

Table S4. Nucleotide Substitutions in *PRB4* 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
11,463,890	Upstream regions	C	C (100%)	T (13%)	T (9%)*	C (100%)	
11,463,868	Upstream regions	G	T (100%)	T (100%)	T (100%)	T (100%)	
11,463,814	Upstream regions	A	T (97%)	T (100%)	T (100%)	T (100%)	
11,463,813	Upstream regions	G	A (100%)	A (100%)	A (100%)	A (97%)	
11,463,806	Upstream regions	G	G (100%)	G (100%)	A (13%)	G (100%)	
11,463,780	Upstream regions	G	G (100%)	A (4%)*	A (13%)	G (100%)	
11,463,693	Upstream regions	C	C (100%)	T (3%)*	T (13%)	C (100%)	
11,463,675	Upstream regions	C	T (3%)*	C (100%)	T (11%)	C (100%)	
11,463,623	Upstream regions	G	G (100%)	A (4%)*	A (11%)	G (100%)	
11,463,613	Upstream regions	T	T (100%)	T (100%)	T (100%)	A (100%)	
11,463,513	Upstream regions	T	T (100%)	T (100%)	T (100%)	C (56%)	
11,463,491	Upstream regions	C	C (100%)	T (5%)*	T (11%)	C (100%)	
11,463,480	Upstream regions	G	T (3%)*	T (4%)*	T (11%) A (11%)	T (4%)*	
11,463,443	Upstream regions	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,463,391	Upstream regions	C	C (100%)	T (13%)	C (100%)	C (100%)	
11,463,375	Upstream regions	G	G (100%)	G (100%)	A (21%)	A (5%)*	
11,463,335	5'UTR	C	T (100%)	T (100%)	T (100%)	T (100%)	
11,463,302	Exon 1 (Signal)	<u>G</u> AC	<u>G</u> AC (100%)	<u>A</u> AC (13%)	<u>A</u> AC (6%)*	<u>G</u> AC (100%)	CUG→L ₁₀ (sp) UUG→L ₁₀ (sp)
11,463,193	Intron 1	C	C (100%)	T (4%)*	T (12%)	C (100%)	
11,463,190	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,463,130	Intron 1	G	G (100%)	A (24%)	A (8%)*	G (100%)	
11,463,113	Intron 1	C	C (100%)	C (100%)	T (13%)	T (2%)*	
11,463,051	Intron 1	T	A (100%)	T (100%)	T (100%)	T (100%)	
11,463,030	Intron 1	C	C (100%)	C (100%)	T (11%)	C (97%)	
11,463,028	Intron 1	C	C (100%)	C (100%)	T (16%)	C (100%)	
11,463,000	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,462,979	Intron 1	C	A (98%)	A (96%)	A (96%)	A (100%)	
11,462,919	Intron 1	G	G (100%)	G (100%)	A (11%)	G (100%)	
11,462,900	Intron 1	C	C (100%)	T (9%)*	T (11%)	C (100%)	

11,462,894	Intron 1	C	C (98%)	C (100%)	T (11%)	C (100%)	
11,462,827	Intron 1	G	G (98%)	G (100%)	A (20%)	G (100%)	
11,462,558	Intron 1	C	C (100%)	T (14%)	C (100%)	C (100%)	
11,462,521	Intron 1	C	C (100%)	C (100%)	T (21%)	C (100%)	
11,462,507	Intron 1	G	G (100%)	A (16%)	A (7%)*	G (100%)	
11,462,505	Intron 1	G	G (100%)	A (11%)	G (100%)	G (100%)	
11,462,504	Intron 1	G	G (100%)	A (15%)	G (94%)	G (100%)	
11,462,487	Intron 1	G	G (100%)	A (14%)	A (7%)*	G (100%)	
11,462,486	Intron 1	G	G (100%)	A (14%)	A (6%)*	G (100%)	
11,462,477	Intron 1	G	G (100%)	A (12%)	G (100%)	G (100%)	
11,462,432	Intron 1	C	C (100%)	T (4%)*	T (11%)	C (100%)	
11,462,430	Intron 1	C	C (100%)	T (3%)*	T (12%)	C (100%)	
11,462,392	Intron 1	C	T (2%)*	C (100%)	T (11%)	C (100%)	
11,462,317	Exon 2 (PGA)	<u>GAG</u>	<u>GAG</u> (100%)	<u>GAA</u> (17%)	<u>GAG</u> (100%)	<u>GAT</u> (4%)*	CUC→L ₁₃ CUU→L ₁₃
11,462,269	Intron 2	G	G (100%)	A (14%)	A (4%)*	G (100%)	
11,462,185	Intron 2	G	G (100%)	A (11%)	G (100%)	G (100%)	
11,462,175	Intron 2	A	A (99%)	A (100%)	A (100%)	G (100%)	
11,462,142	Intron 2	G	G (98%)	G (100%)	A (15%)	G (100%)	
11,462,082	Intron 2	C	C (100%)	C (100%)	T (19%)	C (100%)	
11,462,081	Intron 2	C	C (100%)	C (100%)	T (27%)	C (100%)	
11,462,076	Intron 2	G	G (100%)	A (13%)	G (100%)	G (100%)	
11,462,027	Intron 2	C	C (100%)	T (14%)	C (100%)	C (100%)	
11,462,002	Intron 2	C	A (93%)	A (95%)	A (80%)	A (95%)	
11,461,980	Intron 2	G	A (2%)*	A (13%)	A (3%)*	G (100%)	
11,461,978	Intron 2	G	G (100%)	A (12%)	A (13%)	G (100%)	
11,461,860	Intron 2	A	G (14%)	G (13%)	G (15%)	G (33%)	
11,461,836	Intron 2	T	C (100%)	C (100%)	C (100%)	C (100%)	
11,461,470	Exon 3 (PGA)	<u>CCA</u>	<u>CCT</u> (5%)*	<u>CCT</u> (15%)	<u>CCT</u> (17%)	<u>CCG</u> (11%)	GGU→G ₁₃₃ GGA→G ₁₃₃
11,461,452	Exon 3 (PGA)	<u>GGG</u>	<u>GGG</u> (100%)	<u>GGA</u> (11%)	<u>GGA</u> (4%)*	<u>GGG</u> (100%)	CCC→P ₁₃₉ CCU→P ₁₃₉
11,461,155	3'UTR	C	C (100%)	T (16%)	C (100%)	C (100%)	
11,461,009	Intron 4	C	C (100%)	T (4%)*	T (21%)	C (100%)	
11,461,004	Intron 4	C	C (100%)	T (6%)*	T (11%)	C (100%)	
11,461,002	Intron 4	C	C (100%)	C (96%)	T (16%)	C (100%)	
11,460,987	Intron 4	T	T (100%)	A (35%)	T (100%)	T (100%)	

