

S10 Table. Significant pathways of TMPRSS2 and top 100 similar genes in different tumors

Tumor	Pathway	Gene	p-value	Adjusted p-value	Odds ratio	Combined score
Lung adenocarcinoma						
	Starch and sucrose metabolism	<i>AGL, GANC</i>	0.014	> 0.99	11.00	46.78
	Retrograde endocannabinoid signaling	<i>MAPK10, FAAH, MGLL</i>	0.039	> 0.99	4.01	13.01
Breast invasive carcinoma						
	Proximal tubule bicarbonate reclamation	<i>SLC9A3, ATP1B3</i>	0.006	> 0.99	17.22	88.20
	Protein digestion and absorption	<i>KCNK5, SLC9A3, ATP1B3</i>	0.011	> 0.99	6.60	29.96
	Aldosterone-regulated sodium reabsorption	<i>INSR, ATP1B3</i>	0.015	> 0.99	10.70	44.96
	Mineral absorption	<i>SLC9A3, ATP1B3</i>	0.027	> 0.99	7.77	27.93
	Ras signaling pathway	<i>KSRI, INSR, KIT, PLD1</i>	0.030	> 0.99	3.41	11.96
	Phospholipase D signaling pathway	<i>INSR, KIT, PLD1</i>	0.039	> 0.99	4.01	13.01
Colon adenocarcinoma						
	Glycosphingolipid biosynthesis	<i>B3GALT5, FUT2</i>	0.022	> 0.99	8.80	33.71
	Endocrine and other factor-regulated calcium reabsorption	<i>BDKRB2, DNM2</i>	0.025	> 0.99	8.25	30.60
	Intestinal immune network for IgA	<i>PIGR, CCL28</i>	0.025	> 0.99	8.25	30.60

production					
Caffeine metabolism	<i>XDH</i>	0.025	> 0.99	39.60	146.10
Neomycin, kanamycin and gentamicin biosynthesis	<i>HK2</i>	0.025	> 0.99	39.60	146.10
Basal cell carcinoma	<i>BMP2, FZD5</i>	0.040	> 0.99	6.29	20.17
Central carbon metabolism in cancer	<i>SIRT6, HK2</i>	0.043	> 0.99	6.09	19.21
Retinol metabolism	<i>RETSAT, DHRS9</i>	0.045	> 0.99	5.91	18.31
Prostate adenocarcinoma					
Beta-Alanine metabolism	<i>ALDH1A3, ALDH6A1, ABAT</i>	0.001	0.156	19.16	145.39
Biosynthesis of unsaturated fatty acids	<i>ELOVL7, HACD3</i>	0.008	> 0.99	14.67	70.53
Fatty acid elongation	<i>ELOVL7, HACD3</i>	0.008	0.838	14.67	70.53
Propanoate metabolism	<i>ALDH6A1, ABAT</i>	0.011	0.874	12.38	55.43
Ether lipid metabolism	<i>PLA2G12A, PAFAH2</i>	0.024	> 0.99	8.43	31.59
Valine, leucine and isoleucine degradation	<i>ALDH6A1, ABAT</i>	0.025	> 0.99	8.25	30.60
Lysine degradation	<i>SETD7, DHTKD1</i>	0.036	> 0.99	6.71	22.34
Sulfur metabolism	<i>SUOX</i>	0.045	> 0.99	22.00	68.45
Stomach adenocarcinoma					
Glycerophospholipid metabolism	<i>CDS1, PCYT1A, LPCAT3, LPIN2, AGPAT3</i>	0.000	0.041	10.21	91.13

Tight junction	<i>MAG11, OCLN, CLDN18, CGN, LLGL2</i>	0.002	0.265	5.82	37.08
Glycerolipid metabolism	<i>ALDH2, LPIN2, AGPAT3</i>	0.004	0.374	9.74	54.69
Fc gamma R-mediated phagocytosis	<i>PRKCD, PIP5K1B, DNM2</i>	0.011	0.848	6.53	29.43
Choline metabolism in cancer	<i>SLC44A4, PCYT1A, PIP5K1B</i>	0.014	0.851	6.00	25.69
Fatty acid degradation	<i>CPT2, ALDH2</i>	0.021	> 0.99	9.00	34.85
Sphingolipid metabolism	<i>SPTLC2, SGPP2</i>	0.024	> 0.99	8.43	31.59
Intestinal immune network for IgA production	<i>PIGR, TNFSF13</i>	0.025	0.943	8.25	30.60
N-Glycan biosynthesis	<i>FUT8, MGAT4B</i>	0.026	0.905	7.92	28.78
Phosphonate and phosphinate metabolism	<i>PCYT1A</i>	0.030	0.922	33.00	115.81
Phospholipase D signaling pathway	<i>PIP5K1B, AGPAT3, DNM2</i>	0.039	> 0.99	4.01	13.01
Glycolysis/Gluconeogenesis	<i>PEKL, ALDH2</i>	0.046	> 0.99	5.82	17.89
Liver hepatocellular carcinoma					
Prostate cancer	<i>SPINT1, PDGFD, TGFA, TMPRSS2</i>	0.001	0.456	8.17	53.20
Pathogenic <i>Escherichia coli</i> infection	<i>ITGB1, OCLN, CDH1</i>	0.003	0.418	10.80	63.84
Rap1 signaling pathway	<i>ITGB1, CDH1, PDGFD, CTNND1, CALM2</i>	0.004	0.404	4.81	26.62

Bacterial invasion of epithelial cells	<i>ITGB1, CDH1, ELMO3</i>	0.006	0.481	8.03	40.74
Cell adhesion molecules (CAMs)	<i>ITGB1, OCLN, SDC4, CDH1</i>	0.006	0.387	5.46	27.69
Tight junction	<i>ITGB1, OCLN, MARVELD3, CRB3</i>	0.011	0.558	4.66	21.07
Leukocyte transendothelial migration	<i>ITGB1, OCLN, CTNND1</i>	0.019	0.843	5.30	20.98
Shigellosis	<i>ITGB1, ELMO3</i>	0.043	> 0.99	6.09	19.21

TMPRSS2, transmembrane serine protease 2.