

Table S7. Nucleotide Substitutions in *HTN3* 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
70,893,747	Upstream regions	C	C (100%)	T (4%)*	T (13%)	C (100%)	
70,893,792	Upstream regions	C	C (100%)	C (100%)	T (12%)	T (3%)*	
70,893,878	Upstream regions	C	C (100%)	T (12%)	T (2%)*	C (100%)	
70,893,946	Upstream regions	A	A (100%)	A (100%)	G (27%)	A (100%)	
70,893,955	Upstream regions	G	G (100%)	G (100%)	A (19%)	G (100%)	
70,893,964	Upstream regions	C	C (98%)	C (100%)	T (17%)	C (100%)	
70,893,976	Upstream regions	C	C (100%)	C (100%)	T (17%)	C (100%)	
70,894,056	Upstream regions	C	C (100%)	T (13%)	C (100%)	C (100%)	
70,894,081	Upstream regions	A	C (100%)	C (93%)	C (100%)	A (100%)	
70,894,130	5'UTR	G	G (100%)	A (12%)	A (8%)*	G (100%)	
70,894,131	5'UTR	G	G (100%)	G (100%)	A (13%)	A (3%)*	
70,894,159	5'UTR	G	G (100%)	A (5%)*	A (17%)	G (100%)	
70,894,234	Intron 1	G	A (2%)*	A (11%)	A (8%)*	G (100%)	
70,894,357	Intron 1	C	C (100%)	T (11%)	T (3%)*	C (100%)	
70,894,468	Intron 1	C	C (100%)	T (4%)*	T (12%)	C (100%)	
70,894,547	Intron 1	A	A (100%)	A (100%)	A (100%)	C (100%)	
70,894,581	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
70,894,640	Intron 1	C	C (97%)	C (100%)	T (13%)	C (100%)	
70,894,751	Intron 1	C	C (100%)	T (11%)	C (100%)	C (100%)	
70,894,799	Intron 1	C	C (100%)	C (100%)	T (11%)	C (100%)	
70,894,878	Intron 1	C	C (100%)	C (100%)	T (15%)	C (100%)	
70,894,931	Intron 1	C	T (2%)*	T (13%)	T (5%)*	C (100%)	
70,895,173	Intron 1	G	G (98%)	A (3%)*	A (14%)	G (100%)	
70,895,228	Intron 1	C	C (100%)	T (10%)*	T (18%)	C (100%)	
70,895,232	Intron 1	C	T (2%)*	C (100%)	T (19%)	C (100%)	
70,895,241	Intron 1	C	C (100%)	C (100%)	T (12%)	C (100%)	
70,895,243	Intron 1	G	G (100%)	A (13%)	G (100%)	G (100%)	
70,895,244	Intron 1	G	G (100%)	A (13%)	G (100%)	G (100%)	
70,895,361	Intron 1	A	T (63%)	A (100%)	A (100%)	A (100%)	

70,895,411	Intron 1	C	C (100%)	T (12%)	C (100%)	C (100%)
70,895,437- 70,895,438	Intron 1	AC	delAC (72%)	delAC (72%)**	delAC (83%)**	AC (100%)
70,895,440	Intron 1	G	A (100%)	A (100%)**	A (100%)**	G (100%)
70,895,441	Intron 1	G	T (100%)	T (100%)**	T (100%)**	G (100%)
70,895,444	Intron 1	T	G (100%)	G (80%)**	G (100%)**	T (100%)
70,895,466- 70,895,471	Intron 1	AAAAAC	AAAAAC (100%)	AAAAAC (100%)	delAAAAAC (12%)	AAAAAC (100%)
70,895,478	Intron 1	G	G (100%)	G (100%)	A (14%)	G (100%)
70,895,494	Intron 1	T	A (4%)*	A (11%)	T (100%)	T (100%)
70,895,495	Intron 1		InsTTG (82%)	InsTTG (64%)	InsTTG (95%)	-
70,895,572	Intron 1	G	G (100%)	A (11%)	G (97%)	G (100%)
70,895,628	Intron 1	G	G (98%)	A (8%)*	A (15%)	G (100%)
