

Table S2. Nucleotide Substitutions in *PRB2* 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
11,548,942	Upstream regions	G	G (100%)	G (100%)	A (13%)	G (100%)	
11,548,866	Upstream regions	G	G (100%)	G (100%)	A (13%)	G (100%)	
11,548,855	Upstream regions	G	C (70%)	C (71%)	C (61%)	C (76%)	
11,548,817	Upstream regions	C	C (99%)	T (3%)*	T (12%)	C (100%)	
11,548,807	Upstream regions	G	G (100%)	A (6%)*	A (20%)	A (2%)*	
11,548,679	Upstream regions	G	G (100%)	A (5%)*	A (12%)	G (100%)	
11,548,613	Upstream regions	C	C (100%)	T (18%)	C (100%)	C (100%)	
11,548,610	Upstream regions	C	C (100%)	T (15%)	C (100%)	C (100%)	
11,548,583	Upstream regions	C	C (100%)	C (100%)	T (20%)	C (100%)	
11,548,522	Upstream regions	C	C (100%)	T (11%)	T (7%)*	C (100%)	
11,548,436	Exon 1 (Signal)	<u>A</u> AC	<u>G</u> AC (69%)	<u>G</u> AC (58%)	<u>G</u> AC (60%)	<u>G</u> AC (67%)	UUG→L ^{9(sp)} CUG→L ^{9(sp)}
11,548,358	Intron 1	C	C (100%)	C (100%)	T (15%)	C (100%)	
11,548,273	Intron 1	C	T (2%)*	T (3%)*	T (13%)	C (100%)	
11,548,178	Intron 1	C	C (100%)	T (11%)	C (100%)	C (100%)	
11,548,055	Intron 1	C	C (100%)	T (16%)	T (5%)*	C (100%)	
11,548,051	Intron 1	C	C (100%)	T (17%)	T (7%)*	C (100%)	
11,547,994	Intron 1	C	C (100%)	T (9%)*	T (11%)	C (100%)	
11,547,988	Intron 1	C	C (100%)	T (15%)	T (4%)*	C (100%)	
11,547,770	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,547,743	Intron 1	G	G (100%)	A (7%)*	A (14%)	G (100%)	
11,547,734	Intron 1	C	C (100%)	T (12%)	C (100%)	C (100%)	
11,547,684	Intron 1	C	C (100%)	T (12%)	T (8%)*	C (100%)	
11,547,682	Intron 1	C	C (100%)	T (12%)	T (4%)*	C (100%)	
11,547,651	Intron 1	G	G (100%)	A (4%)*	A (12%)	G (100%)	
11,547,642	Intron 1	G	G (100%)	A (8%)*	A (13%)	G (100%)	
11,547,639	Intron 1	G	G (100%)	A (4%)*	A (15%)	G (100%)	
11,547,624	Intron 1	G	A (2%)*	A (5%)*	A (11%)	G (100%)	
11,547,595	Intron 1	C	C (100%)	T (14%)	T (3%)*	C (100%)	
11,547,570	Intron 1	C	C (100%)	T (7%)*	T (11%)	C (100%)	

