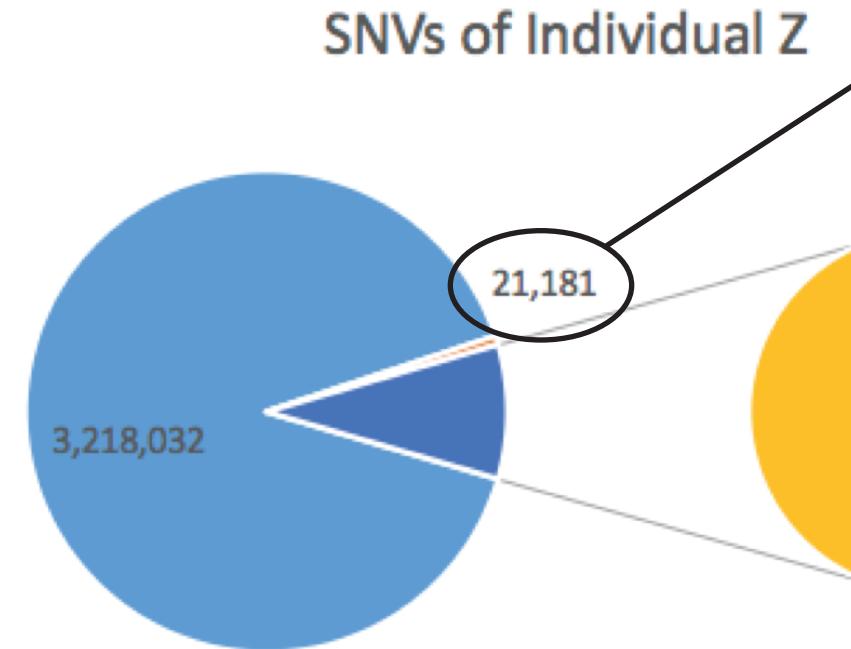
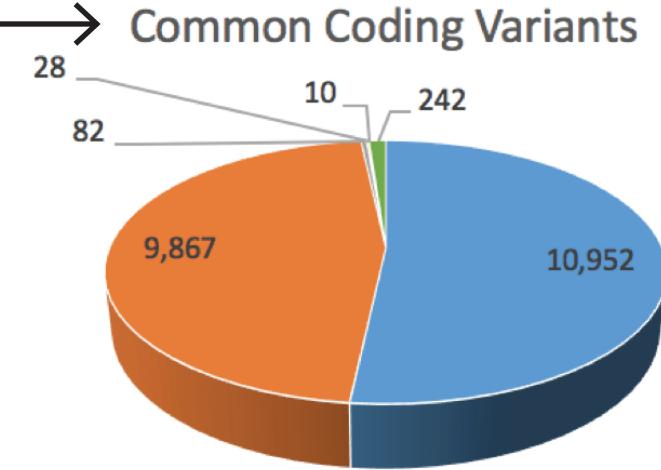


