



prediction tools utilized are MutationAssessor and PolyPhen2, as well as SIFT, PolyPhen2, LRT, MutationAssessor, MutationTaster, FATHMM, CADD, and REVEL. Results submitted to the clinician are interpreted as somatic pathogenic, likely pathogenic, or VUS.

The somatic pathogenicity of a variant was determined by consensus agreement of the above classification interpretation systems. To do this, the following rules were applied:

1. Classifications were transformed to the [ab](#)