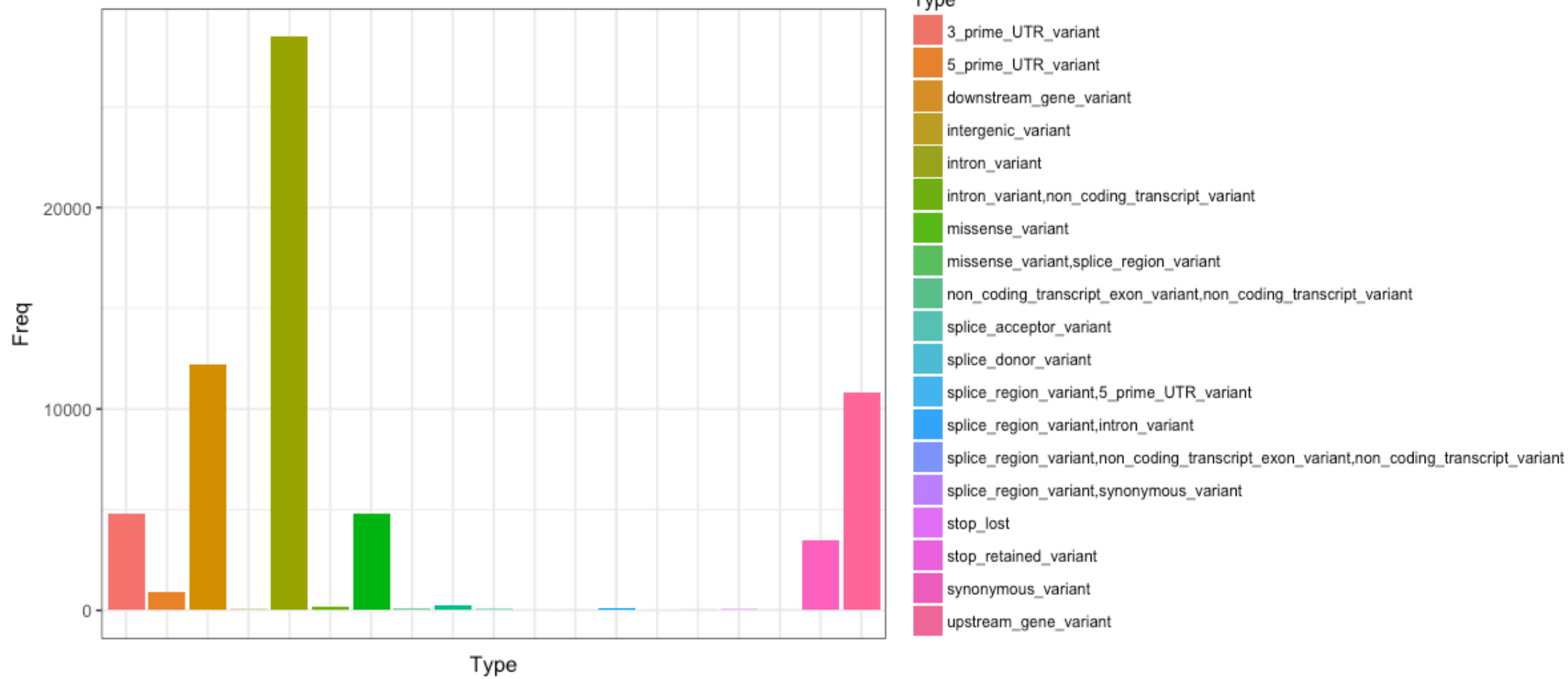
