

Table S10. Nucleotide Substitutions in *SMR3B* gene in introns and regulatory regions

Genomic Coordinates (hg19)	Gene Region			Chagyrskaya	Vindija	Denisovan (Variant Frequency)	Codon → amino acid
				(Variant Frequency)	(Variant Frequency)		
71,248,560	Upstream region	G	G (98%)	G (100%)	A (13%)	G (100%)	
71,248,568	Upstream region	G	G (100%)	A (11%)	A (8%)*	G (100%)	
71,248,590	Upstream region	C	C (100%)	T (11%)	T (7%)*	C (100%)	
71,248,861	5' UTR	G	G (100%)	G (100%)	A (12%)	G (100%)	
71,248,913	5' UTR	C	C (98%)	C (100%)	T (13%)	C (100%)	
71,248,914	5' UTR	A	G (98%)	G (100%)	G (96%)	G (100%)	
71,248,933	Intron 1	G	G (100%)	A (6%)*	A (13%)	G (100%)	
71,248,937	Intron 1	C	C (100%)	T (3%)*	T (13%)	C (100%)	
71,249,018	Intron 1	G	G (100%)	A (11%)	G (100%)	G (100%)	
71,249,052	Intron 1	C	C (100%)	C (100%)	C (100%)	T (100%)	
71,249,061	Intron 1	C	C (100%)	C (100%)	T (14%)	C (100%)	
71,249,065	Intron 1	C	C (98%)	T (3%)*	T (16%)	C (100%)	
71,249,140	Intron 1	G	G (100%)	G (100%)	A (11%)	G (100%)	
71,249,145	Intron 1	G	G (100%)	A (11%)	A (5%)*	G (100%)	
71,249,242	Intron 1	G	G (100%)	A (18%)	G (100%)	G (100%)	
71,249,289	Intron 1	G	G (99%)	A (11%)	A (7%)*	G (100%)	
71,249,361	Intron 1	C	C (100%)	C (100%)	T (12%)	C (100%)	
71,249,365	Intron 1	C	C (100%)	T (11%)	T (8%)*	C (100%)	
71,249,426	Intron 1	G	G (100%)	G (100%)	A (12%)	G (100%)	
71,249,434	Intron 1	C	C (100%)	T (8%)*	T (14%)	C (100%)	
71,249,441	Intron 1	T	T (100%)	T (100%)	T (100%)	A (100%)	
71,249,472	Intron 1	G	A (3%)*	A (7%)*	A (11%)	G (100%)	
71,249,476	Intron 1	A	A (100%)	A (100%)	A (100%)	G (100%)	
71,249,484	Intron 1	C	C (100%)	C (100%)	T (17%)	C (100%)	
71,249,487	Intron 1	G	G (100%)	A (10%)*	A (11%)	G (100%)	
71,249,488	Intron 1	G	G (100%)	A (4%)*	A (11%)	G (100%)	
71,249,593	Intron 1	C	C (95%)	T (3%)*	T (16%)	C (100%)	
71,249,604	Intron 1	G	G (100%)	G (100%)	A (11%)	G (100%)	
71,249,629	Intron 1	T	T (100%)	T (100%)	T (100%)	C (100%)	
71,249,671	Intron 1	G	G (100%)	G (100%)	A (12%)	G (100%)	

