Table S12. Nucleotide Substitutions in *CST2* 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
23,807,611	Upstream region	**C**	**C** (100%)	**T** (15%)	**T** (3%)*	**C** (100%)	
23,807,587	Upstream region	**C**	**C** (100%)	**C** (100%)	**T** (11%)	**C** (100%)	
23,807,544	Upstream region	**G**	**G** (100%)	**G** (100%)	**A** (11%)	**G** (100%)	
23,807,531	Upstream region	**C**	**C** (100%)	**T** (11%)	**T** (6%)*	**C** (100%)	
23,807,528	Upstream region	**C**	**C** (100%)	**T** (12%)	**C** (100%)	**C** (100%)	
23,807,515	Upstream region	**C**	**C** (100%)	**C** (100%)	**T** (14%)	**C** (100%)	
23,807,512	Upstream region	**C**	**T** (2%)*	**T** (14%)	**T** (5%)*	**C** (100%)	
23,807,491	Upstream region	**C**	**C** (100%)	**C** (100%)	**T** (14%)	**C** (100%)	
23,807,480	Upstream region	**C**	**C** (100%)	**T** (4%)*	**T** (14%)	**C** (100%)	
23,807,447	Upstream region	**C**	**C** (100%)	**C** (100%)	**T** (17%)	**C** (100%)	
23,807,423	Upstream region	**C**	**C** (100%)	**C** (100%)	**T** (17%)	**C** (100%)	
23,807,422	Upstream region	**C**	**C** (100%)	**T** (5%)*	**T** (18%)	**C** (100%)	
23,807,416	Upstream region	**C**	**C** (100%)	**C** (100%)	**T** (11%)	**C** (100%)	
23,807,363	Upstream region	**G**	**G** (100%)	**A** (11%)	**G** (100%)	**G** (100%)	
23,807,360	Upstream region	**G**	**G** (98%)	**A** (13%)	**G** (100%)	**G** (100%)	
23,807,259	Exon 1 (Signal)	CG**G**	CG**G** (100%)	CG**A** (8%)*	CG**A** (21%)	CG**G** (100%)	GCC→$A_{12(sp)}$ GCU→ $A_{12(sp)}$
23,807,241	Exon 1 (Signal)	GA**C**	GA**G** (93%)	GA**G** (100%)	GA**G** (82%)	GA**C** (100%)	CUG→$L_{18(sp)}$ CUC→$L_{18(sp}$
23,807,151	Exon 1	GT**G**	GT**G** (100%)	GT**A** (13%)	GT**G** (100%)	GT**G** (100%)	CAC→H_{29} CAU→H_{29}
23,807,145	Exon 1	CA**G**	CA**G** (100%)	CA**A** (13%)	CA**A** (7%)*	CA**G** (100%)	GUC→V_{31} GUU→V_{31}
23,807,100	Exon 1	GC**G**	GC**G** (100%)	GC**A** (4%)*	GC**A** (12%)	GC**G** (100%)	CGC→R_{46} CGU→R_{46}
23,807,076	Exon 1	TC**C**	TC**C** (100%)	TC**C** (100%)	TC**T** (13%)	TC**C** (100%)	AGG→R_{54} AGA→R_{54}
23,807,038	Intron 1	**C**	**C** (100%)	**T** (15%)	**C** (100%)	**C** (100%)	
23,807,028	Intron 1	**A**	**C** (100%)	**C** (100%)	**C** (95%)	**C** (97%)	
23,807,019	Intron 1	**G**	**G** (100%)	**A** (14%)	**A** (4%)*	**G** (100%)	
23,807,018	Intron 1	**G**	**G** (100%)	**A** (14%)	**A** (4%)*	**G** (100%)	
23,806,929	Intron 1	**A**	**A** (100%)	**A** (95%)	**A** (100%)	**C** (100%)	
23,806,880	Intron 1	**G**	**G** (100%)	**G** (100%)	**A** (12%)	**G** (100%)	
23,806,827	Intron 1	**G**	**G** (100%)	**A** (15%)	**A** (5%)*	**G** (100%)	

23,806,821	Intron 1	**G**	**G** (100%)	**G** (100%)	**A** (14%)	**G** (100%)
23,806,811	Intron 1	**G**	**G** (100%)	**G** (100%)	**A** (12%)	**G** (100%)
23,806,715	Intron 1	**G**	**G** (100%)	**G** (100%)	**A** (14%)	**G** (100%)
23,806,695	Intron 1	**G**	**G** (100%)	**A** (12%)	**G** (100%)	**G** (100%)
23,806,690	Intron 1	**G**	**A** (3%)*	**G** (100%)	**A** (18%)	**G** (100%)
