

Table S9. Nucleotide Substitutions in *STATH* gene in introns and regulatory regions

Genomic Coordinates (hg19)	Gene Region	Modern human	Altai Neanderthal (Variant Frequency)	Chagyrskaya	Vindija	Denisovan (Variant Frequency)	Codon → Amino acid
				Neanderthal (Variant Frequency)	Neanderthal (Variant Frequency)		
70,861,286	Upstream region	G	A (7%)*	G (100%)	A (14%)	A (3%)*	
70,861,321	Upstream region	G	G (98%)	G (100%)	A (17%)	G (100%)	
70,861,322	Upstream region	G	G (100%)	G (100%)	A (11%)	G (100%)	
70,861,326	Upstream region	G	G (100%)	A (3%)*	A (16%)	G (100%)	
70,861,343	Upstream region	G	G (100%)	G (100%)	A (14%)	G (100%)	
70,861,345	Upstream region	G	G (100%)	G (100%)	A (21%)	G (100%)	
70,861,354	Upstream region	C	C (100%)	C (100%)	T (11%)	C (100%)	
70,861,408	Upstream region	G	G (100%)	G (96%)	A (11%)	G (100%)	
70,861,449	Upstream region	C	C (100%)	C (100%)	T (12%)	C (100%)	
70,861,482	Upstream region	G	G (100%)	A (19%)	A (4%)*	G (100%)	
70,861,575	Upstream region	G	G (100%)	A (9%)*	A (13%)	G (100%)	
70,861,643	Upstream region	C	C (100%)	C (100%)	T (11%)	C (100%)	
70,861,650	5'UTR	G	G (100%)	A (17%)	A (4%)*	G (100%)	
70,861,675	5'UTR	G	G (100%)	G (100%)	A (11%)	G (100%)	
70,861,702	5'UTR	C	C (100%)	T (15%)	T (5%)*	C (100%)	
70,861,720	5'UTR	T	C (55%)	T (100%)	T (100%)	T (100%)	
70,861,728	5'UTR	C	C (100%)	C (100%)	T (12%)	C (100%)	
70,861,779	Intron 1	A	G (100%)	G (96%)	G (96%)	A (100%)	
70,861,786	Intron 1	G	G (100%)	G (100%)	A (11%)	G (97%)	
70,861,796	Intron 1	C	C (99%)	T (4%)*	T (12%)	C (100%)	
70,861,974	Intron 1	A	G (100%)	G (97%)	G (96%)	G (100%)	
70,862,105	Intron 1	G	A (8%)*	A (9%)*	A (13%)	G (100%)	
70,862,192	Intron 1	C	C (100%)	T (21%)	C (100%)	C (100%)	
70,862,294	Intron 1	C	T (97%)	T (100%)	T (100%)	C (100%)	
70,862,374	Intron 1	G	A (1%)*	A (2%)*	A (13%)	G (100%)	
70,862,380	Intron 1	T	T (100%)	T (100%)	delT (41%)	T (97%)	
70,862,448	Intron 1	G	G (100%)	A (8%)*	A (25%)	G (100%)	
70,862,458	Intron 1	C	C (99%)	C (100%)	T (13%)	C (100%)	
70,862,463	Intron 1	C	T (1%)*	T (13%)	T (4%)*	C (100%)	
70,862,526	Intron 1	C	C (100%)	T (3%)*	T (11%)	C (100%)	

70,862,547	Intron 1	C	T (99%)	T (100%)	T (97%)	C (100%)	
70,862,645	Intron 1	T	delT (44%)	delT (20%)**	delT (25%)	delT (33%)	
70,862,646	Intron 1	T	delT (11%)	delT (20%)**	delT (10%)*	delT (17%)	
70,862,666	Intron 1	T	A (18%)	A (50%)**	A (19%)	A (7%)*	
