**Prognostic values, ceRNA network, and immune regulation function of SDPR in *KRAS*-mutant lung cancer**

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**Tables**

**Table 1. Impact of SDPR expression and clinic pathologic characteristics in lung adenocarcinoma.**

a. SDPR expression associations with overall survival in *KRAS*-mutant patients (GSE72094) using Cox regression.

|  |  |  |  |
| --- | --- | --- | --- |
| **Clinicopathologic variable a** | **HR** | **95% CI** | **p value** |
| **SDPR Expression (Low vs High)** | **0.55** | **0.31-0.98** | **0.04** |

b. Multivariate survival model in *KRAS*-mutant patients (GSE72094) using Cox regression.

|  |  |  |  |
| --- | --- | --- | --- |
| **Clinicopathologic variable b** | **HR** | **95% CI** | **p value** |
| **SDPR Expression (Low vs High)** | **0.53** | **0.29-0.96** | **0.04** |
| **Gender** | **0.77** | **0.41-1.45** | **0.42** |
| **Smoking** | **0.75** | **0.37-1.51** | **0.42** |
| **Pathological Stage (I VS II-IV)** | **2.05** | **1.13-3.70** | **0.02** |

c. Impaction of SDPR and clinicopathologic characteristics on overall survival.



d. SDPR expression associations with overall survival in lung cancer patients (GSE72094) using Cox regression.

|  |  |  |  |
| --- | --- | --- | --- |
| **Clinicopathologic variable a** | **HR** | **95% CI** | **p value** |
| **SDPR Expression (Low vs High)** | **0.44** | **0.30-0.64** | **<0.001** |

e. Multivariate survival model using Cox regression.

|  |  |  |  |
| --- | --- | --- | --- |
| **Clinicopathologic variable b** | **HR** | **95% CI** | **p value** |
| **SDPR Expression (Low vs High)** | **0.47** | **0.32-0.70** | **<0.001** |
| **Gender** | **0.55** | **0.38-0.82** | **<0.001** |
| **Smoking** | **0.78** | **0.503-1.21** | **0.26** |
| **Pathological Stage** |  |  | **<0.001** |
| **Stage I** | **0.75** | **0.16-3.54** | **0.71** |
| **Stage II** | **0.25** | **0.12-0.54** | **<0.001** |
| **Stage III** | **0.48** | **0.21-1.07** | **0.07** |
| **Stage IV** | **0.82** | **0.37-1.83** | **0.63** |

f. Impaction of SDPR and clinicopathologic characteristics on overall survival.



**Table 2. Correlation between SDPR expression and immune infiltration in lung adenocarcinoma.** Significant correlation between immune cell subgroups and SDPR expression were shown in Table 3 based on TIMER, CIBERSORT, quanTIseq, xCell, MCP-counter and EPIC algorithms. Positive correlation was marked in green, while negative correlation was marked in red. P< 0.01 were marked as 0.00.