11,547,569	Intron 1	C	T (2%)*	T (11%)	T (6%)*	C (100%)	
11,547,568	Intron 1	C	C (100%)	T (7%)*	T (16%)	C (100%)	
11,547,565	Intron 1	C	C (100%)	T (4%)*	T (12%)	C (100%)	
11,547,493	Intron 1	C	A (97%)	A (100%)	A (100%)	A (94%)	
11,547,428	Intron 2	C	T (2%)*	T (13%)	T (3%)*	C (100%)	
11,547,411	Intron 2	G	G (100%)	A (13%)	A (3%)*	G (100%)	
11,547,319	Intron 2	C	C (100%)	T (12%)	T (6%)*	C (100%)	
11,547,282	Intron 2	G	A (3%)*	A (6%)*	A (15%)	G (100%)	
11,547,238	Intron 2	C	C (100%)	T (3%)*	T (15%)	C (100%)	
11,547,210	Intron 2	C	C (100%)	T (12%)	T (8%)*	C (100%)	
11,547,206	Intron 2	C	C (100%)	T (4%)*	T (15%)	C (100%)	
11,547,196	Intron 2	G	G (100%)	A (100%)	A (13%)	G (100%)	
11,547,194	Intron 2	G	G (100%)	A (8%)*	A (20%)	G (100%)	
11,547,185	Intron 2	C	C (100%)	C (100%)	T (13%)	C (100%)	
11,547,160	Intron 2	G	A (100%)	A (100%)	G (100%)	G (100%)	
11,547,133	Intron 2	G	A (3%)*	A (11%)	G (100%)	G (100%)	
11,547,130	Intron 2	G	G (100%)	A (11%)	G (100%)	G (100%)	
11,547,117	Intron 2	C	C (100%)	C (100%)	T (11%)	C (97%)	
11,547,581	Intron 2	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,546,742	Exon 3 (IB-1)	G <u>T</u> <u>T</u>	G <u>T</u> <u>C</u> (15%)	G <u>T</u> <u>C</u> (30%)	G <u>T</u> <u>C</u> (9%)*	G <u>T</u> <u>C</u> (35%)	CAA→Q ₇₄ CAG→Q ₇₄
11,546,634	Exon 3 (P-J)	C <u>C</u> <u>G</u>	C <u>C</u> <u>A</u> (3%)*	C <u>C</u> <u>A</u> (15%)	C <u>C</u> <u>A</u> (16%)	C <u>C</u> <u>A</u> (6%)*	GGC→G ₁₄ GGU→G ₁₄
11,546,559	Exon 3 (P-J)	G <u>T</u> <u>T</u>	G <u>T</u> <u>C</u> (8%)*	G <u>T</u> <u>C</u> (18%)	G <u>T</u> <u>C</u> (22%)	G <u>T</u> <u>C</u> (19%)	CAA→Q ₃₉ CAG→Q ₃₉
11,546,553	Exon 3 (P-J)	G <u>G</u> <u>G</u>	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>A</u> (11%)	G <u>G</u> <u>G</u> (100%)	CCC→P ₄₂ CCU→P ₄₂
11,546,523	Exon 3 (P-J)	G <u>G</u> <u>G</u>	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>A</u> (13%)	G <u>G</u> <u>G</u> (100%)	CCC→P ₅₂ CCU→P ₅₂
11,546,373	Exon 3 (IB-8a)	G <u>T</u> <u>T</u>	G <u>T</u> <u>C</u> (10%)	G <u>T</u> <u>T</u> (100%)	G <u>T</u> <u>C</u> (27%)	G <u>T</u> <u>C</u> (5%)*	CAA→Q ₃₉ CAG→Q ₃₉
11,546,367	Exon 3 (IB-8a)	G <u>G</u> <u>G</u>	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>A</u> (11%)	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>G</u> (100%)	CCC→P ₄₁ CCU→P ₄₁
11,546,262	Exon 3 (IB-8a)	C <u>C</u> <u>G</u>	C <u>C</u> <u>A</u> (11%)	C <u>C</u> <u>A</u> (8%)*	C <u>C</u> <u>A</u> (5%)*	C <u>C</u> <u>A</u> (5%)*	GGC→G ₇₆ GGU→G ₇₆
11,546,259	Exon 3 (IB-8a)	T <u>T</u> <u>G</u>	T <u>T</u> <u>G</u> (100%)	T <u>T</u> <u>A</u> (27%)	T <u>T</u> <u>G</u> (100%)	T <u>T</u> <u>G</u> (100%)	AAC→N ₇₇ AAC→N ₇₇
11,546,088	Exon 3 (P-F)	G <u>G</u> <u>G</u>	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>A</u> (17%)	G <u>G</u> <u>G</u> (100%)	CCC→P ₁₀ CCU→P ₁₀
11,546,013	Exon 3 (P-F)	C <u>C</u> <u>G</u>	C <u>C</u> <u>A</u> (3%)*	C <u>C</u> <u>A</u> (15%)	C <u>C</u> <u>G</u> (100%)	C <u>C</u> <u>G</u> (100%)	GGC→G ₃₅ GGU→G ₃₅
11,546,007	Exon 3 (P-F)	T <u>T</u> <u>T</u>	T <u>T</u> <u>T</u> (100%)	T <u>T</u> <u>T</u> (100%)	T <u>T</u> <u>T</u> (100%)	T <u>T</u> <u>C</u> (15%)	AAA→K ₃₇ AAG→K ₃₇
11,546,001	Exon 3 (P-F)	G <u>T</u> <u>T</u>	G <u>T</u> <u>C</u> (11%)	G <u>T</u> <u>C</u> (100%)	G <u>T</u> <u>C</u> (13%)	G <u>T</u> <u>C</u> (11%)	CAA→Q ₃₉ CAG→Q ₃₉
11,545,965	Exon 3 (P-F)	G <u>G</u> <u>G</u>	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>A</u> (14%)	G <u>G</u> <u>G</u> (100%)	G <u>G</u> <u>G</u> (100%)	CCC→P ₅₁ CCU→P ₅₁

11,545,790	Exon 3 (P-H)	CCC	CCC (100%)	CCC (100%)	CCT (14%)	CCC (100%)	GGG→G ₄₈ GGA→G ₄₈
11,544,480	3' UTR	G	A (2%)*	A (11%)	G (100%)	G (97%)	
11,544,389	Downstream regions	G	T (100%)	T (100%)	G (96%)	G (100%)	
11,544,353	Downstream regions	G	G (98%)	A (68%)	A (38%)	G (100%)	
11,544,289	Downstream regions	G	G (100%)	A (13%)	A (6%)*	G (100%)	
11,544,278	Downstream regions	G	G (100%)	A (15%)	A (6%)*	G (100%)	
11,544,213	Downstream regions	G	G (100%)	A (19%)	A (7%)*	G (100%)	
11,544,172	Downstream regions	G	G (100%)	A (3%)*	A (14%)	G (100%)	
11,544,043	Downstream regions	C	C (100%)	T (6%)*	T (11%)	C (100%)	
11,544,014	Downstream regions	G	A (100%)	A (100%)	A (100%)	A (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%. In light orange are underlined the variants fixed at 100% in modern human compared to ancient hominines.