Supplementary Table 1. Alleles and genotype distribution of *WDR46* SNPs

SNP	Position	Allele	Genotype			Heterozygosity	MAF				
							Korean	Caucasian*	Chinese*	Japanese*	African*
rs463260	5' UTR	G>A	G 90	AG 78	A 19	0.428	0.310	0.500	0.350	0.330	0.714
rs446735	Intron 8	T>G	T 91	GT 79	G 19	0.427	0.310	0.500	0.358	0.332	0.719
rs466384	Exon 10	T>C	T 161	CT 24	C 2	0.139	0.075	-	-	-	-
rs455567	Intron 10	C>T	C 90	CT 78	T 19	0.428	0.310	0.500	0.358	0.329	0.732
rs469064	Intron 10	G>T	G 90	GT 79	T 17	0.423	0.304	0.495	0.354	0.324	0.246

SNP, single-nucleotide polymorphism; MAF, minor allele frequency; UTR, untranslated region.
*Data taken from the International HapMap database (version: release #28; http://www.hapmap.org).

Supplementary Table 2. UTRScan output for *rs463260*

SNP	Input sequence length*	UTRSite signal	Start and end positions of signal	Matched nucleotide sequence
rs463260G>A	361bases	Upstream Open Reading Frame	85-348	ATG GCACCTAGAGAGCTTCATACCTGGTACGCTGCTGAT TGGATGAAGGACAGAGGGCTTCCGGGAGTTTTCAAG CCGACTGTGTGGCAGCTGAGA[G/A]GAGTTTTGCACG TGGATCGCCGTTCGGGTGGGCGAGATGGAGACAGCC CCCAAGCCGGGCAAGGATGTCCCGCCCAAGAAAGA CAAACTTCAGACCAAGAGAAAGGTAGAGGCCTCCCT GGGTGGGAAACGAAGTTTTTAGCTGTGGGGTCGGGG GGCGGGGCG TGA

Nucleotide sequence for the UTRsite signal is predicted using the UTRScan program (http://itbtools.ba.itb.cnr.it/utrscan).
*FASTA sequence taken from National Center for Biotechnology Information (NCBI) database (http://www.ncbi.nlm.nih.gov).