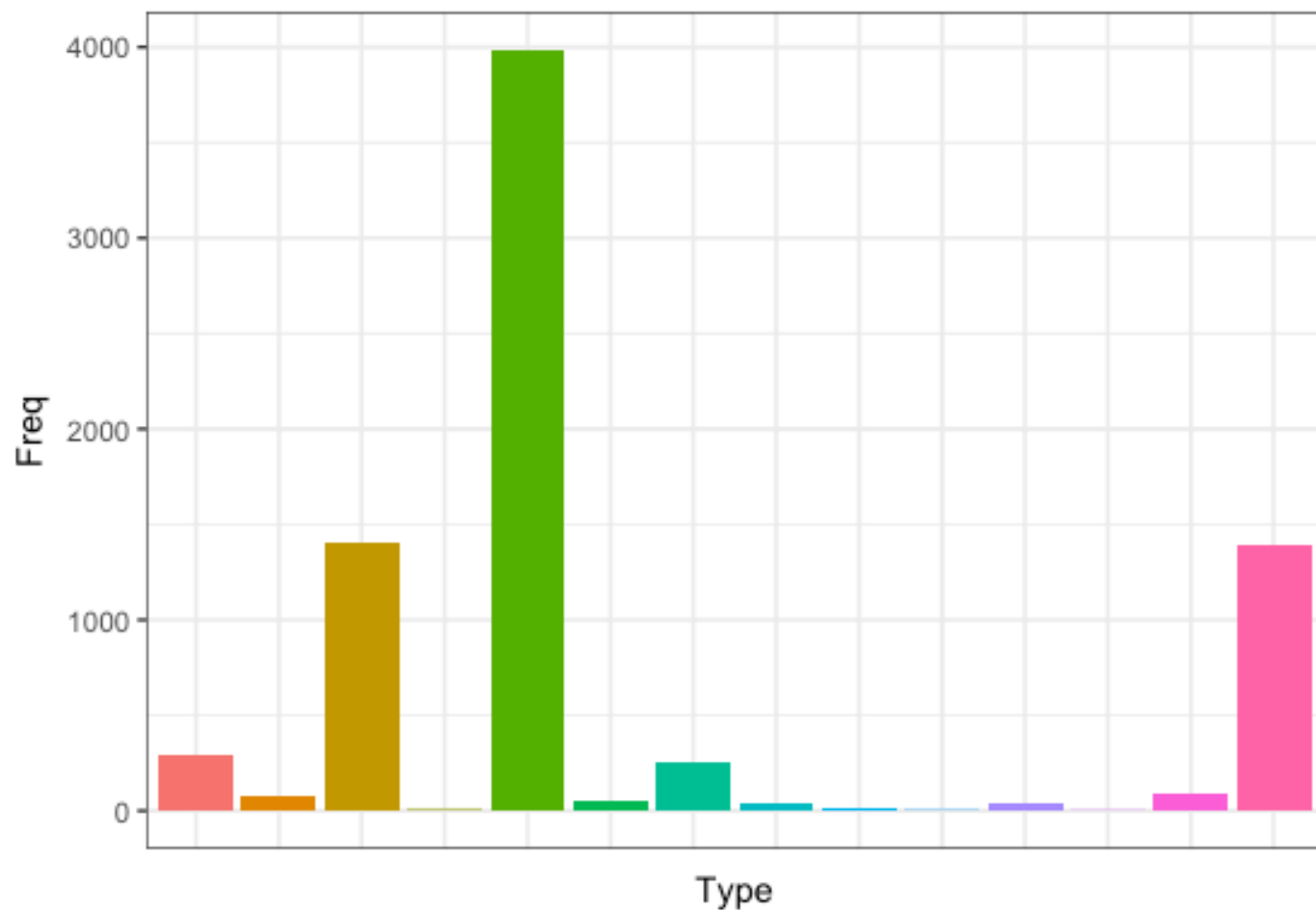


