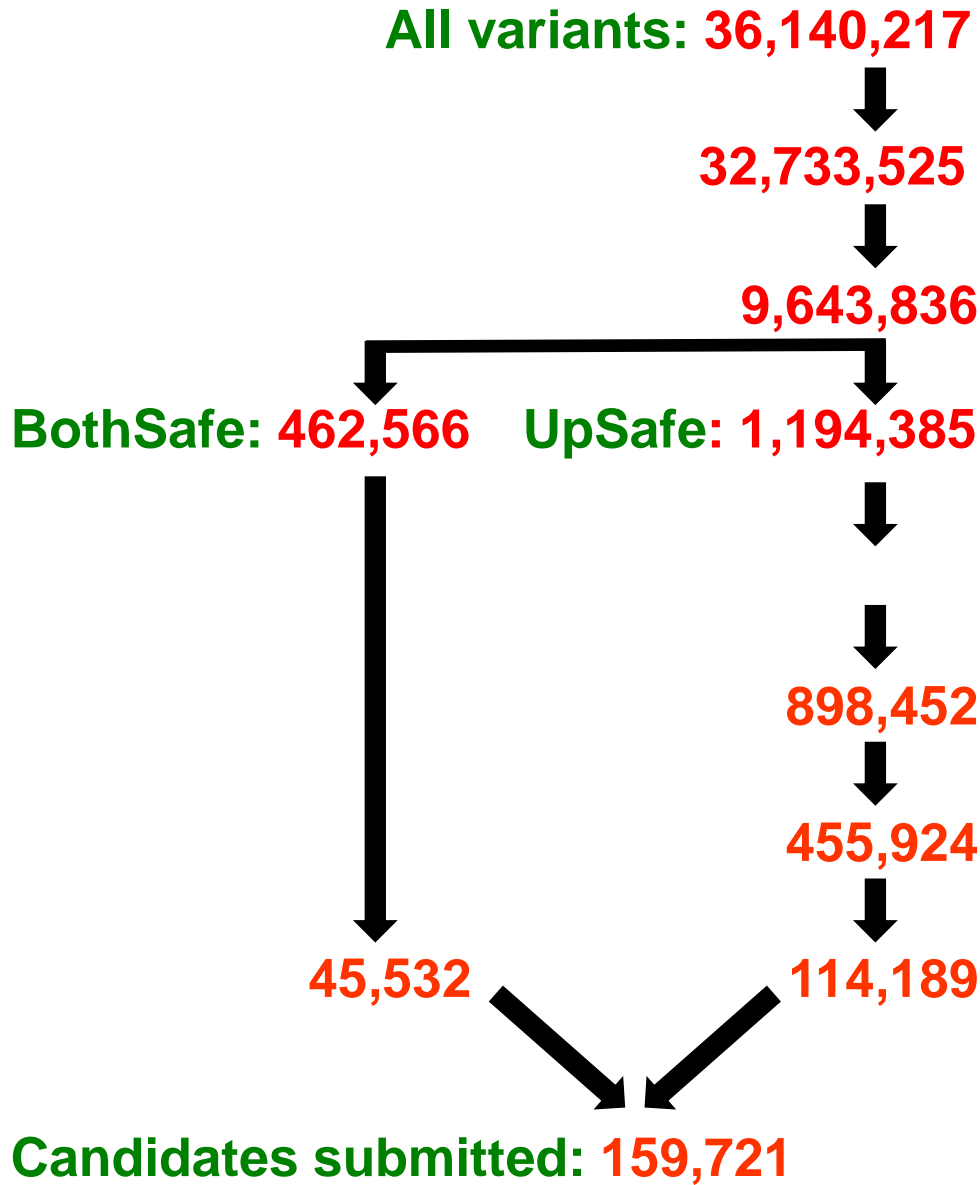


# Di-allelic SNP



## Pipeline steps

1. Retain only *snp* variants.
2. Min. variant read count ( $x=3$ ).
3. UpSafe-DownSafe (24 +/-).
4. A/T – G/C exclusion.
5. Min. GDP presence ( $y = 2$ ).
6. Min. HD-20 absence ( $z = 2$ ).
7. CDS