**SupplementARY figures and tables**

**Validation of the 12-gene predictive signature for Adjuvant Chemotherapy Response in Lung Cancer**

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**Supplementary Table S1**. Summary of Tables and Figures.

|  |  |
| --- | --- |
| Summary of results | |
| Patient cohorts | Table 1. Patient characteristics for the three cohorts.  Suppl. Table S2. Propensity score matching methods  Suppl. Table S3. Propensity score matching results. |
| Assay development | Fig. 1. Assay development and validation flowchart. |
| Suppl. Fig. S1. Determining the cutoff value in risk scores.  Suppl. Table S4. Quality control measures for assay development |
| Prognostic performances | Supp. Fig. S2. Recurrence-free survival curves of high- and low-risk groups for 258 NSCLC patients (pv=0.0114). |
| Fig. 2 (A). Recurrence-free survival curves of high- and low-risk groups for 166 ADC patients (pv=1.25E-5). |
| Fig. 2 (B). Recurrence-free survival curves of high- and low-risk groups for 147 stage I ADC patients (pv=0.000161). |
| Supp. Fig. 2 (A). Time-dependent ROC curve for 166 ADC patients (AUC=0.75). |
| Supp. Fig. 2 (B). Time-dependent ROC curve for 147 stage I ADC patients (AUC=0.74). |
| Table 2. Multivariate analysis for recurrence-free survival prognostic performance in ADC patients. |
| Fig. 2(D). Recurrence-free survival curves in predicted high- and low-risk groups for 90 SCC patients (pv=0.841). |
| Supp. Table S5. Multivariate analysis for recurrence-free survival prognostic performance in stage I ADC patients. |
| Predictive performances | Fig. 3 (A & B) Recurrence-free survival curves in predicted ACT benefit and non-benefit groups. |
| Fig. 3 (C & D) Multivariate survival analysis in predicted ACT benefit and non-benefit groups. |
| Table 3. Multivariate analysis for interaction between predicted groups and ACT. |

**Supplementary Table S2**. Propensity score-matched coefficients for each variable using logistic regression.

|  |  |  |
| --- | --- | --- |
|  | Odds ratio | p value |
| Histology  Other vs. ADC | 1.8E-7 | 0.98 |
| SCC vs. ADC | 0.76 | 0.46 |
| Smoking (Yes vs. No) | 0.79 | 0.66 |
| Age (Year) | 0.93 | 3.66E-04 |
| Gender (M vs. F) | 0.99 | 0.98 |
| Size (>=4cm vs. < 4cm) | 3.22 | 2.50E-03 |
| Stage (II vs. I) | 9.03 | 5.47E-09 |

**Supplementary Table S3. Propensity score matching results.** In the matched patient cohort, there are 138 patients without ACT treatment and 69 patients with ACT. The matching ratio is 2:1, and the variables (Histology, Smoking status, Gender, Tumor stage, Tumor Size and Age at the diagnosis) listed in Supplementary Table S2 were used to estimate the propensity scores.

|  |  |  |
| --- | --- | --- |
|  | Without ACT | ACT |
| All | 258 | 69 |
| Matched | 138 | 69 |
| Unmatched | 120 | 0 |

**Supplementary Table 4. T**he numbers of patients with and without ACT by stage after propensity score matching in ADC and SCC patient groups.

|  |  |  |
| --- | --- | --- |
| ADC | Without ACT | With ACT |
| Stage 1 | 77 | 16 |
| Stage 2 | 19 | 26 |

|  |  |  |
| --- | --- | --- |
| SCC | Without ACT | With ACT |
| Stage 1 | 23 | 5 |
| Stage 2 | 19 | 22 |