variant effect prediction for RNA editing sites in all brains



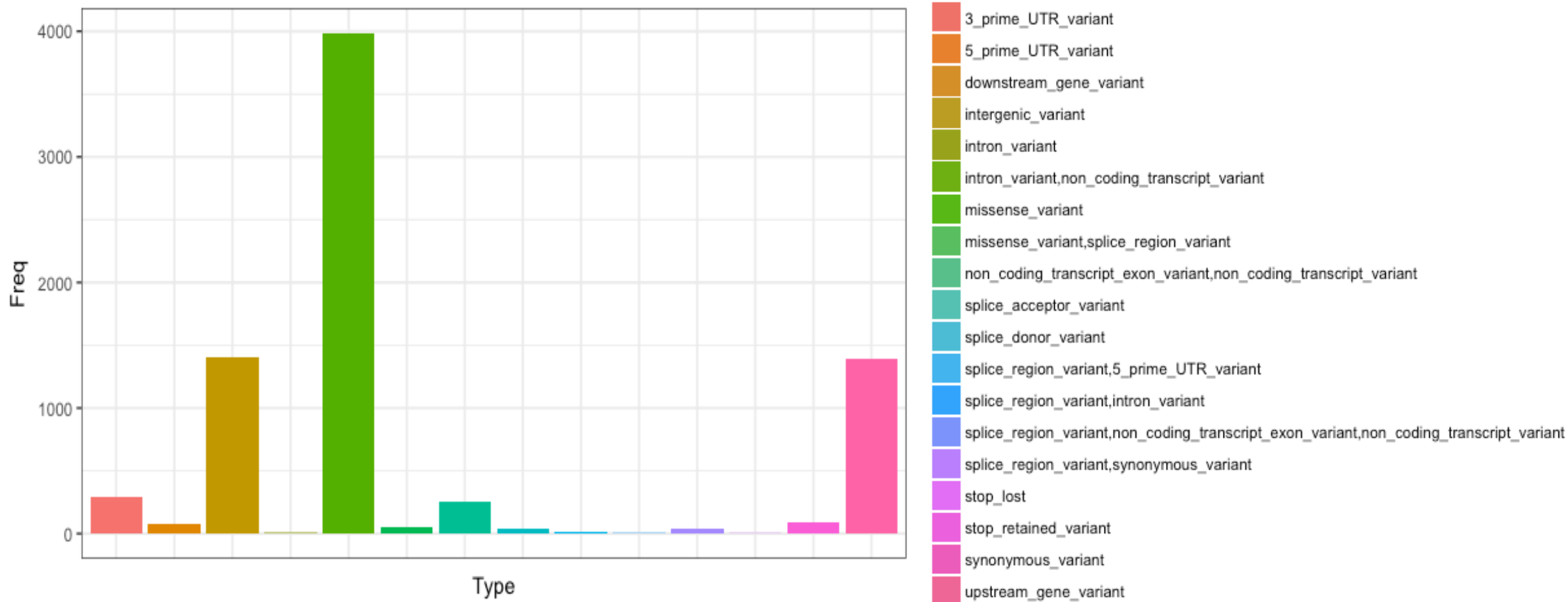
variant effect prediction for RNA editing sites that decrease with age

