**Table S1. PCR Primers used in this study**

|  |  |
| --- | --- |
| **Genesymbol** | **Sequence (5’-3’)** |
| mmu-miR-30f | Forward: 5’-CGGCGTAAACATCCGACTGA-3’ |
| mmu-miR-1a-3p | Forward: 5’-CCGGCTGGAATGTAAAGAAGT -3’ |
| mmu-miR-203-5p | Forward: 5’-CGGCAGTGGTTCTTGACAGT-3’ |
| mmu-miR-212-5p | Forward: 5’-CGGCACCTTGGCTCTAGACTG -3’ |
| mmu-miR-341-3p | Forward: 5’-GCTCGGTCGATCGGTCG-3’ |
| mmu-miR-543-3p | Forward: 5’-GCAAACATTCGCGGTGCA-3’ |
| mmu-miR-504-5p | Forward: 5’-GGCAGACCCTGGTCTGCAC-3’ |
| mmu-miR-133a-5p | Forward: 5’-CGGCGCTGGTAAAATGGAA-3’ |
| mmu-miR-466i-3p | Forward: 5’-GCCGGCATACACACACACATAC-3’ |
| mmu-miR-466f-3p | Forward: 5’-CCGGCCATACACACACACAT-3’ |
| common | Reverse: 5’-ACTGCAGGGTCCGAGGTATT-3’ |
| reverse transcription | 5’-GTCGTATCGACTGCAGGGTCCGAGGTATTCGCAGTCGATACGAC-3’ |

|  |  |  |  |
| --- | --- | --- | --- |
| **Parameters** | **Total** | **No. of patients**† | **Chi-square test*****P* value** |
| **High KCNQ1OT1 (24)** | **Low KCNQ1OT1****(26)** |
| **Gender** |  |  |  | 0.412 |
| Male | 28 | 12 | 16 |  |
| Female | 22 | 12 | 10 |  |
| **Age** |  |  |  | 0.094 |
| ≤60 | 21 | 13 | 8 |  |
| >60 | 29 | 11 | 18 |  |
| **Tumor Size** |  |  |  | 0.011\* |
| ≤5cm | 24 | 7 | 17 |  |
| >5cm | 26 | 17 |  9 |  |
| **Location of Tumor** |  |  |  | 0.981 |
|  Left (upper/lower) | 23 | 11(3/8) | 12(2/10) |  |
| Right(upper/middle/lower) | 27 | 13(2/5/6) | 14(2/6/6) |  |
| **Differentiation** |  |  |  | 0.089 |
|  Well  | 10 | 5 | 5 |  |
| Moderately  | 22 | 7 | 15 |  |
| Poorly  | 18 | 12 | 6 |  |
| **Clinical Stage** |  |  |  | 0.021\* |
| I/II | 23 | 7 | 16 |  |
| III/IV | 27 | 17 | 10 |  |

**Table 1. Correlations between KCNQ1OT1 and clinicopathologic features of LUAD patients**

\**P* <0.05; †The median expression of KCNQ1OT1 in lung adenocarcinoma tissues was used as a cutoff to divide samples into high or low subgroup.