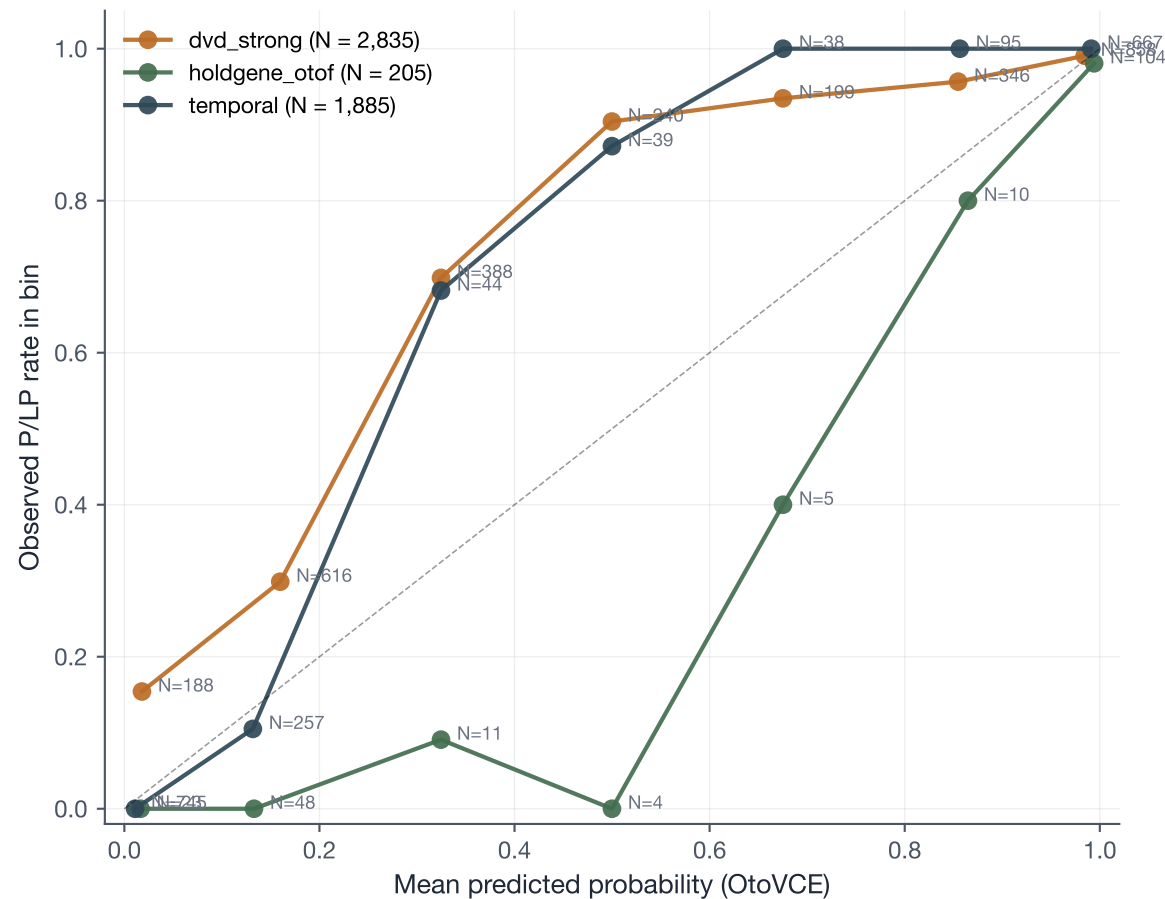
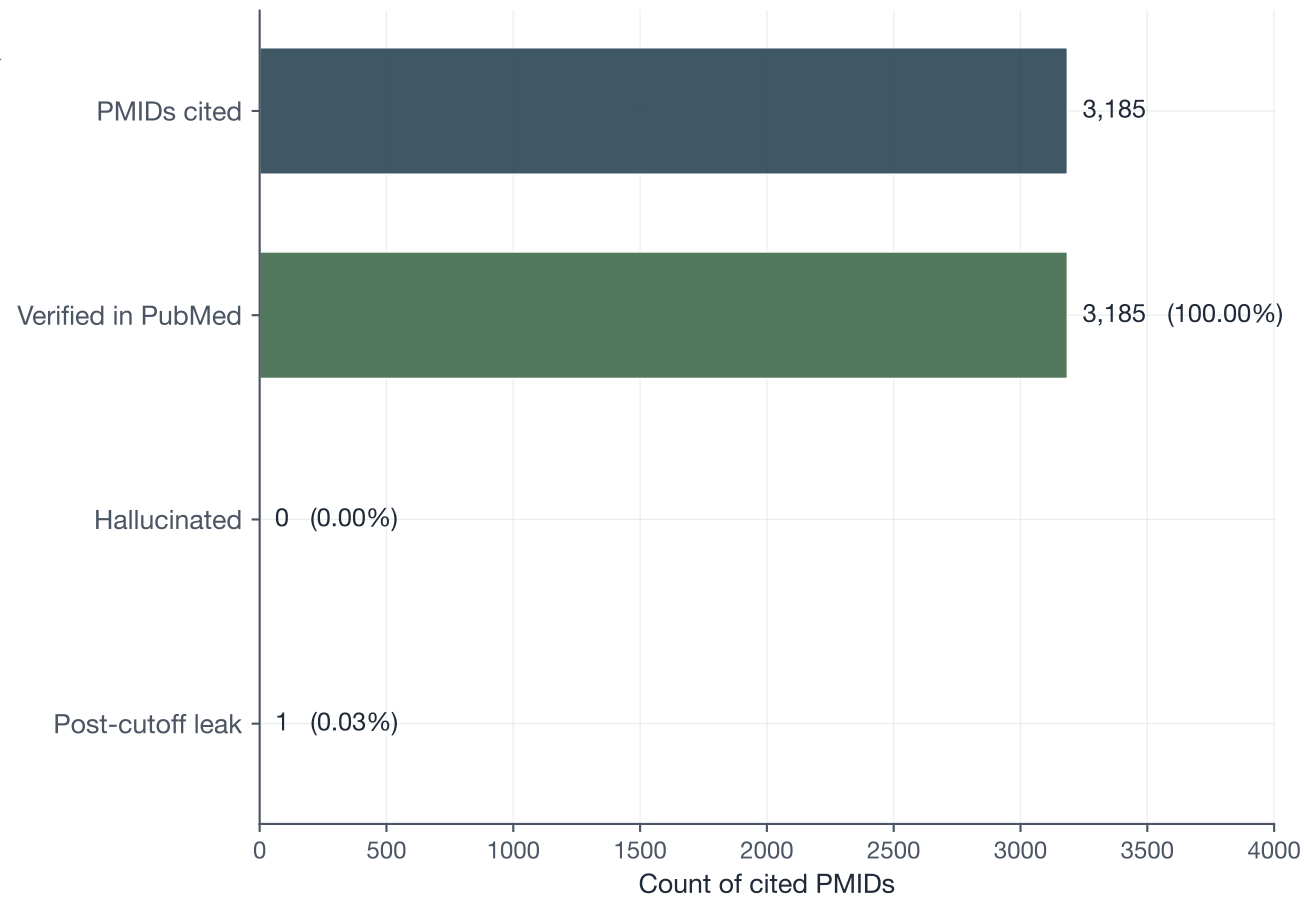


