

Supplementary Materials:

Supplementary Table S1. Detailed characteristics of patients with NSCLC with stages I–III (adenocarcinoma: I–n=3, II–n=4, III–n=3; squamous cell carcinoma I–n=3, II–n=3, III–n=4).

| Adenocarcinoma | | | Squamous Cell Carcinoma | | |
|----------------|-------------|--------------|-------------------------|-------------|--------------|
| I | II | III | I | II | III |
| n=3 | n=4 | n=3 | n=3 | n=3 | n=4 |
| T1bN0M0–IA | T2bN0M0–IIA | T3N2M0–IIIA | T1aNoM0–IA | T2aN1M0–IIA | T1aN2M0–IIIA |
| T1bN1M0–IA | T3N1M0–IIB | T4N1M0–IIIA | T2aN0M0–IB | T3N0M0–IIB | T3N1M0–IIIA |
| T1bN0M0–IA | T1aN1M0–IIA | T2bN2M0–IIIA | T2aN0M0–IB | T2bN0M0–IIA | T3N0M0–IIIA |
| | T2bN0M0–IIA | | | | T3N2M0–IIIA |

A

lncCDH5-3:3

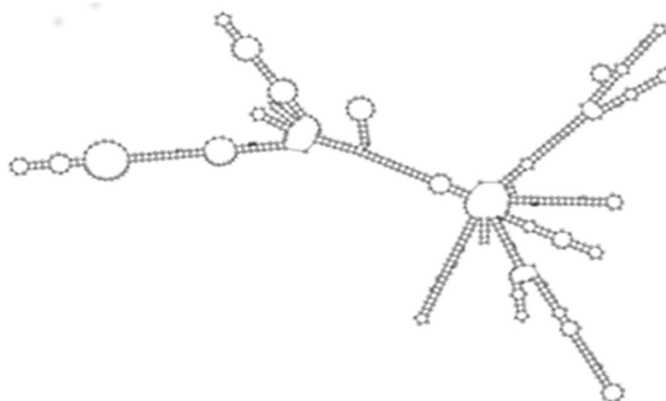
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AGCCUAAUAAAGGGAACUGGGCAGGUGGGGAUACUAAAAGGAGUGCUUA 50
AAAGAGUAUUUUCUGAGUUGGCACUAGAGUUGGGGAGUUUUAAGAGGUUU 100
AGAAGCCUGGCCGUCAAUACCCACAACAGUU AUGGAGGCAAGGGAAACAG 150
GCCCUUGAAAAGAAGGUAAUGUGGAGUGGGUAGCCUCCAUAUUGAUUAAAG 200
AAGGGGACGGGCUUACCUUUCACUGUGAGAGUUACCAAAGCUCGCGCU 250
CGUG AUGGUCUAGGGGGCUUCCGAGGCGAUCGGGCAGUGUCAGUCUUA 300
GCCGCUAGGCCGAGAAGAUUCUGGGAAGGAGUCAGUCAGAGAGCCUUGGGC 350
CAGAGUUCAGGGGGCUCUGGAGUGGCUGCCAGGUAGAUUGAACAGUCCG 400
UUUUCAGUGGGGUCCACACAGAUUGGACGCGGCUUAGGAGGAUCCCGG 450
GCAGCGGGCAUUCUUGGCCAGUGGCCAGAUUCCGGCAGUGUAGCAA 500
GCUCCUGUGGGAGGAGGUUCUGGAGGAACACCUGGCCGCGUCGGUUCAGG 550
CGUUUGGAAGUUCUGUGUCUGGAG AUGUGGCUGGGUUUGUCUCACAG 600
UGAAG 605

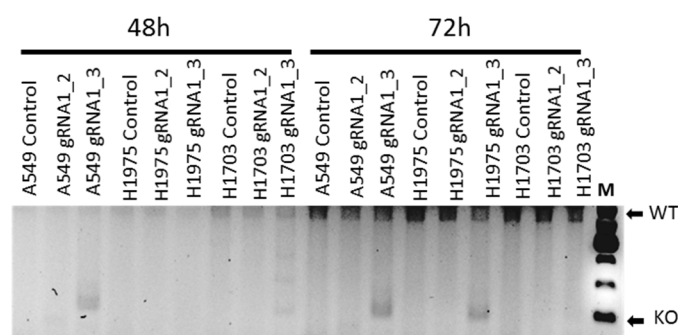
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AUG codons at the positions of 132, 169, 255, 423 and 577
 UAA codons at the positions of 5, 8, 31, 35, 49, 91, 165, 197 and 306
 UAG codons at the positions of 75, 100, 181, 261, 436 and 495
 UGA codons at the positions of 64, 156, 193, 225, 386, 391 and 601

