Reddy analysis [3.8%; N = 973]

CHD1: NM_001270

5

1

CHROMO   DEXDc SNF2_N   HELICc HELIC   DUF4208

1713 aa

1

5
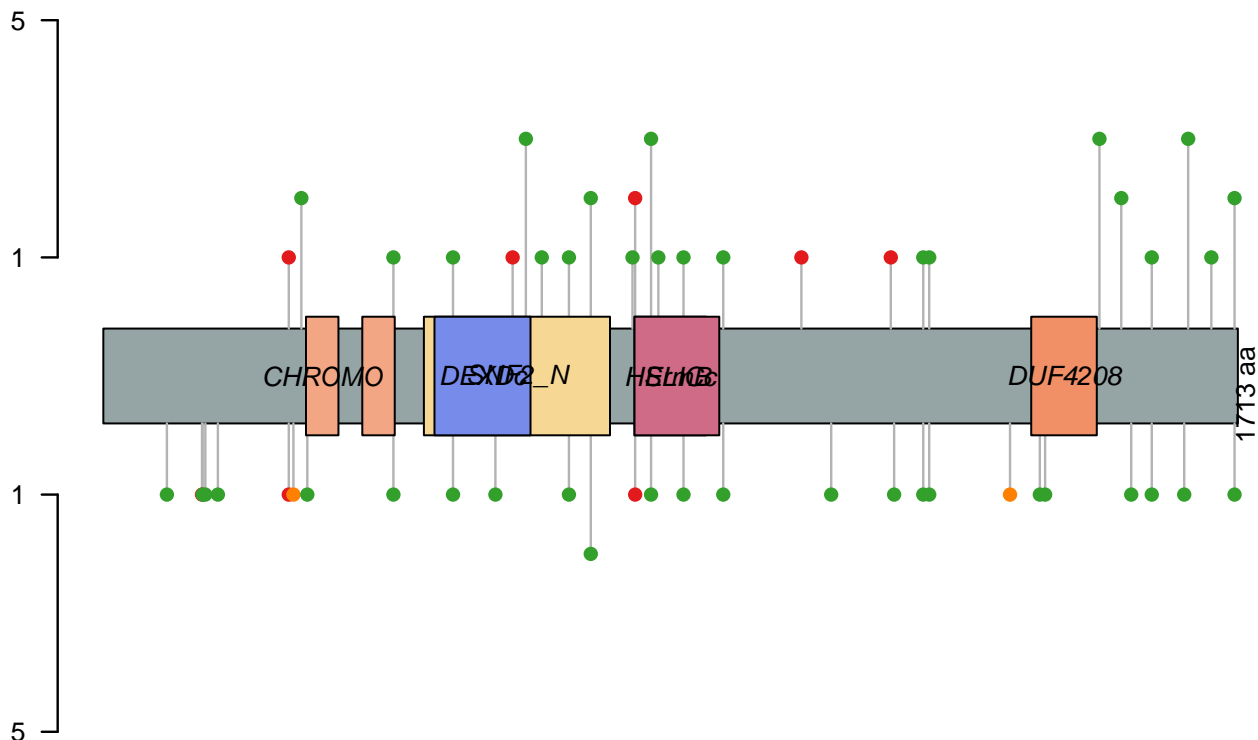
Reanalysis [2.82%; N = 958]

- Nonsense_Mutation
- Missense_Mutation
- Splice_Site