Supplementary Figure S1. Calibration of OtoVCE posterior probabilities and audit of LLM-cited PMIDs

A Calibration

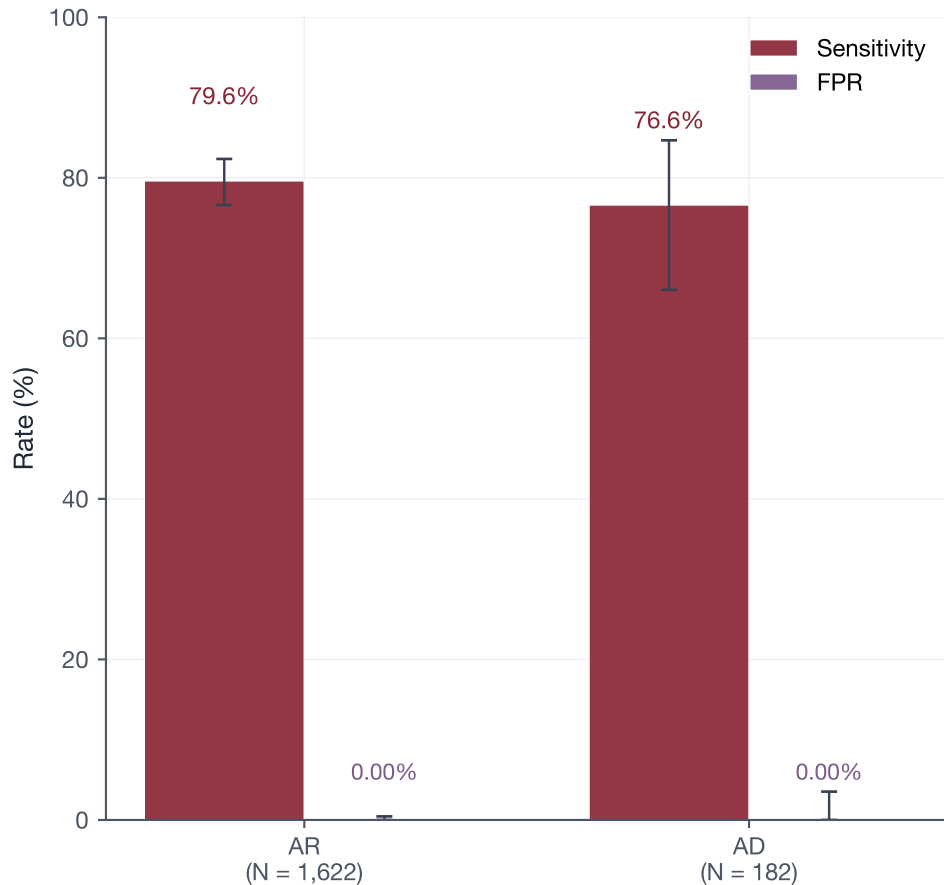


B PMID hallucination audit (3 splits, all LLM citations)

