

**Supplementary Table S1.** Survival associated 33 features selected by log-rank test.

<b>Number</b>	<b>Feature</b>	<b>Likelihood ratio test</b>	<b>Wald test</b>	<b>Log-rank test</b>
1	Feature 1	$p = 0.009$	$p = 0.009$	$p = 0.009$
2	Feature 4	$p = 0.02$	$p = 0.02$	$p = 0.02$
3	Feature 6	$p = 0.01$	$p = 0.01$	$p = 0.01$
4	Feature 7	$p = 0.04$	$p = 0.04$	$p = 0.04$
5	Feature 15	$p = 0.008$	$p = 0.007$	$p = 0.007$
6	Feature 21	$p = 0.05$	$p = 0.05$	$p = 0.05$
7	Feature 23	$p = 0.03$	$p = 0.03$	$p = 0.03$
8	Feature 27	$p = 0.02$	$p = 0.02$	$p = 0.02$
9	Feature 28	$p = 0.02$	$p = 0.02$	$p = 0.02$
10	Feature 33	$p = 0.009$	$p = 0.009$	$p = 0.009$
11	Feature 36	$p = 0.009$	$p = 0.008$	$p = 0.008$
12	Feature 37	$p = 0.009$	$p = 0.01$	$p = 0.01$
13	Feature 38	$p = 1e-04$	$p = 1e-04$	$p = 1e-04$
14	Feature 44	$p = 0.01$	$p = 0.01$	$p = 0.01$
15	Feature 46	$p = 0.01$	$p = 0.01$	$p = 0.01$
16	Feature 48	$p = 0.02$	$p = 0.02$	$p = 0.02$
17	Feature 51	$p = 0.02$	$p = 0.02$	$p = 0.02$
18	Feature 58	$p = 0.005$	$p = 0.005$	$p = 0.005$
19	Feature 59	$p = 0.005$	$p = 0.005$	$p = 0.005$
20	Feature 61	$p = 0.02$	$p = 0.02$	$p = 0.02$
21	Feature 62	$p = 0.007$	$p = 0.007$	$p = 0.007$
22	Feature 65	$p = 0.007$	$p = 0.007$	$p = 0.007$
23	Feature 67	$p = 0.05$	$p = 0.05$	$p = 0.05$
24	Feature 71	$p = 0.003$	$p = 0.003$	$p = 0.003$
25	Feature 72	$p = 0.008$	$p = 0.007$	$p = 0.007$
26	Feature 73	$p = 0.05$	$p = 0.05$	$p = 0.05$
27	Feature 74	$p = 0.01$	$p = 0.01$	$p = 0.01$
28	Feature 79	$p = 3e-04$	$p = 3e-04$	$p = 3e-04$
29	Feature 82	$p = 0.04$	$p = 0.04$	$p = 0.04$
30	Feature 84	$p = 4e-05$	$p = 5e-05$	$p = 5e-05$
31	Feature 87	$p = 0.04$	$p = 0.04$	$p = 0.04$
32	Feature 92	$p = 0.005$	$p = 0.005$	$p = 0.005$
33	Feature 100	$p = 0.04$	$p = 0.04$	$p = 0.04$

**Supplementary Table S2.** ANOVA ranked miRNA and genes (top 20 and 30, respectively) used for SVM.

<b>Number</b>	<b>miRNA</b>	<b>Gene</b>
1	miR-21	<i>SFTPB</i>
2	miR-375	<i>ADAM6</i>
3	miR-143	<i>H19</i>
4	miR-10a	<i>LYZ</i>
5	miR-99b	<i>FTL</i>
6	miR-10b	<i>FN1</i>
7	miR-148a	<i>MUC5B</i>
8	miR-22	<i>SFTPA2</i>
9	Let-7b	<i>S100A9</i>
10	miR-30a	<i>CD74</i>
11	miR-182	<i>CPM</i>
12	miR-183	<i>LOC96610</i>
13	miR-92a-2	<i>IGF2</i>
14	miR-203a	<i>ACTB</i>
15	miR-29a	<i>GAPDH</i>
16	miR-200c	<i>TMSB4XP8</i>
17	Let-7a-2	<i>ALDH1A1</i>
18	miR-100	<i>SLC34A2</i>
19	miR-103a-1	<i>ERBB2</i>
20	miR-30d	<i>FTH1</i>
21	NA	<i>KRT18</i>
22	NA	<i>TPT1</i>
23	NA	<i>COL3A1</i>
24	NA	<i>COL1A1</i>
25	NA	<i>ACTG1</i>
26	NA	<i>KRT8</i>
27	NA	<i>EEF1A1</i>
28	NA	<i>B2M</i>
29	NA	<i>RPL3</i>
30	NA	<i>ENO1</i>

**Supplementary Computer Code.** Keras code we implemented an autoencoder algorithm.

```
inp = Input(shape=(13767,))

encoded = Dense(500, activation='tanh',
               kernel_regularizer=regularizers.l2(10e-3),
               activity_regularizer=regularizers.l1(10e-4))(inp)

encoded = Dropout(0.5)(encoded)
encoded = Dense(100, activation='tanh',
               kernel_regularizer=regularizers.l2(10e-3),
               activity_regularizer=regularizers.l1(10e-4))(encoded)

encoded = Dropout(0.5)(encoded)
decoded = Dense(500, activation='tanh')(encoded)
decoded = Dense(13767, activation='tanh')(decoded)

autoencoder = Model(inp, decoded)
sgd = optimizers.SGD(lr=0.01, decay=1e-6, momentum=0.9, nesterov=True)
autoencoder.compile(optimizer='sgd',
                   loss='mean_squared_error',
                   metrics=['accuracy'])

history = autoencoder.fit(X, X,
                        epochs=150,
                        batch_size=1)
```