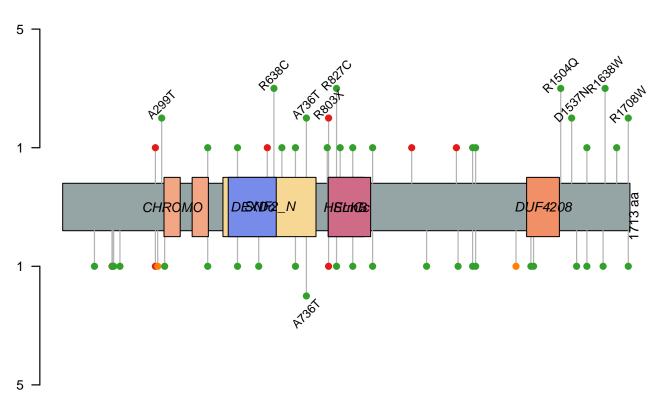
CHD1: NM_001270



Reanalysis [2.82%; N = 958]

- Nonsense_Mutation
- Missense_Mutation
- Splice_Site