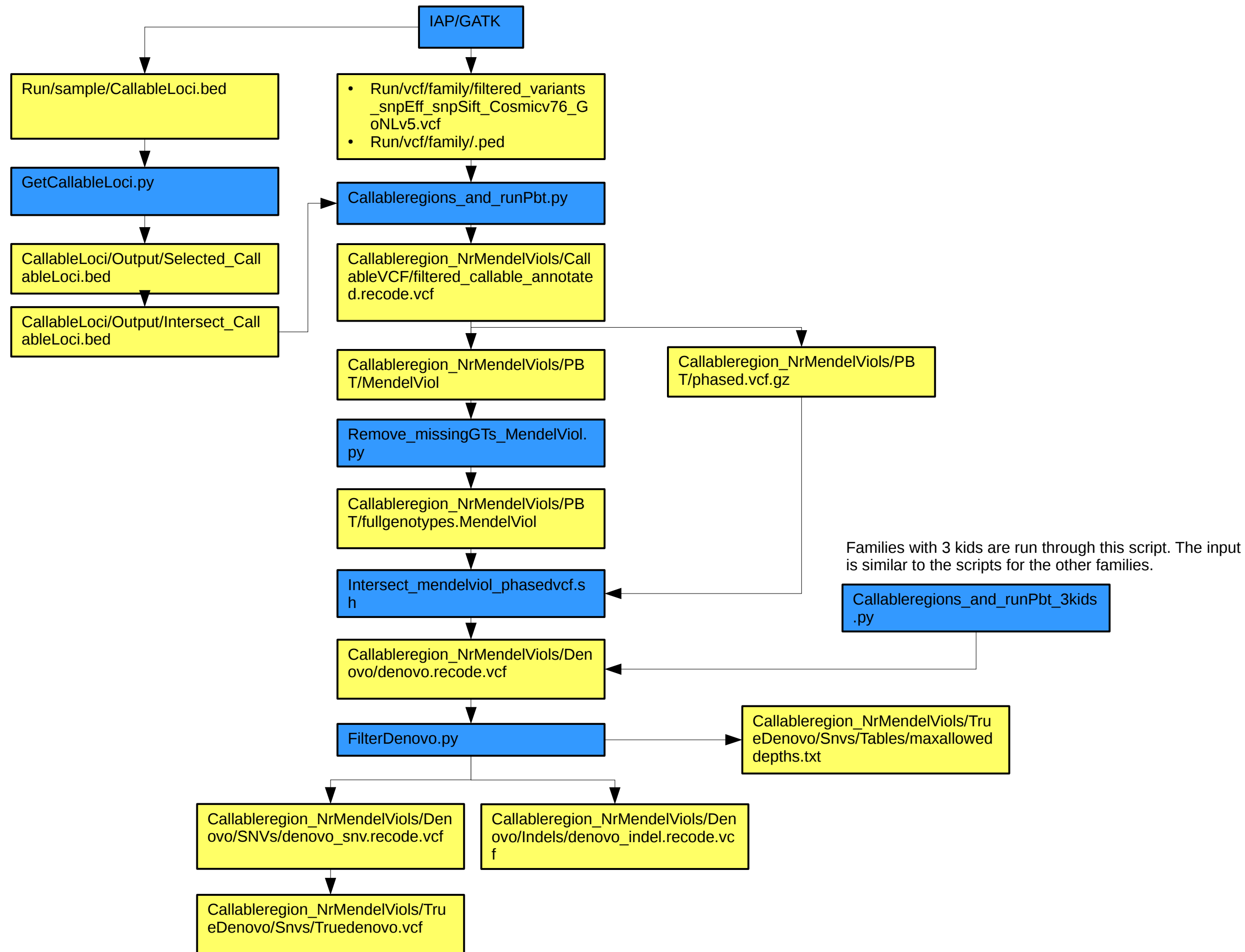


WGS quality control

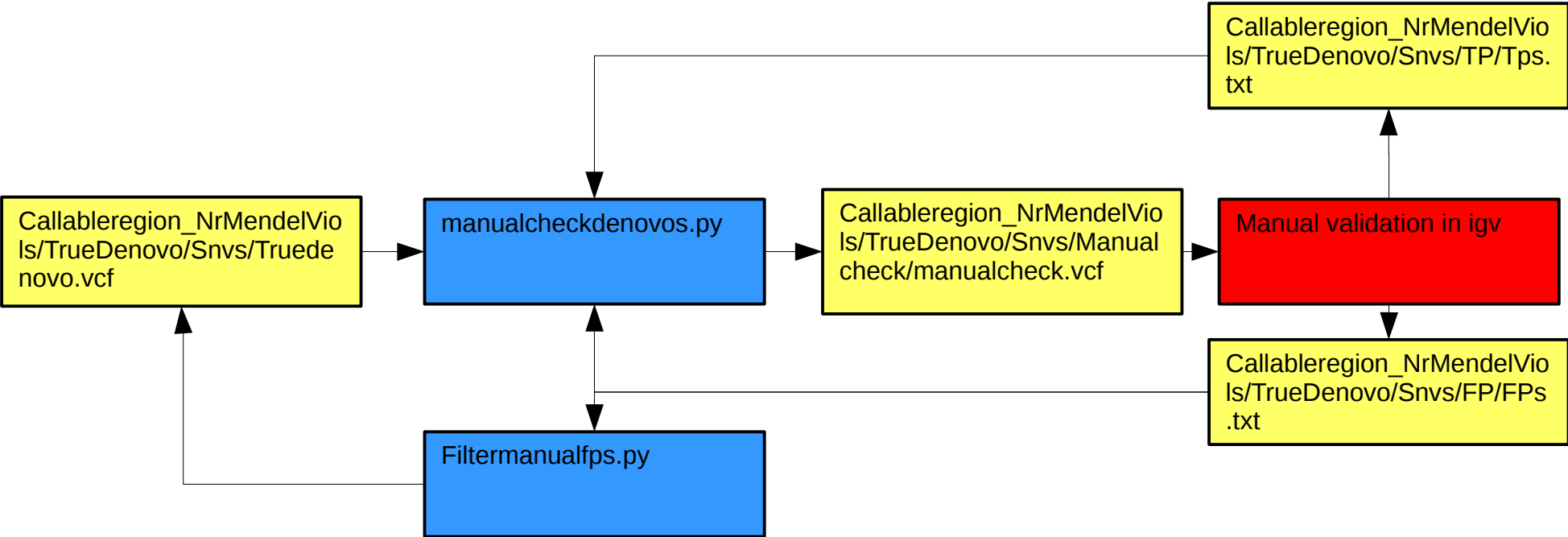


Identification of possibly *de novo* mutations + Filtering *de novo* SNVs

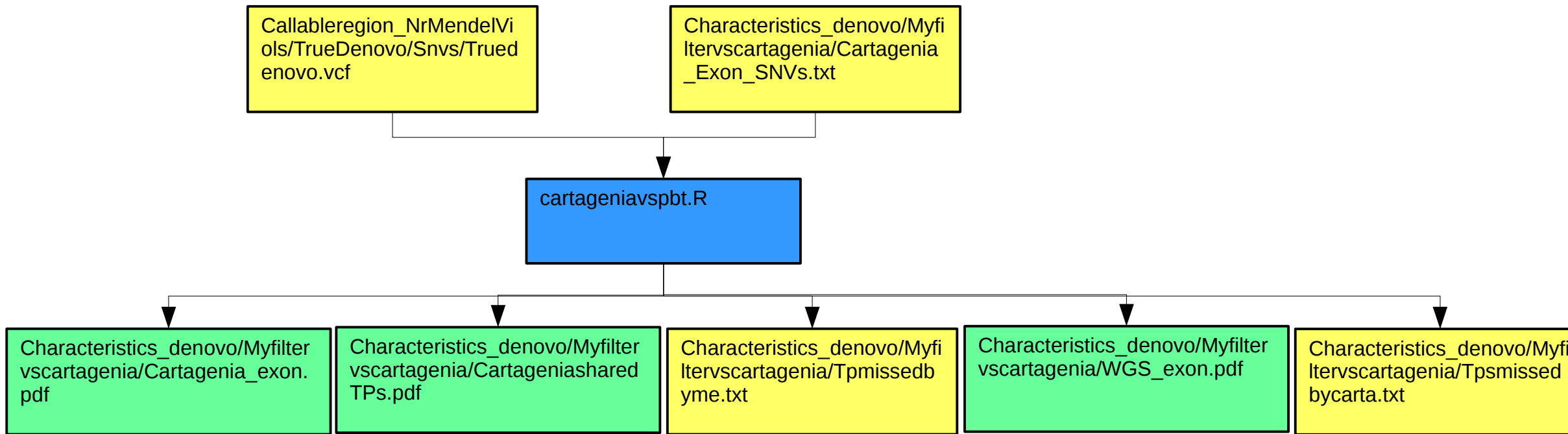


Manual curation of de novo SNVs

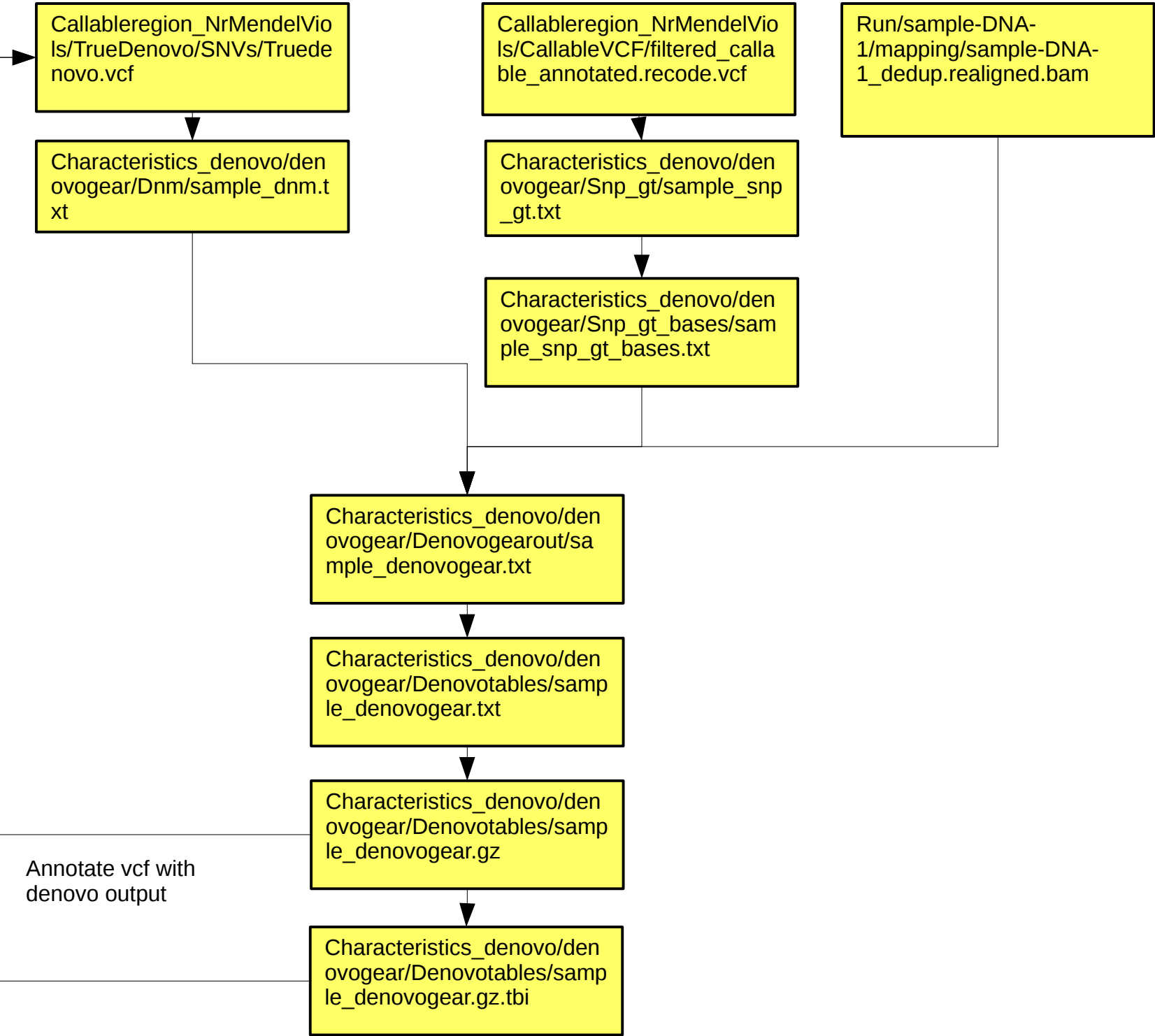
Filter truedenovos on ambiguous phasing, known snps and distance to nearest other denovo (sites in exonic regions are also checked manually).



