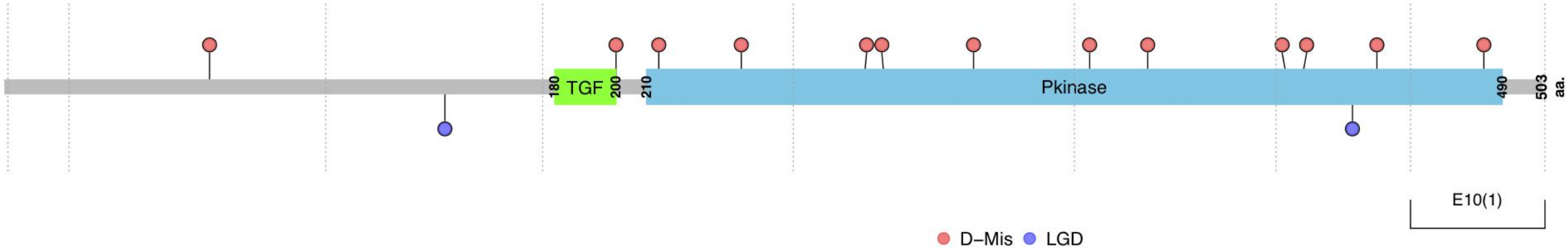
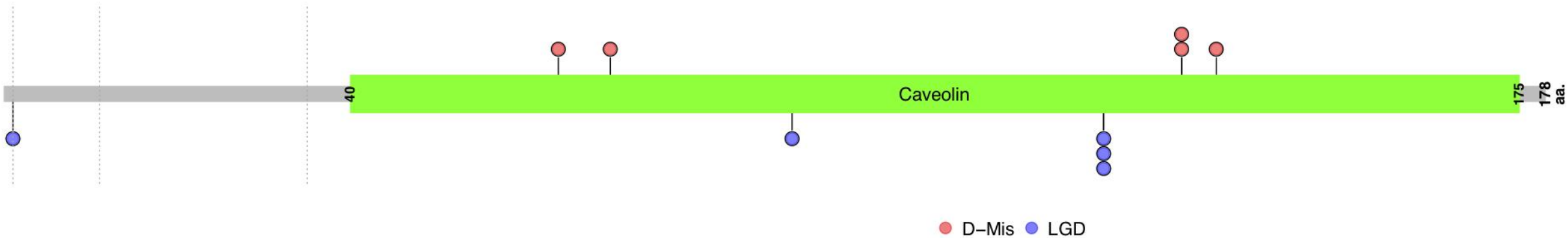
**Figure S4. Locations of rare deleterious PAH patient-derived other previously reported PAH risk gene variants within the two-dimensional protein structures.** Predicted damaging missense (D-Mis) variants are shown above the protein schematics; likely-gene-disrupting (LGD including stopgain, frameshift, in-frame deletion and whole exon deletion) variants are shown below the schematics. The vertical gray lines indicate exon borders. For *ACVRL1*, E10 (1) indicates a deletion of exon 10 identified in one case. For *EIF2AK4*, patients 12-064 and 21-036 are homozygous for the given *EIF2AK4* variants, and patients 12-014, 02-030 and 10-091 are compound heterozygotes.