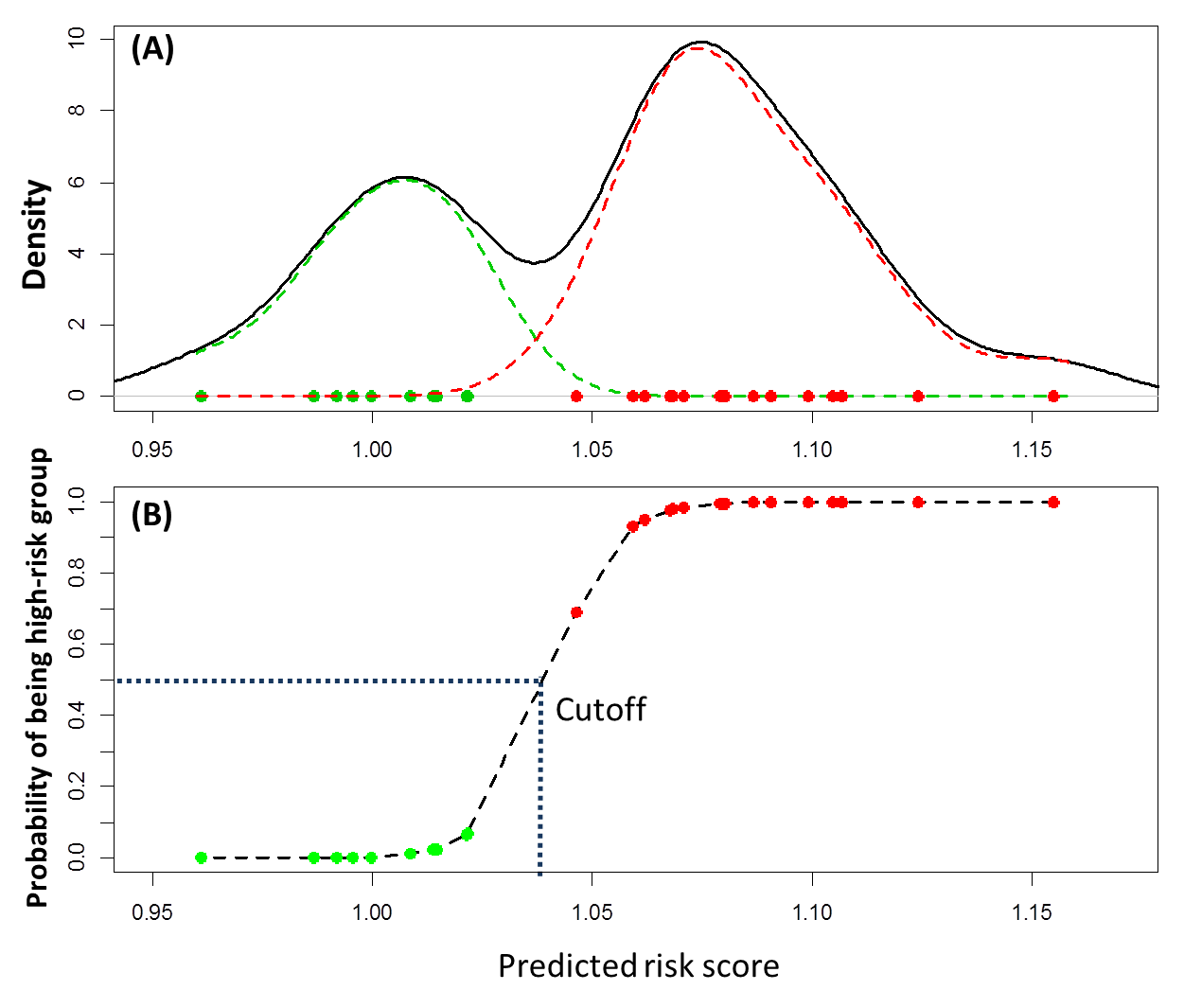
**Supplementary Table S5.** The dynamic range and correlation between expression levels measured in 30 pairs of FFPE and frozen samples of each gene measured by the nCounter gene expression assay.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene Name | Avg Count | Min Count | Max Count | Pearson correlation coefficient |
| ATP8A1 | 695.02 | 24.12 | 4510.31 | 0.62 |
| AURKA | 219.8 | 33.17 | 666.85 | 0.51 |
| C1orf116 | 1279.98 | 45.42 | 7383.24 | 0.65 |
| COL4A3 | 63.56 | 1.12 | 457.18 | 0.52 |
| DOCK9 | 1094.98 | 237.71 | 3107.84 | 0.51 |
| HOPX | 8123.28 | 210.43 | 52256.67 | 0.73 |
| HSD17B6 | 213.1 | 8.32 | 2250.06 | 0.62 |
| IFT57 | 1459.41 | 261.62 | 8044.46 | 0.78 |
| MBIP | 1570.23 | 244.83 | 7832.9 | 0.77 |
| NKX2-1 | 1010.64 | 3.09 | 9669.5 | 0.76 |
| RRM2 | 1240.19 | 146.34 | 4103.03 | 0.68 |
| TTC37 | 995.05 | 261.62 | 1862.19 | 0.80 |

