Table S1 Patient demographics and tumour characteristics. Lung tumour tissues and matched sera were collected from NSCLC patients and stratified into adenocarcinoma or squamous cell carcinoma. Patient demographics and tumour characteristics are represented

Histology	Gender	Age	Smoking	Grade	TMN	Stage
ADC						
1	F	56	Ex	2	pT2aN0	IB
2	F	75	Ex	3	pT4N2M1a	IV
3	F	80	Ex	3	pT1b N0Mx	IA
4	F	57	Current	2	pT1aN0Mx	IA
5	F	75	Current	3	pT1aN1	IIA
6	F	71	Ex	2	pT1bN0	IA
7	M	68	Current	1	pT2aN0	IB
8	F	77	Current	3	pT1bN0	IA
9	M	73	Ex	2	pT1bN0	IA
10	F	78	Ex	2	pT2aN0	IB
SqCC						
1	F	69	Current	2	pT2aN0	IB
2	M	74	Current	2	pT2aN0	IB
3	F	61	Current	2	pT2aN1Mx	IIA
4	M	67	Current	3	pT2aN0	IB
5	F	80	Ex	1	pT3N0	IIB
6	F	64	Current	2	pT1aN0Mx	IA
7	F	58	Current	3	pT1bN1	IIA
8	M	81	Ex	2	pT2aN1Mx	IIA
9	F	71	Ex	2	pT2bN0	IIA
10	F	67	Ex	3	pT2aN1Mx	IIA

Table S2 TCGA analysis of miRNAs in different NSCLC histologies. TCGA data sets were used to examine miRNA expression (miR-30a-3p, miR-30b-5p, miR-30c-5p, miR-34a-5p, miR-4286) in matched normal and tumour lung tissues from adenocarcinoma (normal, n=44; tumour, n=447) and squamous cell carcinoma (normal, n=44; tumour, n=336 patients

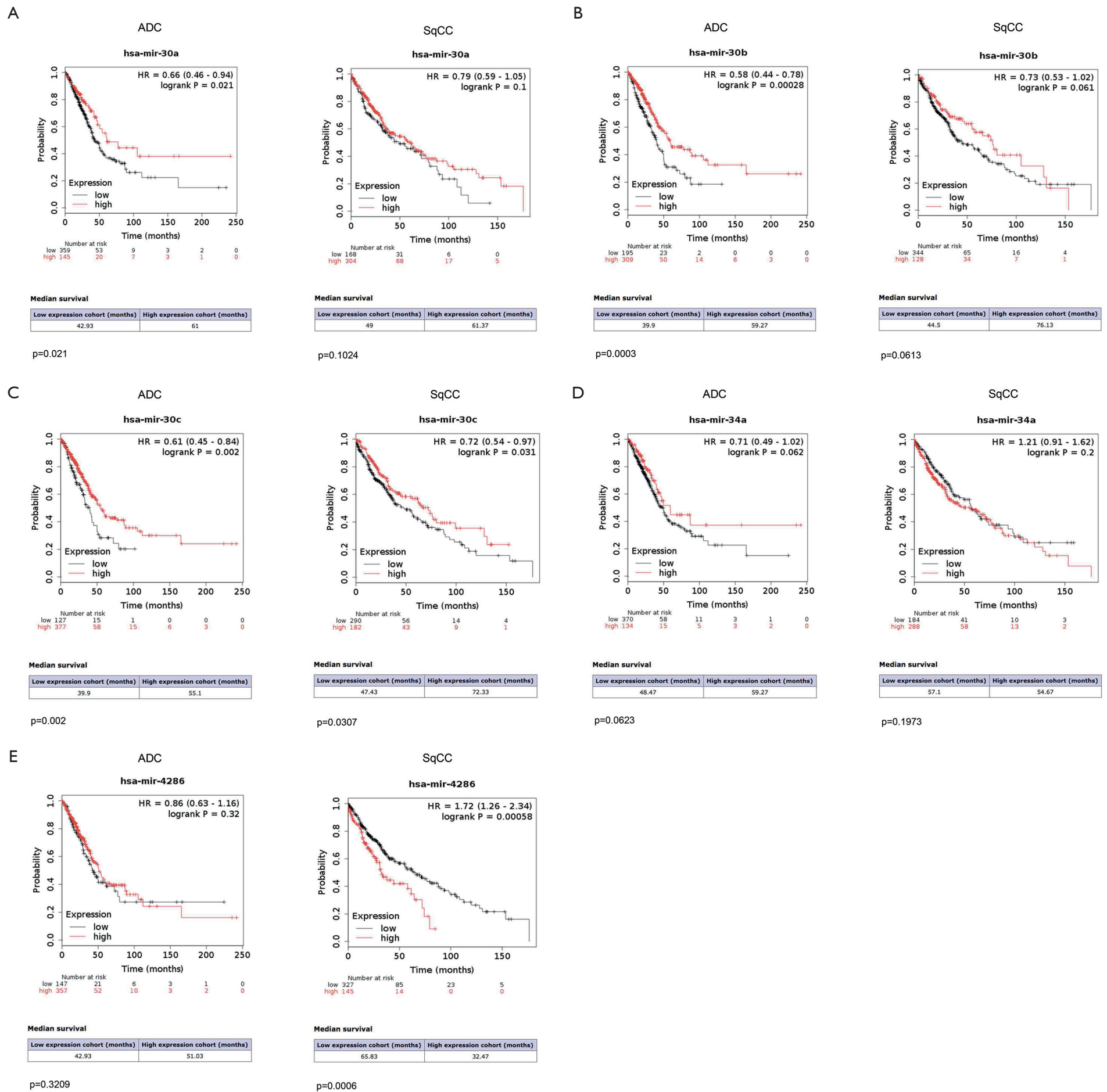| MicroRNA	Expression	ADC	Expression	SqCC
hsa-miR-30a-3p	Down	6.88338275267597e-15	Down	<1e-12
hsa-miR-30b-5p	Unchanged	4.131800e-01	Down	2.97469826548991e-11
hsa-miR-30c-5p	Down	3.783700e-03	Down	2.11869999988679e-07
hsa-miR-34a-5p	Up	1.62447832963153e-12	Down	2.15510000000085e-05
hsa-miR-4286	Unchanged	1.129550e-01	Unchanged	3.266600e-01