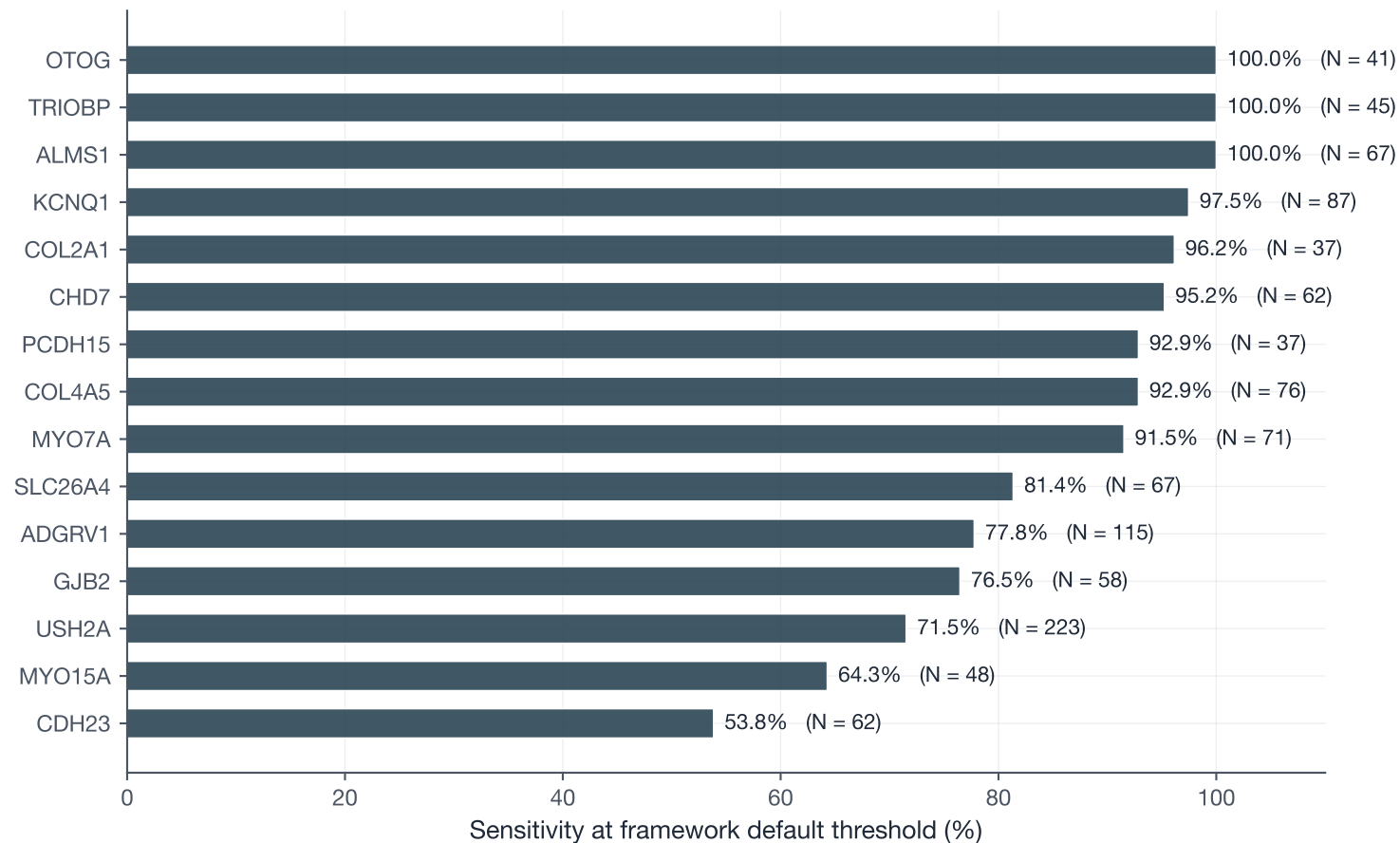


Supplementary Figure S2. Inheritance subgroup and per-gene robustness on val_temporal_extended

A Inheritance subgroup (val_temporal, Wilson 95% CI)

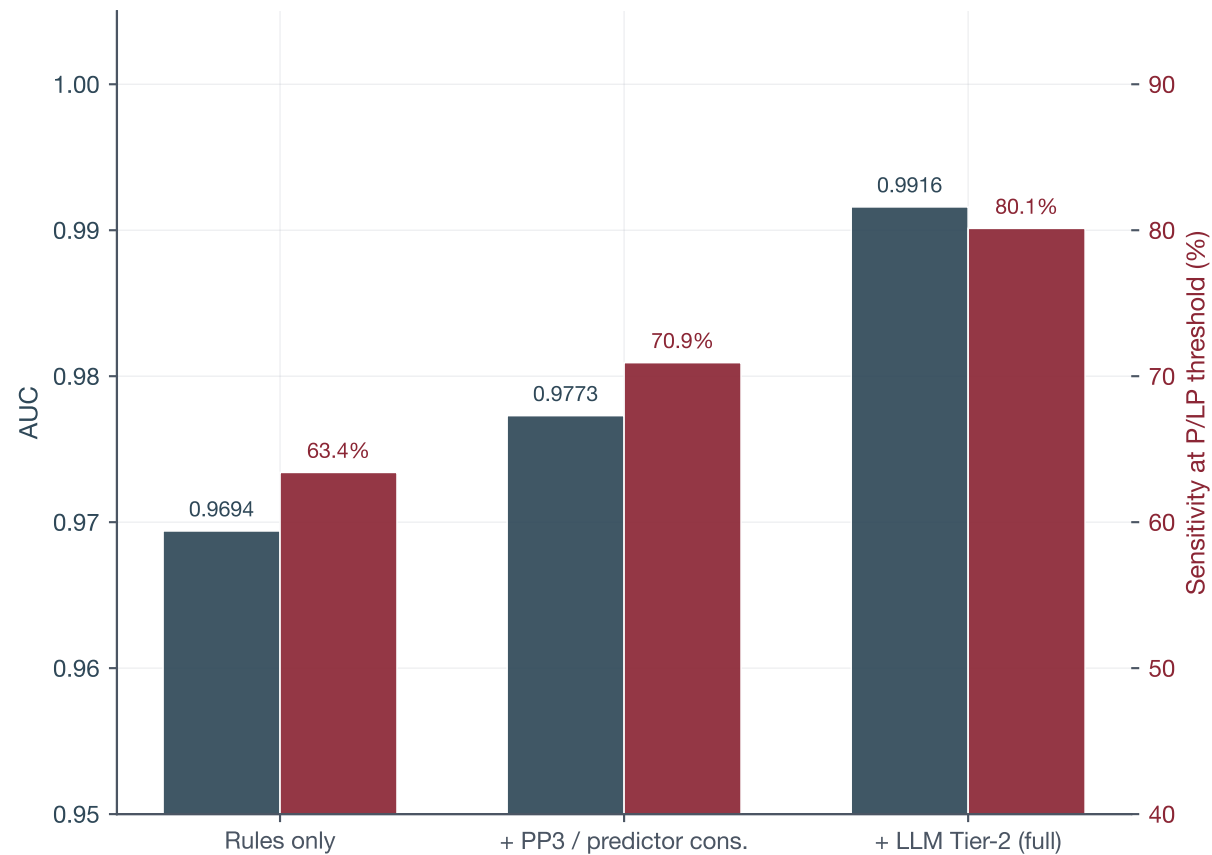


B Per-gene sensitivity (top 15 by N, val_temporal)