70,862,668	Intron 1	A	T (19%)	A (100%)	T (4%)*	A (100%)	
70,862,677	Intron 1	A	G (22%)	G (17%)**	G (20%)	A (100%)	
70,862,684	Intron 1	C	C (96%)	C (100%)	T (20%)	C (100%)	
70,862,700	Intron 1	G	G (100%)	G (100%)	A (15%)	G (100%)	
70,862,715	Intron 1	T	C (45%)	C (47%)	C (13%)	T (100%)	
70,862,730	Intron 1	C	T (3%)*	T (11%)	T (6%)*	T (4%)*	
70,862,732	Intron 1	G	G (100%)	A (11%)	G (100%)	G (100%)	
70,862,736	Intron 1	C	T (3%)*	C (100%)	T (13%)	C (100%)	
70,862,797	Intron 1	G	G (100%)	G (100%)	A (13%)	G (100%)	
70,862,917	Intron 1	C	C (100%)	C (100%)	T (13%)	C (100%)	
70,863,157	Intron 1	C	C (100%)	T (3%)*	T (12%)	C (100%)	
70,863,163	Intron 1	C	C (99%)	T (11%)	T (12%)	T (4%)*	
70,863,200	Intron 1	G	G (100%)	A (13%)	A (5%)*	G (100%)	
70,863,375	Intron 1	G	G (100%)	A (3%)*	A (11%)	G (100%)	
70,863,442	Intron 1	G	A (2%)*	G (100%)	A (11%)	G (100%)	
70,863,443	Intron 1	G	G (98%)	A (8%)*	A (15%)	G (100%)	
70,863,668	Intron 1	C	C (100%)	T (12%)	C (100%)	C (100%)	
70,863,751	Intron 1	C	T (2%)*	C (100%)	T (12%)	C (100%)	
70,863,822	Intron 1	C	C (100%)	T (13%)	C (100%)	C (100%)	
70,863,839	Intron 1	T	C (100%)	C (92%)	C (86%)	C (97%)	
70,863,883	Intron 1	C	C (100%)	T (12%)	T (15%)	C (100%)	
70,863,924	Intron 1	A	T (100%)	T (100%)	T (100%)	A (100%)	
70,863,952	Intron 1	A	G (100%)	G (92%)	G (100%)	A (100%)	
70,863,957	Intron 1	C	T (100%)	T (100%)	T (100%)	C (100%)	
70,864,053	Intron 1	G	G (100%)	A (13%)	G (100%)	G (100%)	
70,864,178	Exon 2 (Signal)	TTC	TTC (100%)	TTC (100%)	TTT (11%)	TTC (100%)	UUC→F _{7(sp)} UUU→F _{7(sp)}
70,864,261	Intron 2	C	C (98%)	T (11%)	T (3%)*	C (100%)	
70,864,274	Intron 2	G	G (100%)	A (15%)	G (100%)	G (100%)	
70,864,349	Intron 2	C	C (100%)	T (12%)	T (8%)*	C (100%)	
70,864,353	Intron 2	C	C (100%)	C (100%)	T (11%)	C (100%)	

70,864,509	Intron 2	C	C (100%)	T (13%)	T (3%)*	C (100%)
70,864,733	Intron 2	T	G (98%)	G (100%)	G (100%)	T (100%)
70,864,751	Intron 2	A	G (97%)	G (100%)	G (89%)	A (100%)
70,864,762	Intron 2	G	A (2%)*	G (100%)	A (13%)	G (100%)
70,864,768	Intron 2	G	G (100%)	A (11%)	A (8%)*	G (100%)
70,864,822	Intron 2	G	G (100%)	G (100%)	A (13%)	G (100%)
70,864,970	Intron 2	C	C (100%)	T (5%)*	T (12%)	C (100%)
70,865,133	Intron 2	C	T (1%)*	C (100%)	T (19%)	C (100%)
70,865,136	Intron 2	C	C (100%)	T (10%)*	T (12%)	C (100%)
70,865,137	Intron 2	C	C (100%)	T (13%)	T (4%)*	C (97%)
70,865,152	Intron 2	C	C (99%)	C (100%)	T (11%)	C (100%)