71,249,733	Intron 1		InsT (78%)	InsT (74%)	InsT (78%)	InsT (7%)*
71,249,743	Intron 1	C	C (100%)	T (11%)	T (3%)*	T (3%)*
71,249,744	Intron 1	C	C (100%)	T (11%)	C (100%)	C (100%)
71,249,756	Intron 1	C	C (100%)	T (15%)	C (100%)	C (100%)
71,249,836	Intron 1	G	G (98%)	G (100%)	A (11%)	G (100%)
71,249,839	Intron 1	T	C (98%)	C (100%)	C (91%)	T (100%)
71,249,901	Intron 1	C	C (100%)	C (100%)	T (12%)	C (100%)
71,249,908	Intron 1	G	G (100%)	A (10%)*	A (15%)	G (100%)
71,249,921	Intron 1	G	G (100%)	A (12%)	A (3%)*	G (100%)
71,249,966	Intron 1	T	T (100%)	T (100%)	C (57%)	T (100%)
71,250,060	Intron 1	C	C (100%)	G (4%)*	G (43%)	C (100%)
71,250,203	Intron 1	C	C (100%)	T (7%)*	T (15%)	C (100%)
71,250,286	Intron 2	G	G (100%)	A (13%)	G (100%)	G (100%)
71,250,287	Intron 2	T	T (100%)	T (100%)	C (15%)	T (100%)
71,250,308	Intron 2	T	A (100%)	A (100%)	A (100%)	A (100%)
71,250,329	Intron 2	C	C (100%)	T (5%)*	T (12%)	C (100%)
71,250,399	Intron 2	A	G (98%)	G (100%)	G (100%)	G (100%)
71,250,415	Intron 2	G	G (100%)	A (12%)	A (9%)*	G (100%)
71,250,521	Intron 2	G	A (2%)*	G (100%)	A (20%)	A (4%)*
71,250,550	Intron 2	C	C (100%)	T (11%)	T (5%)*	C (100%)
71,250,564	Intron 2	G	G (100%)	A (7%)*	A (13%)	G (100%)
71,250,570	Intron 2	C	C (100%)	T (13%)	C (97%)	C (100%)
71,250,583	Intron 2	G	G (99%)	A (14%)	G (100%)	G (100%)
71,250,657	Intron 2	T	C (100%)	C (100%)	C (88%)	T (100%)
71,250,711	Intron 2	G	G (100%)	A (13%)	G (100%)	G (100%)
71,250,716	Intron 2	G	A (100%)	A (100%)	A (100%)	G (100%)
71,250,743	Intron 2	T	T (100%)	T (100%)	C (11%)	T (100%)
71,250,769	Intron 2	G	A (100%)	A (100%)	A (100%)	A (100%)
71,250,835	Intron 2	G	G (100%)	G (100%)	A (13%)	G (100%)
71,250,977	Intron 2	A	A (100%)	A (100%)	A (100%)	T (100%)
71,251,066	Intron 2	C	C (100%)	T (11%)	C (100%)	C (100%)
71,251,115	Intron 2	G	G (100%)	T (20%)	T (7%)*	G (100%)
71,251,116	Intron 2	T	delT (14%)	T (100%)	delT (32%)	delT (46%)
71,251,117	Intron 2	T	delT (12%)	T (100%)**	delT (11%)	delT (43%)
71,251,137	Intron 2	T	G (4%)*	T (100%)**	G (12%)	T (100%)

71,251,138	Intron 2	T	A (4%)*	T (100%)**	A (12%)	T (92%)
71,251,299	Intron 2	T	T (100%)	T (100%)	T (100%)	A (15%)
71,251,313	Intron 2	G	G (100%)	A (5%)*	G (100%)	A (10%)*
71,251,367	Intron 2	A	C (13%)	C (18%)	C (4%)*	C (11%)
71,251,375	Intron 2	C	C (100%)	T (11%)	C (100%)	C (100%)
71,251,469	Intron 2		-	-	InsA (11%)	-
71,251,514	Intron 2	C	C (100%)	T (11%)	C (100%)	C (100%)
71,251,609	Intron 2	C	C (99%)	T (12%)	T (3%)*	C (100%)
71,251,669	Intron 2	T	A (98%)	A (97%)	A (100%)	T (100%)
71,251,716	Intron 2	C	C (100%)	T (11%)	C (100%)	C (100%)
71,251,718	Intron 2	C	C (100%)	T (4%)*	T (13%)	C (100%)
71,251,804	Intron 2	A	G (95%)	G (95%)	G (100%)	A (100%)
71,251,815	Intron 2	C	A (96%)	A (98%)	A (100%)	C (100%)
71,251,848	Intron 2	G	G (98%)	A (12%)	G (100%)	G (100%)
71,251,989	Intron 2		InsA (16%)	-	-	InsA (20%)
71,251,990	Intron 2		InsA (16%)	-	InsA (29%)	InsA (20%)
71,252,145	Intron 2	G	G (100%)	A (4%)*	A (11%)	G (100%)
71,252,158	Intron 2		-	-	-	InsAC (77%)
71,252,168	Intron 2	C	C (100%)	C (100%)	T (11%)	C (100%)
71,252,239	Intron 2	C	C (100%)	C (100%)	T (17%)	C (100%)
71,252,240	Intron 2	C	C (100%)	C (100%)	T (17%)	C (100%)
71,252,241	Intron 2	G	A (100%)	A (100%)	A (100%)	G (97%)
71,252,261	Intron 2	C	C (100%)	T (12%)	T (7%)*	C (100%)
71,252,298	Intron 2	G	G (100%)	G (100%)	A (18%)	G (100%)
71,252,310	Intron 2	C	C (98%)	C (100%)	C (100%)	A (100%)
71,252,311	Intron 2	G	A (100%)	A (100%)	A (100%)	G (100%)
71,252,314	Intron 2	G	G (98%)	A (11%)	A (3%)*	G (100%)
71,252,332	Intron 2	G	G (100%)	G (100%)	A (11%)	G (100%)
71,252,376	Intron 2	G	A (3%)*	G (97%)	A (11%)	G (100%)
71,252,448	Intron 2	C	T (100%)	T (100%)	T (100%)	C (100%)
71,252,470	Intron 2	G	A (4%)*	A (3%)*	A (12%)	G (100%)
71,252,537	Intron 2	A	G (98%)	G (97%)	G (98%)	A (100%)
71,252,694	Intron 2	C	C (98%)	T (3%)*	T (11%)	C (100%)
71,252,882	Intron 2	C	C (100%)	T (12%)	T (5%)*	C (100%)
71,252,947	Intron 2	T	T (100%)	T (100%)	T (100%)	C (100%)

