

Table S4. Functional characterization and allele frequencies for functionally relevant SNPs within ~ 140 kb containing the *FOXII* gene.

SNP ID	Position ^a	Alleles ^b	Africans	Europeans	Asians	Sources	Functional Effect ^d
rs6555882	169401666	G/C	0.683	1	1	HapMap-YRI, CEU, CHB, JPT	ESE (<i>DOCK2</i>)
rs17647491	169416284	C/T	1	0.966	1	HapMap-YRI, CEU, CHB, JPT	ESE (<i>DOCK2</i>)
rs13179480	169428747	A/C	1	1	0.988	HapMap-YRI, CEU, JPT	CNS, ESE (<i>DOCK2</i>)
rs13179490	169428777	A/C	1	1	1	HapMap-YRI, CEU, CHB, JPT	CNS (<i>DOCK2</i>)
rs2270900	169435654	T/C	1	1	0.989	HapMap-YRI, CEU, CHB, JPT	ESE (<i>DOCK2</i>)
rs1045168	169437321	T/C	0.619	0.758	0.895	HGDP-Yoruba, HapMap- CEU, JPT	ESE (<i>DOCK2</i>)
rs2270898	169441471	T/A	1	1	0.989	HapMap-YRI, CEU, CHB, JPT	CNS, ESE (<i>DOCK2</i>)
rs1045176	169442598	G/T	0.595	0.121	0.478	HapMap-YRI, CEU, CHB	ESE (<i>DOCK2</i>)
rs9307	169442601	A/G	0.080	0.361	0.330	1000 genomes (dbSNP)-YRI, CEU, CHB, JPT	ESE (<i>DOCK2</i>)
rs17072089	169461251	C/G	0.978	0.979	1	Afr-Am, European, Asian (Perlegen)	New TFBS (<i>FOXII</i>)
rs7704953	169461667	C/T	0.929	0.583	0.818	HGDP-Yor, HapMap- JPT, 1000 ge (dbSNP)-CEU	New TFBS (<i>FOXII</i>)
rs34218925	169465509	G/T	NA ^c	NA ^c	NA ^c		ESE (<i>FOXII</i>)
rs2277944	169465818	A/G	0.714	0.188	0.479	HGDP-Yor, European, Asian (Perlegen)	ESE (<i>FOXII</i>)
rs35678180	169467782	G/A	0.974	NA ^c	NA ^c	Afr-Am (Applera)	ESE (<i>FOXII</i>)
rs10063424	169468100	T/C	0.024	0.092	0.044	HGDP-Yoruba, HapMap- CEU, CHB	ESE (<i>FOXII</i>)
rs3828625	169468141	T/C	1	1	0.988	HGDP-Yoruba, HapMap- CEU, JPT	CNS, ESE (<i>FOXII</i>)
rs6873124	169468312	A/C	0.575	0.164	0.489	HapMap-YRI, CEU, CHB	ESE (<i>FOXII</i>)
rs6555887	169468633	A/G	0.847	0.908	0.978	HapMap-YRI, CEU, JPT	ESS, ESE, miRNA (<i>FOXII</i>)
rs6555888	169468728	G/A	0.842	0.808	0.944	HapMap-YRI, CEU, JPT	miRNA (<i>FOXII</i>)

^aSNP positions are based on NCBI build 36.3, ^bAncestral allele in bold, ^cNot available, ^dFunctional effect as predicted by PupaSuite [40, 41]: ESE, exonic splicing enhancer; CNS, coding non-synonymous SNPs; TFBS, transcription factor binding sites; ESS, exonic splicing silencer; miRNA, microRNAs and their targets.