70,865,189	Intron 2	C	C (98%)	C (100%)	T (14%)	C (100%)
70,865,193	Intron 2	C	C (100%)	C (100%)	T (11%)	C (100%)
70,865,261	Intron 2	G	G (100%)	A (11%)	A (3%)*	G (100%)
70,865,284	Intron 2	C	C (100%)	C (100%)	T (11%)	C (100%)
70,865,285	Intron 2	C	C (100%)	C (100%)	T (13%)	C (100%)
70,865,405	Intron 3	G	A (3%)*	A (2%)*	A (13%)	G (100%)
70,865,533	Intron 4	G	A (100%)	A (100%)	A (100%)	G (100%)
70,865,633	Intron 4	C	T (1%)*	T (11%)	C (100%)	C (100%)
70,865,638	Intron 4	G	G (100%)	A (13%)	G (100%)	G (100%)
70,865,677	Intron 4	A	C (100%)	C (100%)	C (81%)	C (100%)
70,865,748	Intron 4	C	T (2%)*	T (14%)	T (5%)*	C (100%)
70,865,768	Intron 4	C	C (100%)	T (4%)*	T (14%)	C (100%)
70,865,853	Intron 4	G	G (100%)	A (11%)	G (100%)	G (100%)
70,866,032	Intron 4	G	G (100%)	G (100%)	A (13%)	G (100%)
70,866,033	Intron 4	G	G (98%)	G (100%)	A (13%)	G (100%)
70,866,034	Intron 4	G	G (100%)	G (100%)	A (19%)	G (100%)
70,866,046	Intron 4	C	C (100%)	C (100%)	T (13%)	C (100%)
70,866,061	Intron 4	G	G (100%)	G (100%)	A (14%)	G (100%)
70,866,109	Intron 4	G	G (98%)	A (4%)*	A (15%)	G (100%)
70,866,118	Intron 4	T	C (96%)	C (95%)	C (94%)	T (100%)
70,866,221	Intron 4	T	A (97%)	A (100%)	A (100%)	A (100%)
70,866,267	Intron 4	G	G (100%)	G (100%)	A (13%)	G (100%)
70,866,278	Intron 4	G	A (2%)*	A (6%)*	A (11%)	G (100%)
70,866,503	Intron 4	C	C (100%)	T (12%)	C (100%)	C (100%)

70,866,529	Intron 4	C	C (100%)	T (11%)	T (5%)*	C (100%)	
70,866,660	Exon 5	ACC	ACC (98%)	ACT (11%)	ACC (100%)	ACC (100%)	ACC→T ₄₂ ACU→T ₄₂
70,866,707	Intron 5	G	G (100%)	G (100%)	A (12%)	G (100%)	
70,866,776	Intron 5	A	C (100%)	C (100%)	C (98%)	A (100%)	
70,866,862	Intron 5	G	G (100%)	T (11%)	G (100%)	G (100%)	
70,866,864	Intron 5	T	T (100%)	A (11%)	T (100%)	T (100%)	
70,866,865	Intron 5		InsAA (92%)	InsAA (55%)	InsAA (100%)	InsAA (100%)	
70,866,866	Intron 5	G	G (100%)	A (28%)	G (100%)	G (100%)	
70,866,867	Intron 5	T	T (100%)	A (28%)	T (100%)	T (100%)	
70,866,868	Intron 5	C	C (100%)	C (100%)	G (18%)	C (100%)	
70,866,893	Intron 5	A	T (100%)	T (100%)	T (100%)	A (100%)	
70,866,917	Intron 5	G	A (3%)*	G (100%)	A (15%)	G (100%)	
70,866,944	Intron 5	C	C (100%)	T (7%)*	T (17%)	C (100%)	
70,866,954	Intron 5	G	G (100%)	G (100%)	A (15%)	G (100%)	
70,866,963	Intron 5	C	C (100%)	C (100%)	T (11%)	C (100%)	
70,866,979	Intron 5	T	C (98%)	C (100%)	C (100%)	T (100%)	
70,866,980	Intron 5	G	A (2%)*	G (100%)	A (11%)	G (100%)	
