

Table S3. Nucleotide Substitutions in *PRB3* 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
11,422,912	Upstream regions	A	A (100%)	G (4%)*	A (100%)	G (100%)	
11,422,899	Upstream regions	G	G (100%)	A (13%)	A (19%)	G (97%)	
11,422,898	Upstream regions	G	G (100%)	A (4%)*	A (16%)	A (3%)*	
11,422,897	Upstream regions	C	C (100%)	T (8%)*	T (13%)	T (3%)*	
11,422,894	Upstream regions	G	G (100%)	A (12%)	G (100%)	G (100%)	
11,422,892	Upstream regions	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,422,827	Upstream regions	C	C (98%)	C (100%)	T (11%)	C (100%)	
11,422,768	Upstream regions	C	C (100%)	C (100%)	T (15%)	C (100%)	
11,422,763	Upstream regions	G	G (100%)	A (11%)	A (6%)*	G (100%)	
11,422,756	Upstream regions	G	T (95%)	T (96%)	T (100%)	T (94%)	
11,422,745	Upstream regions	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,422,701	Upstream regions	C	C (98%)	C (100%)	T (15%)	C (100%)	
11,422,661	Upstream regions	C	C (100%)	T (4%)*	T (11%)	C (100%)	
11,422,660	Upstream regions	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,422,598	Exon 1 (Signal)	<u>GAT</u>	<u>GAC</u> (2%)*	<u>GAC</u> (8%)*	<u>GAC</u> (18%)	<u>GAC</u> (11%)	CUA→L _{9(sp)} CUG→L _{9(sp)}
11,422,513	Intron 1	C	C (100%)	T (18%)	C (100%)	C (100%)	
11,422,471	Intron 1	C	C (100%)	T (13%)	C (100%)	C (100%)	
11,422,316	Intron 1	C	C (100%)	T (12%)	T (6%)*	C (100%)	
11,422,294	Intron 1	C	C (100%)	T (17%)	T (7%)*	C (98%)	
11,422,265	Intron 1	C	C (100%)	T (12%)	T (11%)	C (100%)	
11,422,251	Intron 1	C	C (100%)	T (4%)*	T (15%)	C (100%)	
11,422,190	Intron 1	A	C (100%)	C (100%)	C (91%)	C (100%)	
11,422,174	Intron 1	G	G (100%)	G (96%)	A (15%)	G (100%)	
11,422,040	Intron 1	G	G (100%)	A (14%)	A (4%)*	G (100%)	
11,422,039	Intron 1	G	G (97%)	A (11%)	G (100%)	G (100%)	
11,422,020	Intron 1	C	C (100%)	T (17%)	T (7%)*	C (100%)	
11,422,013	Intron 1	C	T (2%)*	T (12%)	T (4%)*	C (100%)	
11,422,003	Intron 1	C	C (100%)	T (11%)	T (12%)	C (100%)	
11,422,002	Intron 1	C	C (100%)	C (100%)	T (12%)	C (100%)	

11,421,951	Intron 1	C	C (100%)	T (11%)	C (100%)	C (100%)	
11,421,787	Intron 1	C	T (4%)*	C (100%)	T (11%)	C (100%)	
11,421,775	Intron 1	G	G (97%)	A (13%)	A (6%)*	G (100%)	
11,421,729	Intron 1	C	C (100%)	C (100%)	T (13%)	C (100%)	
11,421,721	Intron 1	A	G (94%)	G (100%)	G (100%)	G (96%)	
11,421,713	Intron 1	G	G (100%)	A (17%)	G (100%)	G (100%)	
11,421,668	Intron 1	C	C (100%)	C (100%)	T (16%)	C (100%)	
11,421,611	Intron 1	G	G (100%)	A (6%)*	A (12%)	G (100%)	
11,421,577	Exon 2 (GI-5)	AG <u>G</u>	AG <u>G</u> (100%)	AG <u>A</u> (11%)	AG <u>G</u> (100%)	AG <u>G</u> (100%)	UCC→S ₁₄ UCU→S ₁₄
11,421,454	Intron 1	C	T (2%)*	T (6%)*	T (16%)	C (100%)	
11,421,371	Intron 1	C	C (100%)	C (100%)	A (56%)	A (3%)*	
11,421,352	Intron 1	C	C (100%)	C (100%)	T (18%)	C (100%)	
11,421,344	Intron 1	C	C (100%)	C (100%)	T (18%)	C (100%)	
11,421,329	Intron 1	C	C (100%)	C (100%)	T (17%)	C (100%)	