Exonic SNVs



Phasing: all steps performed by denovogear.py



Visualize: phasing + Parental age

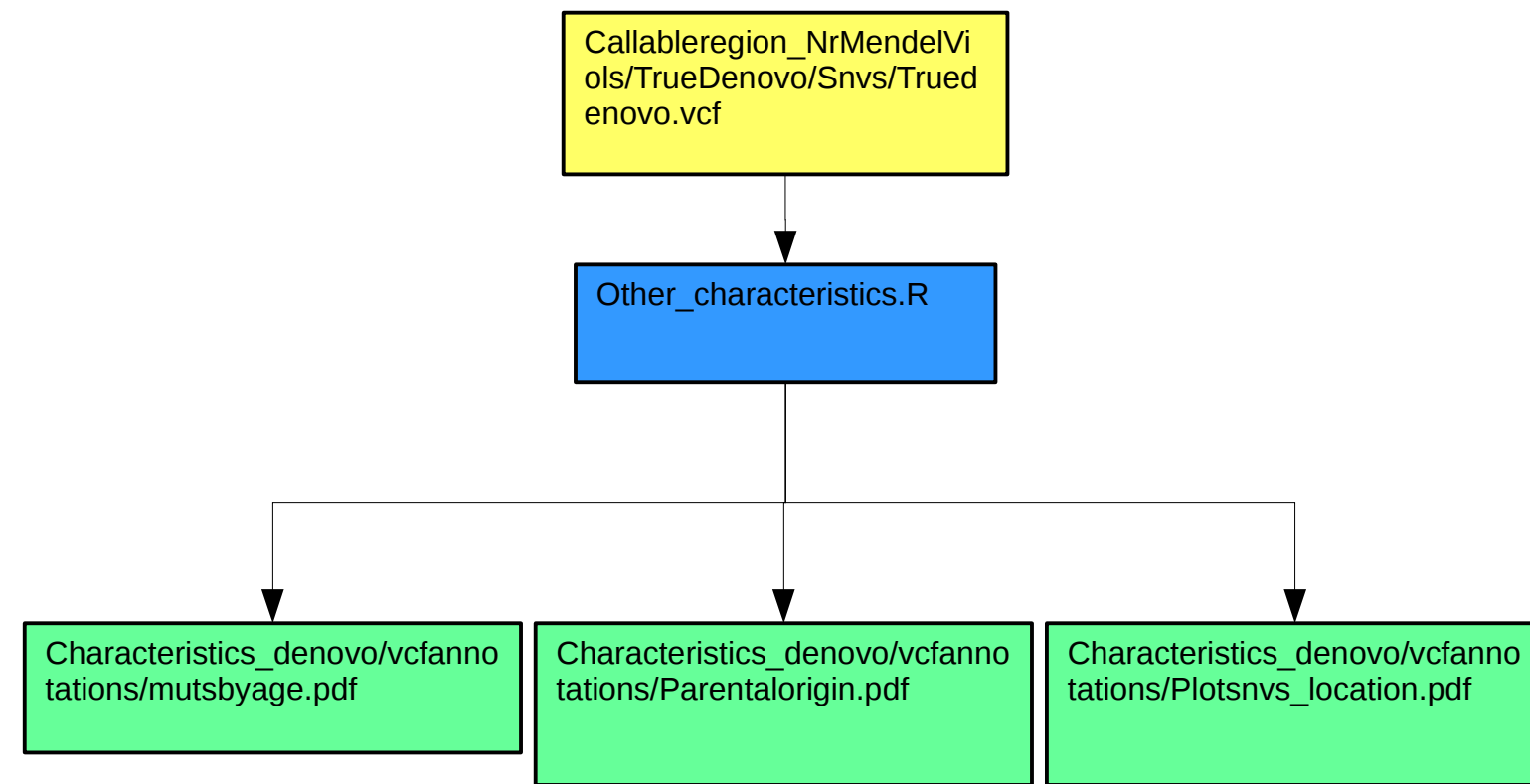
Callableregion_NrMendelVi
ols/TrueDenovo/Snvs/Trued
enovo.vcf