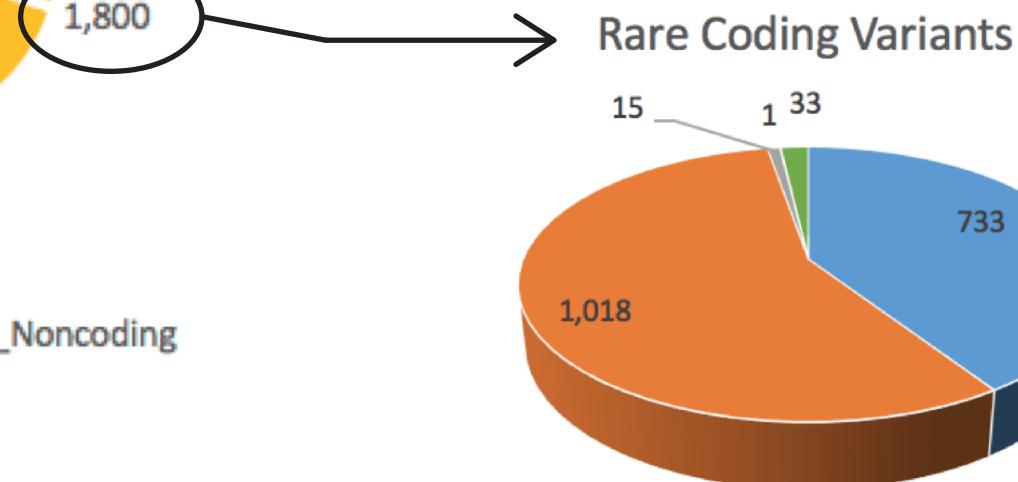
Overview & Coding Variants



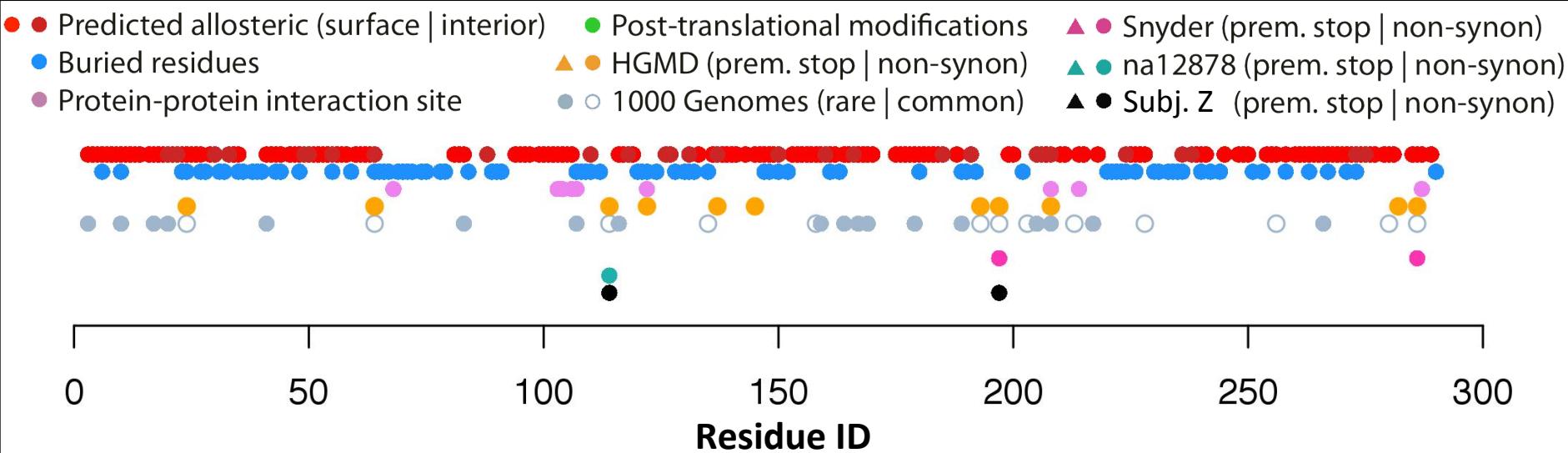
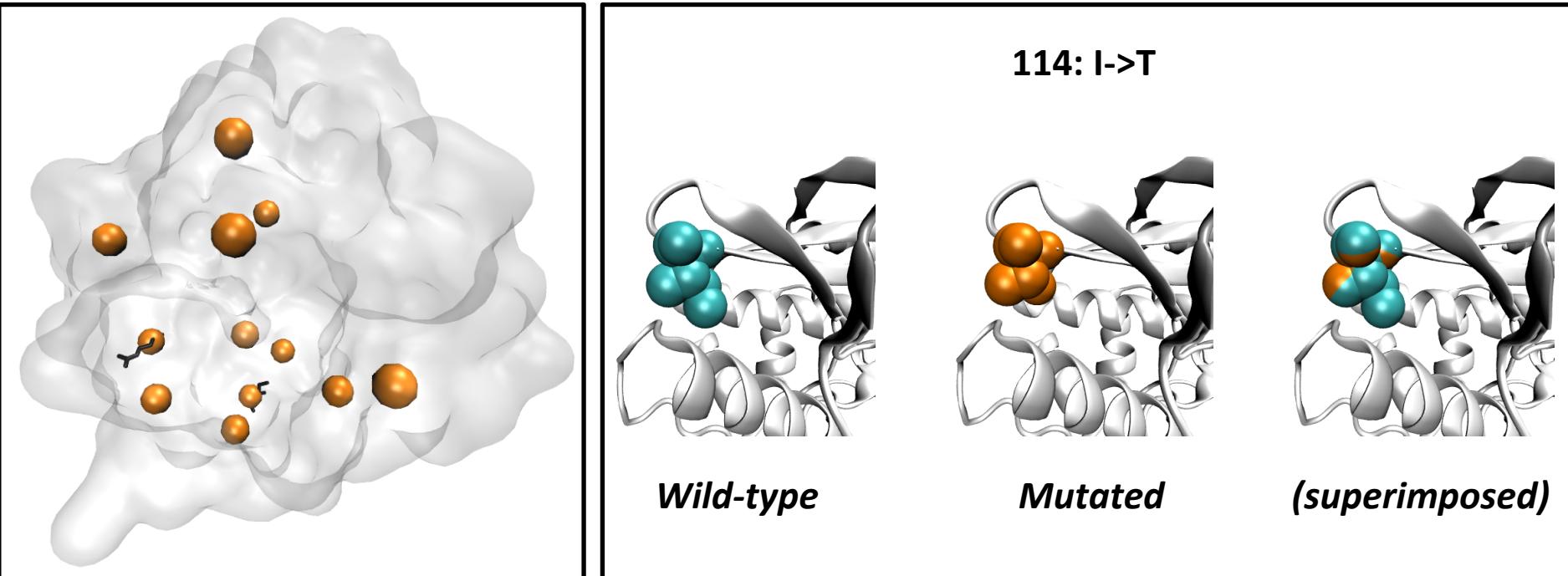
■ Common_Noncoding ■ Common_Coding ■ Rare_Coding ■ Rare_Noncoding