11,421,325	Intron 1	C	C (100%)	C (100%)	T (14%)	C (100%)	
11,421,322	Intron 1	C	T (2%)*	C (100%)	T (13%)	C (100%)	
11,421,318	Intron 2	G	G (100%)	A (18%)	A (6%)*	G (100%)	
11,421,295	Intron 2	C	C (100%)	T (13%)	T (4%)*	C (100%)	
11,421,294	Intron 2	C	C (100%)	T (27%)	C (100%)	C (100%)	
11,421,286	Intron 2	G	G (100%)	A (13%)	G (100%)	G (100%)	
11,421,265	Intron 2	C	C (100%)	A (8%)*	C (97%)	A (13%)	
11,421,102	Intron 2	G	G (100%)	G (100%)	A (16%)	G (100%)	
11,421,099	Intron 2	C	C (100%)	C (100%)	T (13%)	C (100%)	
11,420,967	Exon 3 (GI-5)	GG <u>T</u>	GG <u>T</u> (100%)	GG <u>C</u> (36%)	GG <u>T</u> (100%)	GG <u>T</u> (100%)	CCA→P ₅₆ CCG→P ₅₆
11,420,841	Exon 3 (GI-5)	GG <u>T</u>	GG <u>C</u> (27%)	GG <u>T</u> (100%)	GG <u>T</u> (100%)	GG <u>T</u> (100%)	CCA→P ₉₈ CCG→P ₉₈
11,420,799	Exon 3 (GI-5)	CC <u>T</u>	CC <u>T</u> (100%)	CC <u>T</u> (100%)	CC <u>G</u> (20%)	CC <u>T</u> (100%)	GGA→G ₁₁₂ GGC→G ₁₁₂
11,420,781	Exon 3 (GI-5)	GG <u>G</u>	GG <u>G</u> (100%)	GG <u>A</u> (11%)	GG <u>A</u> (5%)*	GG <u>G</u> (100%)	CCC→P ₁₁₈ CCU→P ₁₁₈
11,420,736	Exon 3 (GI-5)	CC <u>T</u>	CC <u>T</u> (100%)	CC <u>G</u> (27%)	CC <u>G</u> (14%)	CC <u>T</u> (100%)	GGA→G ₁₃₃ GGC→G ₁₃₃
11,420,715	Exon 3 (GI-5)	GG <u>C</u>	GG <u>T</u> (2%)*	GG <u>T</u> (24%)	GG <u>T</u> (4%)*	GG <u>C</u> (100%)	CCG→P ₁₄₀ CCA→P ₁₄₀
11,420,601	Exon 3 (GI-2)	AG <u>G</u>	AG <u>G</u> (100%)	AG <u>G</u> (100%)	AG <u>A</u> (11%)	AG <u>G</u> (100%)	UCC→S ₁₇₈ UCU→S ₁₇₈
11,420,496	Exon 3 (GI-2)	GG <u>G</u>	GG <u>A</u> (12%)	GG <u>G</u> (97%)	GG <u>A</u> (3%)*	GG <u>A</u> (8%)*	CCC→P ₂₁₃ CCU→P ₂₁₃
11,420,458	Intron 3	C	T (16%)	T (4%)*	T (33%)	T (15%)	
11,420,454	Intron 3	T	T (100%)	C (37%)	C (18%)	T (100%)	
11,420,440	Intron 3	C	C (100%)	T (4%)*	T (14%)	C (100%)	

11,420,432	Intron 3	G	G (100%)	G (100%)	A (11%)	G (100%)	
11,420,407	Intron 3	C	C (100%)	T (16%)	C (100%)	C (100%)	
11,420,403	Intron 3	G	A (2%)*	A (14%)	G (100%)	G (100%)	
11,420,399	Intron 3	G	A (9%)*	A (13%)	G (98%)	G (100%)	
11,420,395	Intron 3	C	T (6%)*	C (100%)	T (15%)	C (100%)	
11,420,372	Intron 3	G	G (100%)	A (8%)*	A (13%)	G (100%)	
11,420,337	Intron 3	T	T (100%)	G (18%)	G (17%)**	T (100%)	
11,420,336	Intron 3	G	G (100%)	T (24%)	T (17%)**	G (100%)	
11,420,334	Intron 3	G	delG (91%)	delG (77%)	delG (50%)** A (50%)**	delG (89%)	
11,420,306	Exon 4 (Gl-2)	GGG	GGG (100%)	GGA (12%)	GGA (5%)*	GGG (100%)	CCC→P ₂₃₄ CCU→P ₂₃₄
11,420,246	Exon 4 (Gl-2)	GGG	GGG (100%)	GGG (100%)	GGA (14%)	GGG (100%)	CCC→P ₂₅₄ CCU→P ₂₅₄
11,420,225	Exon 4 (Gl-2)	GTC	GTC (100%)	GTC (100%)	GTT (12%)	GTC (100%)	CAG→Q ₂₆₁ CAA→Q ₂₆₁
11,420,218	Exon 4 (Gl-2)	GAC	GAC (100%)	GAC (100%)	AAC (15%)	GAC (100%)	CUG→L ₂₆₄ UUG→L ₂₆₄
11,420,109	3'UTR	C	C (100%)	T (4%)*	T (11%)	C (100%)	
11,420,006	Intron 4	G	delG (95%)	delG (88%)	delG (97%)	delG (100%)	
11,419,970	Intron 4	G	G (100%)	A (12%)	A (5%)*	G (100%)	
