MBE, 19 (8): 8361–8379.  
DOI: 10.3934/mbe.2022389  
Received: 21 March 2022

Revised: 06 May 2022  
Accepted: 19 May 2022  
Published: 09 June 2022

http://www.aimspress.com/journal/MBE

***Research article***

**TRPV1 is a potential biomarker for the prediction and treatment of multiple cancers based on a pan-cancer analysis**

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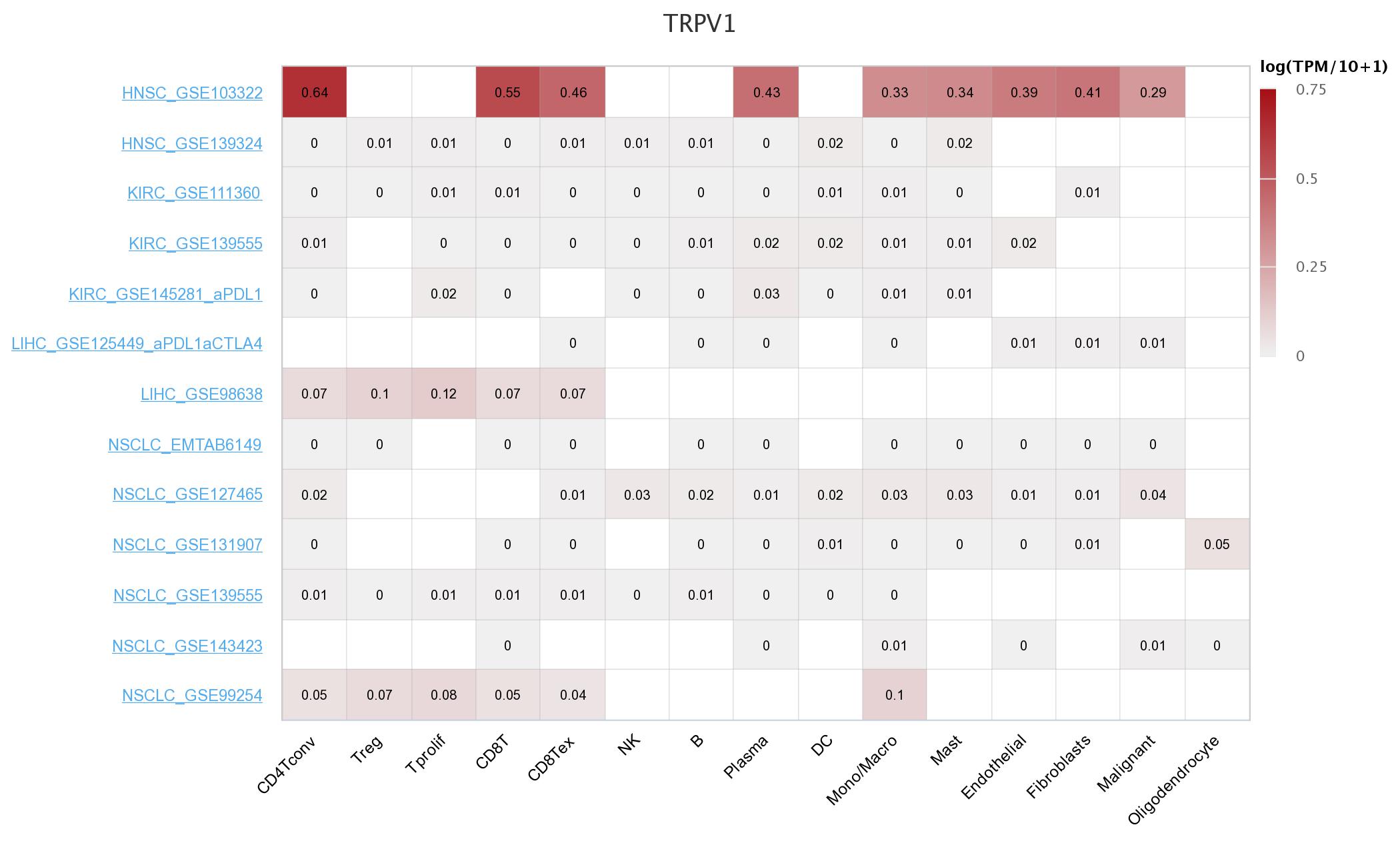
**Supplementary**