70,895,643	Intron 1	C	C (100%)	C (100%)	T (13%)	C (100%)
70,895,697	Intron 1	C	C (100%)	C (100%)	T (16%)	C (100%)
70,895,736	Intron 1	G	G (98%)	A (7%)*	A (12%)	G (100%)
70,895,787	Intron 1	G	G (98%)	A (3%)*	A (11%)	G (100%)
70,895,846	Intron 1	G	A (2%)*	A (11%)	G (100%)	G (100%)
70,895,900	Intron 1	C	C (100%)	T (14%)	T (5%)*	T (3%)*
70,895,902	Intron 1	C	C (100%)	T (14%)	T (12%)	C (100%)
70,895,905	Intron 1	C	C (100%)	T (5%)*	T (13%)	C (100%)
70,895,912	Intron 1	C	C (100%)	T (14%)	T (13%)	C (100%)
70,895,962	Intron 1	C	C (100%)	T (5%)*	T (11%)	C (100%)
70,896,213	Intron 1	G	G (100%)	A (15%)	A (5%)*	G (100%)
70,896,255	Intron 1	G	G (100%)	A (11%)	G (100%)	G (100%)
70,896,257	Intron 1	C	C (100%)	C (100%)	T (14%)	C (100%)
70,896,285	Intron 1	G	G (100%)	G (100%)	A (16%)	G (100%)
70,896,365	Intron 1	G	G (100%)	G (100%)	A (11%)	G (100%)
70,896,509	Intron 2	G	G (100%)	G (100%)	A (11%)	G (100%)
70,896,812	Intron 2	C	C (100%)	T (18%)	T (4%)*	C (100%)
70,896,813	Intron 2	C	C (100%)	T (17%)	T (5%)*	C (100%)
70,896,839	Intron 2	G	G (100%)	A (11%)	A (4%)*	G (100%)
70,896,875	Intron 2	G	G (100%)	G (100%)	A (11%)	G (100%)
70,896,876	Intron 2	G	G (100%)	A (6%)*	A (11%)	G (100%)
70,896,877	Intron 2	G	G (100%)	G (100%)	A (11%)	G (100%)
70,896,879	Intron 2	G	G (100%)	G (100%)	A (13%)	G (100%)

70,897,046	Intron 2	G	G (98%)	G (100%)	A (13%)	G (100%)	
70,897,113	Intron 2	C	C (100%)	T (14%)	C (100%)	C (100%)	
70,897,179	Intron 2	C	T (2%)*	T (6%)*	T (14%)	C (100%)	
70,897,184	Intron 2	C	C (100%)	C (100%)	T (18%)	C (100%)	
70,897,340	Intron 2	G	G (100%)	G (100%)	A (12%)	G (100%)	
70,897,444	Intron 2	C	C (100%)	T (3%)*	T (11%)	C (100%)	
70,897,522	Intron 2	C	C (100%)	C (100%)	T (11%)	C (97%)	
70,897,523	Intron 2	C	C (98%)	C (100%)	T (11%)	C (100%)	
70,897,571	Intron 2	A	G (98%)	G (100%)	G (96%)	A (100%)	
70,897,695	Intron 2	G	G (100%)	A (4%)*	A (11%)	G (100%)	
70,897,717	Intron 3	G	G (100%)	A (10%)*	A (12%)	G (100%)	
70,897,806	Exon 4	GGG	GGG (100%)	GGA (12%)	GGA (5%)*	GGG (100%)	GGG→G ₉ GGA→G ₉
70,897,829	Intron 4	G	G (100%)	A (5%)*	A (13%)	G (100%)	
70,898,014	Intron 4	C	G (100%)	G (96%)*	G (95%)	C (100%)	
70,898,016	Intron 4	G	A (2%)*	A (17%)	A (5%)*	G (100%)	
70,898,027	Intron 4	A	C (100%)	C (100%)	C (98%)	A (100%)	
70,898,115	Intron 4	C	C (100%)	C (100%)	T (11%)	C (97%)	
70,898,122	Intron 4	C	C (98%)	T (13%)	T (3%)*	C (100%)	
70,898,177	Intron 4	G	A (2%)*	A (11%)	A (10%)*	G (100%)	
70,898,289	Intron 4	G	G (100%)	G (100%)	A (11%)	G (100%)	
70,898,340	Intron 4	G	A (98%)	A (100%)	A (100%)	G (100%)	
70,898,459	Intron 4	G	G (100%)	A (3%)*	A (11%)	G (100%)	