11,460,919	Intron 4	C	C (100%)	T (14%)	C (100%)	C (100%)
11,460,891	Intron 4	G	G (100%)	G (100%)	T (11%)	G (100%)
11,460,868	Intron 4	G	G (100%)	A (4%)*	A (14%)	G (100%)
11,460,860	Intron 4	C	C (100%)	C (100%)	T (12%)	C (100%)
11,460,821	Intron 4	G	G (99%)	A (13%)	A (6%)*	G (100%)
11,460,819	Intron 4	G	A (3%)*	A (8%)*	A (11%)	G (100%)
11,460,683	Intron 4	G	G (100%)	A (19%)	G (100%)	G (100%)
11,460,647	Intron 4	C	C (100%)	T (15%)	T (13%)	C (100%)
11,460,636	Intron 4	G	G (98%)	A (13%)	A (6%)*	G (100%)
11,460,532	Intron 4	G	G (100%)	A (8%)*	A (22%)	G (100%)
11,460,531	Intron 4	G	G (100%)	G (100%)	A (13%)	G (100%)
11,460,498	Intron 4	C	C (99%)	T (15%)	T (12%)	C (100%)
11,460,445	Intron 4	C	C (100%)	T (5%)*	T (13%)	C (100%)
11,460,394	Intron 4	G	G (100%)	A (11%)	A (10%)*	G (100%)
11,460,245	Intron 4	C	C (100%)	T (14%)	C (100%)	C (100%)
11,460,244	Intron 4	G	G (98%)	A (5%)*	A (13%)	G (100%)
11,460,231	Intron 4	C	T (98%)	T (100%)	T (100%)	T (100%)
11,460,224	Intron 4	G	A (11%)	G (98%)	G (100%)	G (100%)
11,460,070	3'UTR	C	C (98%)	C (100%)	T (13%)	C (100%)
11,460,054	3'UTR	C	C (100%)	T (9%)*	T (17%)	C (100%)
11,459,932	Downstream regions	G	G (100%)	A (14%)	A (5%)*	G (100%)
11,459,865	Downstream regions	T	C (99%)	C (97%)	C (93%)	C (100%)
11,459,793	Downstream regions	G	A (2%)*	A (5%)*	A (11%)	G (100%)
11,459,750	Downstream regions	G	G (98%)	A (12%)	G (100%)	G (100%)
11,459,722	Downstream regions	G	G (100%)	G (100%)	A (11%)	A (4%)*
11,459,713	Downstream regions	G	G (100%)	A (21%)	A (6%)*	G (100%)
11,459,706	Downstream regions	G	G (100%)	A (4%)*	A (11%)	G (100%)
11,459,689	Downstream regions	C	C (100%)	T (9%)*	T (18%)	C (97%)
11,459,685	Downstream regions	G	G (98%)	G (100%)	A (14%)	G (100%)
11,459,684	Downstream regions	G	G (100%)	A (3%)*	A (14%)	G (100%)
11,459,683	Downstream regions	G	A (2%)*	G (100%)	A (13%)	G (100%)
11,459,645	Downstream regions	C	C (100%)	C (100%)	T (11%)	C (100%)
11,459,633	Downstream regions	G	G (100%)	A (11%)	A (5%)*	G (100%)

11,459,625	Downstream regions	C	C (100%)	C (100%)	T (12%)	C (100%)
11,459,615	Downstream regions	C	C (100%)	C (100%)	T (14%)	C (100%)
11,459,596	Downstream regions	C	C (100%)	C (100%)	T (11%)	C (100%)
11,459,588	Downstream regions	C	G (18%)	C (100%)	C (100%)	G (5%)*
11,459,568	Downstream regions	C	A (25%)	C (100%)	A (4%)*	A (6%)*
11,459,566	Downstream regions	C	C (100%)	C (100%)	T (11%)	C (100%)
11,459,565	Downstream regions	A	G (20%)	A (100%)	A (3%)*	A (100%)
11,459,556	Downstream regions	G	G (100%)	A (38%)	A (7%)*	G (100%)
11,459,551	Downstream regions	T	G (22%)	G (6%)*	T (100%)	G (3%)*
11,459,531	Downstream regions	G	G (100%)	G (100%)	A (13%)	G (97%)

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.