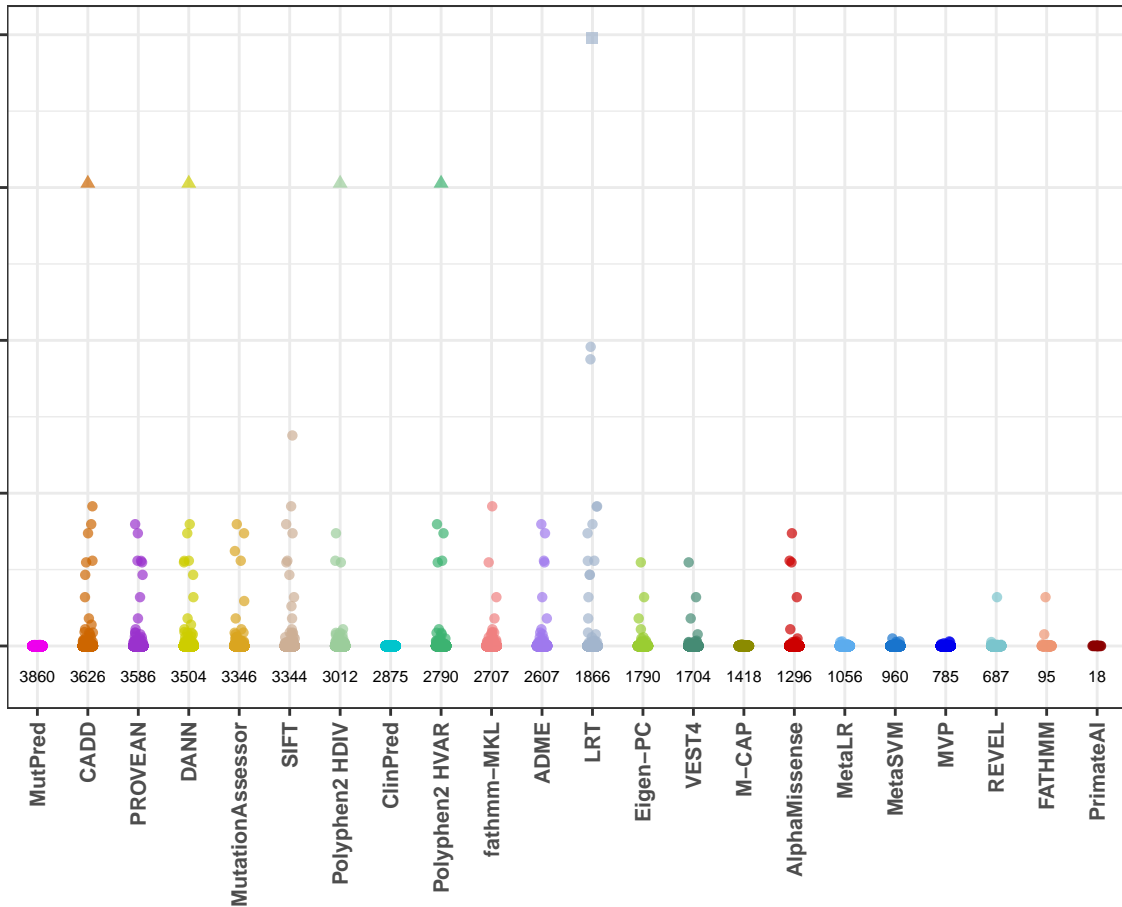


**GMAF of missense variants predicted as deleterious**



**Variant ID (GMAF>0.5)**

- 4-115589302-A-G
- ▲ 4-69795626-C-T