Supplementary data 1: Genotyping

DNA was isolated from EDTA blood samples. Genotyping of the Ex1f-VNTR was carried out at the department of Human Genetics of the Radboud University Nijmegen Medical Centre. PCR was performed with 1 μl 10x PCR buffer II (Applied Biosystems, Nieuwerkerk a/d IJssel, The Netherlands), 1 μl of 25 mM MgCl₂, 1 μl dNTPs (2.5 mM of each dNTP; GE Healthcare, Zeist, The Netherlands), 0.50 μl forward and reverse primer together (10 pmol/μl of each primer, VIC®-labeled 5’-CCCTGCGTGCTACTACTACATT-3’ and 5’-CTGGGCTCCAAAGCATACAT-3’ with ‘PIG’-tail; Applied Biosystems) and 0.08 μl AmpliTaq Gold polymerase (Applied Biosystems). The cycling conditions were: 12 min 95 ºC, 10 amplification cycles of 30 sec at 94ºC, 54ºC for 30 sec and 72ºC for 1 min, followed by 22 cycles of 30 sec at 89ºC, 54ºC for 30 sec and 1 min at 72ºC, followed by a final 10 min at 72ºC. After the PCR, fragment length analysis was performed on the ABI prism 3730 Genetic Analyser (Applied Biosystems) and results were analyzed with GeneMapper® Software, version 4.0 (Applied Biosystems). After testing for Hardy-Weinberg equilibrium¹, ², the resulting genotypes were converted to short (S) and long (L) alleles (see table below). The frequency of the dichotomous NOS1 ex1f-VNTR genotype in Caucasian populations is as follows: SS=21.0%; SL=51.4%; LL=27.6% (n=7847 population-based subjects from Germany, Italy, Norway, Sweden, Estonia, Spain, The Netherlands and Austria) (Prof. Dr. A. Reif, personal communication).

NOS1 Ex1f-VNTR³

| Allele size | Reif | freq | Allele size | Reif | freq |
|-------------|------|------|-------------|------|------|
| 138         | -    | 1    | 178         | 198  | 2    |
| 161         | 182  | 36   | 180         | 200  | 40   |
| 163         | 184  | 9    | 182         | 202  | 31   |
| 169         | 188  | 1    | 184         | 204  | 82   |
| 172         | 192  | 57   | 186         | 206  | 5    |
| 174         | 194  | 7    |             |      |      |
| 176         | 196  | 1    |             |      |      |

³Displayed are the size of the alleles found in the current study sample (allele size), the corresponding allele size from the study of Reif et al. 2009 (Reif) and frequency of these alleles in the current study sample (freq).
References

1. Raymond, M. & Rousset, F. GENEPOP (version 1.2): population genetics software for exact tests and ecumenism. *Journal of heredity* **86**, 248-249 (1995).
2. Rousset, F. GENEPOP ' 007: a complete re-implementation of the GENEPOP software for Windows and Linux. *Molecular Ecology Resourses* **8**, 103-106 (2008).