Other_characteristics.R

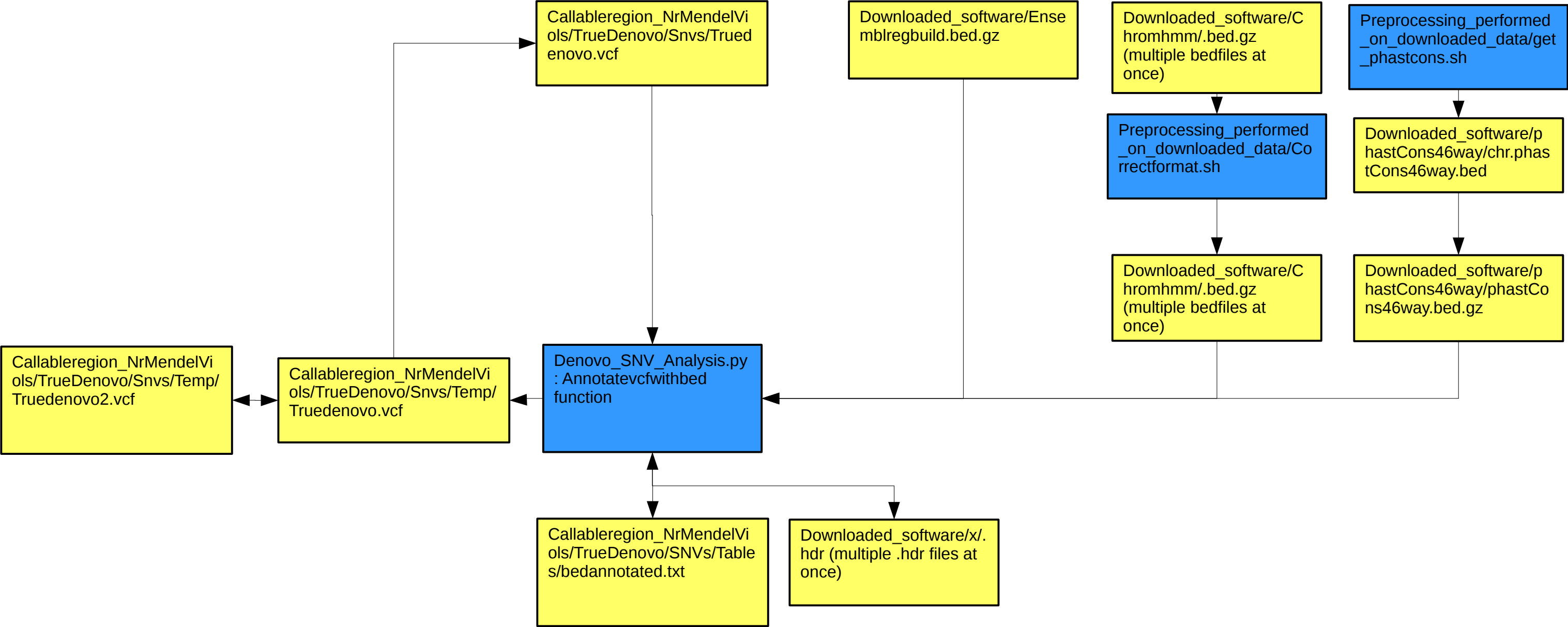
Characteristics_denovo/vcfanno
tations/mutsbyage.pdf

