Table S10

Amino acid changes at the AVPR2 positions with a higher probability (> 65%) of being under positive selection and/or having relaxed functional constraints.

Protein region	Nucleotide	Amino acid	Grantham score	Mammalian species																																		
				Human	Chimpanzee	Gorilla	Orangutan	Gibbon	Macaque	Baboon	Squirrel monkey	Marmoset	Bushbaby	Mouse	Rat	Kangaroo rat	Naked mole rat	Guinea pig	Squirrel	Rabbit	Pika	Orca	Cow	Sheep	Pig	Panda	Ferret	Dog	Cat	Horse	Rhinoceros	Microbat	Megabat	Shrew	Manatee	Elephant	Lesser hedgehog tenrec	Armadillo
ICL3	AGG->GTA	249 Arg->Val	96	0_{abd}	0_{abd}	0_{abd}	0_{abd}	0_{abd}	0_{abd}	0_{abd}				0	0	0	0_{a}	0_{ad}	0_{bcd}		1_{a}		0	0	0							0_{ab}		0				0_{a}
	AGG->CCG	249 Arg->Pro	103								1_{a}	1_{a}																										
	AGG->AGC	249 Arg->Ser	110																																	1_{abd}		
	AGG->GGG	249 Arg->Gly	125										1													1			1									
	AGG->GGA	249 Arg->Gly	125																	1_{a}		1_{a}				1	1	1		1	1_{a}		1_{a}					
	AGG->GGC	249 Arg->Gly	125																																1_{ad}		1_{a}	
	GGT->AGT	257 Gly->Ser	56	0_{fg}	0_{fg}	0_{fg}	0_{fg}	0_{fg}	1	0						1_{g}										1_{eg}			1_{eg}			0	0		1			
	GGT->AGC	257 Gly->Ser	56								1	1	1_{g}	1_{efg}	1_{efg}					1		1_{eg}					1_{eg}	1_{eg}								1	1	
	GGT->TCC	257 Gly->Ser	56																															1				
	GGT->GCC	257 Gly->Ala	60																				1_{g}															
	GGT->GCT	257 Gly->Ala	60																					1														
	GGT->CAT	257 Gly->His	98																		1																	
	GGT->CGC	257 Gly->Arg	125																						1_{g}													1
	GGT->AGA	257 Gly->Arg	125														1_{g}	1_{g}	1_{eg}											1_{g}	1_{g}							
TM6	GTC->ATA	278 Val->Ile	29	0	0	0	0	0	0	0		0										1	1	1														
	GTC->ATT	278 Val->Ile	29											1	1	1	1			1	1					1			1	1	1		1		1			1
	GTC->ATC	278 Val->Ile	29										1					1	1								1	1				1		1		1		
	GTC->GTA	278 Val->Ile	29								1																											
	GTC->GCT	278 Val->Ala	64																						1													
C-terminal	GGA->AGT	345 Gly->Ser	56	0_{j}	0_{j}	0	0	0	0	0																0	1	1										
	GGA->AGC	345 Gly->Ser	56														1_{j}																					
	GGA->GGC	345 Gly->Ser	56															1_{j}																				
	GGA->ACG	345 Gly->Thr	59																			1_{n}																
	GGA->GCA	345 Gly->Ala	60																																		1_{j}	
	GGA->GCC	345 Gly->Ala	60																																			1
	GGA->GTA	345 Gly->Val	109																1																			
	GGA->AGG	345 Gly->Arg	125								1_{a}	1_{aj}	1_{aj}	1	1	1_{ai}				1	1_{a}		1_{a}	1_{a}	1_{aj}					1_{a}	1_{a}	1_{a}	1_{j}	1_{a}	1_{a}	1_{a}		
	GGA->AAA	345 Gly->Lys	127																										1_{ah}									

Sites identified in the Bayes Empirical Bayes (BEB) analysis with a probability higher than 65% of being under ω > 1, which indicates positive selection. + Positively selected sites (*p* >95%); bold text indicates positively selected sites (*p* >99%). AVPR2 regions: ICL 3 = Intracellular 3; TM 6 = Transmembrane 6; and C-terminal = Carboxy-terminus. Zero (0) indicates the amino acid present in the *Homo sapiens* reference sequence, whereas 1 indicates a variant amino acid.

The nature of the modification does not represent an ancestry and descendant relationship. Grantham scores are predicted as conservative (0–50), moderately conservative (51–100), moderately radical (101–150), or radical (>151). Subscripted letters indicate the predicted presence of specific Eukaryotic Linear Motifs (as depicted using the code shown in Table S11). Scientific names of the species can be found in Table S1.