

**Supplementary Table 1.** Correlation between HR survival curves between Microarray based versus RNA-seq based analysis.

Gene	Connexin	HR Array LUSC	HR RNA- seq LUSC	Dis- Cordance	HR Array LUAD	HR RNA- seq LUAD	Dis- Cordance
GJA1	Cx43	0,78	0.85		0,64	1.34	**
GJA3	Cx46	0,77	0.75		1,48	1.2	
GJA4	Cx37	0,83	1.43	*	0,67	1.28	**
GJA5	Cx40	1,20	1.58		1,86	0.7	**
GJA8	Cx50	1,16	0.73	*	0,60	0.8	
GJA10	Cx62	0,77	0.73		1,62	1.57	
GJB1	Cx32	1,38	1.38		0,60	0.79	
GJB3	CX31	1,27	1.24		2,39	1.94	
GJB4	Cx30.3	1,18	0.84	*	1,88	1.59	
GJB5	Cx31.1	1,12	0.77	*	1,63	1.49	
GJB6	Cx30	0,75	0.77		0,82	1.35	*
GJB2	Cx26	0,87	0.7		2,12	2.09	
GJC1	Cx45	1,22	0.78	*	0,66	1.41	**
GJC2	Cx47	0,81	1.34	*	1,45	0.7	**
GJC3	Cx30.2	0,78	1.34	*	1,76	1.43	
GJD2	Cx36	1,14	1.46		2,13	0.82	**
GJD3	Cx31.9	0,66	1.49	***	1,26	1.23	
GJD4	Cx40.1	0,83	0.86		1,49	0.8	**

<sup>1</sup> Abbreviations: HR; hazard ratio, LUSC; squamous cell lung cancer, LUAD; Adeno Carcinoma lung cancer, <sup>2</sup> The table depicts the patient hazard ratio, where the cohort expressing high levels of connexin mRNA is either associated with better survival (depicted in green, HR less than 1, i.e., less chance of death) or with worse survival (red, HR greater than 1, i.e., higher chance of death). Those associations that have a significant statistical difference ( $p < 0.01$ ) are shown in bold. Correlation between HR survival curves between Microarray based versus RNA-seq based analysis. Samples in bold show significant statistical significance ( $P < 0.01$ ). One star suggest discordance in cohorts that don't reach statistical significance on their own; two stars suggests discordance where either the microarray or the RNA-seq cohort have reported statistical significance; and three stars denotes situations where both the microarray and RNA-seq analysis cohort reported the finding as significant.