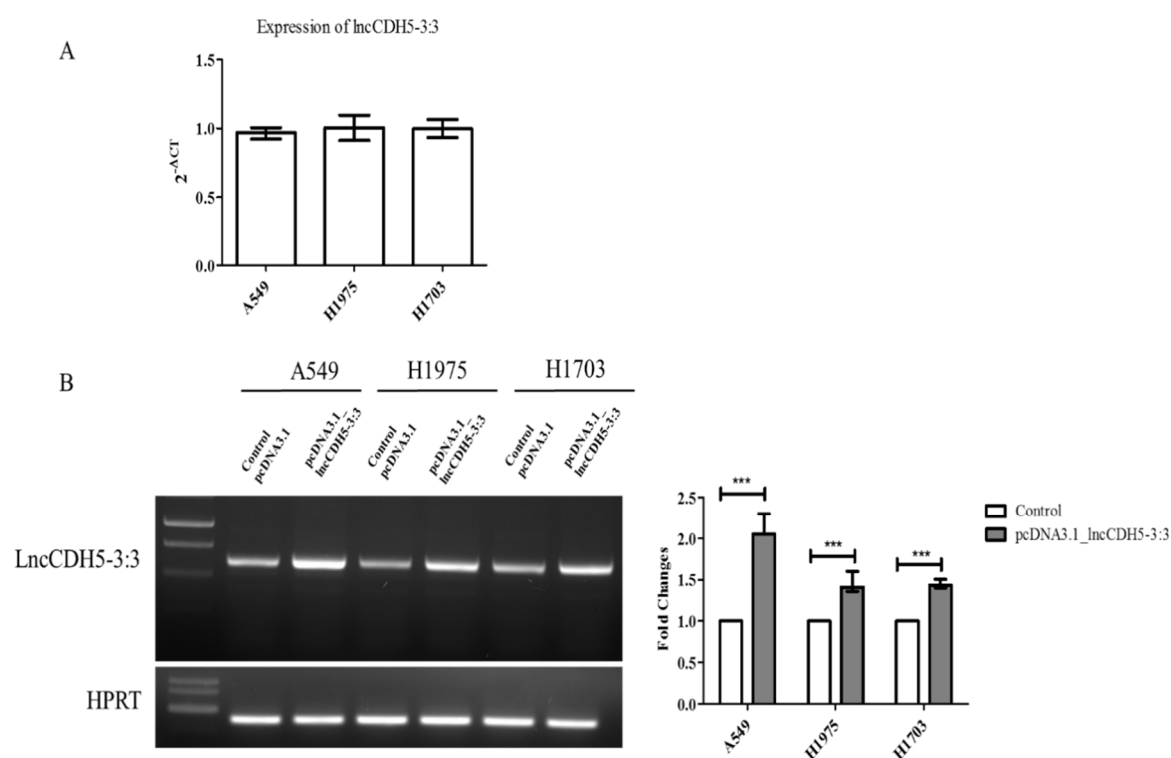
B



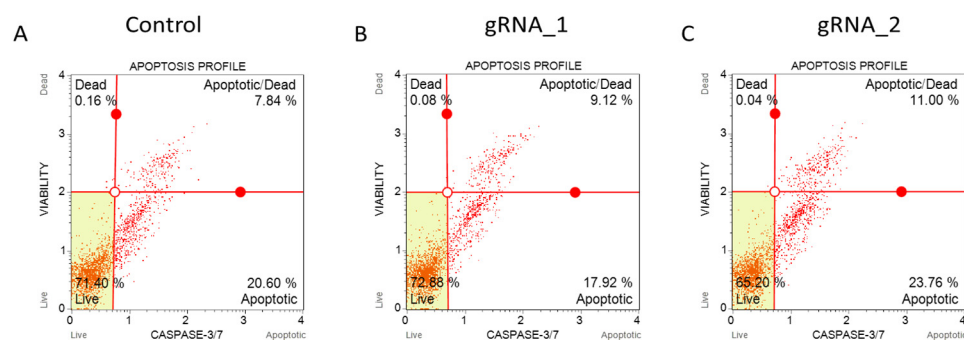
Supplementary Figure S1. The sequence and structure of lncCDH5-3:3. (A) The lncCDH5-3:3 primary sequence and stop codons (marked on yellow), five AUG codons at positions 132, 169, 255, 423, and 577 (marked on blue) are indicated. (B) Predicted optimal secondary structure consists of multiple stem-loop structures.