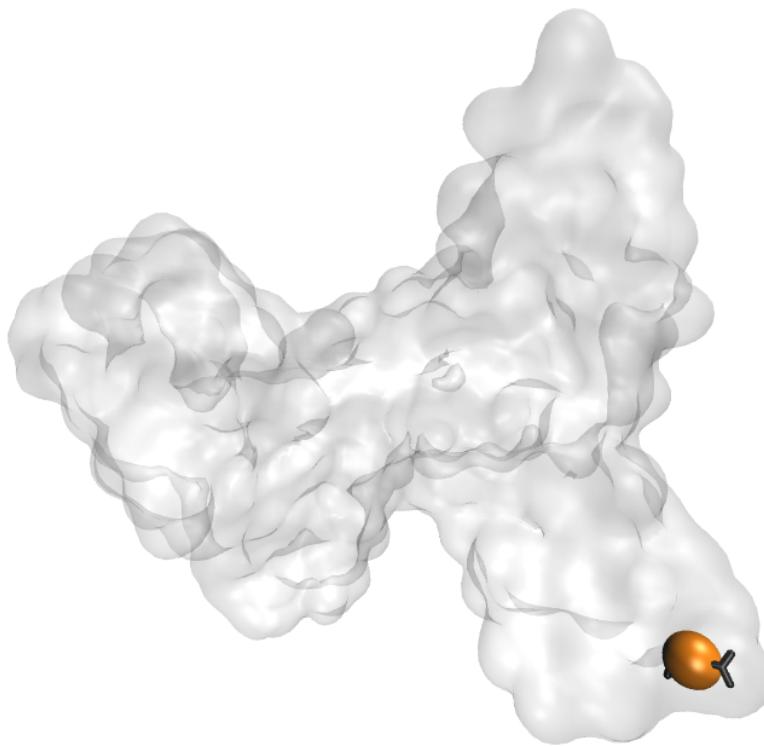


■ Synonymous ■ Nonsynonymous ■ PrematureStop
■ RemovedStop ■ SpliceOverlap ■ NA



Arylamine N-acetyltransferase (PDB: 2PFR_A ; gene: NAT2)





- ● Predicted allosteric (surface | interior)
- Buried residues
- Protein-protein interaction site
- Post-translational modifications
- ▲ ● HGMD (prem. stop | non-synon)
- ○ 1000 Genomes (rare | common)
- ▲ ● Snyder (prem. stop | non-synon)
- ▲ ● na12878 (prem. stop | non-synon)
- ▲ ● Subj. Z (prem. stop | non-synon)

Vitamin D-binding protein (1KW2_A: gene = GC)