23,806,685	Intron 1	**G**	**G** (100%)	**A** (12%)	**A** (17%)	**G** (100%)
23,806,655	Intron 1	**C**	**C** (100%)	**C** (100%)	**T** (15%)	**C** (100%)
23,806,653	Intron 1	**C**	**C** (100%)	**C** (100%)	**T** (12%)	**C** (100%)
23,806,536	Intron 1	**T**	**T** (100%)	**T** (100%)	**T** (100%)	**C** (100%)
23,806,513	Intron 1	**G**	**G** (100%)	**A** (13%)	**G** (100%)	**G** (100%)
23,806,507	Intron 1	**A**	**G** (100%)	**G** (100%)	**A** (13%)	**G** (100%)
23,806,506	Intron 1	**G**	**A** (3%)*	**G** (100%)	**A** (17%)	**G** (100%)
23,806,468	Intron 1	**G**	**G** (100%)	**A** (17%)	**A** (9%)*	**G** (100%)
23,806,466	Intron 1	**G**	**G** (100%)	**G** (100%)	**A** (13%)	**G** (100%)
23,806,452	Intron 1	**A**	**G** (97%)	**G** (100%)	**G** (89%)	**A** (96%)
23,806,416	Intron 1	**G**	**G** (100%)	**A** (11%)	**A** (7%)*	**G** (100%)
23,806,387	Intron 1	**G**	**G** (100%)	**A** (25%)	**A** (4%)*	**G** (100%)
23,806,383	Intron 1	**C**	**C** (100%)	**T** (17%)	**T** (9%)*	**C** (100%)
23,806,310	Intron 1	**C**	**C** (100%)	**C** (100%)	**T** (12%)	**T** (3%)*
23,806,290	Intron 1	**C**	**C** (100%)	**T** (11%)	**C** (100%)	**T** (4%)*
23,806,278	Intron 1	**C**	**C** (100%)	**C** (100%)	**T** (18%)	**C** (100%)
23,806,274	Intron 1	**C**	**C** (100%)	**T** (6%)*	**T** (11%)	**C** (100%)
23,806,273	Intron 1	**C**	**C** (100%)	**C** (100%)	**T** (11%)	**C** (100%)
23,806,183	Intron 1	**A**	**A** (100%)	**A** (100%)	**A** (100%)	**G** (100%)
23,806,108	Intron 1	**C**	**C** (100%)	**C** (100%)	**T** (15%)	**C** (100%)
23,806,105	Intron 1	**C**	**C** (100%)	**C** (100%)	**T** (18%)	**C** (100%)
23,806,095	Intron 1	**C**	**G** (76%)	**G** (22%)	**C** (100%)	**C** (100%)
23,806,079	Intron 1	**G**	**G** (98%)	**A** (11%)	**G** (100%)	**G** (100%)
23,806,071	Intron 1	**G**	**G** (100%)	**G** (97%)	**A** (12%)	**G** (100%)
23,806,039	Intron 1	**G**	**G** (100%)	**A** (4%)*	**G** (100%)	**A** (28%)
23,805,961	Intron 1	**C**	**T** (2%)*	**T** (14%)	**C** (100%)	**C** (100%)
23,805,846	Intron 2	**C**	**C** (100%)	**T** (6%)*	**T** (11%)	**C** (100%)
23,805,832	Intron 2	**G**	**A** (92%)	**A** (93%)	**A** (92%)	**A** (97%)
23,805,800	Intron 2	**C**	**C** (100%)	**T** (4%)*	**T** (11%)	**C** (100%)
23,805,798	Intron 2	**C**	**C** (100%)	**T** (11%)	**C** (94%)	**C** (100%)

23,805,785	Intron 2	**A**	**G** (14%)	**G** (3%)*	**A** (100%)	**G** (4%)*
23,805,773	Intron 2	**T**	**T** (100%)	**G** (11%)	**G** (6%)*	**G** (2%)*
23,805,769	Intron 2	**C**	**C** (100%)	**T** (11%)	**C** (100%)	**C** (100%)
23,805,758	Intron 2	**C**	**C** (100%)	**T** (3%)*	**T** (20%)	**C** (100%)
23,805,754	Intron 2	**C**	**C** (100%)	**C** (100%)	**T** (24%)	**C** (100%)
23,805,750	Intron 2		**InsAC** (25%)	**InsAC** (6%)*	**InsAC** (9%)*	**InsAC** (15%)
23,805,746	Intron 2	**C**	**C** (100%)	**T** (10%)*	**T** (15%)	**C** (100%)
23,805,738	Intron 2	**C**	**T** (44%)	**T** (13%)	**T** (26%)	**C** (100%)
23,805,720	Intron 2	**T**	**C** (49%)	**C** (67%)	**C** (48%)	**C** (59%)
23,805,712	Intron 2	**T**	**C** (46%)	**C** (31%)	**C** (45%)	**C** (36%)
