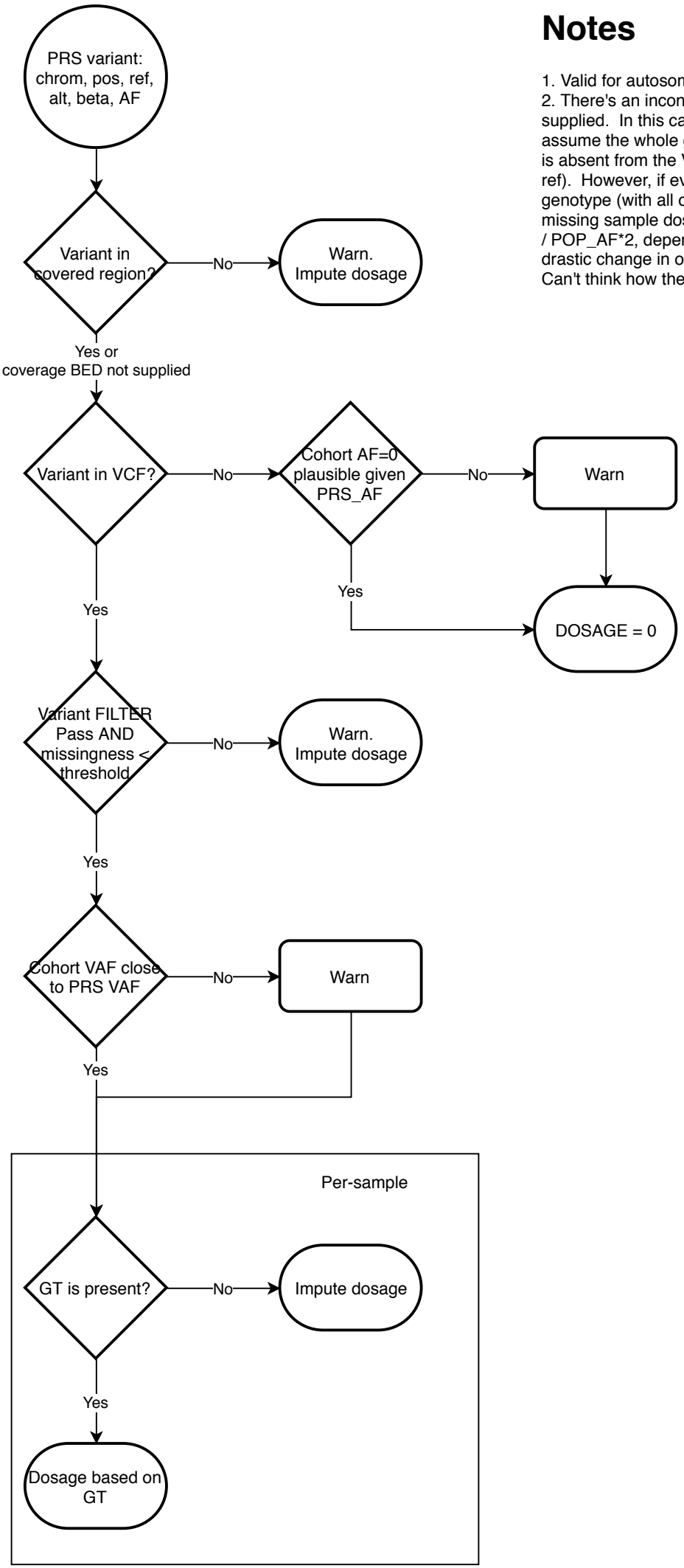

Notes

1. Valid for autosomes only
2. There's an inconsistency when a coverage BED is not supplied. In this case the current behaviour is to assume the whole genome is covered. Then if a variant is absent from the VCF, dosage is imputed to 0 (hom-ref). However, if even a single sample has a called genotype (with all other samples missing GT), then the missing sample dosage is imputed to NAN / PRS_AF*2 / POP_AF*2, depending on imputation setting. This is a drastic change in output for a small change in input. Can't think how the behaviour can be improved though.