Table S1. List of primers information

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| Gene | Sequence (5’-3’) |
| NRF2 | F: ACGGTATGCAACAGGACATTGAGC |
|  | R: TTGGCTTCTGGACTTGGAACCATG |
| HO1 | F: CCTCCCTGTACCACATCTATGT |
|  | R: GCTCTTCTGGGAAGTAGACAG |
| SOD1 | F: ATCCTCTATCCAGAAAACACGG |
|  | R: GCGTTTCCTGTCTTTGTACTTT |
| GST | F: TCTCCAGATTCCCATCCACTTCCC |
|  | R: CTGCGGCTCGGTGATGTCTTC |
| NRF2\_M1 | F: TTATTATGATGGATTTGGAGTTGTC |
|  | R: CTAACCAAACGTAAAAAAAACCG |
| NRF2\_U1 | F: ATTATGATGGATTTGGAGTTGTTGT |
|  | R: CTAACCAAACATAAAAAAAACCAAT |
| NRF2\_M2 | F: TGTCGGTAAAAATGTGTTTAGTTAC |
|  | R: CTCAAAACTACCAAAAAATAATCCG |
| NRF2\_U2 | F: TTGGTAAAAATGTGTTTAGTTATGG |
|  | R: AAAACTACCAAAAAATAATCCAAA |

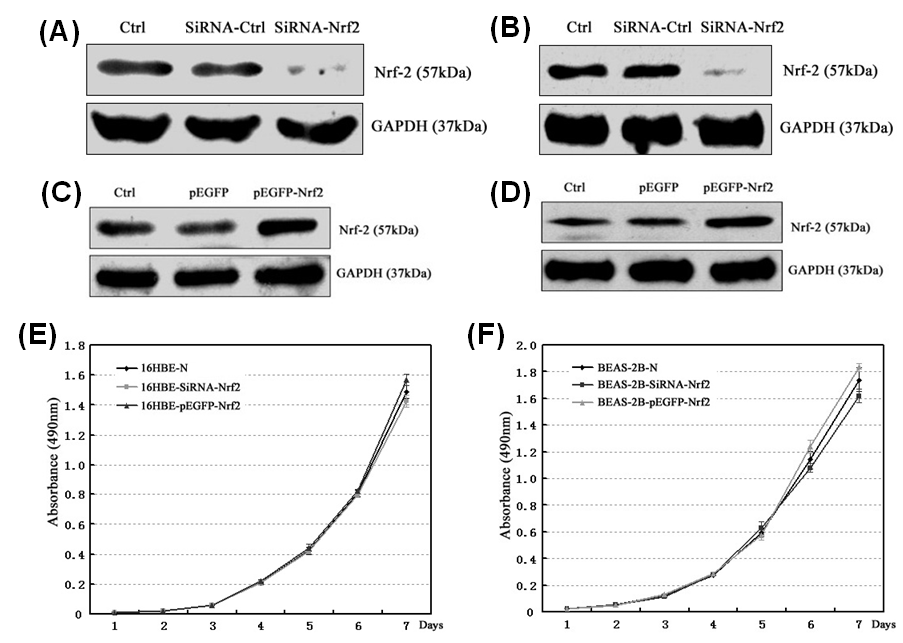


Figure S1. Knockdown and overexpression of *NRF2* in human bronchial epithelial cells. Expression of NRF2 protein was identified in 16HBE cells (A and C) and BEAS-2B cells (B and D) by Western blotting. GAPDH was used as the internal control for normalization. (E-F) Line plots showing that either knockdown or overexpression of *NRF2* has no effects on cell growth curve when compared with the normal cells (16HBE-N or BEAS-2B-N).