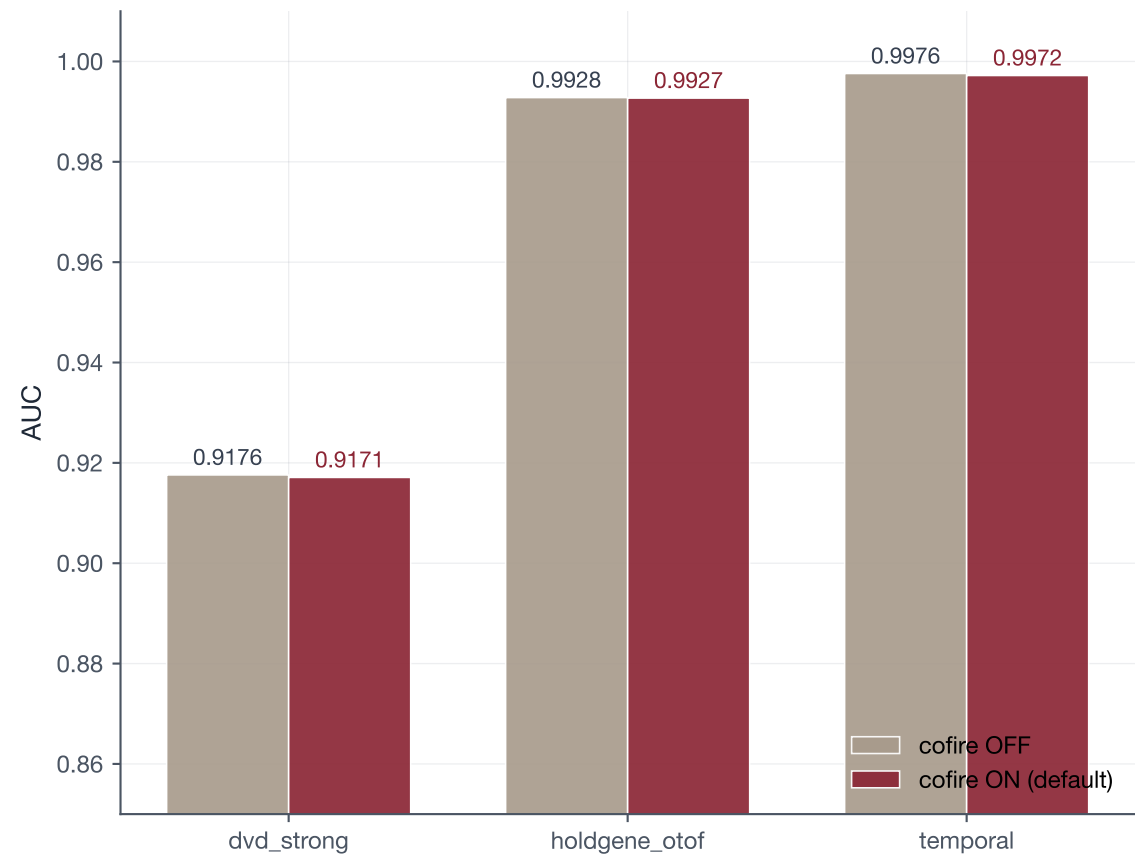


Supplementary Figure S3. Stage-by-stage and cofire-safeguard ablation

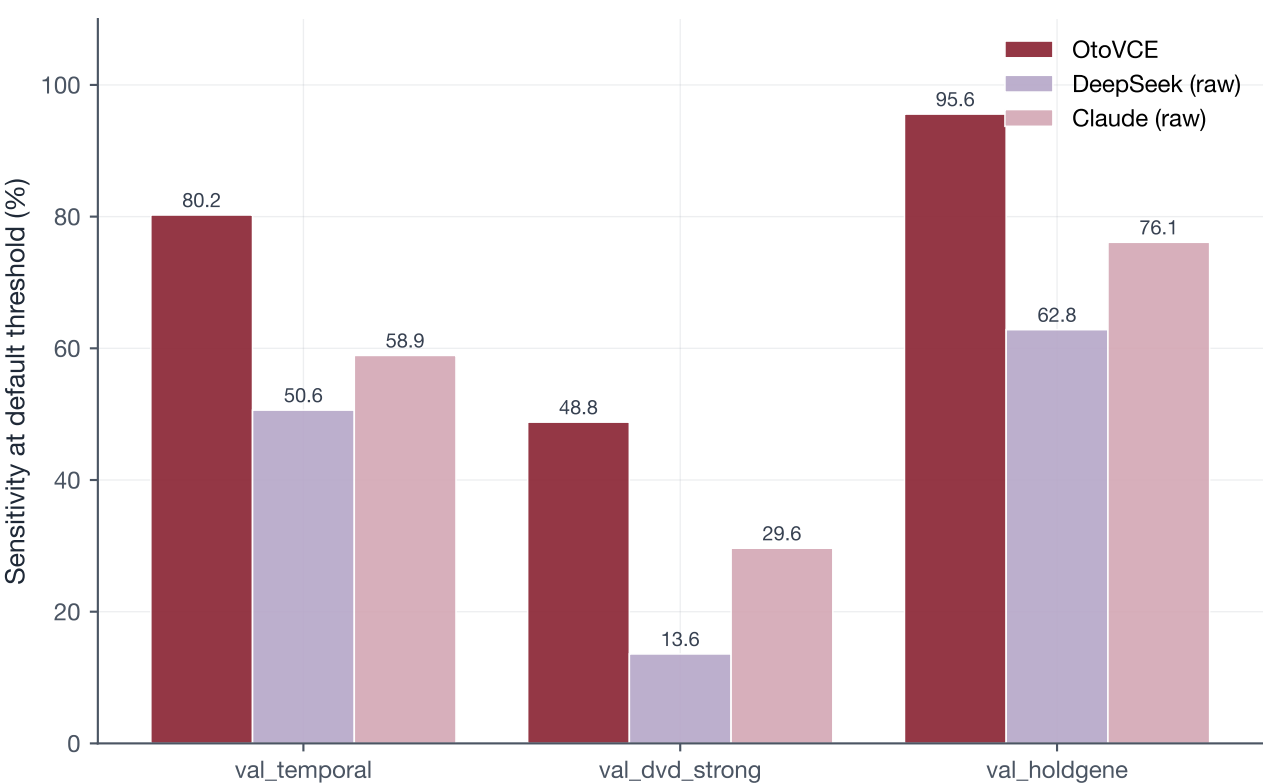
A Stage-by-stage ablation (val_temporal)



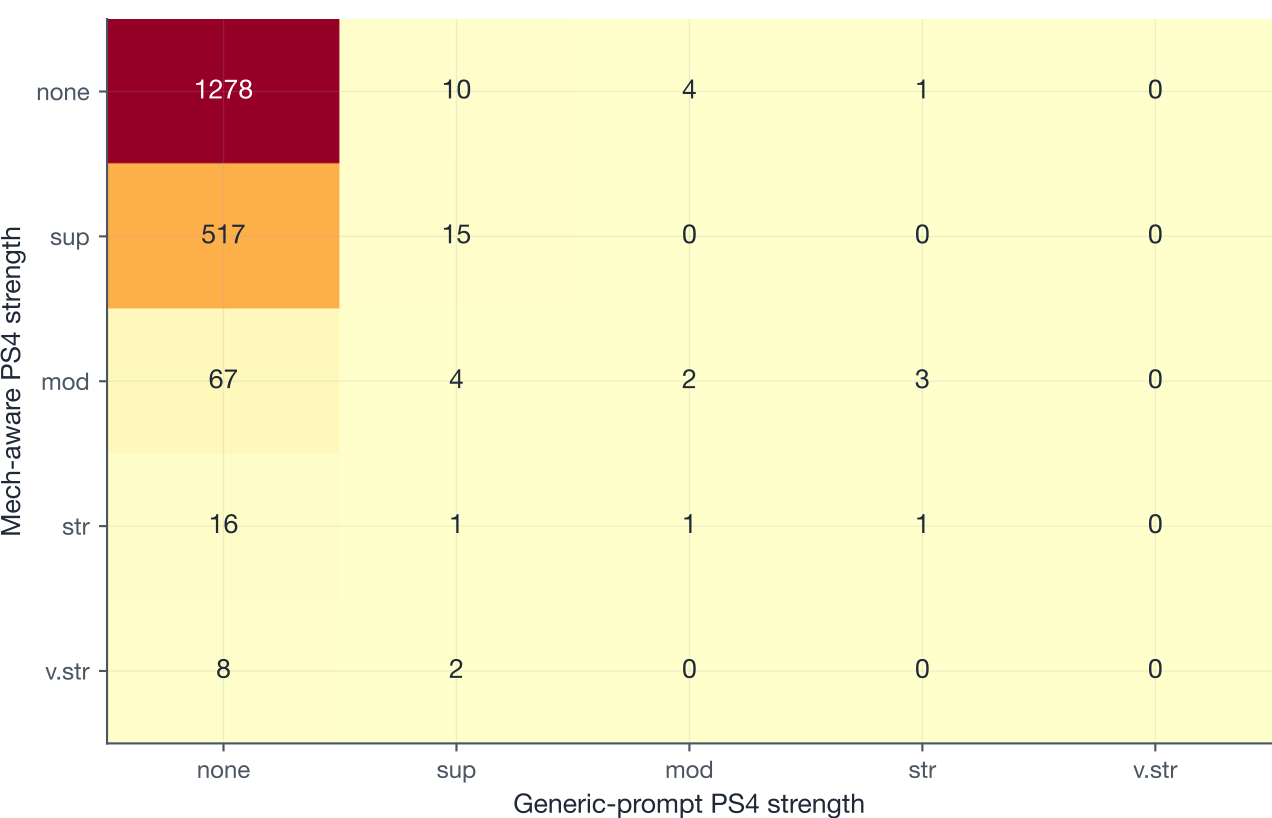
B Cofire safeguard ablation (minimal effect)