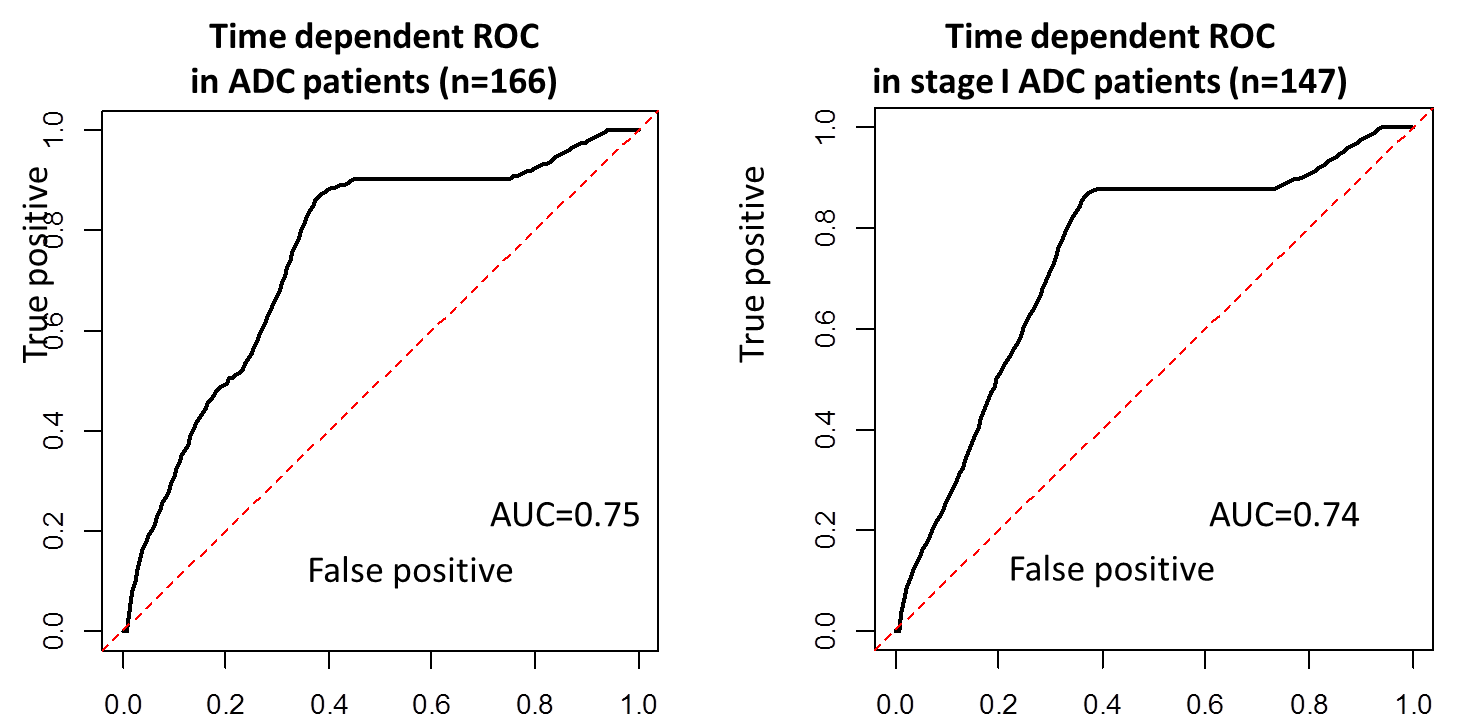
**Supplementary Table S6.** Multivariate analysis for validating the prognostic performance of the 12-gene signature measured from FFPE samples after adjusting for other patient characteristics in the 147 stage I ADC patients without ACT.

|  |  |  |
| --- | --- | --- |
|  | HR | p-value |
| Smoking status (Yes vs. No) | 2.06 (0.47, 8.99) | 0.34 |
| Age (Year) | 1.03 (0.98, 1.08) | 0.21 |
| Gender (M vs. F) | 3.08 (1.30, 7.28) | 0.011 |
| Size (>=4cm vs. < 4cm) | 1.92 (0.41, 9.03) | 0.41 |
| Group (High risk vs. Low risk) | 3.23 (1.26, 8.30) | 0.015 |

**Supplementary Figure S1**. Determining the cutoff value of pre-defined risk scores for predicted high-risk and low-risk groups using the assay development cohort. (A) Density plot of the predicted risk score in the assay development cohort (solid black line). The predicted risk scores were fitted with a mixture of two normal distributions using a model-based clustering algorithm. One normal distribution corresponds to the low-risk group (dashed green line), and the other corresponds to the high-risk group (dashed green line). In the figure, each dot represents a patient, and the axis is the predicted risk score for each patient in the assay development cohort. The green dots are the patients in the predicted low-risk group and the red dots are patients in the predicted high-risk group. The risk groups are defined using a model-based clustering method. (B) The predicted risk score of a patient vs. the probability that the patient is in the predicted high-risk group. The functional relationship was determined by the model-based clustering result. The patients whose probabilities of being in the high-risk group were greater than 0.5 are defined as the predicted high-risk group (presented as red dots), and the predicted low-risk group (green dots) otherwise. The corresponding risk score cutoff value is 1.035.



**Supplementary Figure S2**. (C) Time-dependent ROC curves in (A) ADC patients and (B) stage I ADC patients.



**Supplementary Figure S3**. The ROC curve for the predictive analysis. The ROC curve was estimated based on the R package tsm (Huang et. al. Biometrics 2012). The AUC for the predictive performance is 0.806 and the 95% confidence interval is (0.694, 0.865).

