## Supplemental Method

### MTT cell viability assay

The viability of NCI-H295A cells were detected using MTT assay kit purchased from Cayman Chemical Company (Ann Arbor, Michigan) following the manufacturer's instruction. In brief, NCI-H295A cells were treated with nicotine at different doses (0, 1, 10, and 100 μM) for 7 days. At the end of incubation, cell cultures were incubated with 20 μl of 5 mg/ml MTT solution for 4 hours at 37°C in a humidified, 5 % $CO_2$ atmosphere. The medium was aspirated, and the precipitated formazan was solubilized with 200 μl DMSO. The absorbance at 570 nm was measured and used to calculate the relative ratio of cell viability.

**Supplemental Results**

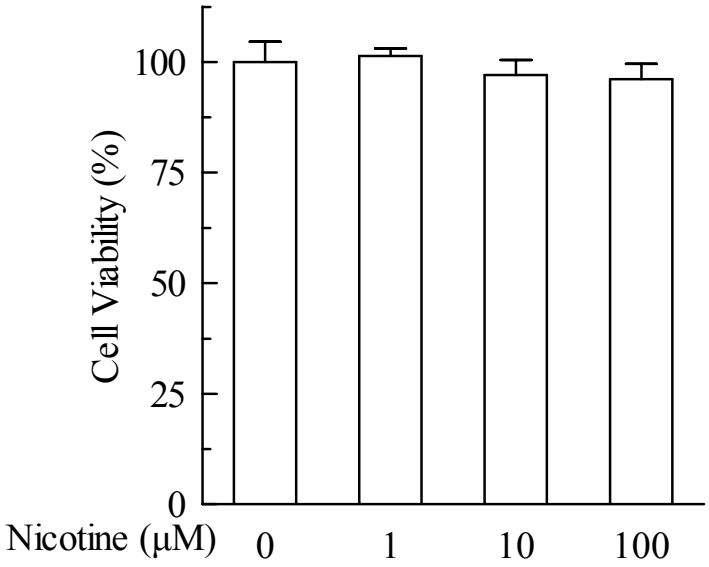


Fig S1. **Effect of nicotine on the viability of NCI-H295A cells by MTT assay.** NCI-H295A cells were treated with nicotine at different doses (0, 1, 10, and 100 μM) for 7 days. The absorbance at 570 nm was measured and used to calculate the relative ratio of cell viability. Data are expressed as mean ± S.E.M. (n=7).

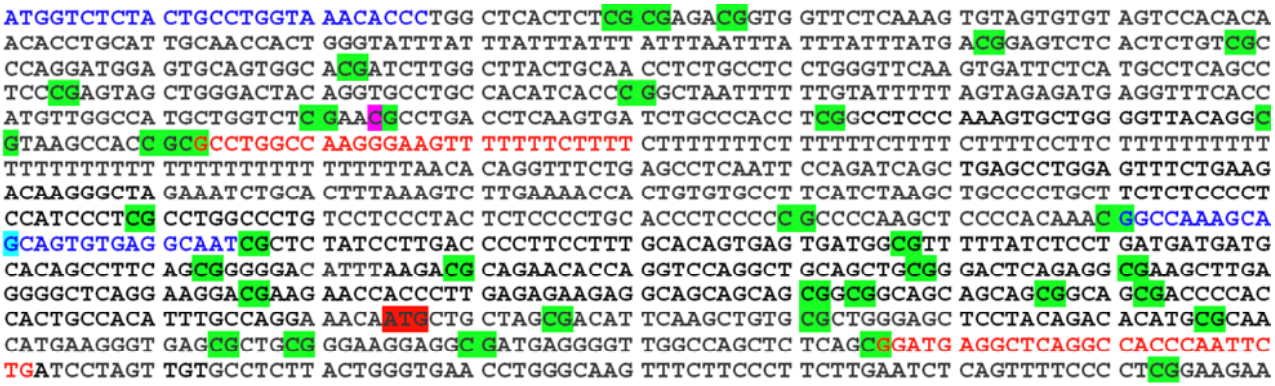


Fig S2. **Human StAR gene proximal promoter sequence and CpG map.** Pink highlighted, nt -377; Cyan, transcription initiation site; Red, translation start codon; green, CpG dinucletides. Two subregions from nucleotides labeled in blue (forward primer sequence) to nucleotides labeled in red (reverse primer sequence) indicate nt -719 to -280 and nt -9 to +402, respectively.


**Fig S3. Bioinformatics analysis of human StAR promoter region.** MacVector, software for gene analysis, and some online web services such as PROMO, TFBIND, TFSEARCH and Match were utilized for prediction the potential binding site of transcription factors. The result showed that several gene consensus sequences, including a glucagon-G3 promoter consensus (CGCCTGA), were predicted as potential binding site of transcription factors. The nucleotide sequence CGCCTGA labeled in yellow indicates the glucagon-G3 promoter consensus, tentative Pax6 binding motif.