

Resveratrol suppresses myofibroblast activity of human buccal mucosal fibroblasts through the epigenetic inhibition of ZEB1 expression

Supplementary Information

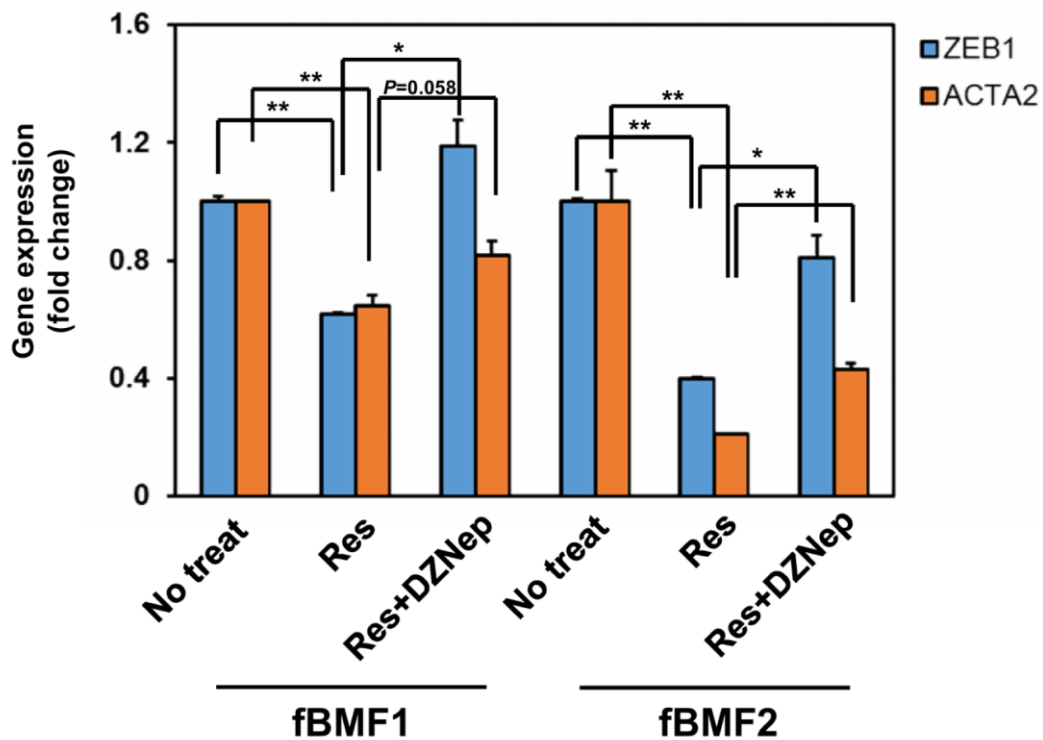


Figure S1: 3-Deazaneplanocin A (DZNep) reverses the inhibitory effect of resveratrol on ZEB1 expression. fBMF1 or fBMF2 cells were seeded into 6-well-plate as 1×10^5 cells/well and cultured in 0.5 % FBS/DMEM at 37°C with 0.1% ethanol/DMAO (No treat), 0.1%DMSO/100 μ M resveratrol (Res), or 100 μ M resveratrol/10 μ M DZNep for 48 hours. The expression of *ZEB1* and *ACTA2* was determined by SYBR-Green based qRT-PCR method. *, $p < 0.05$; **, $p < 0.01$.