70,866,996	Intron 5	G	A (98%)	A (100%)	A (100%)	G (100%)	
70,867,021	Intron 5	C	C (100%)	T (7%)*	T (13%)	C (100%)	
70,867,092	Intron 5	G	G (100%)	A (13%)	A (6%)*	G (100%)	
70,867,137	Intron 5	C	C (100%)	T (4%)*	T (14%)	C (100%)	
70,867,142	Intron 5	G	G (100%)	A (14%)	A (5%)*	G (100%)	
70,867,237	Intron 5	C	C (100%)	T (13%)	T (4%)*	C (100%)	
70,867,238	Intron 5	C	C (100%)	C (100%)	T (14%)	C (100%)	
70,867,289	Intron 5	C	T (1%)*	T (6%)*	T (12%)	T (3%)*	
70,867,343	Intron 5	C	C (100%)	T (3%)*	T (11%)	C (100%)	
70,867,424	Intron 5	G	A (1%)*	A (11%)	A (3%)*	G (100%)	
70,867,426	Intron 5	G	G (100%)	A (11%)	A (3%)*	G (100%)	
70,867,431	Intron 5	G	G (100%)	A (10%)*	A (12%)	G (100%)	
70,867,457	Intron 5	G	G (100%)	G (100%)	A (11%)	G (100%)	
70,867,522	Intron 5	G	A (100%)	A (100%)	A (100%)	G (100%)	
70,867,531	Intron 5	G	A (2%)*	A (12%)	A (2%)*	G (100%)	
70,867,535	Intron 5	G	G (100%)	A (11%)	A (2%)*	G (100%)	
70,867,537	Intron 5	G	G (97%)	A (11%)	A (5%)*	G (100%)	

70,867,623	Intron 5	G	G (100%)	G (100%)	A (13%)	G (100%)
70,867,656	Intron 5	T	C (98%)	C (100%)	C (97%)	T (100%)
70,867,787	Intron 5	C	C (100%)	T (6%)*	T (12%)	C (100%)
70,867,856	Intron 5	C	C (100%)	T (3%)*	T (13%)	C (100%)
70,867,859	Intron 5	G	G (100%)	A (6%)*	A (17%)	G (100%)
70,867,886	Intron 5		-	-	InsT (23%)	-
70,867,898	Intron 5	C	C (98%)	C (100%)	T (12%)	T (2%)*
70,867,971	3'UTR	C	C (100%)	C (100%)	T (13%)	C (100%)
70,868,014	3'UTR	C	C (100%)	T (7%)*	T (11%)	C (100%)
70,868,162	3'UTR	A	G (98%)	G (97%)	G (94%)	A (100%)
70,868,247	Downstream regions	C	C (100%)	T (9%)*	T (11%)	C (100%)
70,868,250	Downstream regions	G	G (100%)	G (100%)	A (16%)	G (100%)
70,868,280	Downstream regions	C	C (100%)	T (12%)	T (4%)*	C (100%)
70,868,378	Downstream regions	C	C (100%)	T (12%)	C (97%)	C (100%)
70,868,397	Downstream regions	C	C (100%)	C (100%)	T (12%)	C (100%)
70,868,398	Downstream regions	C	C (100%)	T (11%)	T (6%)*	C (100%)
70,868,410	Downstream regions	G	A (2%)*	A (3%)*	A (11%)	G (100%)
70,868,420	Downstream regions	C	T (2%)*	T (6%)*	T (11%)	C (100%)
70,868,471	Downstream regions	C	C (100%)	T (11%)	C (100%)	C (100%)
70,868,546	Downstream regions	T	C (99%)	C (100%)	C (96%)	T (100%)
70,868,550	Downstream regions	C	T (99%)	T (100%)	T (100%)	C (100%)
70,868,585	Downstream regions	T	G (98%)	G (91%)	G (100%)	T (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.