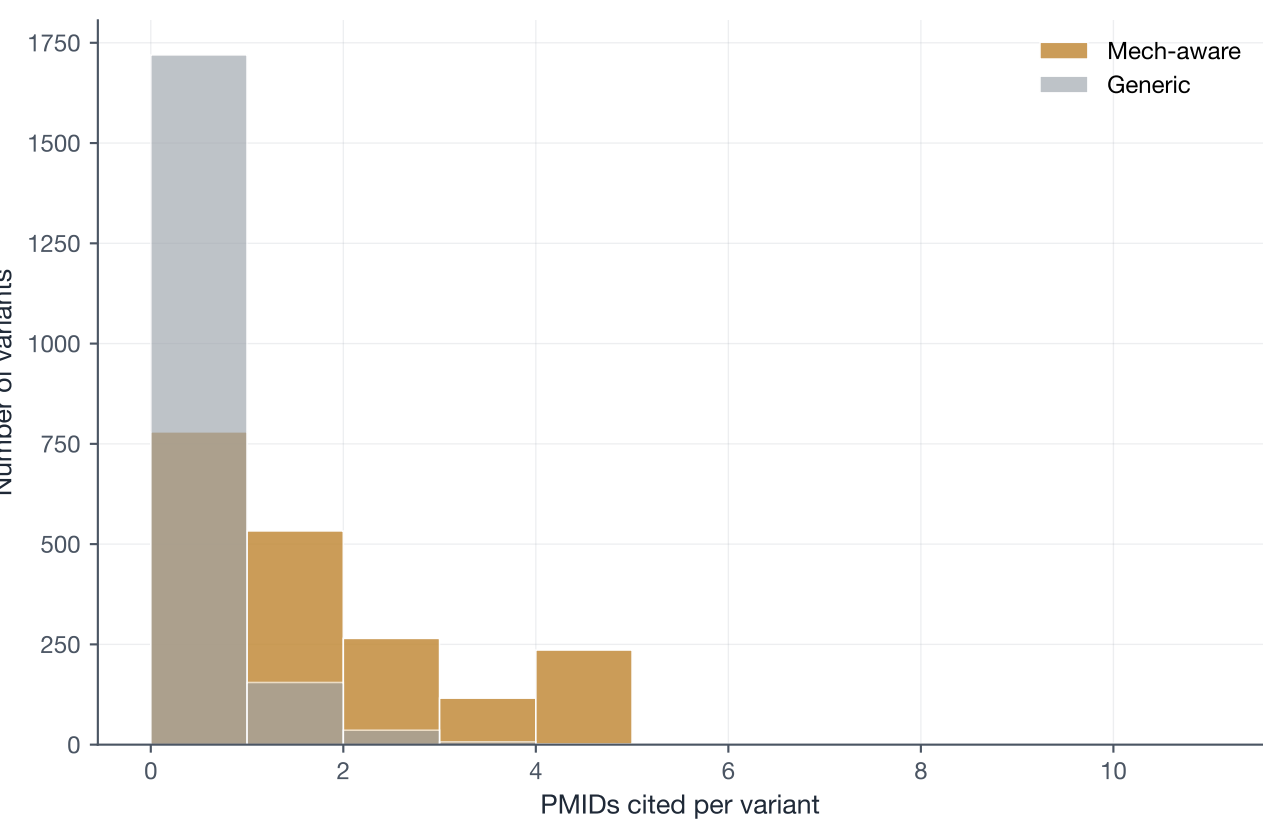
A OtoVCE vs raw single-shot LLMs across cohorts



B PS4 strength agreement (paired N = 1,930, 67% diagonal)



C PMID-per-variant distribution (paired N = 1,930)



D Worked-example rationale comparison (COL2A1 p.Arg565Cys)

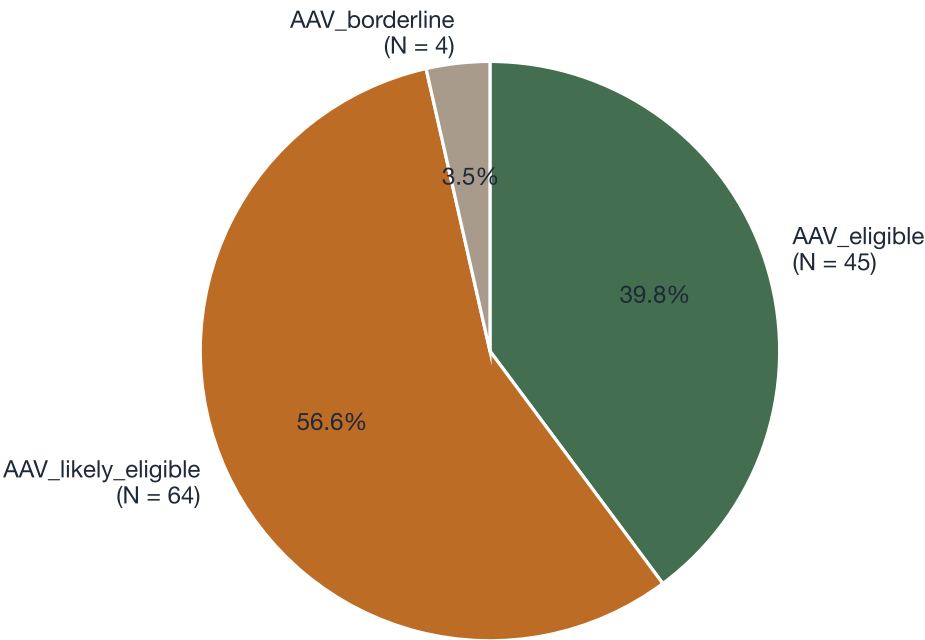
Mech-aware (PS3 = moderate, PS4 = strong; 4 PMIDs):

