

Table S5. Nucleotide Substitutions in *PRH2* gene in introns and regulatory regions

Genomic Coordinates (hg19)	Gene Region	Modern human	Altai Neanderthal (Variant Frequency)	Chagyrskaya Neanderthal (Variant Frequency)	Vindija Neanderthal (Variant Frequency)	Denisovan (Variant Frequency)	Codon → amino acid
11,081,651	Upstream regions	C	C (100%)	C (100%)	T (16%)	C (100%)	
11,081,653	Upstream regions	C	C (100%)	T (4%)*	T (15%)	C (100%)	
11,081,672	Upstream regions	C	A (4%)*	T (11%)	C (100%)	C (100%)	
11,081,681	Upstream regions	C	C (100%)	T (15%)	C (100%)	C (100%)	
11,081,759	Upstream regions	G	G (100%)	A (15%)	A (13%)*	G (100%)	
11,081,788	Upstream regions	G	A (4%)*	A (100%)	G (100%)	G (100%)	
11,081,803	Upstream regions	G	G (100%)	G (100%)	A (17%)	G (96%)	
11,081,840	5'UTR	A	G (98%)	A (100%)	A (100%)	A (100%)	
11,081,842	5'UTR	A	A (100%)	A (100%)	A (100%)	T (100%)	
11,081,856	5'UTR	C	C (100%)	C (100%)	T (13%)	C (100%)	
11,081,997	Intron 1	G	G (100%)	A (4%)*	A (11%)	G (100%)	
11,082,013	Intron 1	G	G (100%)	A (14%)	G (100%)	G (100%)	
11,082,167	Intron 1	G	G (100%)	A (11%)	A (6%)*	G (100%)	
11,082,201	Intron 1	G	G (100%)	A (3%)*	A (11%)	G (100%)	
11,082,210	Intron 1	A	A (100%)	G (89%)	G (100%)	A (100%)	
11,082,254	Intron 1	C	C (100%)	A (100%)	A (100%)	C (100%)	
11,082,310	Intron 1	T	T (100%)	C (100%)	C (97%)	T (100%)	
11,082,355	Intron 1	G	G (97%)	A (15%)	A (3%)*	G (100%)	
11,082,462	Intron 1	C	T (100%)	T (4%)*	T (7%)*	T (3%)*	
11,082,479	Intron 1	G	G (100%)	G (100%)	A (14%)	G (100%)	
11,082,514	Intron 1	G	A (3%)*	G (100%)	A (11%)	G (100%)	
11,082,598	Intron 1	C	C (100%)	T (12%)	T (10%)*	C (100%)	
11,082,599	Intron 1	C	C (100%)	T (16%)	C (97%)	C (100%)	
11,082,615	Intron 1	A	A (100%)	A (100%)	A (100%)	G (97%)	
11,082,650	Intron 1	G	G (100%)	A (11%)	A (3%)*	G (100%)	
11,082,651	Intron 1	G	G (100%)	A (11%)	G (100%)	G (100%)	
11,082,652	Intron 1	C	C (100%)	T (3%)*	T (22%)	C (100%)	
11,082,653	Intron 1	C	C (100%)	T (6%)*	T (11%)	C (100%)	
11,082,654	Intron 1	C	C (100%)	T (3%)*	T (12%)	C (100%)	
11,082,661	Intron 1	G	G (100%)	A (3%)*	A (13%)	G (100%)	