Figure S1 *In silico* analysis of lung tumour tissue miRNAs and survival. miRNA expression and survival data from a meta-analysis of lung ADC (n=513) and SqCC (n=478) patient tissues were examined using a validated pan-Cancer miRNA Kaplan Meier Plotter. Each miRNA (A-E) was stratified as high (red) or low (black) expression and examined across the main NSCLC histological subtypes, ADC and SqCC. Data are presented as a time-to-event analysis. Median survival is presented in months. Statistical analysis was performed by Cox-Regression using online software via the validated pan-Cancer miRNA Kaplan-Meier Plotter to produce a Hazard Ratio (HR) with 95% confidence intervals (CI), a HR less than or greater than 1 with CI that do not include 1 were considered significant. Log rank regression was also carried out to determine significance, P<0.05 was considered significant.

Table S3 *In silico* meta-analysis of the top 10 miR-4286 target genes associated with cancer proliferation for altered expression in LUSC, as determined using Lung Cancer Explorer

| Symbol	Expression Change	SMD	SMD lower	SMD upper	pv	p.adj
PARVG	Down	−2.25	−3.38	−1.11	1e-04	0.00029
PHF1	Down	−1.07	−1.38	−0.76	2.3e-11	2×10^{-10}
APLN	Down	−0.94	−1.44	−0.45	2e-04	0.00052