PMID 38073514 demonstrates that COL2A1 mutants (including p.Arg565Cys) form large aggregates in the ER and elevate ER stress, with wild-type negative control — qualitative loss-of-function in a validated assay (PS3 moderate). For PS4, the variant is reported across 4 PMIDs as a recurrent allele in 11 unrelated Stickler probands.

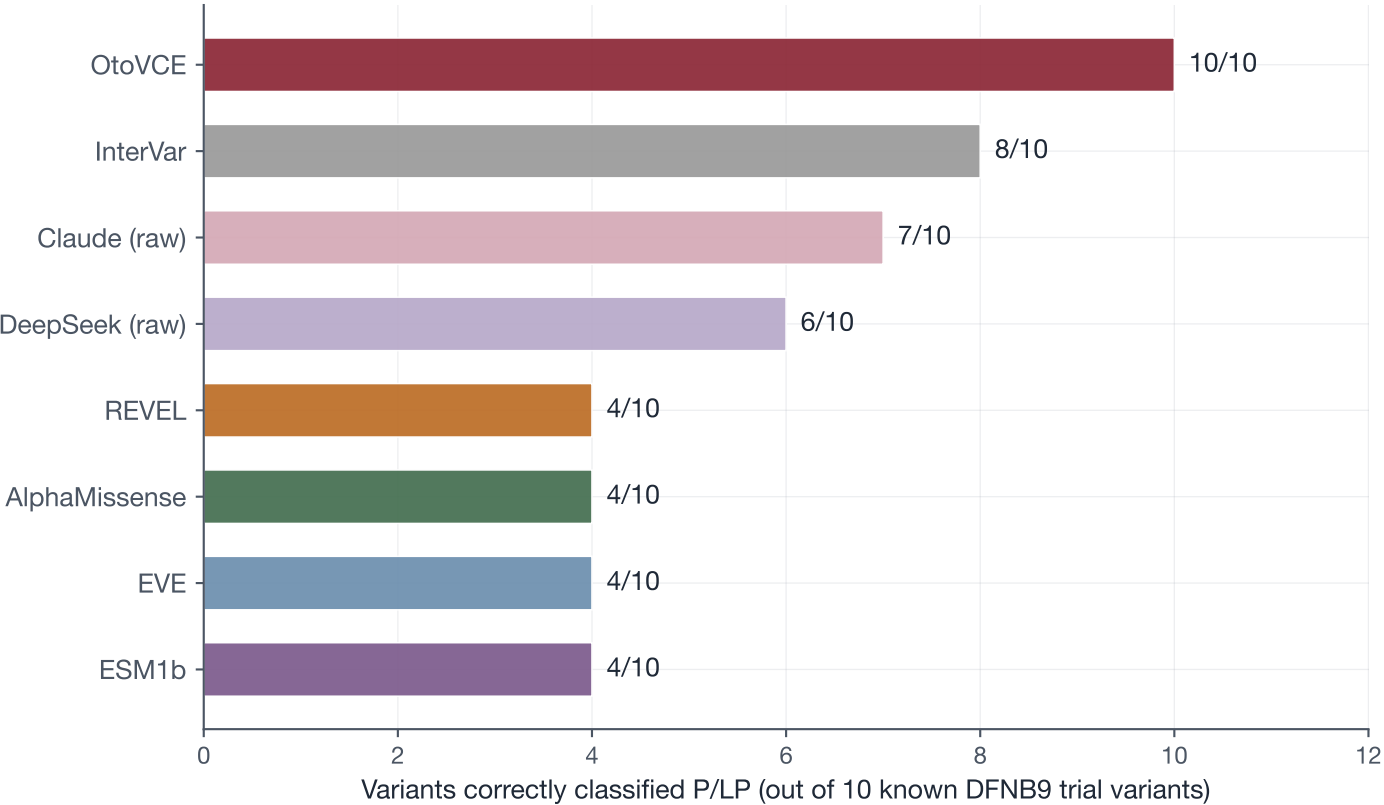
Generic (PS3 = none, PS4 = none; 0 PMIDs):

No retrieved literature provides functional data or proband counts for the specific variant COL2A1 p.Arg565Cys. The papers focus on Stickler syndrome diagnosis and other COL2A1 mutations.

