

Table S1. Nucleotide Substitutions in *PRB1* 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
11,508,879	Upstream regions	G	C (10%) *	C (15%)	C (26%)	C (26%)	
11,508,854	Upstream regions	C	C (100%)	T (11%)	T (3%) *	C (100%)	
11,508,728	Upstream regions	G	A (1%)*	A (13%)	A (7 %)*	G (100%)	
11,508,703	Upstream regions	G	G (100%)	A (11%)	A (6%)*	G (100%)	
11,508,622	Upstream regions	C	C (100%)	T (2%)*	T (13%)	T (2%)*	
11,508,557	Upstream regions	G	G (100%)	G (100%)	A (11%)	G (100%)	
11,508,523	5' UTR	G	G (100%)	G (100%)	A (11%)	G (100%)	
11,508,460	Exon 1 (Signal)	<u>A</u> AC	<u>G</u> AC (27%)	<u>G</u> AC (17%)	<u>G</u> AC (34%)	<u>G</u> AC (31%)	UUG→L _{9(sp)} CUG→L _{9(sp)}
11,508,383	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,508,382	Intron 1	C	C (98%)	T (12%)	T (6%)*	C (100%)	
11,508,345	Intron 1	C	C (97%)	T (13%)	C (100%)	C (100%)	
11,508,296	Intron 1	C	C (100%)	T (13%)	T (4%)*	C (100%)	
11,508,289	Intron 1	C	C (100%)	T (14%)	T (5%)*	C (100%)	
11,508,283	Intron 1	G	G (100%)	A (11%)	A (12%)	G (100%)	
11,508,217	Intron 1	G	G (100%)	G (100%)	A (11%)	G (100%)	
11,508,167	Intron 1	C	C (98%)	C (100%)	T (11%)	C (100%)	
11,508,026	Intron 1	C	C (100%)	C (100%)	T (13%)	C (100%)	
11,508,014	Intron 1	G	G (100%)	A (11%)	G (100%)	G (100%)	
11,507,986	Intron 1	G	G (100%)	A (12%)	A (10%)*	G (100%)	
11,507,916	Intron 1	G	G (100%)	A (11%)	A (7%)*	G (100%)	
11,507,833	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,507,830	Intron 1	G	G (98%)	G (100%)	A (11%)	G (100%)	
11,507,811	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,507,810	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,507,801	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,507,768	Intron 1	G	G (100%)	A (15%)	A (5%)*	G (100%)	
11,507,652	Intron 1	G	G (100%)	G (100%)	A (14%)	G (100%)	
11,507,607	Intron 1	G	G (100%)	G (100%)	A (16%)	G (100%)	
11,507,594	Intron 1	C	C (100%)	T (11%)	C (100%)	C (100%)	
11,507,592	Intron 1	C	C (97%)	T (14%)	C (100%)	C (100%)	
11,507,584	Intron 1	C	C (100%)	T (11%)	C (100%)	C (100%)	