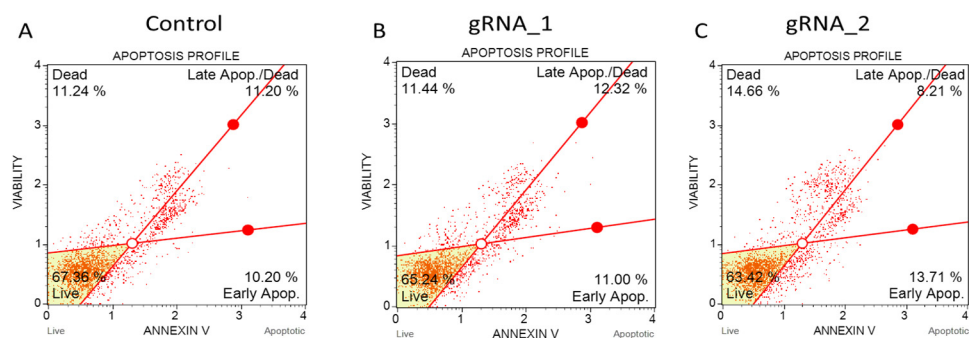
Supplementary Figure S2. Electrophoresis of cleavage products obtained after CRISPR-Cas9-mediated lncCDH5-3:3 knockout using gRNAs presented in Table 1. The arrows are showing PCR product (~200bp) after lncCDH5-3:3 silencing.



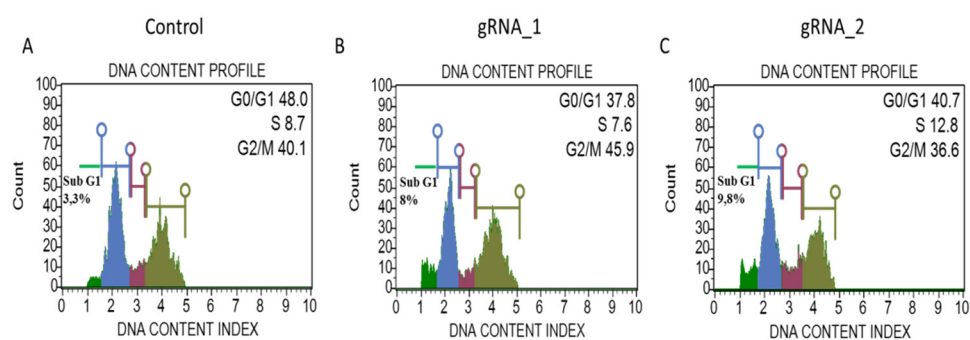
Supplementary Figure S3. Expression of lncCDH5-3:3. (A) Basal expression of A549, H1975, and H1703 cells. (B) Changes in expression of lncCDH5-3:3 after stable overexpression of lncCDH5-3:3 gathered from transfection pools of NSCLC cells.



Supplementary Figure S4. Exemplary dot-plots of lncCDH5-3:3 silencing effect on caspase-3/7 activation in lung cancer cells: control (A) and knockout of the lncCDH5-3:3 with the first (B) and second (C) pair of gRNAs.



Supplementary Figure S5. Exemplary dot-plots of lncCDH5-3:3 silencing effect on the viability of lung cancer cells: control (A) and knockout of the lncCDH5-3:3 with the first (B) and second (C) pair of gRNAs.



Supplementary Figure S6. Exemplary dot-plots of lncCDH5-3:3 silencing effect on lung cancer cell cycle: control (A) and knockout of the lncCDH5-3:3 with the first (B) and second (C) pair of gRNAs.