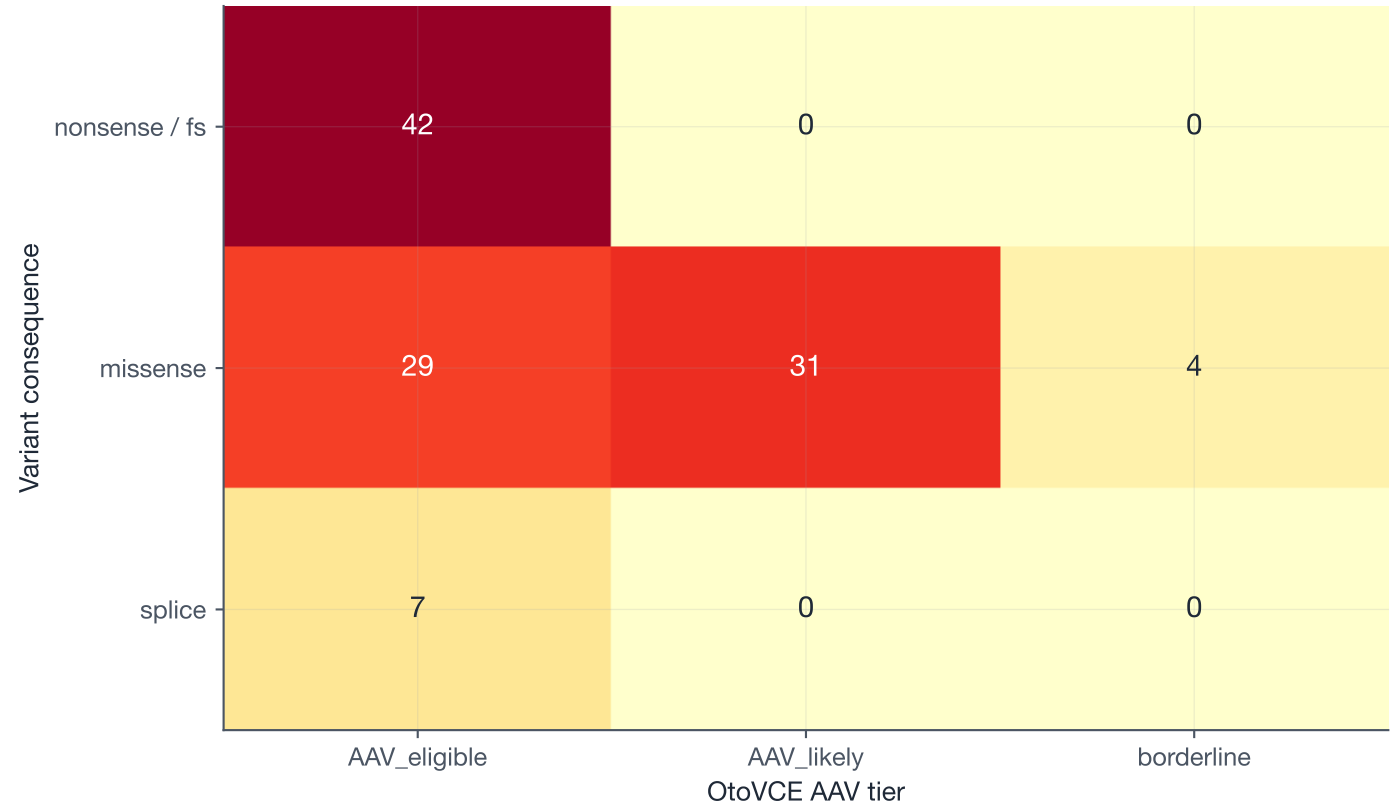
A OTOF P/LP variants by AAV-eligibility tier (N = 113)



B 10 known DFNB9 trial variants — tool comparison



C AAV tier × variant consequence (N = 113 OTOF P/LP)



D Illustrative AAV-OTOF case (OTOF p.Pro490Arg, recurrent in clinical trials)

Step 2 — rules engine: VUS (net 3 pts)

Step 3 — multi-agent debate: Likely pathogenic (moderate confidence)

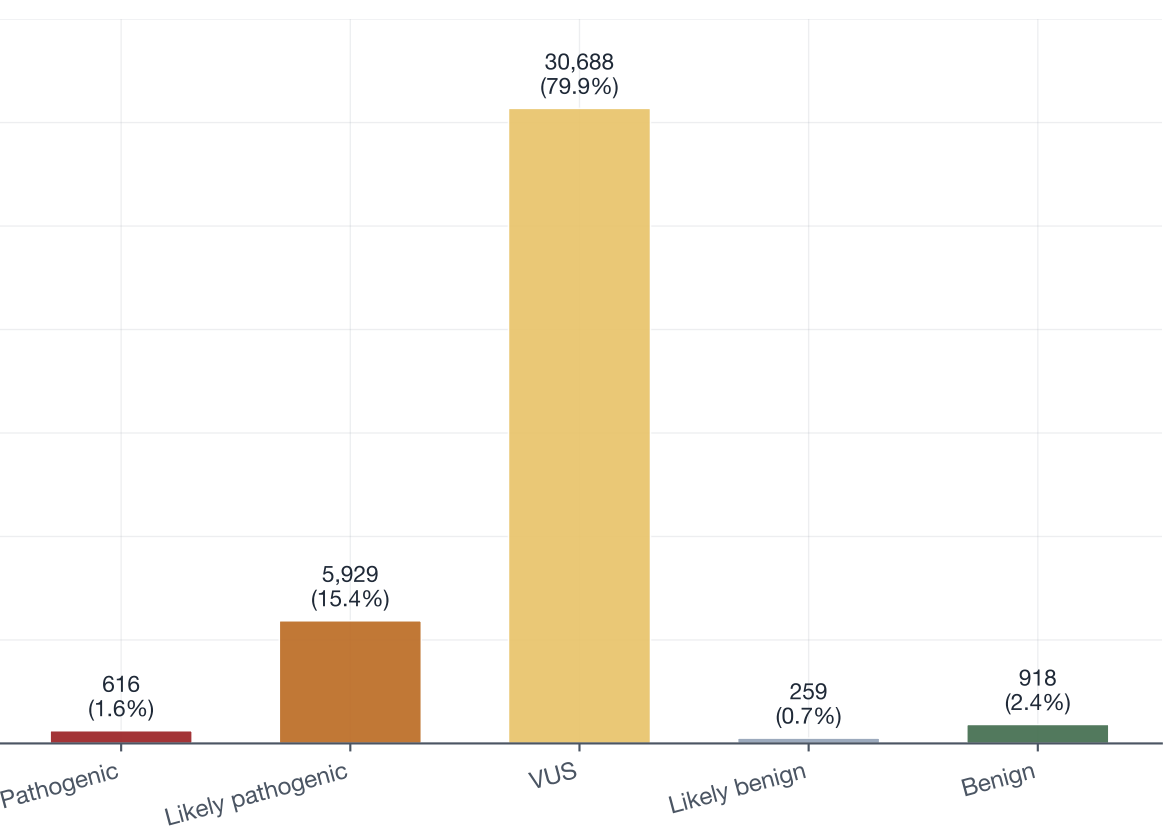
Rationale (excerpt):

C2-3 calcium-binding fold; Pro-to-Arg substitution introduces charge and disrupts the beta-sandwich, mechanistically aligned with otoferlin loss-of-function. Computationally convergent (AlphaMissense 0.979, EVE 0.842, ESM1b strong, HL-PLM 0.979 with LoF as top mechanism head), AF functionally absent in gnomAD.

