

Appendix Table 3. Genotype and allele frequencies for SNPs in *PRKAA2* in case and control samples (Joint samples)

		Joint (initial + replication + Hiroshima) samples					
SNP ID	genotype	genotype frequency		p value ^a	minor allele frequency case/control	p value ^b	
		Case (n=1205)	Control (n=824)				
SNP1	rs2051040	GG	435 (0.36)	314 (0.38)	0.083	0.40/0.38	0.07
		GA	558 (0.46)	396 (0.48)			
		AA	211 (0.18)	114 (0.14)			
SNP2	rs2796495	GG	442 (0.37)	276 (0.33)	0.33	0.40/0.41	0.22
		GA	561 (0.47)	405 (0.49)			
		AA	200 (0.16)	142 (0.17)			
SNP3	rs2143754	TT	395 (0.33)	237 (0.29)	0.12	0.43/0.45	0.16
		TC	572 (0.48)	424 (0.51)			
		CC	234 (0.19)	163 (0.20)			
SNP4	rs1418442	AA	690 (0.57)	472 (0.57)	0.87	0.24/0.25	0.78
		AG	432 (0.36)	293 (0.36)			
		GG	79 (0.07)	59 (0.07)			
SNP5	rs932447	AA	697 (0.58)	505 (0.61)	0.39	0.23/0.22	0.22
		AG	441 (0.37)	281 (0.34)			
		GG	58 (0.05)	38 (0.05)			
SNP6	rs3738568	TT	884 (0.73)	590 (0.71)	0.63	0.14/0.15	0.43
		TC	296 (0.25)	218 (0.27)			
		CC	24 (0.02)	16 (0.02)			

a)b) p values for genotype frequency(^a) and allele frequency(^b).