**Supplementary Table 1**:

|  |
| --- |
| Patient information |
| Variable  | Number |
| Gender (female/male) | 166/142 |
| TNM Stage (stage I/stage II) | 212/96 |
| Lymph node metastasis (positive/negative) | 61/247 |
| Age (>60/<=60/missing) | 221/78/9 |
| TP53 Status (WT/MUT) | 210/98 |
| Smoking (no/yes/missing) | 15/93/200 |

**Supplementary Table 2**:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Survival analysis |  |  |  |  |  |
|  | Univariate Cox analysis | Mulvariate Cox analysis |
| Variable  | HR | 95% CI | P-value | HR | 95% CI | P-value |
| Gender (female vs male) | 1.04 | 0.69-1.58 | 0.85 |  |  |  |
| KRAS Status (WT vs MUT) | 1.01 | 0.62-1.56 | 0.95 |  |  |  |
| EGFR Status (WT vs MUT) | 1.35 | 0.73-2.48 | 0.33 |  |  |  |
| Age(Old vs Young) | 1.70 | 1.10-2.58 | 0.016\* | 2.10 | 1.34-3.30 | 0.001\* |
| TP53 Status (WT vs MUT) | 2.07 | 1.33-3.20 | 0.001\* | 1.58 | 0.97-2.59 | 0.07 |
| TNM Stage (Stage II vs Stage I) | 2.34 | 1.53-3.57 | <0.0001\* | 1.80 | 1.28-3.13 | 0.002\* |
| Immune signature-based risk score | 6.35 | 3.82-10.55 | <0.0001\* | 4.53 | 2.62-7.81 | <0.0001\* |

**Doc. S1 Neural network-based deep learning framework.**

**Doc. S2** **Differently expressed immune-related genes.**