11,082,689	Intron 1	G	G (100%)	G (100%)	A (16%)	G (100%)	
11,082,705	Intron 1	C	C (100%)	T (12%)	T (4%)*	C (100%)	
11,082,740	Intron 1	G	A (2%)*	A (3%)*	A (16%)	G (100%)	
11,082,774	Intron 1	G	G (100%)	G (94%)	A (11%)	G (100%)	
11,082,775	Intron 1	G	G (100%)	A (7%)*	A (16%)	G (100%)	
11,082,787	Intron 1	G	G (100%)	G (100%)	A (17%)	G (100%)	
11,082,831	Intron 1	C	C (100%)	A (100%)	A (100%)	C (100%)	
11,082,869	Exon 2 (PRP-1)	GAT	GAC (100%)	GAT (100%)	GAT (100%)	GAT (100%)	GAU→D ₆ GAC→D ₆
11,082,884	Exon 2 (PRP-1)	GAC	GAC (100%)	GAT (11%)	GAT (8%)*	GAC (100%)	GAC→D ₁₁ GAU→D ₁₁
11,082,932	Intron 2	C	C (100%)	T (3%)*	T (11%)	C (100%)	
11,082,971	Intron 2	G	G (100%)	A (11%)	A (3%)*	G (100%)	
11,083,014	Intron 2	C	C (97%)	T (14%)	C (100%)	C (100%)	
11,083,015	Intron 2	C	C (100%)	T (14%)	C (100%)	C (97%)	
11,083,054	Intron 2	G	G (100%)	G (100%)	A (13%)	G (100%)	
11,083,088	Intron 2	C	C (100%)	T (6%)*	T (12%)	C (100%)	
11,083,089	Intron 2	C	C (98%)	C (100%)	T (11%)	C (100%)	
11,083,090	Intron 2	C	C (100%)	C (100%)	T (13%)	C (100%)	
11,083,134	Intron 2	G	G (100%)	T (93%)	T (83%)	C (79%)	
11,083,177	Intron 2	C	C (100%)	T (6%)*	T (13%)	C (100%)	
11,083,180	Intron 2	C	C (100%)	C (100%)	T (12%)	C (100%)	
11,083,313	Exon 3 (PRP-1)	TTG	TTG (98%)	TTA (12%)	TTA (5%)*	TTG (94%)	UUG→L ₃₅ UUA→L ₃₅
11,083,445	Exon 3 (PRP-1)	CCC	CCC (100%)	CCT (11%)	CCC (100%)	CCC (100%)	CCC→P ₇₉ CCU→P ₇₉
11,083,502	Exon 3 (PRP-1)	CAG	CAG (98%)	CAG (100%)	CAA (20%)	CAG (100%)	CAG→Q ₉₈ CAA→Q ₉₈
11,083,613	Exon 3 (PRP-1)	CCC	CCC (100%)	CCC (100%)	CCC (100%)	CCT (60%)	CCC→P ₁₃₅ CCU→P ₁₃₅
11,083,622	Exon 3 (PRP-1)	GGC	GGC (100%)	GGC (100%)	GGT (11%)	GGC (100%)	GGC→G ₁₃₈ GGU→G ₁₃₈
11,083,671	3'UTR	C	C (100%)	C (100%)	T (12%)	C (100%)	
11,083,677	3'UTR	T	C (100%)	C (100%)	C (85%)	C (93%)	
11,083,679	3'UTR	G	G (100%)	G (100%)	A (12%)	G (100%)	
11,083,689	Intron 3	C	C (100%)	T (14%)	T (4%)*	C (100%)	
11,083,700	Intron 3	C	C (100%)	C (100%)	T (3%)*	T (86%)	
11,083,709	Intron 3	G	G (98%)	A (13%)	A (3%)*	G (100%)	
11,083,819	Intron 3	T	T (100%)	T (100%)	T (100%)	C (39%)	
11,083,828	Intron 3	G	G (100%)	A (11%)	A (5%)*	G (100%)	
11,083,870	Intron 3	C	C (100%)	C (100%)	T (12%)	C (100%)	

11,083,899	Intron 3	C	C (100%)	T (4%)*	T (13%)	C (100%)
11,083,900	Intron 3	C	C (100%)	T (3%)*	T (13%)	C (100%)
11,083,951	Intron 3	G	G (100%)	A (13%)	G (100%)	G (100%)
11,083,962	Intron 3	C	C (100%)	C (100%)	T (12%)	C (100%)
11,083,967	Intron 3	C	C (100%)	T (5%)*	T (11%)	C (100%)
11,084,096	Intron 3	C	C (98%)	T (13%)	T (4%)*	C (100%)
11,084,126	Intron 3	C	C (100%)	T (12%)	C (100%)	C (100%)
11,084,167	Intron 3	C	C (100%)	T (11%)	C (100%)	C (100%)
11,084,228	Intron 3	C	C (100%)	T (13%)	T (6%)*	C (100%)
11,084,229	Intron 3	C	C (100%)	T (13%)	T (5%)*	C (100%)
11,084,419	Intron 3	T	InsT (2%)* delT (7%)*	InsT (16%)	InsT (8%)* delT (6%)*	delT (14%)
11,084,464	Intron 3	A	G (96%)	G (96%)	G (98%)	G (100%)
11,084,646	Intron 3	C	C (100%)	C (100%)	T (16%)	C (100%)
11,084,671	Intron 3	G	G (100%)	A (3%)*	A (3%)*	G (100%)
11,084,698	Intron 3	G	G (100%)	A (7%)*	A (11%)	G (100%)
11,084,701	Intron 3	G	G (100%)	A (3%)*	A (18%)	G (100%)
11,084,702	Intron 3	G	G (100%)	G (100%)	A (13%)	G (100%)
11,084,711	Intron 3	G	A (2%)*	A (13%)	G (100%)	G (100%)
11,084,750	Intron 3	C	C (98%)	C (95%)	A (17%)	C (97%)
11,084,798	Intron 3	G	G (100%)	G (100%)	A (13%)	G (100%)
11,084,799	Intron 3	C	C (100%)	T (4%)*	T (13%)	C (100%)
11,084,807	Intron 3	C	C (100%)	T (11%)	C (100%)	C (100%)
11,084,825	3'UTR	G	G (100%)	A (4%)*	A (11%)	G (100%)
11,084,960	3'UTR	G	G (100%)	G (100%)	A (13%)	G (100%)
11,084,999	3'UTR	G	G (100%)	A (3%)*	A (14%)	G (100%)
11,085,183	3'UTR	G	G (100%)	A (100%)	G (100%)	G (100%)
11,085,272	3'UTR	C	C (100%)	C (100%)	T (11%)	C (100%)
11,085,302	3'UTR	C	T (2%)*	C (100%)	T (13%)	C (100%)
11,085,303	3'UTR	C	T (2%)*	C (100%)	T (13%)	C (100%)
11,085,331	3'UTR	G	G (100%)	G (100%)	A (11%)	G (97%)
11,085,392	3'UTR	C	C (100%)	T (7%)*	T (11%)	C (100%)
11,085,499	3'UTR	G	G (100%)	G (97%)	A (15%)	G (100%)
11,085,555	3'UTR	C	C (98%)	T (3%)*	T (17%)	C (100%)
11,085,557	3'UTR	C	T (100%)	T (2%)*	T (13%)	T (100%)