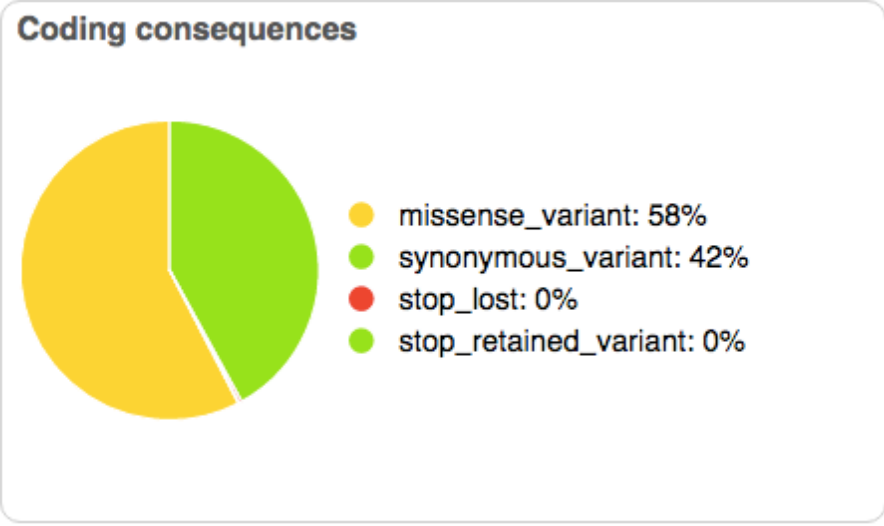


Type

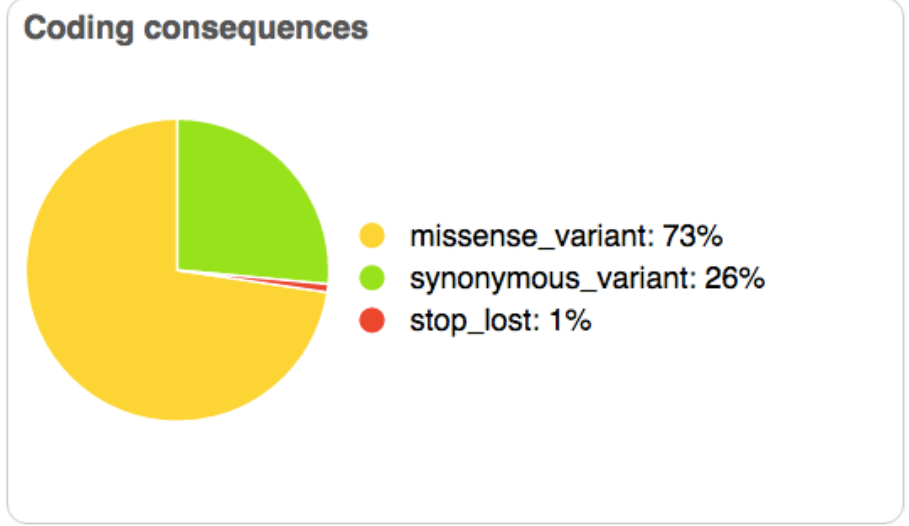
- 3_prime_UTR_variant
- 5_prime_UTR_variant
- downstream_gene_variant
- intergenic_variant
- intron_variant
- missense_variant,non_coding_transcript_variant
- missense_variant
- missense_variant,splice_region_variant
- non_coding_transcript_exon_variant,non_coding_transcript_variant
- splice_acceptor_variant
- splice_donor_variant
- splice_region_variant,5_prime_UTR_variant
- splice_region_variant,intron_variant
- splice_region_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant
- splice_region_variant,synonymous_variant
- stop_lost
- stop_retained_variant
- synonymous_variant
- upstream_gene_variant

variant effect prediction for RNA editing sites that increase with age

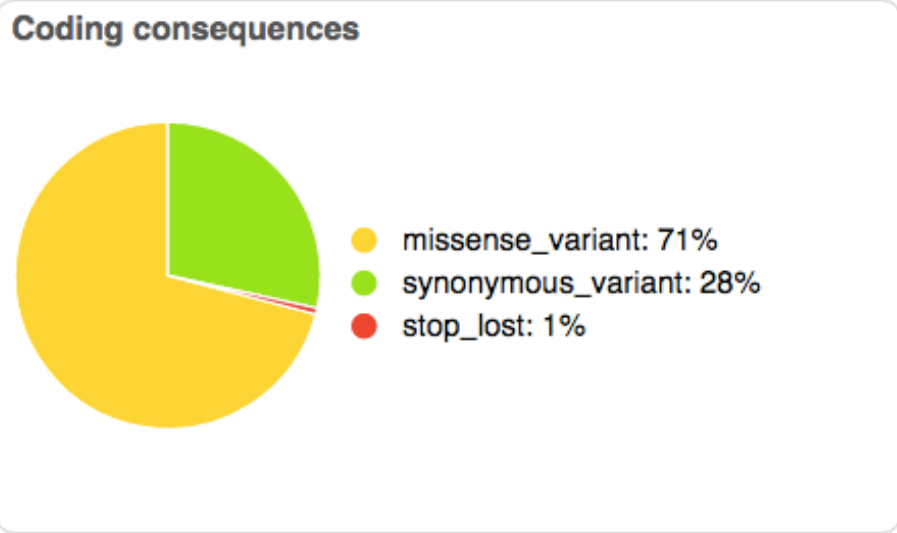




Editing sites- all



Editing sites- *decrease* with age



Editing sites- *increase* with age

	X-squared	Df	P-value
All v decrease	83.69	1	2.2*10-16
All v increase	85.338	1	2.2*10-16
Decrease v increase	1.0946	1	0.2955

2-sample (missense and other) test for equality of proportions with continuity correction