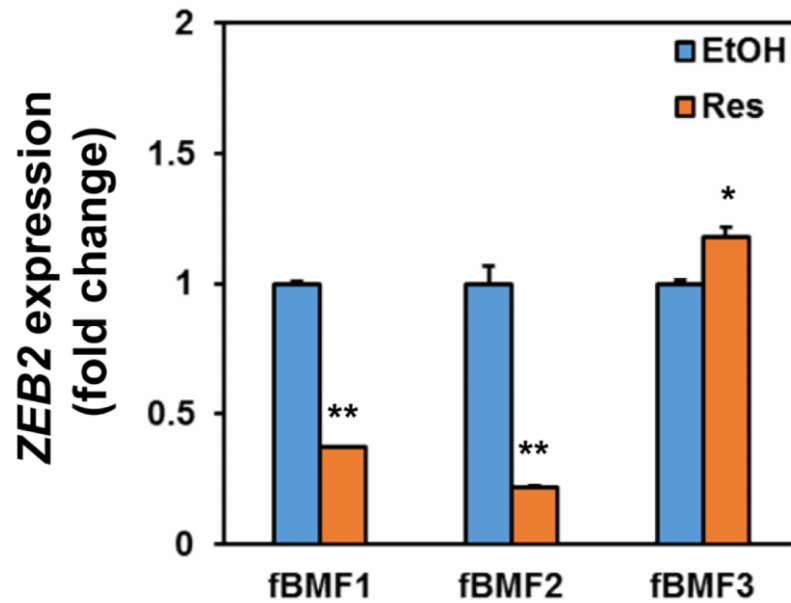


Figure S2: ZEB2 expression in resveratrol treated fibrotic BMFs. fBMF1, fBMF2 or fBMF3 cells were seeded into 6-well-plate as 1×10^5 cells/well and cultured in 0.5 % FBS/DMEM at 37°C with 0.1% ethanol (EtOH) or 100 μ M resveratrol (Res) for 48 hours. The expression of *ZEB2* was determined by SYBR-Green based qRT-PCR method. *, $p < 0.05$; **, $p < 0.01$ as comparison between EtOH and Res.

IUPAC/Regular Expression Analysis Results

Results for your IUPAC string (*CANNTG*) search (match highlighted):

>S100A4:chr1:150345377 [-700..299](-) [human, Homo sapiens]

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ATGGGGATCCCCACCCCAGTTTTTGTCTGAATCTTTATTTTTTTAAGA      50
GACAAGGTCCTCTGTGTTGCTCAGGCTGGAGAGCAGTGGCTTGAGCATAG     100
CCAACTGCAGTCTCGAACTCCTGGGCTCAAATGATCCTCCTGTCTCAGCT    150
TCCTGACTAGCTGGGACTACAGGCTACAGCCATGCTGCCAGCTAATTAA      200
AAAAAAAAAATTGTTTTTCCTTTTATAGAGACAGAAGTCTCTCTATGTTG     250
CCTAGGCTGGTCTTGAACCTCGGCTCAGGCGATCCTCCATCTCCCC        300
CTAGCTTTTGTGTCAACCACATTTCCAGGGCAATCTCCCACCTGTACCCA    350
CCACCCCTGCATCTCCTTTCCTAGGTCCTCCATGGGACTACTCCCTGTCC    400
CCCATGCTCCAGGCACAGGCTGCCCTTCTCCACCTCTCTAAACTCAG       450
GCTGAGCTATGTACACTGGGTGGTGGCCATCTCATCCAGTCCCCTGCTAG    500
TAACCGCTAGGGCTTACCCGTTACCCACGGGTGCCCACCTGGGAACAGGA    550
GGCTTGGTCCACGGCTGGGCTGGTGGAGGGTGTGTGGCACTTACCGCA     600
TCAGCCACAGCAGGAAGGCAGTATCCGCTCTCCCCTGTCCCCTGCTATG    650
GGCAGGGCCTGGCTGGGGTATAAATAGGTCAGACCTCTGGGCCGTCCCA    700
TTCTTCCCCTCTCTACAACCCTCTCTCCTCAGCGTTCTTCTTTCTTGGT    750
TTGGTGAGTTGTGTTGGCCTGACTGGCATGCAAGGGGTGTCAGAGGCCAG    800
GGCTGGGGAAGGAGAAGGGGAGGCTGGTGGGGGCCAGATGTGCTAAAGAG   850
ATCAGATGTGAGATTCTGATGTGGAACCTGGGTGGATTGTGTGCGTGG     900
GTGTGCATGGCACACACACACATGCACGTAAGACGGAGGAAAAACAAC     950
AGAAAAGTGAGCAAGTGACTGAATTTGAGCTCTCCAGGTGCTTCTGAGAT  1000
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1 [101 .. 106] CAACTG
2 [127 .. 132] CAAATG
3 [337 .. 342] CACCTG
4 [535 .. 540] CACCTG
5 [834 .. 839] CAGATG
6 [853 .. 858] CAGATG
7 [918 .. 923] CACATG
8 [961 .. 966] CAAGTG
9 [984 .. 989] CAGGTG
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Figure S3: The analysis of putative E-box domains in S100A4 promoter. E-box domain is defined as sequences contain CANNTG. The bioinformatics analysis of E-box domains within S100A4 promoter was conducted by Transcriptional Regulatory Element Database

(<https://cb.utdallas.edu/cgi-bin/TRED/tred.cgi?process=home>).