23,805,686	Intron 2	**A**	**C** (24%)	**C** (12%)	**C** (27%)	**C** (10%)*
23,805,680	Intron 2	**T**	**G** (23%)	**G** (9%)*	**G** (24%)	**G** (7%)*
23,805,674	Intron 2	**T**	**C** (18%)	**C** (6%)*	**C** (23%)	**C** (3%)*
23,805,632	Intron 2	**C**	**C** (98%)	**C** (100%)	**T** (13%)	**C** (100%)
23,805,630	Intron 2	**C**	**C** (100%)	**T** (19%)	**T** (6%)*	**C** (100%)
23,805,599	Intron 2	**G**	**G** (98%)	**A** (15%)	**A** (3%)*	**G** (100%)
23,805,548	Intron 2	**C**	**C** (98%)	**C** (100%)	**C** (100%)	**G** (88%)
23,805,532	Intron 2	**C**	**T** (2%)*	**C** (100%)	**T** (11%)	**T** (5%)*
23,805,507	Intron 2	**C**	**C** (100%)	**C** (100%)	**T** (11%)	**C** (100%)
23,805,506	Intron 2	**C**	**C** (100%)	**C** (100%)	**T** (11%)	**C** (100%)
23,805,505	Intron 2	**C**	**C** (100%)	**T** (13%)	**T** (17%)	**C** (100%)
23,805,497	Intron 2	**C**	**C** (100%)	**C** (100%)	**T** (11%)	**C** (100%)
23,805,494	Intron 2	**C**	**C** (98%)	**T** (6%)*	**T** (13%)	**C** (100%)
23,805,491	Intron 2	**C**	**C** (100%)	**T** (6%)*	**T** (11%)	**C** (100%)
23,805,490	Intron 2	**C**	**C** (100%)	**T** (6%)*	**T** (11%)	**C** (100%)
23,805,489	Intron 2	**C**	**C** (100%)	**T** (12%)	**T** (11%)	**C** (100%)
23,805,487	Intron 2	**C**	**C** (100%)	**C** (100%)	**T** (11%)	**C** (100%)
23,805,469	Intron 2	**C**	**C** (100%)	**T** (17%)	**C** (100%)	**C** (100%)
23,805,468	Intron 2	**C**	**C** (100%)	**T** (11%)	**T** (4%)*	**C** (100%)
23,805,465	Intron 2	**C**	**C** (100%)	**T** (11%)	**C** (100%)	**C** (100%)
23,805,464	Intron 2	**G**	**G** (100%)	**A** (13%)	**G** (100%)	**G** (100%)
23,805,409	Intron 2	**G**	**G** (100%)	**A** (23%)	**A** (4%)*	**G** (100%)
23,805,369	Intron 2	**C**	**C** (100%)	**C** (100%)	**T** (13%)	**C** (100%)
23,805,365	Intron 2	**C**	**C** (100%)	**T** (14%)	**C** (100%)	**C** (100%)
23,805,356	Intron 2	**C**	**C** (100%)	**T** (10%)*	**T** (13%)	**C** (100%)

23,805,329	Intron 2	**G**	**G** (100%)	**A** (6%)*	**A** (15%)	**G** (100%)
23,805,283	Intron 2	**C**	**C** (100%)	**C** (100%)	**T** (20%)	**C** (100%)
23,805,282	Intron 2	**C**	**C** (100%)	**T** (7%)*	**T** (20%)	**C** (100%)
23,805,280	Intron 2	**G**	**G** (100%)	**A** (19%)	**G** (100%)	**G** (100%)
23,805,269	Intron 2	**C**	**T** (2%)*	**T** (17%)	**C** (100%)	**C** (100%)
23,805,258	Intron 2	**G**	**G** (100%)	**A** (15%)	**G** (100%)	**G** (100%)
23,805,176	Intron 2	**G**	**G** (100%)	**G** (100%)	**A** (20%)	**G** (100%)
23,805,167	Intron 2	**G**	**G** (98%)	**G** (100%)	**A** (11%)	**G** (100%)
23,805,154	Intron 2	**G**	**G** (98%)	**A** (14%)	**A** (8%)*	**G** (100%)
23,805,057	Intron 2	**C**	**G** (4%)*	**G** (6%)*	**T** (14%) **G** (11%)	**C** (100%)
23,805,032	Intron 2	**G**	**G** (100%)	**A** (10%)*	**A** (11%)	**G** (100%)
23,805,026	Intron 2	**C**	**C** (100%)	**C** (100%)	**T** (11%)	**C** (100%)
23,804,923	Intron 2	**A**	**A** (100%)	**A** (100%)	**A** (100%)	**delA** (76%)
23,804,918	Intron 2	**C**	**T** (4%)*	**T** (12%)	**T** (10%)*	**C** (100%)
