Identification and Genotyping of repetitive sequences in and around *NOS2A*

The primers were designed using PrimerSelect (DNASTAR) software except for M1, for which primers and conditions were used as described previously[1]. Primer specificity was checked by BLASTing the primer sequence to the NCBI database (http://www.ncbi.nlm.nih.gov/blast/). PCR amplification (1 cycle at 94ºC for 5 min and then 94ºC for 30 sec, annealing at temp mentioned in table 1 for 30 sec, and extending at 72ºC for 30 sec for 30 cycles) were carried out in a total volume of 5µl reaction containing 25ng of genomic DNA, 0.5 pmol each of a 6-FAM-labeled forward primer and a non-labeled reverse primer, 1.5mM $MgCl_2$, 0.25mM of each dNTP, 0.03U/µl of Taq DNA polymerase (Bangalore Genie, India) and the buffer recommended by the supplier on a PE 9700 thermocycler (Applied Biosystems, Foster City, Calif). PCR products were sequenced on an ABI 3100 capillary sequencer (Applied Biosystems, Foster City, CA, USA) by Big Dye terminator kit V 3.1 using unlabeled forward primer for each repeat.

Reference:

1.Xu W, Liu L, Emson PC, *et al.* Evolution of a homopurine-homopyrimidine pentanucleotide repeat sequence upstream of the human inducible nitric oxide synthase gene. *Gene*1997;204:165-70