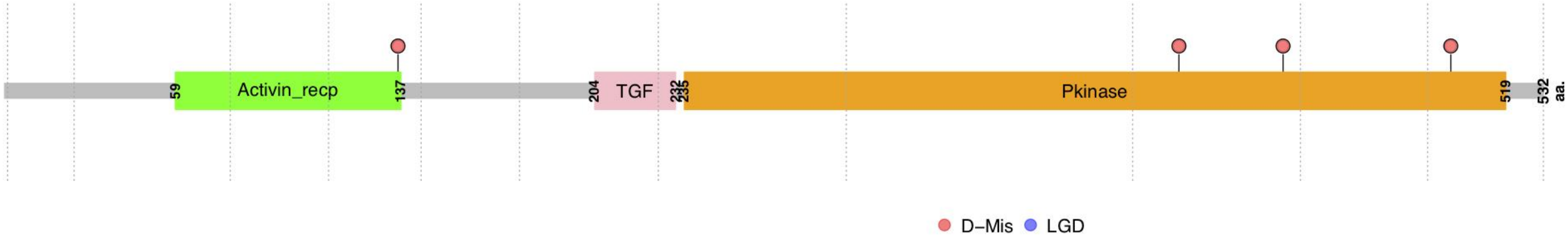
***ACVRL1***


180
TGF
200
210
Pkinase
490
503
aa.
E10(1)
D−Mis
LGD

***CAV1***

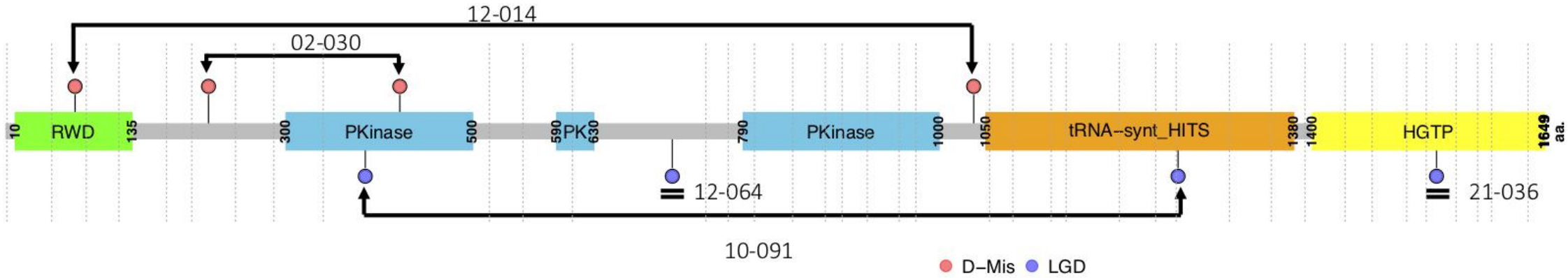

40
Caveolin
175
178
aa.
D−Mis
LGD

***BMPR1A***

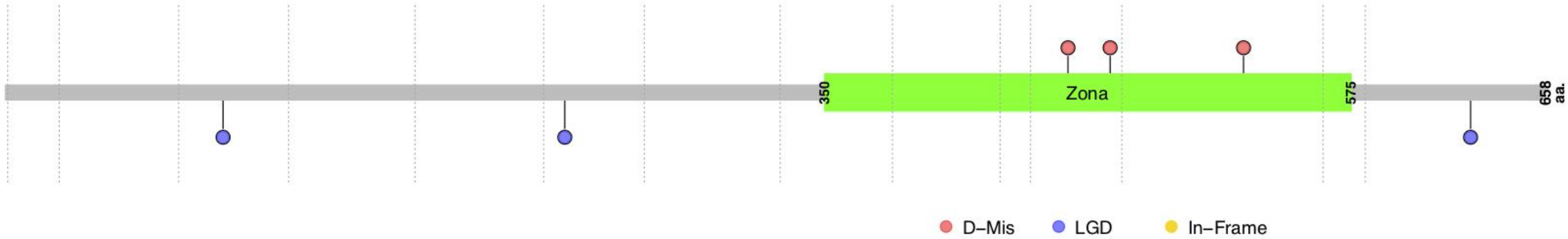



