at |
| breast | Ductal Breast Carcinoma vs. Normal | -0,72 | 6,00E-03 | 40 vs 7 | GSE3744 | 244472_at |
| bone marrow | Smoldering Myeloma vs. Normal | -0,77 | 6,00E-03 | 12 vs 22 | GSE5900 | 244472_at |
| rectum and colon | Colon Adenocarcinoma vs. Normal | -0,80 | 1,63E-05 | 101 vs 22 | TCGA RNA-seq | A_32_P232218 |
| synovial tissues | disease state: 'rheumatoid arthritis' vs 'normal' | -0,89 | 2,70E-02 | 4 vs 4 | GDS1857 | 12558 |
| rectum and colon | Rectal Mucinous Adenocarcinoma vs. Normal | -1,00 | 1,70E-02 | 6 vs 22 | TCGA RNA-seq | A_32_P232218 |
| breast | Invasive Breast Carcinoma vs. Normal | -1,31 | 6,83E-10 | 76 vs 61 | TCGA RNA-seq | A_32_P232214 |
| skin | Cutaneous Melanoma vs. Normal | -1,45 | 1,80E-02 | 14 vs 4 | GSE7553 | 244472_at |
| breast | Invasive Ductal Breast Carcinoma vs. Normal | -1,51 | 4,83E-22 | 389 vs 61 | TCGA RNA-seq | A_32_P232218 |
| ductal breast cell | Invasive Ductal Breast Carcinoma vs. Normal | -2,00 | 4,30E-02 | 5 vs 10 | GSE5764 | 244472_at |
| bone | disease:'osteosarcoma' vs 'normal' on A-AFFY-44 | -2,44 | 1,10E-05 | 14 vs 4 | E-MEXP-3628 | 244472_at |
| breast | Mucinous Breast Carcinoma vs. Normal | -2,46 | 6,00E-03 | 4 vs 61 | TCGA RNA-seq | A_32_P232218 |

In order to gain insights into the expression alteration of *TIKI1* (TRABD2A) and *TIKI2* (TRABD2B) in human diseases, a gene-based analysis was performed using public accessible databases of NCBI Geo Profiles (Barrett *et al.*, 2013), ArrayExpress (Parkinson *et al.*, 2011), and Oncomine (Rhodes *et al.*, 2007). A threshold of 1.5 times fold change ($\log_2(\text{fold change}) \geq -0.585$) and $p\text{-value} < 0.05$ was applied to identify differentially expressed genes. The result, ranked by gene expression fold changes, is summarized in the table. According to this analysis, *TIKI1* and *TIKI2* are both down-regulated in breast and colon carcinoma, up-regulated in kidney and testis tumors, which may reflect altered Wnt signaling in these diseases. In addition, *TIKI1* expression increases in gastric cancer, endometrial tissue of patients with endometriosis, prostate carcinoma, and thyroid gland papillary carcinoma, and decreases in osteosarcoma, ovarian adenocarcinoma, and brain tumors. The differential expression of *TIKI1* in various kinds of lymphoma and leukemia might result from the population drift of different B cell or T cell subtypes (Piccaluga *et al.*, 2007). *TIKI2* increases in skin carcinoma, melanoma, and vulvar neoplasia, while it decreases in osteosarcomas, rheumatoid arthritis and gastric cancer. Similar to that seen with other Wnt inhibitors, *TIKI2* downregulation appears to correlate with osteosarcoma growth (Li *et al.*, 2014).