70,898,488	Intron 4	T	T (100%)	T (100%)	T (100%)	C (100%)	
70,898,561	Intron 4	G	G (100%)	G (100%)	A (11%)	G (100%)	
70,898,562	Intron 4	G	G (100%)	A (3%)*	A (11%)	G (100%)	
70,898,563	Intron 4	G	G (100%)	A (6%)*	A (11%)	G (100%)	
70,898,617	Intron 4	G	G (100%)	G (97%)	A (11%)	G (100%)	
70,898,619	Intron 4	G	G (100%)	G (100%)	A (12%)	G (100%)	
70,898,620	Intron 4	G	G (100%)	A (10%)*	A (16%)	G (100%)	
70,898,623	Intron 4	G	G (100%)	G (100%)	A (13%)	G (100%)	
70,898,722	Intron 4	G	A (99%)	A (100%)	A (100%)	G (100%)	
70,898,811	Intron 4	G	G (100%)	A (9%)*	A (11%)	G (100%)	
70,898,954	3'UTR	G	A (100%)	A (100%)	A (100%)	G (100%)	
70,899,036	Intron 5	T	T (100%)	delT (12%)	T (97%)	T (100%)	

70,899,037	Intron 5	T	A (100%)	A (88%)	A (100%)	A (95%)
70,899,067	Intron 5	C	T (1%)*	T (6%)*	T (12%)	C (100%)
70,899,203	Intron 5	C	T (9%)*	T (18%)	C (100%)	T (7%)*
70,899,225	Intron 5	C	C (96%)	C (100%)	T (19%)	C (100%)
70,899,239	Intron 5	G	G (100%)	A (4%)*	A (11%)	G (100%)
70,899,368	Intron 5	T	C (98%)	C (91%)	C (85%)	T (100%)
70,899,602	Intron 5	G	G (100%)	G (100%)	A (11%)	G (100%)
70,899,668	Intron 5	G	G (98%)	A (3%)*	A (11%)	G (100%)
70,899,676	Intron 5	G	G (98%)	A (3%)*	A (12%)	G (100%)
70,899,819	Intron 5	C	C (100%)	T (17%)	T (3%)*	C (100%)
70,899,836	Intron 5	G	G (97%)	A (6%)*	A (16%)	G (100%)
70,899,837	Intron 5	G	G (100%)	G (100%)	A (14%)	G (100%)
70,900,035	Intron 5	G	G (100%)	A (13%)	G (100%)	G (100%)
70,900,037	Intron 5	G	G (100%)	G (100%)	A (18%)	G (100%)
70,900,040	Intron 5	G	G (100%)	A (3%)*	A (11%)	G (100%)
70,900,108	Intron 5	A	G (96%)	G (88%)	G (86%)	G (90%)
70,900,280	Intron 5	G	G (100%)	A (3%)*	A (11%)	G (100%)
70,900,305	Intron 5	C	T (2%)*	T (3%)*	T (15%)	C (100%)
70,900,315	Intron 5	G	G (100%)	G (100%)	A (11%)	G (100%)
70,900,319	Intron 5	G	G (100%)	A (3%)*	A (21%)	G (100%)
70,900,396	Intron 5	C	C (100%)	C (100%)	T (11%)	C (100%)
70,900,408	Intron 5	G	A (90%)	A (85%)	A (63%)	G (100%)
70,900,563	Intron 5	C	C (98%)	T (3%)*	T (13%)	C (97%)
70,900,602	Intron 5	C	C (98%)	C (100%)	T (4%)*	T (100%)
70,900,603	Intron 5	C	C (100%)	A (100%)	A (41%)	C (100%)
70,900,622	Intron 5	G	G (100%)	G (100%)	A (15%)	G (100%)
70,900,681	Intron 5	C	C (100%)	T (11%)	C (100%)	C (100%)
70,900,683	Intron 5	C	C (100%)	C (100%)	T (11%)	C (100%)
70,900,728	Intron 5	G	G (100%)	A (11%)	G (100%)	G (100%)
70,900,729	Intron 5	G	G (100%)	A (5%)*	A (27%)	G (100%)
70,900,731	Intron 5	G	G (100%)	A (14%)	G (100%)	G (100%)
70,900,734	Intron 5	G	G (100%)	A (5%)*	A (20%)	G (100%)
70,900,751	Intron 5	G	G (100%)	A (12%)	G (100%)	G (100%)