11,507,578	Intron 1	G	G (100%)	G (100%)	A (13%)	G (100%)	
11,507,536	Intron 1	T	A (16%)	A (27%)	A (18%)	A (20%)	
11,507,532	Intron 1	C	C (100%)	T (23%)	T (8%)*	C (100%)	
11,507,236	Intron 2	C	C (100%)	T (4%)*	T (11%)	C (100%)	
11,507,234	Intron 2	C	C (100%)	T (14%)	T (8%)*	C (100%)	
11,507,230	Intron 2	C	T (3%)*	T (13%)	C (100%)	C (100%)	
11,507,214	Intron 2	C	T (2%)*	T (15%)	C (100%)	C (100%)	
11,507,202	Intron 2	G	T (100%)	T (100%)	T (100%)	T (100%)	
11,507,199	Intron 2	G	G (100%)	A (13%)	G (100%)	G (100%)	
11,507,196	Intron 2	C	C (100%)	T (11%)	T (8%)*	C (100%)	
11,507,180	Intron 2	C	C (100%)	T (4%)*	T (14%)	C (100%)	
11,507,074	Intron 2	A	C (100%)	C (100%)	C (98%)	C (100%)	
11,506,905	Exon 3 (II-2)	CC <u>G</u>	CC <u>G</u> (100%)	CC <u>A</u> (11%)	CC <u>A</u> (4%)*	CC <u>G</u> (100%)	GGC→G ₂₈ GGU→G ₂₈
11,506,887	Exon 3 (II-2)	GG <u>G</u>	GG <u>G</u> (100%)	GG <u>A</u> (11%)	GG <u>G</u> (100%)	GG <u>G</u> (100%)	CCC→P ₃₄ CCU→P ₃₄
11,506,794	Exon 3 (II-2)	GG <u>G</u>	GG <u>G</u> (100%)	GG <u>A</u> (12%)	GG <u>G</u> (100%)	GG <u>G</u> (100%)	CCC→P ₆₅ CCU→P ₆₅
11,506,785	Exon 3 (II-2)	CC <u>C</u>	CCT (4%)*	CCT (17%)	CC <u>C</u> (100%)	CCT (5%)*	GGG→G ₆₈ GGA→G ₆₈
11,506,749	Exon 3 (P-E)	TT <u>T</u>	TT <u>C</u> (17%)	TT <u>C</u> (9%)*	TT <u>T</u> (100%)	TT <u>C</u> (10%)*	AAA→K ₅ AAG→K ₅
11,506,533	Exon 3 (Ps-1)	GT <u>T</u>	GTC (5%)*	GTC (5%)*	GTC (4%)*	GTC (14%)	CAA→Q ₁₆ CAG→Q ₁₆
11,506,356	Exon 3 (Ps-1)	CC <u>G</u>	CC <u>G</u> (100%)	CC <u>A</u> (17%)	CC <u>A</u> (17%)	CC <u>A</u> (12%)	GGC→G ₇₅ GGU→G ₇₅
11,506,260	Exon 3 (Ps-1)	TT <u>C</u>	TT <u>C</u> (100%)**	TT <u>T</u> (18%)	TT <u>C</u> (100%)	TT <u>C</u> (100%)	AAG→K ₁₀₇ AAA→K ₁₀₇
11,506,245	Exon 3 (Ps-1)	GG <u>G</u>	GG <u>G</u> (100%)**	GG <u>A</u> (18%)	GG <u>A</u> (6%)*	GG <u>G</u> (100%)	CCC→P ₁₁₂ CCU→P ₁₁₂
11,506,040	3' UTR	G	G (100%)	A (5%)*	A (13%)	G (100%)	
11,505,908	Intron 3	C	C (100%)	T (11%)	T (5%)*	C (100%)	
11,505,736	Intron 3	G	G (98%)	A (13%)	G (90%)	G (100%)	
11,505,708	Intron 3	G	A (1%)*	A (12%)	A (6%)*	G (100%)	
11,505,389	Intron 3	G	G (100%)	A (14%)	G (100%)	G (100%)	
11,505,375	Intron 3	G	A (65%)	A (59%)	A (59%)	A (47%)	
11,505,362	Intron 3	G	G (100%)	G (100%)	A (11%)	G (100%)	
11,505,347	Intron 3	C	C (100%)	T (11%)	C (100%)	C (100%)	
11,505,277	Intron 3	C	C (100%)	T (2%)*	T (14%)	T (2%)*	
11,505,249	Intron 3	G	A (2%)*	A (3%)*	A (17%)	G (100%)	
11,505,246	Intron 3	G	A (2%)*	A (8%)*	A (12%)	G (100%)	
11,505,168	Intron 3	C	C (100%)	T (13%)	T (5%)*	C (100%)	
11,505,069	Intron 3	G	A (58%)	A (46%)	A (51%)	A (49%)	

11,504,999	Intron 3	C	C (100%)	T (4%)*	T (21%)	C (100%)
11,504,988	Intron 3	C	C (99%)	T (11%)	C (100%)	C (100%)
11,504,987	Intron 3	C	T (1%)*	T (4%)*	T (17%)	C (100%)
11,504,980	Intron 3	C	C (100%)	T (12%)	C (100%)	C (100%)
11,504,970	Intron 3	C	C (100%)	T (12%)	C (100%)	C (100%)
11,504,952	Intron 3	C	C (100%)	C (100%)	T (15%)	C (100%)
11,504,942	Intron 3	C	C (100%)	C (100%)	T (13%)	C (100%)
11,504,691	Downstream regions	C	C (100%)	T (13%)	T (7%)*	C (100%)
11,504,589	Downstream regions	G	G (100%)	A (12%)	A (5%)*	G (100%)
11,504,563	Downstream regions	G	G (100%)	A (13%)	A (13%)	G (100%)
11,504,561	Downstream regions	G	G (100%)	G (100%)	A (17%)	G (100%)
11,504,548	Downstream regions	C	C (100%)	C (100%)	T (12%)	C (100%)
11,504,493	Downstream regions	G	G (100%)	A (11%)	A (4%)*	G (100%)
11,504,491	Downstream regions	G	G (100%)	A (12%)	A (4%)*	G (100%)
11,504,470	Downstream regions	G	G (100%)	A (13%)	G (100%)	G (100%)
11,504,425	Downstream regions	A	G (100%)	G (96%)	G (91%)	G (100%)
11,504,388	Downstream regions	C	T (3%)*	T (5%)*	T (13%)	C (100%)
11,504,360	Downstream regions	G	G (98%)	A (17%)	G (100%)	G (100%)
11,504,295	Downstream regions	C	C (100%)	C (100%)	T (14%)	C (100%)
11,504,272	Downstream regions	G	G (100%)	G (100%)	A (23%)	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.