***BMPR1B***

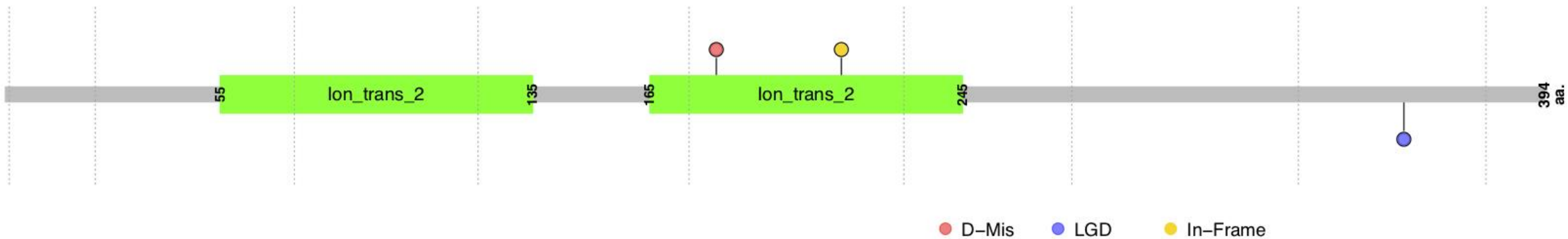
## *EIF2AK4*



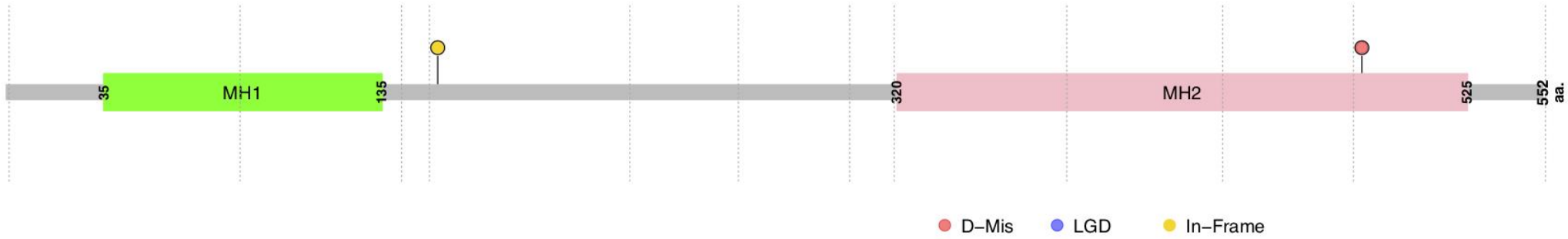

## *ENG*



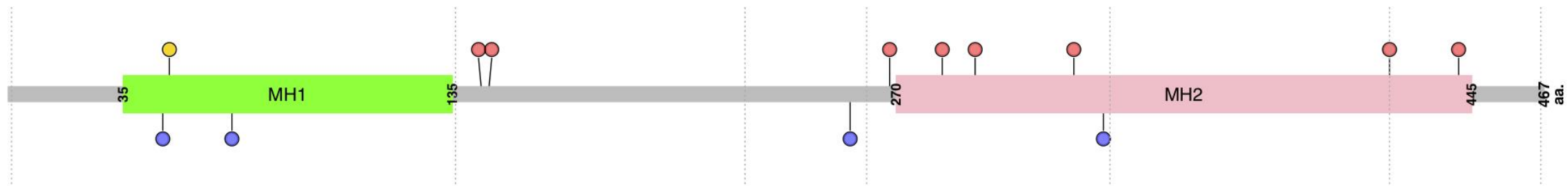

## *KCNK3*



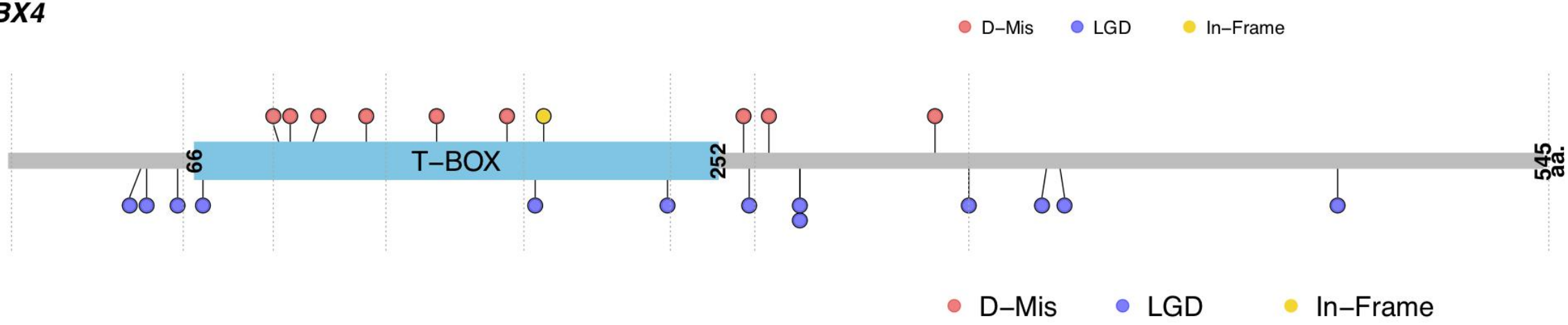
***SMAD4***



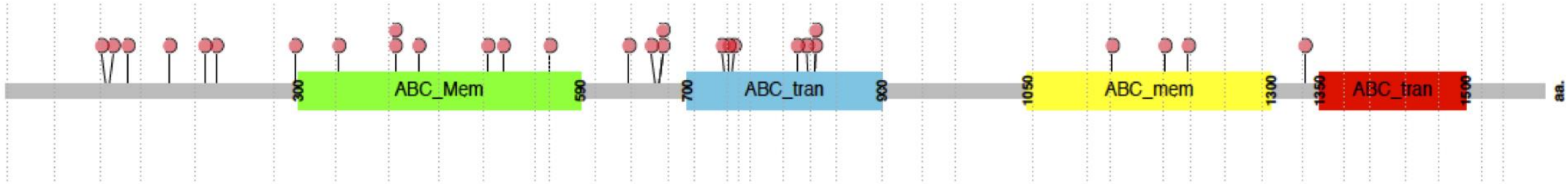