11,419,953	Intron 4	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,419,836	Intron 4	G	G (100%)	A (6%)*	A (13%)	G (100%)	
11,419,782	Intron 4	G	G (100%)	A (12%)	G (100%)	G (100%)	
11,419,678	Intron 4	G	G (100%)	A (15%)	A (3%)*	G (100%)	
11,419,650	Intron 4	G	A (2%)*	A (11%)	A (4%)*	G (100%)	
11,419,630	Intron 4	C	T (100%)	T (100%)	T (98%)	T (100%)	
11,419,573	Intron 4	G	G (100%)	A (17%)	A (8%)*	G (100%)	
11,419,509	Intron 4	C	C (100%)	T (7%)*	T (16%)	C (100%)	
11,419,513	Intron 4	G	G (100%)	A (12%)	G (100%)	G (100%)	
11,419,505	Intron 4	A	G (100%)	A (100%)	A (100%)	A (100%)	
11,419,379	Intron 4	C	C (100%)	C (100%)	T (11%)	C (100%)	
11,419,295	Intron 4	G	G (100%)	G (100%)	A (12%)	G (100%)	
11,419,132	Intron 4	G	G (100%)	G (100%)	A (12%)	G (100%)	
11,419,080	Intron 4	C	C (100%)	T (17%)	C (100%)	C (100%)	
11,419,079	Intron 4	C	C (100%)	T (13%)	T (8%)*	C (100%)	
11,419,072	Intron 4	C	T (3%)*	T (10%)*	T (11%)	C (100%)	
11,419,071	Intron 4	C	C (100%)	T (14%)	T (5%)*	C (100%)	

11,419,031	Intron 4	G	G (100%)	G (100%)	A (14%)	G (100%)
11,419,011	Intron 4	G	G (100%)	G (100%)	A (13%)	G (100%)
11,419,001	Intron 4	G	G (100%)	A (14%)	A (4%)*	G (100%)
11,418,969	Intron 4	C	C (100%)	T (13%)	C (100%)	C (100%)
11,418,876	3'UTR	G	G (100%)	A (5%)*	A (27%)	G (100%)
11,418,771	Downstream regions	G	A (2%)*	G (100%)	A (11%)	G (100%)
11,418,769	Downstream regions	G	G (100%)	A (13%)	A (4%)*	G (100%)
11,418,741	Downstream regions	G	G (100%)	A (11%)	A (8%)*	G (100%)
11,418,740	Downstream regions	G	G (98%)	G (100%)	A (15%)	G (100%)
11,418,645	Downstream regions	C	C (100%)	C (100%)	T (14%)	C (100%)
11,418,639	Downstream regions	G	G (98%)	A (11%)	G (100%)	G (100%)
11,418,631	Downstream regions	G	A (4%)*	A (11%)	A (14%)	G (100%)
11,418,630	Downstream regions	G	G (98%)	A (17%)	G (100%)	A (4%)*
11,418,627	Downstream regions	C	C (100%)	C (100%)	T (13%)	C (100%)
11,418,626	Downstream regions	C	C (100%)	C (100%)	T (17%)	C (100%)
11,418,570	Downstream regions	C	C (100%)	T (11%)	T (11%)	C (100%)
11,418,557	Downstream regions	G	A (3%)*	A (3%)*	A (12%)	G (100%)
11,418,555	Downstream regions	G	G (98%)	G (100%)	A (12%)	G (100%)
11,418,546	Downstream regions	G	A (3%)*	G (100%)	A (15%)	G (100%)
11,418,508	Downstream regions	C	C (100%)	C (100%)	T (11%)	C (100%)
11,418,414	Downstream regions	G	G (100%)	G (100%)	A (15%)	G (100%)
11,418,410	Downstream regions	T	C (98%)	C (95%)	C (90%)	C (100%)
11,418,406	Downstream regions	C	C (100%)	C (100%)	T (11%)	C (100%)
11,418,394	Downstream regions	C	T (6%)*	C (100%)	T (17%)	C (100%)
11,418,393	Downstream regions	C	C (100%)	T (13%)	T (6%)*	C (100%)
11,418,386	Downstream regions	G	G (100%)	G (100%)	A (14%)	G (100%)
11,418,372	Downstream regions	G	G (100%)	A (18%)	A (7%)*	G (100%)
11,418,368	Downstream regions	G	G (100%)	G (100%)	A (14%)	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.