71,252,977	Intron 2	G	G (100%)	A (5%)*	A (13%)	G (100%)
71,252,994	Intron 2	G	G (100%)	A (11%)	G (100%)	A (3%)*
71,253,001	Intron 2	G	G (98%)	A (11%)	G (100%)	G (100%)
71,253,017	Intron 2	G	G (100%)	A (3%)*	A (12%)	G (100%)
71,253,024	Intron 2	C	T (2%)*	C (97%)	T (11%)	C (100%)
71,253,074	Intron 2	T	A (100%)	A (100%)	A (100%)	T (100%)
71,253,085	Intron 2	G	G (100%)	A (14%)	G (100%)	G (100%)
71,253,153	Intron 2	G	A (98%)	A (100%)	A (100%)	G (100%)
71,253,270	Intron 2	G	G (100%)	A (11%)	A (8%)*	G (100%)
71,253,281	Intron 2	G	A (2%)*	G (100%)	A (17%)	G (100%)
71,253,283	Intron 2	G	G (100%)	G (100%)	A (11%)	G (100%)
71,253,291	Intron 2	C	C (100%)	C (100%)	T (13%)	C (100%)
71,253,481	Intron 2	A	T (97%)	T (96%)	T (98%)	A (100%)
71,253,518	Intron 2	G	G (98%)	A (13%)	A (7%)*	G (100%)
71,253,561	Intron 2	C	C (100%)	T (3%)*	T (12%)	C (100%)
71,253,609	Intron 2	C	C (100%)	T (3%)*	T (13%)	C (100%)
71,253,619	Intron 2	G	G (100%)	A (11%)	G (100%)	G (100%)
71,253,709	Intron 2	G	G (100%)	G (100%)	A (52%)	G (100%)
71,253,747	Intron 2	C	C (100%)	T (11%)	T (10%)*	C (100%)
71,253,752	Intron 2	G	A (100%)	A (100%)	A (100%)	G (100%)
71,253,816	Intron 2	C	C (100%)	T (13%)	C (100%)	C (100%)
71,253,817	Intron 2	C	C (100%)	T (12%)	C (100%)	C (100%)
71,253,830	Intron 2	G	G (100%)	A (7%)*	A (11%)	G (100%)
71,253,893	Intron 2	G	A (2%)*	G (100%)	A (11%)	G (100%)
71,253,934	Intron 2	C	C (100%)	T (13%)	T (3%)*	C (100%)
71,253,991	Intron 2		InsT (80%)	InsT (47%)	InsT (73%)	InsTT (92%)
71,254,001	Intron 2	A	T (2%)*	T (19%)	A (100%)	A (97%)
71,254,078	Intron 2	C	C (100%)	T (11%)	T (3%)*	C (100%)
71,254,160	Intron 2	C	T (100%)	T (100%)	T (100%)	C (100%)
71,254,169	Intron 2	C	C (100%)	T (3%)*	T (11%)	C (100%)
71,254,246	Intron 2	G	G (100%)	A (4%)*	A (15%)	G (100%)
71,254,247	Intron 2	G	A (2%)*	A (13%)	A (12%)	G (100%)
71,254,378	Intron 2	C	C (100%)	T (4%)*	T (13%)	C (100%)
71,254,420	Intron 2	T	C (98%)	C (100%)	C (96%)	T (100%)
71,254,472	Intron 2	C	C (100%)	C (100%)	T (12%)	C (100%)