Characteristics_denovo/vcfanno
tations/Parentalorigin.pdf

Characteristics_denovo/vcfanno
tations/Plotsnvs_location.pdf

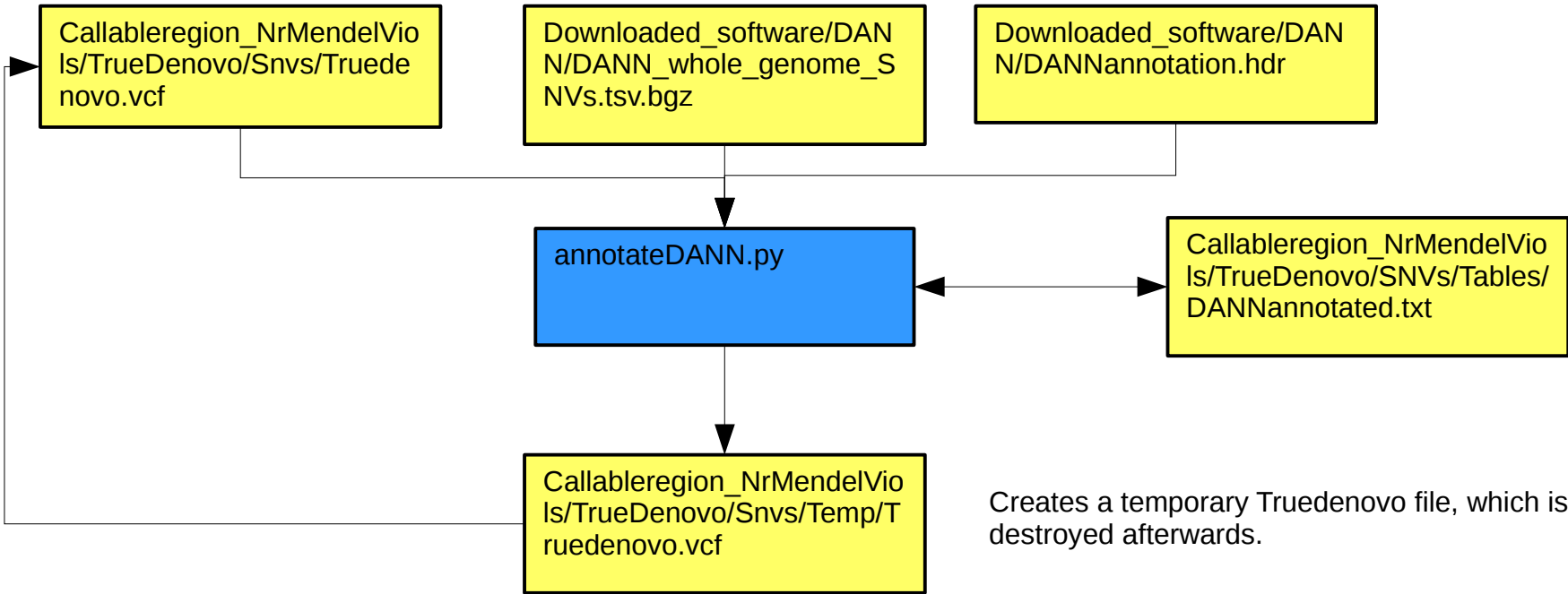


Annotating: Ensembl regbuild, chromhmm tracks from the Roadmap Epigenomics project and phastCons_46way scores

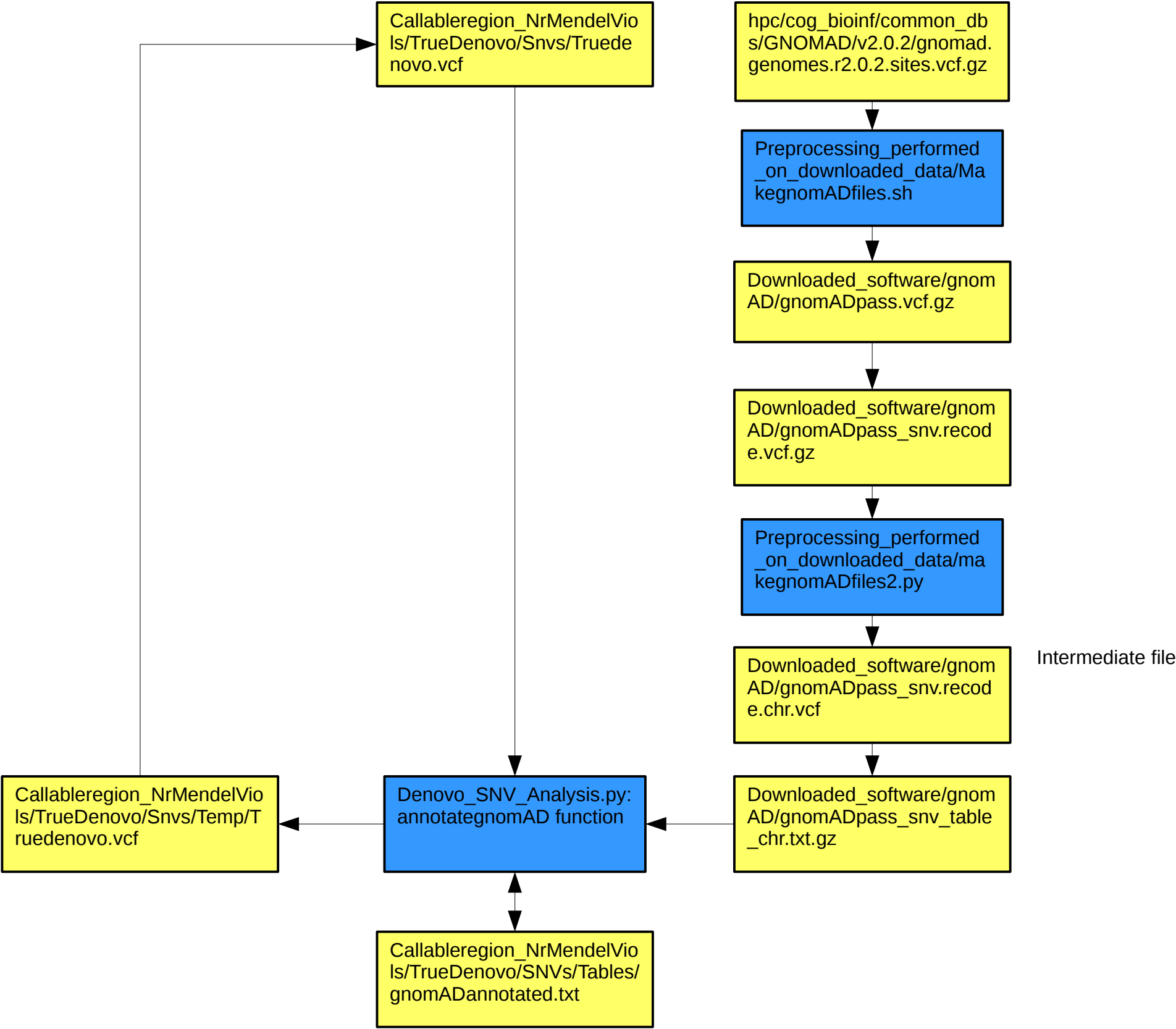


.hdr files are created by the script and used for the annotation. They are no longer needed after use, but it might be useful to see what has been added to the header of the annotated vcf.