11,085,704	3'UTR	G	G (100%)	A (17%)	A (6%)*	G (97%)
11,085,705	3'UTR	G	G (100%)	A (13%)	G (100%)	G (100%)
11,085,739	3'UTR	T	T (100%)	C (100%)	C (100%)	T (100%)
11,085,747	3'UTR	G	A (1%)*	G (100%)	A (13%)	G (100%)
11,085,925	3'UTR	C	T (100%)	T (6%)*	T (13%)	T (100%)
11,085,964	3'UTR	C	T (100%)	T (3%)*	T (13%)	T (100%)
11,086,132	3'UTR	G	A (2%)*	A (13%)	A (3%)*	G (100%)
11,086,145	3'UTR	C	T (100%)	T (97%)	T (97%)	T (100%)
11,086,323	3'UTR	G	A (3%)*	G (100%)	A (14%)	G (100%)
11,086,491	3'UTR	G	G (100%)	G (100%)	A (13%)	G (100%)
11,086,570	3'UTR	G	G (100%)	C (100%)	C (100%)	G (100%)
11,086,646	3'UTR	C	C (100%)	T (3%)*	T (11%)	T (3%)*
11,086,828	3'UTR	C	C (100%)	T (14%)	T (4%)*	C (100%)
11,086,844	3'UTR	C	C (100%)	T (11%)	C (100%)	C (100%)
11,086,849	3'UTR	C	C (100%)	T (11%)	T (3%)*	T (5%)*
11,086,882	3'UTR	C	C (100%)	T (11%)	T (5%)*	C (100%)
11,086,908	3'UTR	C	C (100%)	T (16%)	T (8%)*	C (100%)
11,086,910	3'UTR	C	C (100%)	T (4%)*	T (11%)	C (100%)
11,086,966	3'UTR	G	G (100%)	G (100%)	A (13%)	G (100%)
11,086,987	3'UTR	C	G (100%)	T (4%)*	C (100%)	C (100%)
11,087,001	3'UTR	C	C (100%)	T (12%)	T (12%)	C (100%)
11,087,003	3'UTR	C	C (100%)	C (100%)	T (11%)	C (100%)
11,087,039	3'UTR	C	C (100%)	T (13%)	T (3%)*	C (100%)
11,087,080	3'UTR	G	G (100%)	A (15%)	A (8%)*	G (100%)
11,087,107	3'UTR	G	G (100%)	G (100%)	A (13%)	G (100%)
11,087,118	3'UTR	G	T (3%)*	A (11%)	A (7%)*	G (100%)
11,087,172	3'UTR	C	A (2%)*	T (16%)	C (100%)	A (3%)*
11,087,173	3'UTR	C	T (100%)	T (11%)	T (16%)	T (100%)
11,087,199	3'UTR	G	G (100%)	G (100%)	A (13%)	G (100%)
11,087,215	3'UTR	C	C (99%)	T (11%)	C (100%)	C (100%)
11,087,216	3'UTR	C	C (100%)	T (17%)	T (5%)*	C (97%)
11,087,220	3'UTR	A	delA (91%)	T (29%) delA (45%)	delA (82%)	delA (82%)
11,087,260	3'UTR	T	T (100%)	C (100%)	C (100%)	T (100%)
11,087,348	3'UTR	G	G (100%)	C (100%)	C (88%) T (12%)	G (100%)

11,087,467	Downstream regions	C	C (100%)	T (3%)*	T (11%)	C (100%)
11,087,570	Downstream regions	G	G (100%)	A (14%)	G (100%)	G (100%)
11,087,615	Downstream regions	G	G (100%)	A (12%)	G (100%)	G (100%)
11,087,625	Downstream regions	G	G (100%)	A (13%)	A (8%)*	G (100%)
11,087,626	Downstream regions	G	G (98%)	A (12%)	A (7%)*	G (100%)
11,087,765	Downstream regions	C	T (2%)*	C (100%)	T (11%)	C (100%)
11,087,766	Downstream regions	G	A (2%)*	G (100%)	A (11%)	G (100%)
11,087,811	Downstream regions	G	G (100%)	A (12%)	G (100%)	G (100%)

n.a.: not available; the variant frequency is referred to the percentage of the highlighted base in the sequenced ancient hominine genome, with* frequency≤10% and ** counts<10. In light orange are underlined the variants fixed at 100% in modern human compared to ancient hominines.