71,254,486	Intron 2	C	C (100%)	T (13%)	T (4%)*	C (100%)	
71,254,512	Intron 2	G	G (98%)	G (100%)	A (14%)	G (100%)	
71,254,543	Intron 2	G	G (100%)	G (93%)	G (97%)	T (100%)	
71,254,578	Intron 2	G	G (100%)	A (12%)	G (100%)	G (100%)	
71,254,609	Intron 2	G	G (100%)	A (16%)	A (4%)*	G (100%)	
71,254,610	Intron 2	G	G (100%)	A (11%)	G (100%)	G (97%)	
71,254,612	Intron 2	C	C (100%)	C (100%)	T (13%)	C (100%)	
71,254,658	Intron 2	G	G (100%)	A (14%)	G (100%)	G (100%)	
71,254,797	Intron 2	G	A (2%)*	A (5%)*	A (13%)	G (100%)	
71,254,910	Intron 2	G	G (100%)	A (6%)*	A (13%)	G (100%)	
71,254,963	Intron 2	C	C (100%)	C (100%)	T (15%)	T (3%)*	
71,254,997	Intron 2	G	G (100%)	G (100%)	A (16%)	G (100%)	
71,255,001	Intron 2	G	A (2%)*	G (100%)	A (11%)	G (100%)	
71,255,043	Intron 2	C	C (98%)	T (16%)	C (100%)	C (100%)	
71,255,051	Intron 2	C	T (100%)	T (100%)	T (100%)	C (100%)	
71,255,071	Intron 2	G	G (100%)	A (11%)	A (9%)*	G (100%)	
71,255,079	Intron 2	C	C (100%)	T (5%)*	T (13%)	C (100%)	
71,255,081	Intron 2	C	C (100%)	T (11%)	T (9%)*	C (100%)	
71,255,093	Intron 2	C	C (100%)	T (6%)*	T (11%)	C (100%)	
71,255,108	Intron 2	C	C (100%)	T (13%)	T (8%)*	C (100%)	
71,255,118	Intron 2	G	A (97%)	A (100%)	A (90%)	G (100%)	
71,255,119	Intron 2	C	C (100%)	T (15%)	T (11%)**	C (100%)	
71,255,211	Intron 2	G	G (100%)	G (100%)	A (14%)	G (100%)	
71,255,267	Intron 2	G	A (2%)*	G (97%)	A (11%)	G (100%)	
71,255,322	Intron 2	C	T (2%)*	T (15%)	C (100%)	C (100%)	
71,255,370	Intron 2	A	T (99%)	T (100%)	T (100%)	A (100%)	
71,255,427	Exon 3	<u>CCG</u>	CCA (6%)*	CCG (100%)	CCA (11%)	CCG (100%)	CCG→P ₁₂ CCA→P ₁₂
71,255,496	Exon 3	<u>GGG</u>	GGG (100%)	GGA (11%)	GGA (8%)*	GGG (100%)	GGG→G ₃₅ GGA→G ₃₅
71,255,593	3' UTR	G	A (100%)	A (100%)	A (100%)	G (100%)	
71,255,614	3' UTR	C	C (100%)	C (100%)	T (19%)	C (100%)	
71,255,623	3' UTR	C	C (100%)	T (13%)	T (5%)*	C (100%)	
71,255,675	3' UTR	C	C (100%)	T (4%)*	T (16%)	C (100%)	
71,255,677	3' UTR	C	T (2%)*	C (100%)	T (15%)	C (100%)	
71,255,679	3' UTR	C	C (100%)	T (4%)*	T (16%)	C (100%)	

71,255,680	3' UTR	C	C (100%)	T (4%)*	T (11%)	C (100%)
71,255,719	3' UTR	G	G (100%)	A (12%)	G (100%)	G (100%)
71,255,739	3' UTR	C	C (100%)	T (5%)*	T (11%)	C (100%)
71,255,767	3' UTR	A	G (100%)	G (97%)	G (100%)	A (100%)
71,255,989	Downstream region	G	G (100%)	A (13%)	A (9%)*	G (100%)
71,256,001	Downstream region	C	C (100%)	C (100%)	T (13%)	C (100%)
71,256,002	Downstream region	C	C (100%)	C (100%)	T (13%)	C (100%)
71,256,003	Downstream region	C	C (100%)	T (4%)*	T (13%)	C (100%)
71,256,123	Downstream region	G	A (2%)*	G (100%)	A (11%)	G (100%)
71,256,203	Downstream region	C	C (100%)	T (4%)*	T (17%)	C (100%)
71,256,204	Downstream region	C	C (100%)	T (4%)*	T (17%)	C (100%)
71,256,209	Downstream region	G	G (100%)	G (100%)	A (11%)	G (100%)
71,256,210	Downstream region	G	G (100%)	A (10%)*	A (12%)	G (100%)
71,256,289	Downstream region	C	C (100%)	T (14%)	C (100%)	C (100%)
71,256,397	Downstream region	C	C (100%)	T (11%)	T (6%)*	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.