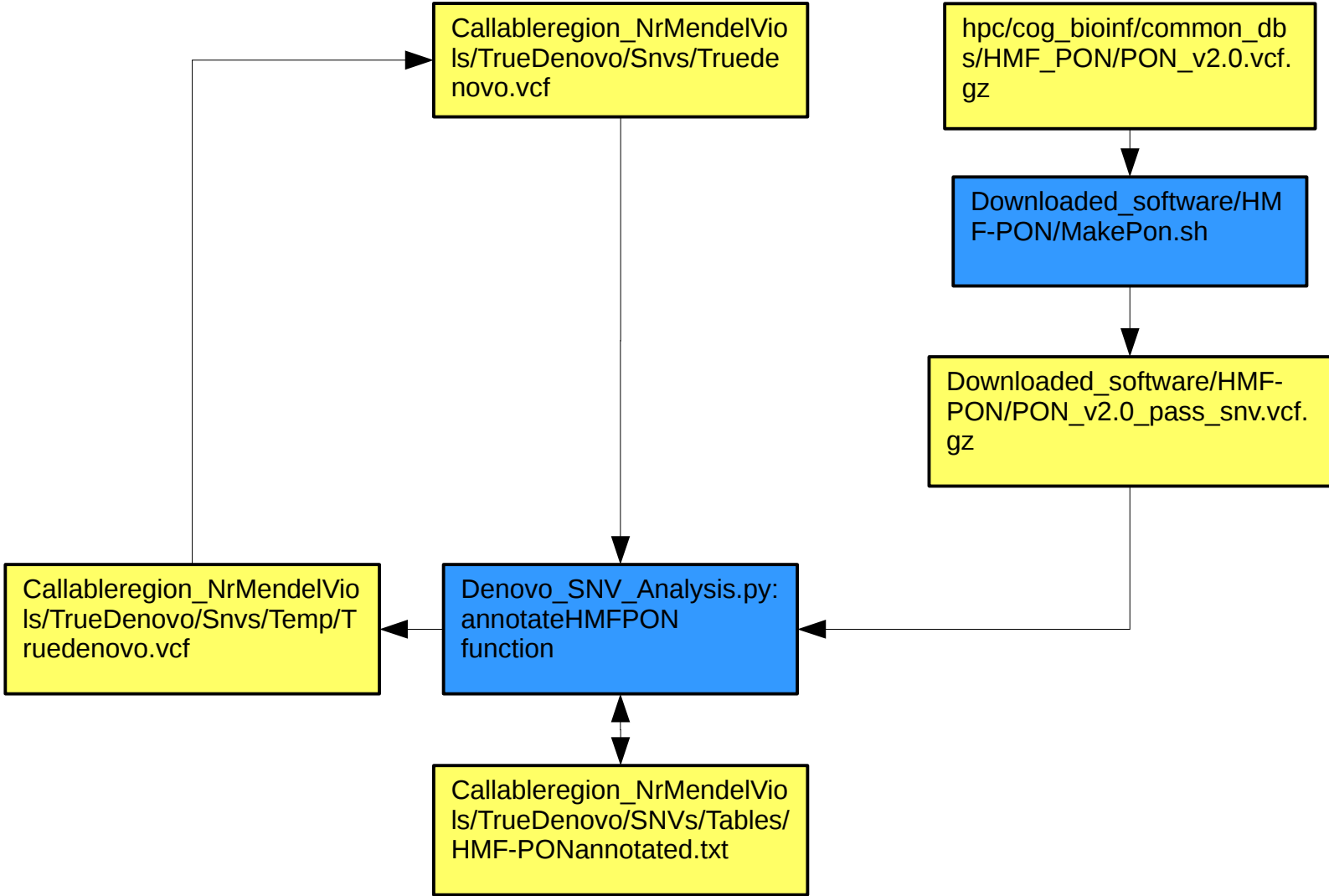
Annotating: DANN scores



Annotating: gnomAD



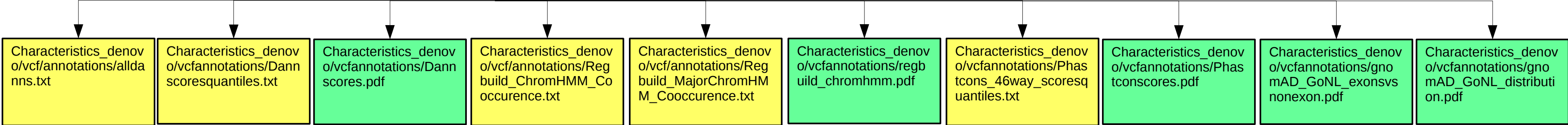