**Supplementary Appendix 1.** Cancers were included in the study.

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| The full name of cancer | Abbreviation |
| Adrenocortical Carcinoma | ACC |
| Bladder Urothelial Carcinoma | BLCA |
| Breast Invasive Carcinoma | BRCA |
| Cholangiocarcinoma | CHOL |
| Colon Adenocarcinoma | COAD |
| Lymphoid Neoplasm Diffuse Large B-Cell Lymphoma | DLBC |
| Esophageal Carcinoma | ESCA |
| Glioblastoma Multiforme | GBM |
| Head and Neck Squamous Cell Carcinoma | HNSCC |
| Kidney Chromophobe | KICH |
| Kidney Renal Clear Cell Carcinoma | KIRC |
| Kidney Renal Papillary Cell Carcinoma | KIRP |
| Acute Myeloid Leukemia | LAML |
| Brain Lower Grade Glioma | LGG |
| Liver Hepatocellular Carcinoma | LIHC |
| Lung Adenocarcinoma | LUAD |
| Lung Squamous Cell Carcinoma | LUSC |
| Mesothelioma | MESO |
| Ovarian Serous Cystadenocarcinoma | OV |
| Pancreatic Adenocarcinoma | PAAD |
| Pheochromocytoma and Paraganglioma | PCPG |
| Prostate Adenocarcinoma | PRAD |
| Rectum Adenocarcinoma | READ |
| Sarcoma | SARC |
| Skin Cutaneous Melanoma | SKCM |
| Stomach Adenocarcinoma | STAD |
| Testicular Germ Cell Tumors | TGCT |
| Thyroid Carcinoma | THCA |
| Thymoma | THYM |
| Uterine Corpus Endometrial Carcinoma | UCEC |
| Uterine Carcinosarcoma | UCS |
| Uveal Melanoma | UVM |



**Supplementary Appendix 2.** Cancers selected in the study and their sample number.



**Supplementary Appendix 3.** Analyses based on single cell RNA-seq data to explore cell types highly express TRPV1. The figure was obtained from Tumor Immune Single-cell Hub (http://tisch.comp-genomics.org/home/). Blank cell represents no relevant data.



**Supplementary Appendix 4.** Selection ofpossible hub genes of TRPV1 in ACC. Panel A: The clustering tree diagram indicates that specific samples (above the red line) with distinct outliers should be excluded; the remaining samples (below the red line) were utilized for subsequent analysis. Panel B: The soft threshold was set as 4. Panels C–D: Modules were determined in hierarchical clustering, of which the “brown” module had the strongest correlation with the TRPV1 expression by Pearson correlation coefficient. Panel E: A significant positive correlation between gene significance of TRPV1 expression and module membership in the “brown” module. Panel F: CDCA8 was the hub gene of the “brown” module; the network was constructed in Cytoscape with the “degree” algorithm. In Cytoscape, the visualization network was constructed based on the top 100 genes (rank by the weight values) of the “brown” module; genes not in the most extensive network are not displayed.



**Supplementary Appendix 5.** Selection ofpossible hub genes of TRPV1 in ACC. Panel A: The clustering tree diagram indicates that specific samples (above the red line) with distinct outliers should be excluded; the remaining samples (below the red line) were utilized for subsequent analysis. Panel B: The soft threshold was set as 3. Panels C–D: Modules were determined in hierarchical clustering, of which the “brown” module (except for the grey module) had the strongest correlation with the TRPV1 expression by Pearson correlation coefficient. Panel E: A significant positive correlation between gene significance of TRPV1 expression and module membership in the “brown” module. Panel F: HID1 was the hub gene of the “brown” module; the network was constructed in Cytoscape with the “degree” algorithm. In Cytoscape, the visualization network was constructed based on the top 100 genes (rank by the weight values) of the “brown” module; genes not in the most extensive network are not displayed.



