

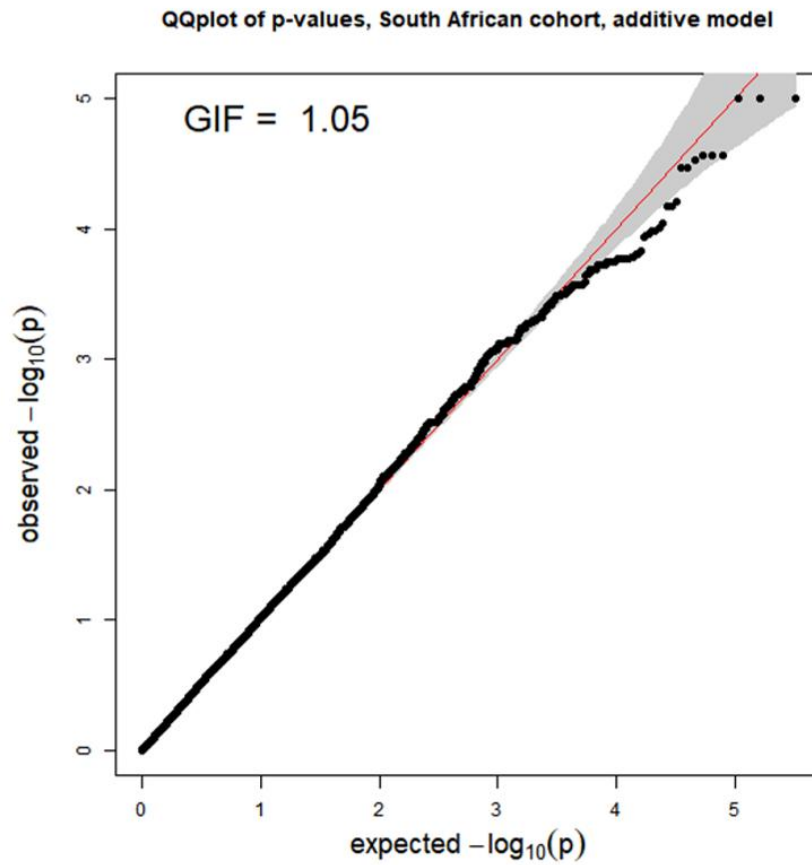


Fig. S1: Quantile-quantile plot showing distribution of p -values as a function of the expected p -values for the additive model in the South African cohort

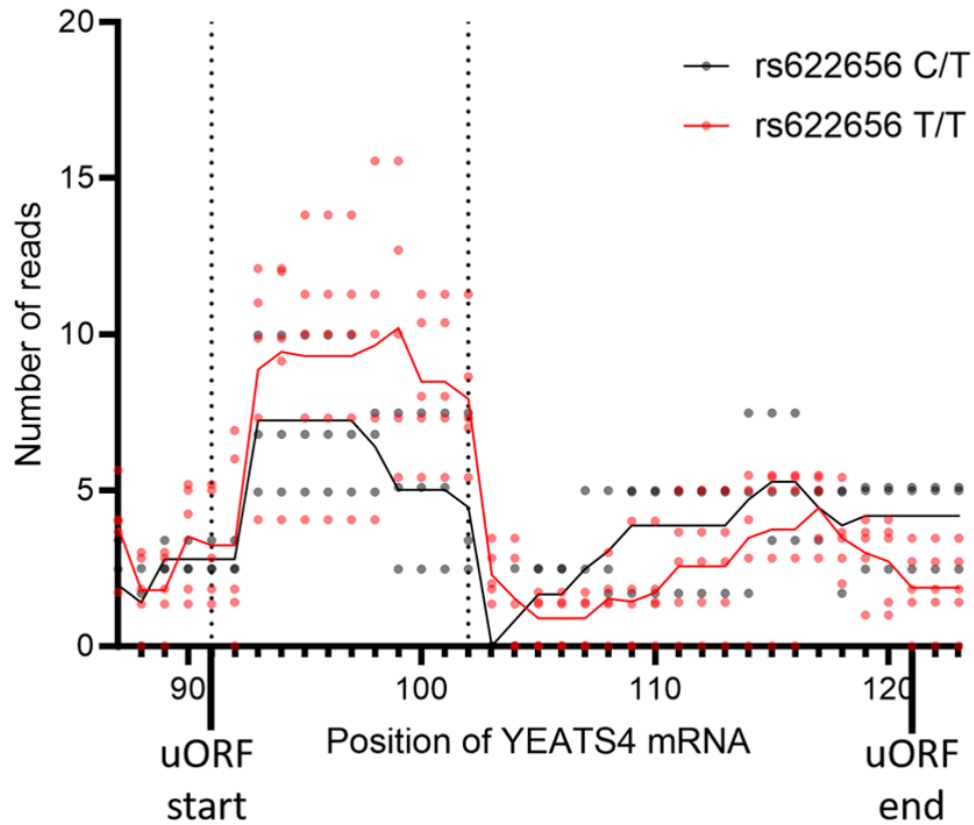


Fig. S2: Number of reads observed in Ribo-sequencing the by position on the transcript ENST00000247843 of YEATS4. Three individuals C/T and five T/T at rs622656 were sequenced. Value shown is the number of reads on the position+10bp sliding window. uORF size from start to stop codons is 30bp. We tested the hypothesis that the mean count of reads in T/T group would be higher compared to the C/T group in the window starting at the uORF start codon up to 3 codons forward in the uORF (i.e. 4 codons, 12bp, dashed lines) using a one-tailed Wilcoxon Mann-Whitney test (see Methods). Ribo-sequencing data suggesting that the uORF disrupted by rs622656 is actually translated, increasing the count of ribosome footprints in rs622656-TT (red) individuals relative to rs622656-CT (black) individuals.