***SMAD9***




***TBX4***

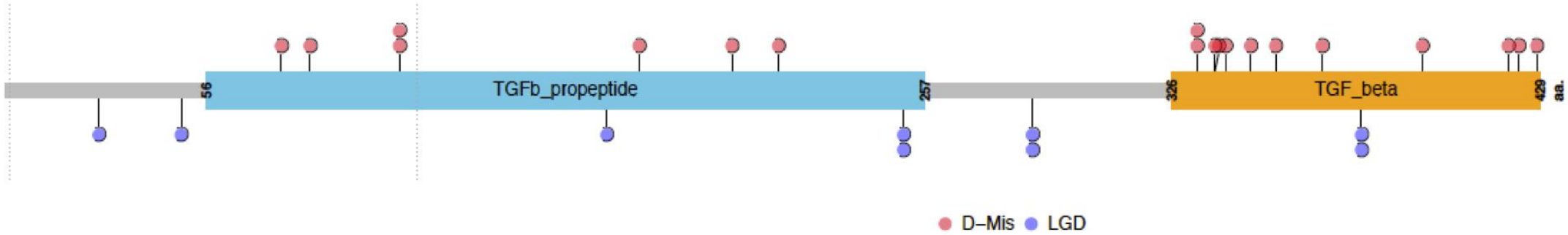


***ABCC8***

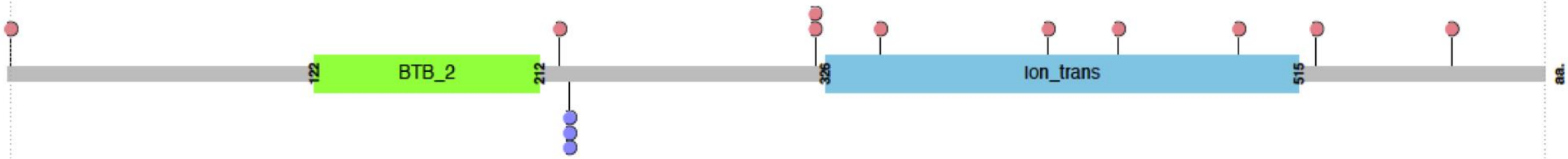



***ATP13A3***

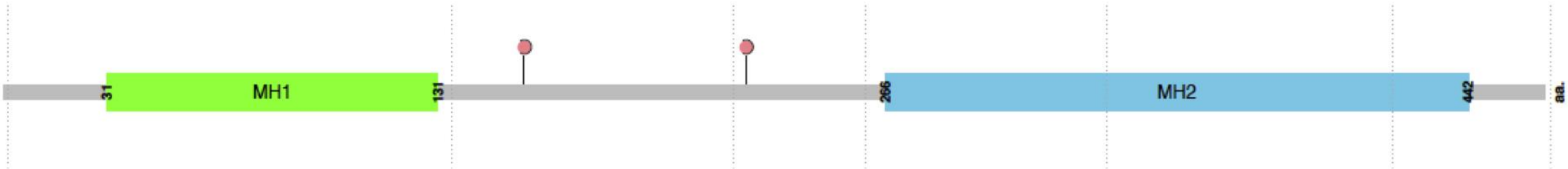

***GDF2***



***KCNA5***




***SMAD1***




***SOX17***