**Supplementary Appendix 6.** Selection ofpossible hub genes of TRPV1 in ACC. Panel A: The clustering tree diagram indicates that specific samples (above the red line) with distinct outliers should be excluded; the remaining samples (below the red line) were utilized for subsequent analysis. Panel B: The soft threshold was set as 4. Panels C–D: Modules were determined in hierarchical clustering, of which the “yellow” module had the strongest correlation with the TRPV1 expression by Pearson correlation coefficient. Panel E: A significant positive correlation between gene significance of TRPV1 expression and module membership in the “yellow” module. Panel F: LY6G5B was the hub gene of the “yellow” module; the network was constructed in Cytoscape with the “degree” algorithm. In Cytoscape, the visualization network was constructed based on the top 100 genes (rank by the weight values) of the “yellow” module; genes not in the most extensive network are not displayed.



**Supplementary Appendix 7.** Selection ofpossible hub genes of TRPV1 in ACC. Panel A: The clustering tree diagram indicates that specific sample (above the red line) with distinct outliers should be excluded; the remaining samples (below the red line) were utilized for subsequent analysis. Panel B: The soft threshold was set as 4. Panels C–D: Modules were determined in hierarchical clustering, of which the “blue” module (except for the grey module) had the strongest correlation with the TRPV1 expression by Pearson correlation coefficient. Panel E: A significant positive correlation between gene significance of TRPV1 expression and module membership in the “blue” module. Panel F: EFR3B, TMSB15B, and EFS were the hub gene of the “blue” module; the network was constructed in Cytoscape with the “degree” algorithm. In Cytoscape, the visualization network was constructed based on the top 100 genes (rank by the weight values) of the “blue” module; genes not in the most extensive network are not displayed.

**Supplementary Appendix 8.** Correlation between *TRPV1* expression level and IC50 of drugs with a *p*-value less than 0.01.

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| --- | --- | --- |
| Drug | Spearman Correlation Coefficient | *p*-value |
| I-BET-762 | -0.461 | <0.001 |
| INCB-057643 | -0.388 | 0.003 |
| DOLASTATIN 10 | -0.364 | 0.005 |
| AEW-541 | -0.358 | 0.006 |
| ABBV-075 | -0.348 | 0.008 |
| OTX-015 | -0.335 | 0.011 |
| ADW-742 | -0.335 | 0.011 |
| Bet-BAY-002 | -0.331 | 0.012 |
| AMG-51 | -0.329 | 0.013 |
| Selumetinib | -0.328 | 0.013 |
| Defactinib | -0.328 | 0.013 |
| BMS-986158 | -0.328 | 0.013 |
| AZD-5153 | -0.315 | 0.017 |
| HPI-1 | -0.313 | 0.018 |
| GSK-2194069 | -0.304 | 0.022 |
| ARRY-162 | -0.303 | 0.022 |
| Cs-1730 | -0.303 | 0.022 |
| I-BET-151 | -0.301 | 0.023 |
| PYRAZOLOACRIDINE | 0.298 | 0.024 |
| Dabrafenib | -0.296 | 0.025 |
| Sulfatinib | -0.294 | 0.027 |
| PFI-1 | -0.290 | 0.028 |
| ABBV-744 | -0.288 | 0.030 |
| JNJ-28312141 | -0.288 | 0.030 |
| Cyclophosphamide | -0.279 | 0.036 |
| RG-7602 | -0.278 | 0.037 |
| CEP-9722 | 0.275 | 0.039 |
| ST-3595 | 0.274 | 0.039 |
| Tandutinib | -0.273 | 0.040 |
| Adavosertib | -0.269 | 0.043 |
| Ensartinib | -0.268 | 0.044 |
| CH-7057288 | -0.267 | 0.045 |
| Refametinib | -0.264 | 0.048 |
| Bafetinib | -0.263 | 0.048 |