Supplementary table. Primers and restriction enzymes used in defining *HTT* haplogroups and haplogroup A variants.

SNP	rs code	F primer	R primer	Restriction enzyme	Fragment lengths (bp)
1	rs2857936	TGGGGGCTGCTTTTC**G**TT	CCTACAGTAATGCCCTGTGCGT	n.a.	516
		TGGGGGCTGCTTTTC**A**TT			
11	rs762855	TAACAGCAGAGAACTGGGAAC	CAGAGAGGAGCCCAGTAAAGC	PvuII	A: 464, 183 G: 647
33	rs2798235	AGTACCCTTGGCTCTGAAGTTTA	GGGCCTCCTCAGGTCTAATC	AccI (XmiI)	A: 113, 106 G: 219
n.a.	rs1143646	TGACATGCCTTCCTCTTGGAAT	AACTGAGGGGCTATATTGGGA	n.a.	475
89	rs4690073	GATCAGTTCCCCTGTTGTTCT	CAAGAAATGTGCAAGAGCTATGT	AseI	A: 93, 166 G: 256
94	rs363144	ACATCACCACATCACCTCGT	ACTAGGATCCCTGGGAGAAATCA	n.a.	469
95	rs3025838	ACATCACCACATCACCTCGT	ACTAGGATCCCTGGGAGAAATCA	Alw26I	C: 195, 150, 124 T: 319, 150
112	rs363096	TCTACCTGCTGCCTCCGAAC	TGATTGCCTCTGATTCCCTAA**A**A	n.a.	236
			TGATTGCCTCTGATTCCCTA**G**A		
176	rs2276881	AACAGCGCGATTCTCCCCTT	GTCGCTGAACCCCCTCCAT	n.a.	379
176	rs2276881	AGCT**G**ATGTATGTGACGCTGA	GTCGCTGAACCCCCTCCAT	n.a.	290
		TGAGCT**A**ATGTATGTGACGCTGA			292
182	rs362307	AGGAAGCCCATATCACCGGC	AAGCCTGCTCACGGCACCT	n.a.	474

SNPs are numbered according to Warby et al., 2009 (10). SNP, single nucleotide polymorphism; rs code, reference SNP ID number. The LNA bases in the primers are typed in bold. The SNP 176 was determined using both sequencing (upper row) and allele-specific amplification (lower row).