23,804,864	Intron 2	**C**	**T** (2%)*	**T** (11%)	**T** (5%)*	**C** (100%)
23,804,863	Intron 2	**C**	**C** (100%)	**T** (12%)	**T** (6%)*	**C** (100%)
23,804,860	Intron 2	**C**	**C** (100%)	**C** (100%)	**T** (21%)	**C** (100%)
23,804,858	Intron 2	**C**	**T** (5%)*	**T** (17%)	**C** (100%)	**C** (100%)
23,804,856	Intron 2	**C**	**T** (2%)*	**T** (15%)	**C** (100%)	**C** (100%)
23,804,854	Intron 2	**C**	**C** (100%)	**T** (15%)	**T** (14%)	**C** (100%)
23,804,843	Intron 2	**G**	**G** (100%)	**A** (11%)	**A** (10%)*	**G** (100%)
23,804,839	Intron 2	**G**	**G** (98%)	**A** (11%)	**A** (20%)	**G** (100%)
23,804,838	Intron 2	**G**	**G** (100%)	**A** (11%)	**A** (9%)*	**G** (100%)
23,804,828	Intron 2	**G**	**G** (100%)	**G** (100%)	**A** (13%)	**G** (100%)
23,804,794	Intron 2	**G**	**G** (100%)	**A** (12%)	**A** (6%)*	**G** (100%)
23,804,750	Intron 2	**G**	**G** (100%)	**A** (11%)	**A** (6%)*	**G** (100%)
23,804,655	3′UTR	**C**	**C** (100%)	**C** (100%)	**T** (13%)	**C** (100%)
23,804,647	3′UTR	**G**	**G** (100%)	**G** (100%)	**A** (17%)	**G** (100%)
23,804,612	3′UTR	**G**	**G** (100%)	**A** (15%)	**A** (10%)*	**G** (100%)
23,804,575	3′UTR	**G**	**A** (3%)*	**A** (18%)	**G** (100%)**	**G** (100%)
23,804,515	3′UTR	**G**	**G** (100%)	**A** (13%)	**G** (100%)	**G** (100%)
23,804,501	3′UTR	**G**	**G** (100%)	**A** (14%)	**G** (100%)	**G** (100%)
23,804,465	3′UTR	**G**	**G** (98%)	**G** (100%)	**A** (14%)	**G** (96%)
23,804,408	3′UTR	**T**	**C** (11%)	**C** (4%)*	**T** (100%)	**C** (5%)*

23,804,370	Downstream region	**T**	**C** (25%)	**C** (21%)	**C** (23%)	**C** (19%)
23,804,355	Downstream region	**C**	**C** (98%)	**T** (3%)*	**T** (4%)*	**T** (68%)
23,804,286	Downstream region	**C**	**C** (100%)	**C** (100%)	**T** (11%)	**C** (100%)
23,804,245	Downstream region	**C**	**C** (100%)	**C** (100%)	**T** (15%)	**C** (100%)
23,804,180	Downstream region	**C**	**C** (100%)	**T** (13%)	**T** (6%)*	**C** (100%)
23,804,169	Downstream region	**C**	**C** (100%)	**T** (20%)	**C** (100%)	**C** (100%)
23,804,167	Downstream region	**C**	**C** (100%)	**C** (100%)	**T** (15%)	**C** (100%)
23,804,157	Downstream region	**C**	**C** (100%)	**C** (100%)	**T** (18%)	**C** (100%)
23,804,155	Downstream region	**C**	**C** (100%)	**T** (8%)*	**T** (20%)	**C** (100%)
23,804,147	Downstream region	**G**	**G** (100%)	**A** (6%)*	**A** (18%)	**G** (100%)
23,804,131	Downstream region	**C**	**C** (100%)	**T** (11%)	**T** (5%)*	**C** (100%)
23,804,128	Downstream region	**C**	**C** (100%)	**T** (15%)	**C** (100%)	**C** (100%)
23,804,089	Downstream region	**C**	**C** (100%)	**C** (100%)	**T** (17%)	**C** (100%)
23,804,080	Downstream region	**C**	**C** (100%)	**T** (11%)	**C** (100%)	**C** (100%)
23,804,991	Downstream region	**G**	**G** (100%)	**A** (3%)*	**A** (12%)	**G** (100%)
23,804,983	Downstream region	**C**	**T** (2%)*	**T** (11%)	**T** (3%)*	**C** (98%)
23,804,931	Downstream region	**C**	**C** (98%)	**T** (4%)*	**T** (13%)	**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.