70,900,766	Intron 5	G	G (100%)	A (10%)*	A (17%)	G (100%)
70,900,770	Intron 5	C	C (100%)	C (100%)	T (13%)	C (100%)

70,900,775	Intron 5	G	G (100%)	G (100%)	A (19%)	G (100%)
70,900,776	Intron 5	G	G (100%)	A (5%)*	A (13%)	G (100%)
70,900,799	Intron 5	G	A (3%)*	A (7%)*	A (12%)	A (4%)*
70,900,856	Intron 5	C	C (100%)	T (3%)*	T (12%)	C (100%)
70,900,966	Intron 5	C	C (98%)	T (4%)*	T (14%)	C (100%)
70,901,006	Intron 5	C	C (100%)	T (11%)	T (3%)*	C (100%)
70,901,013	Intron 5	G	G (100%)	A (11%)	A (3%)*	G (100%)
70,901,058	Intron 5	C	C (100%)	T (5%)*	T (15%)	C (100%)
70,901,107	Intron 5	G	G (100%)	A (14%)	G (100%)	G (100%)
70,901,208	Intron 5	C	C (100%)	T (12%)	C (100%)	C (100%)
70,901,275	Intron 5	A	G (95%)	G (89%)	G (98%)	A (100%)
70,901,313	Intron 5	G	G (100%)	A (14%)	G (100%)	G (100%)
70,901,362	Intron 5	A	G (93%)	G (100%)	G (97%)	A (100%)
70,901,432	Intron 5	C	C (100%)	T (12%)	T (2%)*	C (100%)
70,901,488	Intron 5	G	G (100%)	A (14%)	G (100%)	G (100%)
70,901,496	Intron 5	C	T (1%)*	T (11%)	T (6%)*	C (100%)
70,901,552	Intron 5	G	G (100%)	G (100%)	A (14%)	G (100%)
70,901,583	Intron 5	C	T (100%)	T (100%)	T (100%)	T (100%)
70,901,598	Intron 5	G	G (100%)	A (3%)*	A (13%)	A (3%)*
70,901,610	Intron 5	A	C (8%)*	C (8%)*	C (30%)	A (100%)
70,901,729- 70,901,731	Intron 5	GAT	delGAT (88%)	delGAT (72%)	delGAT (85%)	GAT (100%)
70,901,736	Intron 5	A	A (100%)	G (13%)	A (100%)	A (100%)
70,901,737	Intron 5	T	T (100%)	A (13%)	T (100%)	T (100%)
70,901,738	Intron 5	G	G (98%)	A (13%)	G (100%)	G (100%)
70,901,739	Intron 5	G	G (100%)	A (11%)	G (100%)	G (100%)
70,901,925	Intron 5	A	T (100%)	T (100%)	T (100%)	A (100%)
70,901,940	Intron 5	A	G (100%)	G (96%)	G (92%)	A (100%)
70,902,051	3'UTR	C	C (100%)	T (11%)	T (4%)*	C (100%)
70,902,079	3'UTR	C	A (99%)	A (100%)	A (100%)	C (100%)
70,902,127	3'UTR	C	C (100%)	T (6%)*	T (14%)	C (100%)
70,902,228	3'UTR	C	C (100%)	T (2%)*	T (11%)	C (100%)
70,902,290	Downstream region	C	C (100%)	T (2%)*	T (13%)	C (100%)
70,902,355	Downstream region	C	T (9%)*	T (12%)	T (35%)	C (100%)
70,902,357	Downstream region	T	C (8%)*	C (4%)*	C (29%)	T (100%)

70,902,601	Downstream region	C	C (100%)	C (100%)	T (12%)	C (100%)
70,902,634	Downstream region	G	G (100%)	G (100%)	A (11%)	G (100%)
70,902,651	Downstream region	C	T (2%)*	T (7%)*	T (18%)	C (100%)
70,902,661	Downstream region	C	C (100%)	T (12%)	C (100%)	C (100%)
70,902,690	Downstream region	C	C (100%)	T (4%)*	T (12%)	C (100%)
70,902,692	Downstream region	C	C (100%)	T (4%)*	T (13%)	C (100%)
70,902,694	Downstream region	C	C (100%)	C (100%)	T (17%)	C (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.