

Table S9. Validation for the difference in gene expression level between adenocarcinoma and squamous-cell carcinoma in the USA2 and KOR cohorts

Gene symbol	USA2		KOR	
	Fold change <sup>a</sup>	Adjusted P-value <sup>b</sup>	Fold change <sup>a</sup>	Adjusted P-value <sup>b</sup>
<i>CACNA1D</i>	1.83	1.4E-07	1.62	6.7E-06
<i>CACNA2D1</i>	0.49	4.3E-05	0.35	2.0E-06
<i>CACNA2D2</i>	1.37	1.5E-01	4.31	2.1E-05
<i>CACNB3</i>	1.50	6.2E-05	1.31	4.1E-03
<i>CLCC1</i>	1.14	4.2E-02	1.27	7.7E-04
<i>CLCN7</i>	1.25	8.4E-03	1.47	7.7E-10
<i>CLIC1</i>	1.10	2.6E-01	1.26	7.7E-04
<i>CLIC4</i>	0.95	5.7E-01	0.90	7.6E-02
<i>CLIC5</i>	1.07	1.7E-02	2.00	1.3E-05
<i>CLIC6</i>	3.10	7.6E-04	7.30	2.2E-08
<i>GLRB</i>	1.27	1.4E-02	2.31	8.8E-09
<i>KCNJ2</i>	0.63	5.6E-03	0.39	2.4E-07
<i>KCNJ8</i>	1.32	2.6E-02	0.79	7.2E-01
<i>KCNK1</i>	0.83	3.2E-01	0.78	8.8E-02
<i>KCNK17</i>	1.19	1.4E-02	2.04	1.9E-02
<i>KCNK5</i>	3.26	5.0E-12	11.52	6.4E-21
<i>KCNQ3</i>	1.55	4.3E-06	2.20	2.1E-07
<i>MCOLN3</i>	0.72	5.9E-02	0.77	7.4E-02
<i>P2RX4</i>	1.27	3.4E-02	1.85	2.9E-08
<i>SCN7A</i>	1.56	2.7E-03	2.29	1.0E-06
<i>SCNN1A</i>	1.97	9.6E-05	1.78	5.6E-04
<i>SCNN1B</i>	1.71	1.4E-02	4.19	9.3E-10
<i>SCNN1G</i>	1.25	1.7E-01	1.84	7.7E-04
<i>TPCN1</i>	1.55	5.9E-08	1.78	2.1E-13
<i>TRPC6</i>	1.98	4.3E-05	1.32	7.5E-02
<i>TRPM7</i>	0.87	4.9E-02	0.75	1.0E-06
<i>TRPV2</i>	1.26	7.0E-03	1.08	1.4E-01
<i>VDAC1</i>	0.82	2.2E-02	0.87	6.5E-03
<i>VDAC2</i>	0.62	2.1E-04	0.51	3.6E-11
<i>VDAC3</i>	0.76	2.0E-03	0.68	1.2E-04

<sup>a</sup> Fold change is calculated by dividing the expression in adenocarcinoma by the expression in squamous-cell carcinoma.

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