CBX2	Up	1.94	1.39	2.48	3.9e-12	3.7×10^{-11}
PRX	Down	−2.58	−3.7	−1.46	6.3e-06	2.2×10^{-05}
FOXO4	Down	−1.24	−1.71	−0.77	2.2e-07	1×10^{-06}
CCR7	Unchanged	−0.07	−0.41	0.26	0.67	0.73
STAC	Down	−2.24	−3	−1.48	6.5e-09	3.8×10^{-08}
ZNF23	Trending Down	−0.76	−1.1	−0.42	9.9e-06	3.4×10^{-05}
WLS	Down	−0.81	−1.17	−0.44	1.4e-05	4.7×10^{-05}
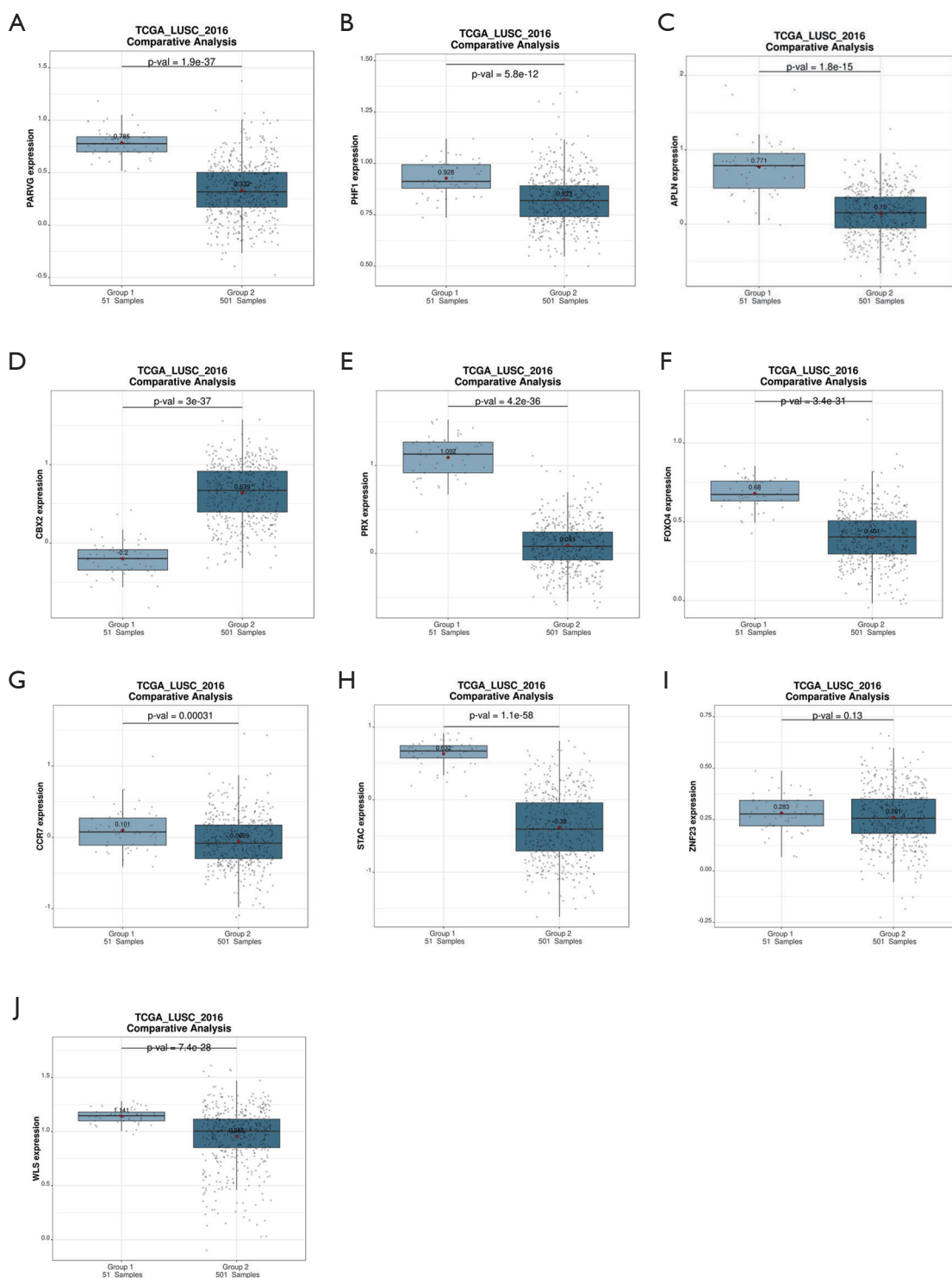
Figure S2 Altered expression of miR-4286 target genes. Following the identification of potential miR-4286 gene targets using TargetScan, the expression of the top 10 candidate genes associated with cellular proliferation were examined for changes in expression in the TCGA-LUSC (SqCC) dataset. The results are shown as follows: (A) PARVG, (B) PHF4, (C) APLN, (D) CBX2, (E) PRX, (F) FOXO4, (G) CCR7, (H) STAC, (I) ZNF23, (J) WLS.

Table S4 *In silico* meta-analysis of the top 10 miR-4286 target genes associated with cancer proliferation for survival associations in LUSC, as determined using Lung Cancer Explorer

Gene symbol	HR	Z	P	P.adj
PARVG	0.91	−1.4	0.16	0.76
PHF1	0.95	−1.04	0.3	0.85
APLN	1.08	1.4	0.16	0.76
CBX2	1.04	0.6	0.55	0.93
PRX	0.99	−0.26	0.79	0.98
FOXO4	0.97	−0.74	0.46	0.9
CCR7	0.9	−2.3	0.022	0.43
STAC	0.96	−1	0.32	0.86
ZNF23	1.01	0.24	0.81	0.98
WLS	0.98	−0.37	0.71	0.96