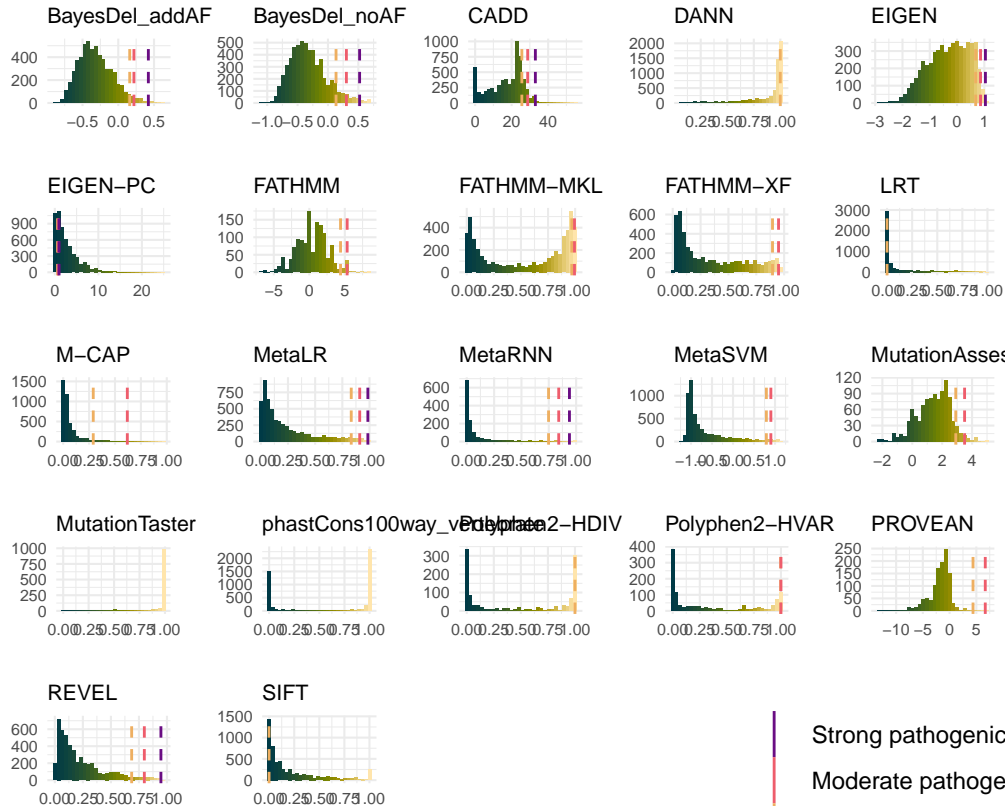


No. qualifying variants



in silico prediction score

Strong pathogenic

Moderate pathogenic

Supporting pathogenic