**Table 2.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Infiltrates** | **rho** | **p** | **adj.p** |
| B cell memory\_CIBERSORT | 0.14 | 0.00 | 0.00 |
| B cell memory\_CIBERSORT-ABS | 0.18 | 0.00 | 0.00 |
| B cell plasma\_XCELL | -0.21 | 0.00 | 0.00 |
| B cell\_EPIC | 0.10 | 0.03 | 0.07 |
| B cell\_MCPCOUNTER | 0.15 | 0.00 | 0.00 |
| B cell\_QUANTISEQ | 0.12 | 0.01 | 0.02 |
| Cancer associated fibroblast\_EPIC | -0.09 | 0.04 | 0.10 |
| Cancer associated fibroblast\_XCELL | 0.36 | 0.00 | 0.00 |
| Common lymphoid progenitor\_XCELL | -0.21 | 0.00 | 0.00 |
| Common myeloid progenitor\_XCELL | 0.17 | 0.00 | 0.00 |
| Endothelial cell\_EPIC | 0.51 | 0.00 | 0.00 |
| Endothelial cell\_MCPCOUNTER | 0.61 | 0.00 | 0.00 |
| Endothelial cell\_XCELL | 0.47 | 0.00 | 0.00 |
| Eosinophil\_XCELL | 0.15 | 0.00 | 0.00 |
| Granulocyte-monocyte progenitor\_XCELL | 0.39 | 0.00 | 0.00 |
| Hematopoietic stem cell\_XCELL | 0.62 | 0.00 | 0.00 |
| Macrophage M0\_CIBERSORT | -0.33 | 0.00 | 0.00 |
| Macrophage M0\_CIBERSORT-ABS | -0.22 | 0.00 | 0.00 |
| Macrophage M1\_CIBERSORT | -0.12 | 0.01 | 0.03 |
| Macrophage M1\_QUANTISEQ | 0.24 | 0.00 | 0.00 |
| Macrophage M2\_CIBERSORT | 0.22 | 0.00 | 0.00 |
| Macrophage M2\_CIBERSORT-ABS | 0.38 | 0.00 | 0.00 |
| Macrophage M2\_QUANTISEQ | 0.40 | 0.00 | 0.00 |
| Macrophage M2\_XCELL | 0.29 | 0.00 | 0.00 |
| Macrophage\_EPIC | 0.14 | 0.00 | 0.01 |
| Macrophage\_TIMER | 0.19 | 0.00 | 0.00 |
| Macrophage\_XCELL | 0.10 | 0.03 | 0.07 |
| Mast cell activated\_CIBERSORT | 0.38 | 0.00 | 0.00 |
| Mast cell activated\_CIBERSORT-ABS | 0.42 | 0.00 | 0.00 |
| Mast cell resting\_CIBERSORT | -0.23 | 0.00 | 0.00 |
| Mast cell resting\_CIBERSORT-ABS | -0.20 | 0.00 | 0.00 |
| Mast cell\_XCELL | 0.32 | 0.00 | 0.00 |
| MDSC\_TIDE | -0.50 | 0.00 | 0.00 |
| Monocyte\_CIBERSORT | 0.34 | 0.00 | 0.00 |
| Monocyte\_CIBERSORT-ABS | 0.40 | 0.00 | 0.00 |
| Monocyte\_QUANTISEQ | -0.22 | 0.00 | 0.00 |
| Monocyte\_XCELL | 0.18 | 0.00 | 0.00 |
| Myeloid dendritic cell activated\_CIBERSORT | 0.13 | 0.00 | 0.01 |
| Myeloid dendritic cell activated\_CIBERSORT-ABS | 0.17 | 0.00 | 0.00 |
| Myeloid dendritic cell activated\_XCELL | 0.15 | 0.00 | 0.00 |
| Myeloid dendritic cell resting\_CIBERSORT | 0.13 | 0.00 | 0.01 |
| Myeloid dendritic cell resting\_CIBERSORT-ABS | 0.17 | 0.00 | 0.00 |
| Myeloid dendritic cell\_MCPCOUNTER | 0.29 | 0.00 | 0.00 |
| Myeloid dendritic cell\_QUANTISEQ | -0.19 | 0.00 | 0.00 |
| Myeloid dendritic cell\_TIMER | 0.17 | 0.00 | 0.00 |
| Myeloid dendritic cell\_XCELL | 0.29 | 0.00 | 0.00 |
| Neutrophil\_MCPCOUNTER | 0.33 | 0.00 | 0.00 |
| Neutrophil\_QUANTISEQ | 0.18 | 0.00 | 0.00 |
| Neutrophil\_TIMER | 0.11 | 0.01 | 0.03 |
| NK cell activated\_CIBERSORT-ABS | 0.09 | 0.04 | 0.10 |
| NK cell\_EPIC | -0.10 | 0.03 | 0.07 |
| Plasmacytoid dendritic cell\_XCELL | -0.15 | 0.00 | 0.00 |
| T cell CD4+ (non-regulatory)\_XCELL | 0.09 | 0.04 | 0.08 |
| T cell CD4+ effector memory\_XCELL | 0.12 | 0.01 | 0.02 |
| T cell CD4+ memory activated\_CIBERSORT | -0.24 | 0.00 | 0.00 |
| T cell CD4+ memory activated\_CIBERSORT-ABS | -0.23 | 0.00 | 0.00 |
| T cell CD4+ memory resting\_CIBERSORT | 0.28 | 0.00 | 0.00 |
| T cell CD4+ memory resting\_CIBERSORT-ABS | 0.37 | 0.00 | 0.00 |
| T cell CD4+ Th1\_XCELL | -0.38 | 0.00 | 0.00 |
| T cell CD4+ Th2\_XCELL | -0.38 | 0.00 | 0.00 |
| T cell CD4+\_EPIC | 0.30 | 0.00 | 0.00 |
| T cell CD8+ naive\_XCELL | -0.21 | 0.00 | 0.00 |
| T cell CD8+\_CIBERSORT-ABS | 0.16 | 0.00 | 0.00 |
| T cell CD8+\_EPIC | 0.24 | 0.00 | 0.00 |
| T cell CD8+\_TIMER | 0.17 | 0.00 | 0.00 |
| T cell follicular helper\_CIBERSORT | -0.11 | 0.01 | 0.03 |
| T cell regulatory (Tregs)\_CIBERSORT | -0.17 | 0.00 | 0.00 |
| T cell regulatory (Tregs)\_QUANTISEQ | 0.34 | 0.00 | 0.00 |