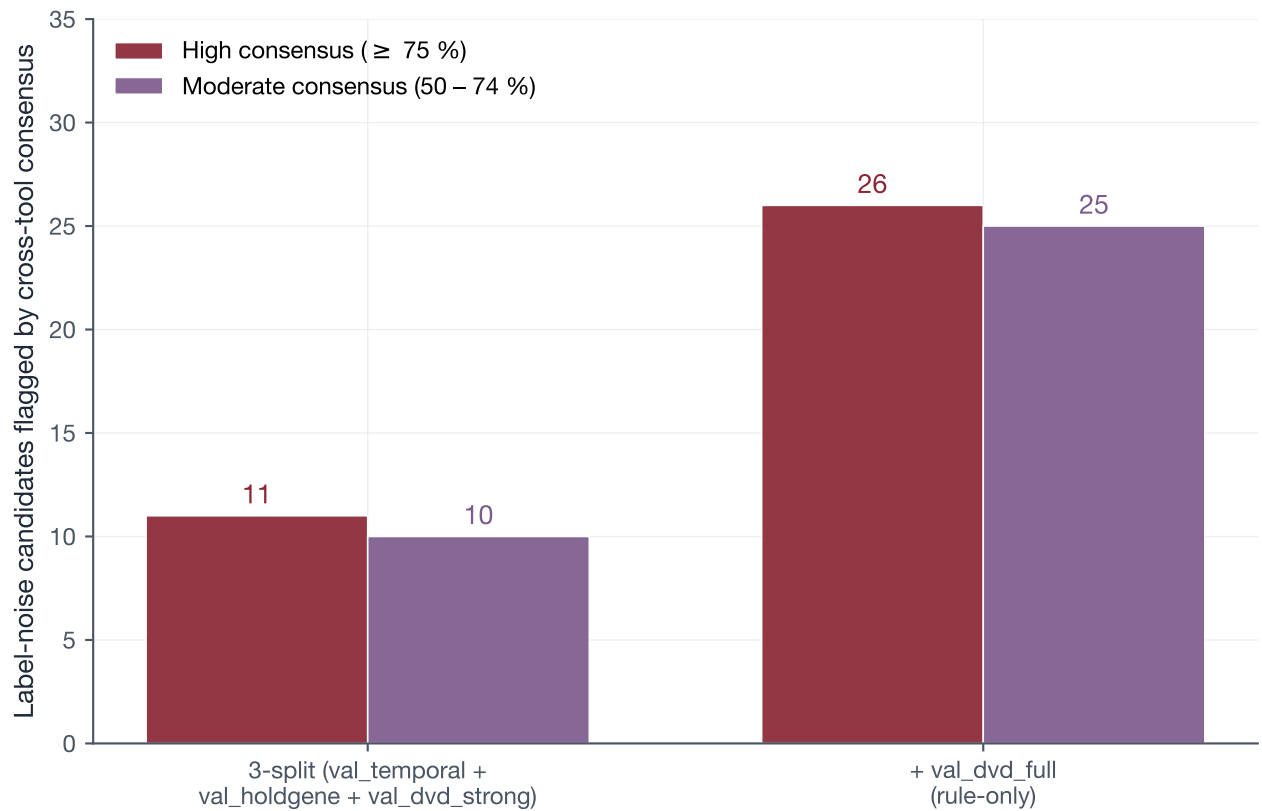
AAV-OTOF eligibility:

In trans with a second pathogenic allele, this variant supports trial enrollment as biallelic pathogenic genotype.

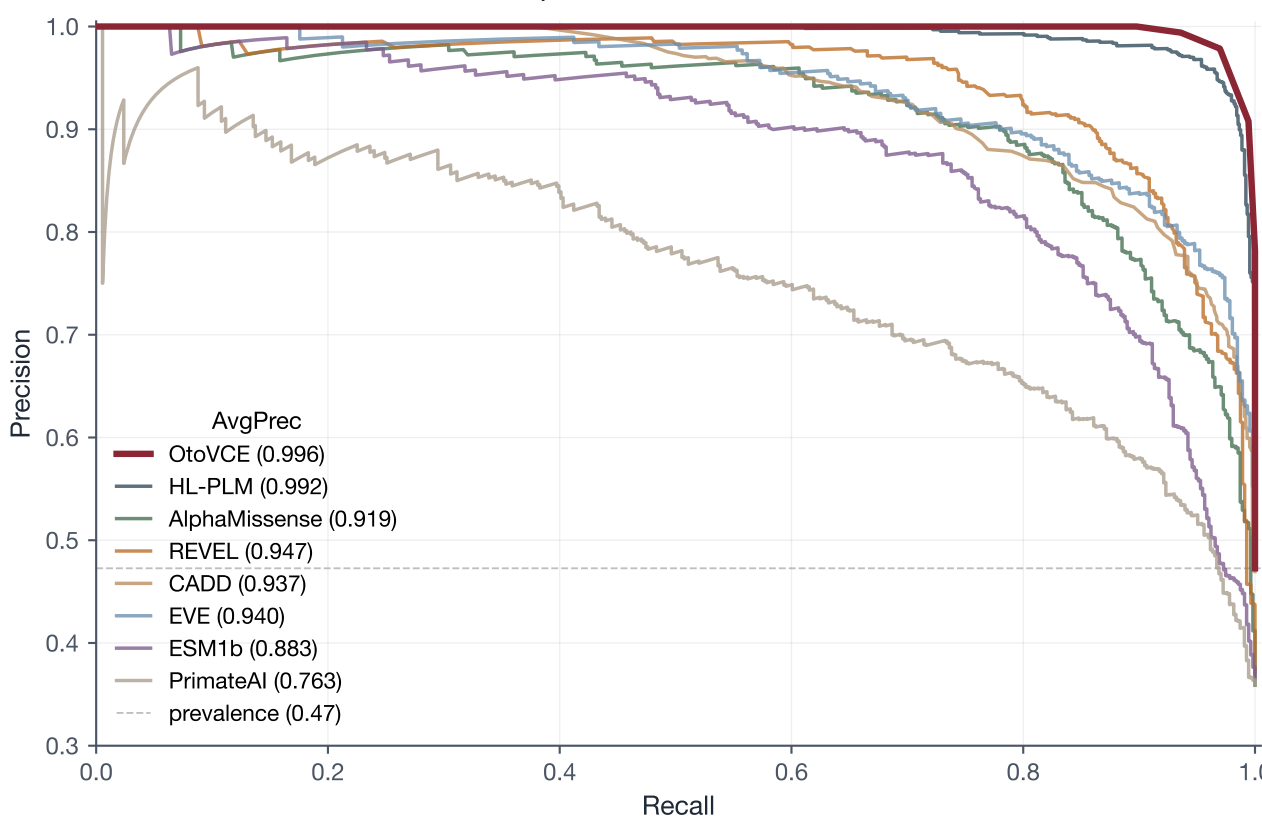
A val_dvd_full step-2 rule-only class distribution (N = 38,410)



B Label-noise candidate growth with val_dvd_full expansion



C Precision-recall on val_temporal_extended



D Classification × ground truth (val_temporal)

