

Table S4. Validation for the difference in gene expression level between normal and tumor tissues in the USA1 cohort

Gene symbol	Gene title	Fold change <sup>a</sup>	Adjusted P-value <sup>b</sup>
<i>ANO1</i>	anoctamin 1, calcium activated chloride channel	0.92	7.3E-01
<i>CACNA1C</i>	calcium channel, voltage-dependent, L type, alpha 1C subunit	1.01	4.6E-01
<i>CACNA1D</i>	calcium channel, voltage-dependent, L type, alpha 1D subunit	0.57	7.3E-03
<i>CACNA2D2</i>	calcium channel, voltage-dependent, alpha 2/delta subunit 2	0.08	9.2E-11
<i>CACNB3</i>	calcium channel, voltage-dependent, beta 3 subunit	1.64	5.5E-04
<i>CLCC1</i>	chloride channel CLIC-like 1	1.16	3.8E-01
<i>CLCN3</i>	chloride channel, voltage-sensitive 3	1.37	4.8E-03
<i>CLCN7</i>	chloride channel, voltage-sensitive 7	1.41	6.4E-05
<i>CLIC3</i>	chloride intracellular channel 3	0.08	2.9E-12
<i>CLIC4</i>	chloride intracellular channel 4	0.62	1.8E-05
<i>CLIC5</i>	chloride intracellular channel 5	0.05	6.2E-13
<i>KCNAB1</i>	potassium voltage-gated channel, shaker-related subfamily, beta member 1	0.37	3.6E-07
<i>KCNAB2</i>	potassium voltage-gated channel, shaker-related subfamily, beta member 2	0.49	2.9E-07
<i>KCNJ2</i>	potassium inwardly-rectifying channel, subfamily J, member 2	0.55	6.5E-03
<i>KCNJ8</i>	potassium inwardly-rectifying channel, subfamily J, member 8	0.43	4.5E-11
<i>KCNK1</i>	potassium channel, subfamily K, member 1	5.29	4.2E-08
<i>KCNK3</i>	potassium channel, subfamily K, member 3	0.03	1.2E-20
<i>KCNK5</i>	potassium channel, subfamily K, member 5	2.12	2.9E-04
<i>KCNMB4</i>	potassium large conductance calcium-activated channel, subfamily M, beta member 4	1.00	9.7E-01
<i>KCNQ3</i>	potassium voltage-gated channel, KQT-like subfamily, member 3	1.06	1.4E-01
<i>MCOLN1</i>	mucolipin 1	0.45	1.8E-05
<i>MCOLN3</i>	mucolipin 3	0.78	9.4E-02
<i>PKD1</i>	polycystic kidney disease 1 (autosomal dominant)	0.59	2.2E-06
<i>PKD2</i>	polycystic kidney disease 2 (autosomal dominant)	0.76	3.4E-03
<i>SCN7A</i>	sodium channel, voltage-gated, type VII, alpha subunit	0.81	5.5E-02
<i>SCNN1B</i>	sodium channel, non-voltage-gated 1, beta subunit	0.26	3.0E-06
<i>SCNN1G</i>	sodium channel, non-voltage-gated 1, gamma subunit	1.00	3.8E-01
<i>TPCN1</i>	two pore segment channel 1	1.05	4.7E-01
<i>TRPC1</i>	transient receptor potential cation channel, subfamily C, member 1	0.64	4.7E-03
<i>TRPC6</i>	transient receptor potential cation channel, subfamily C, member 6	0.63	2.8E-02
<i>TRPM2</i>	transient receptor potential cation channel, subfamily M, member 2	1.06	1.2E-01
<i>TRPV2</i>	transient receptor potential cation channel, subfamily V, member 2	0.27	5.4E-12
<i>VDAC1</i>	voltage-dependent anion channel 1	1.54	2.8E-05

<sup>a</sup> Fold change is calculated by dividing the expression of tumor tissue by the expression of normal tissue.

<sup>b</sup> P-value is calculated by paired t-test and adjusted by Benjamini & Hochberg correction.