SUPPLEMENTAL INFORMATION

Genotyping measurement procedure

EDTA anticoagulated peripheral blood samples were obtained from three cases. Genomic DNA was extracted from peripheral blood using the Puregene DNA extraction kit (Qiagen, Hilden, Germany) following the manufacturer's protocol.

5-HTTLPR polymorphism

Direct polymerase chain reaction (PCR) was used to determine the insertion/deletion polymorphism (L/S allele). We designed a pair of PCR primers by the Primer3 Software Online Program (http://frodo. wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). Oligonucleotide primers: forward 5'-CGGGATGCGGGGGAATACTGGT-3' and reverse 5'-TTGCCGCTCTGAATGCCAGCAC-3' were used to amplify the 5-HTTLPR region. PCR amplification was carried out in a final volume of 10 μ l consisting of 3 μ l of DNA solution (Qiagen Inc.), PCR buffer (Qiagen Inc.), 0.2 mM deoxynucleotide triphosphates, 1 μ l primers (2 μ M), 1 U HotStar Taq polymerase (Qiagen Inc.) and 1 μ l of 10 ng μ l genomic DNA. The PCR system consisted of 2 min of initial denaturation at 95°C, followed by 35 cycles of 20s of denaturation at

94°C and 2 min of extension at 68°C, and a final extension of 60 min at 68°C, and 4°C forever.

STin2 VNTR polymorphism

Primers as follows: forward 5'-TGGCGAGATTTGACTTTTCTACC-3' and reverse 5'-CTGAGCTTCATCAAGGGGAAC-3' were used to amplify the STin2 VNTR region. A 20 μ l mixture was prepared for each reaction and included HotStar Taq buffer, 3.0 mM Mg²⁺, 0.3 mM dNTP, 0.1 μ M of primers, 1 U HotStar Taq polymerase (Qiagen Inc.) and 1 μ l template DNA. PCR conditions were as follows: 15 min of initial denaturation at 95°C; 11 cycles of 94°C for 20s and 62°C–0.5°C per cycle for 40s and 68°C for 2 min; followed by 24 cycles of 20s of denaturation at 94°C, 56°C for 40s and 2 min of extension at 68°C, and a final extension of 60 min at 60°C.

Polymorphisms analysis

The products were analyzed on a 3730 DNA analyzer (Applied Biosystems, Carlsbad, California). Two technicians called genotypes independently by visual observation of peak sizes using GeneMapper 4.0 (Applied Biosystems, Carlsbad, California, USA) with referring to explicit standards.