

Table S1. Summary information of all included allele genotypes and polymorphic sites of the network analyzed.

	rs8177352	rs8177364	rs1893352	rs8177399	rs595209	rs3802813	rs3802814	rs8177374	rs7932766	rs8177375	rs8177376	rs625413				
	A	B	C	J	D	E	K	L	F	G	H	I	N	Africa	Europe	Asia
Allele genotype													N			
1	A	C	A	C	A	G	G	C	C	A	T	C	53	x		x
2	A	C	A	C	A	G	G	C	C	G	T	C	60	x	x	x
3	A	C	G	C	A	G	G	C	C	A	T	C	13	x		
4	A	C	A	C	A	G	G	C	C	A	T	T	34	x	x	
5	A	C	A	C	C	G	G	C	C	A	T	C	148	x	x	x
6	A	C	A	C	A	G	G	C	T	A	T	C	5	x		
7	A	C	A	C	A	G	G	C	T	A	G	C	39	x	x	x
8	G	C	A	C	A	A	G	C	C	A	T	C	37	x	x	x
9	A	A	A	C	A	G	G	C	C	G	T	C	2	x		
10	A	C	A	C	A	A	G	C	C	A	T	C	1	X		
12	G	C	A	C	A	G	G	C	C	A	T	C	1	x		
13	A	C	A	T	C	G	G	C	C	A	T	C	1			x
14	G	C	A	C	C	G	G	C	C	A	T	C	2			x
15	A	C	A	T	A	G	G	C	C	G	T	C	3		x	
16	G	C	G	C	A	G	G	C	C	A	T	C	3		x	
17	G	C	G	C	A	G	A	T	C	A	T	C	16		x	x
18	A	C	G	C	A	G	G	C	C	G	T	C	1	X		

All allele genotypes are composed of the different polymorphic sites they contain. The TIRAP 180L polymorphism is shown in bold (L) and in the HapMap data it is only found in the European and Asian populations. For all allele genotypes, number of alleles and in which population they are found are presented.

From the HapMap Genome browser (HapMap Data Rel 23a/phaseIIMar08, on NCBI B36 assembly, dbSNP b126) all phased haplotype data of the TIRAP gene, from each population, were downloaded. Hereby filters were set on all population-specific polymorphic sites. After downloading, all polymorphic sites were converted

to the allele states, having a total of 120 alleles from African (YRI) and European (CEU) and 180 from Asian (JPT+CHB). Missing polymorphic sites in a population were filled in as the ancient nucleotide of that position.

Each polymorphic site was given a letter and all different allele genotypes numbers. Before performing the network analysis, all polymorphic sites were checked on their nucleotide surroundings if they were part of a CpG, because of the influence the higher mutation rate could have on the homoplasy. Two included SNPs, namely rs8177352 and rs817739, were therefore left out of the network analysis. Also, networks were analyzed that weighed the mutation rate of transversion and transition sites differently. With these weightings, no difference was seen in the network outcome.