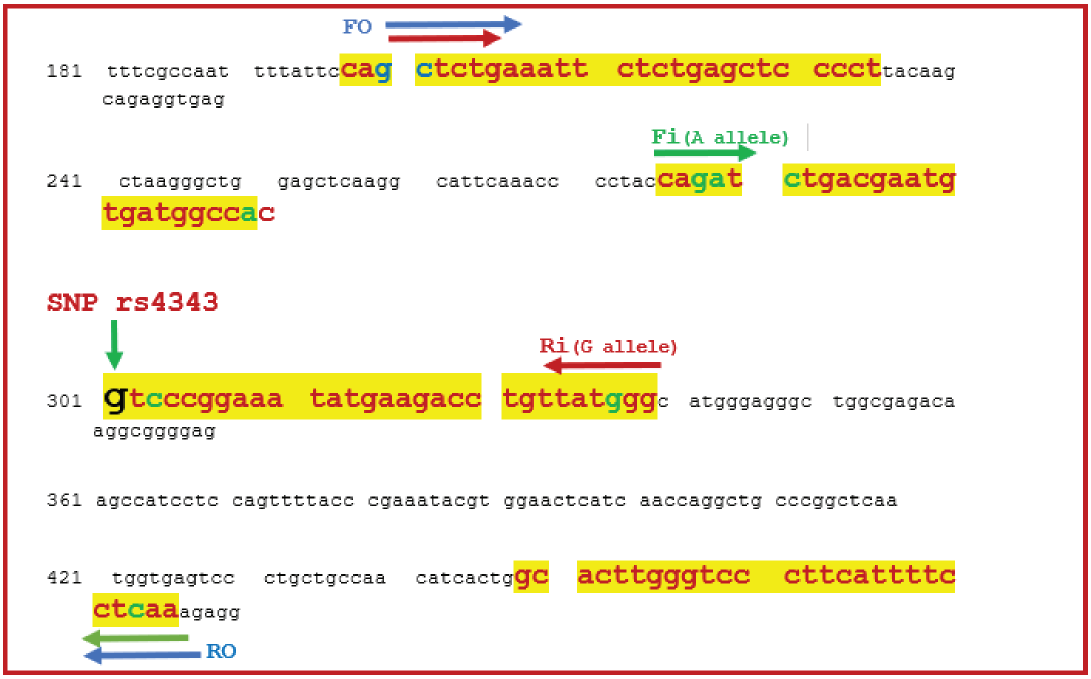
Supplementary 1.

Reference sequence detail for ACE gene 600 bps within rs4343 (gen bank, NCBI databased). Ref|NC_000017.11|:63488370-63488970 Homo sapiens chromosome 17, GRCh38.p14 Primary Assembly. SNP rs4343 located at: Chr17: 63.488.670 (located at 301 base sequences in this figure which represent G alelle)

1 aaaaaaaaaa aaggagagga gagagactca agcacgcccc tcacaggact gctgaggccc

61 tgcaggtgtc tgcagcatgt ggccccaggc cggggactct gtaagccact gctggagagc

121 cactcccatc ctttctccca tttctctaga cctgctgcct atacagtcac ttttatgtgg



181 tttcgccaat tttattccag ctctgaaatt ctctgagctc ccctacaag cagaggtgag

241 ctaagggctg gagctcaagg cattcaaacc cctaccagat ctgacgaatg tgatggccac

301 gtcccggaaa tatgaagacc tgttatgggc atgggagggc tggcgagaca aggcggggag

361 agccatcctc cagttttacc cgaaatacgt ggaactcatc aaccaggctg cccggctcaa

421 tggtgagtcc ctgctgccaa catcactggc acttgggtcc cttcattttc ctcaaagagg

481 tgctgtgaaa ccccaagcct aggaaaaggt agatccctgg aggaggcagg taatgtggtg

541 ttgggagagc ctggctgtgt cccctctgta ggctatgtag atgcagggga ctcgtggagg

601 t

Primer design for this study

Fi: 5' CATATTTGACGAATGTGATGGCCCCA 3' *(276-301 forward inner primer for A allele with 5 base mismatch from gen bank reference sequences, colored in green letter).*

Ri: 5'CCAATAACAGGTCTTCATATTTCCGGTAC 3' *(301-330 reverse inner primer for G allele, with 2 base mismatch from gen bank sequences, colored in green letter)*

FO: 5' CATTTCTGAAATTCTCTGAGCTCCCCT 3' *(198-224 forward outer primer with 2 base mismatch from gen bank reference sequences in 3' side, colored in green letter)*

RO: 5' TTTAGGAAAATGAAGGGACCCAAGTGC 3' *(449-476 reverse outer primer with 1 base mismatch from gen bank reference sequences in 5' side, colored in green letter)*

Product size for A allele: 202 (located at 276-476; Fi-RO)
Product size for G allele: 134 (located at 198-330; FO-Ri)
Product size of two outer primers: 280 (located at 198-476; FO-RO)

Tetra Primer specific for SNP rs4343 *ACE* gene used in TETRA ARMS PCR, anneal in reference sequences and the PCR product size.