S9 Table. Significant KEGG pathways of ACE2 and top 100 similar genes in different tumors

Tumor	Pathway	Gene	p-value	Adjusted p-value	Odds ratio	Combined score
Lung adenocarcinoma						
	Phenylalanine metabolism	*MAOA, ALDH3B1*	0.003	> 0.99	23.30	133.34
	Histidine metabolism	*MAOA, ALDH3B1*	0.006	0.918	17.22	88.20
	beta-Alanine metabolism	*ALDH6A1, ALDH3B1*	0.011	> 0.99	12.78	58.00
	Propanoate metabolism	*ALDH6A1, SUCLG2*	0.011	0.874	12.38	55.43
	Tyrosine metabolism	*ASH2L*	0.014	0.876	11.00	46.78
Breast invasive carcinoma						
	Tryptophan metabolism	*AADAT, HAAO, KYNU*	0.001	0.383	14.14	94.62
	PPAR signaling pathway	*FABP6, FABP7, DBI*	0.006	0.963	8.03	40.74
	Arachidonic acid metabolism	*GGT1, ALOX15B*	0.040	> 0.99	6.29	20.17
Colon adenocarcinoma						
	Vitamin digestion and absorption	*SLC5A6, SCARB1, SLC23A1, SLC19A3*	<0.001	0.002	33.00	396.70
	Sulfur relay system	*NFS1, MOCS3*	0.001	0.107	49.50	360.11
	Fat digestion and absorption	*SCARB1, PLA2G12B, DGAT2*	0.001	0.119	14.49	97.95
	Renin-angiotensin system	*ACE2, AGT*	0.006	0.459	17.22	88.20
	Progesterone-mediated oocyte maturation	*RPS6KA3, RPS6KA6, AURKA*	0.014	0.851	6.00	25.69

Insulin resistance	*RPS6KA3, RPS6KA6, AGT*	0.017	0.894	5.50	22.28
Bladder cancer	*SRC, MYC*	0.018	0.802	9.66	38.69
Proteasome	*ADRM1, PSMA7*	0.022	0.836	8.80	33.71
Oocyte meiosis	*RPS6KA3, RPS6KA6, AURKA*	0.026	0.873	4.75	17.44
Cholesterol metabolism	*SCARB1, VAPB*	0.026	0.814	7.92	28.78
Central carbon metabolism in cancer	*PDHA1, MYC*	0.043	> 0.99	6.09	19.21
Cortisol synthesis and secretion	*SCARB1, AGT*	0.043	> 0.99	6.09	19.21
Acute myeloid leukemia	*CEBPA, MYC*	0.044	> 0.99	6.00	18.75
Long-term potentiation	*RPS6KA3, RPS6KA6*	0.045	0.993	5.91	18.31
Prostate adenocarcinoma					
Steroid hormone biosynthesis	*UGT1A1, AKR1C3, UGT1A6*	0.003	> 0.99	9.90	56.07
Ascorbate and aldarate metabolism	*UGT1A1, UGT1A6*	0.008	> 0.99	14.67	70.53
Pentose and glucuronate interconversions	*UGT1A1, UGT1A6*	0.013	> 0.99	11.65	50.81
Porphyrin and chlorophyll metabolism	*UGT1A1, UGT1A6*	0.019	> 0.99	9.43	37.34
Glycerolipid metabolism	*DGAT2, GK*	0.038	> 0.99	6.49	21.21
Arachidonic acid metabolism	*PLA2G16, AKR1C3*	0.040	> 0.99	6.29	20.17
Retinol metabolism	*UGT1A1, UGT1A6*	0.045	> 0.99	5.91	18.31
Stomach adenocarcinoma					
Fat digestion and absorption	*FABP1, MTTP, APOA4*	0.001	0.337	14.78	100.78
Vitamin digestion and absorption	*RBP2, APOA4*	0.006	0.960	16.84	85.48

Liver hepatocellular carcinoma					
Renin-angiotensin system	*ACE2, MME*	0.006	> 0.99	17.22	88.20
Amphetamine addiction	*MAOB, CAMK2A*	0.046	> 0.99	5.82	17.89

ACE2, angiotensin-converting enzyme 2; KEGG, Kyoto Encyclopedia of Genes and Genomes.