Annotating: HMF database



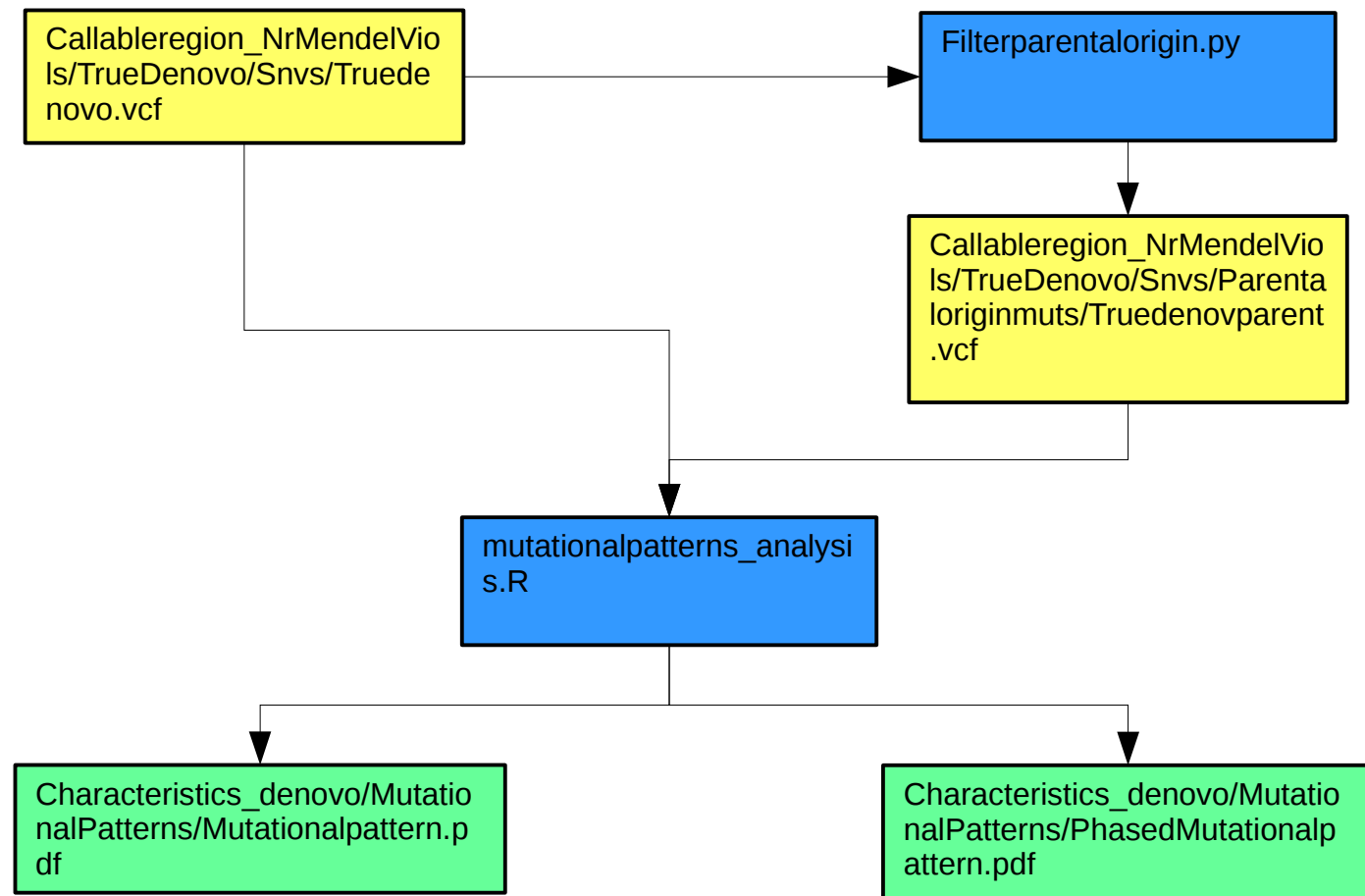
Visualize: annotations

Callableregion_NrMendelVi
ols/TrueDenovo/Snvs/Trued
enovo.vcf

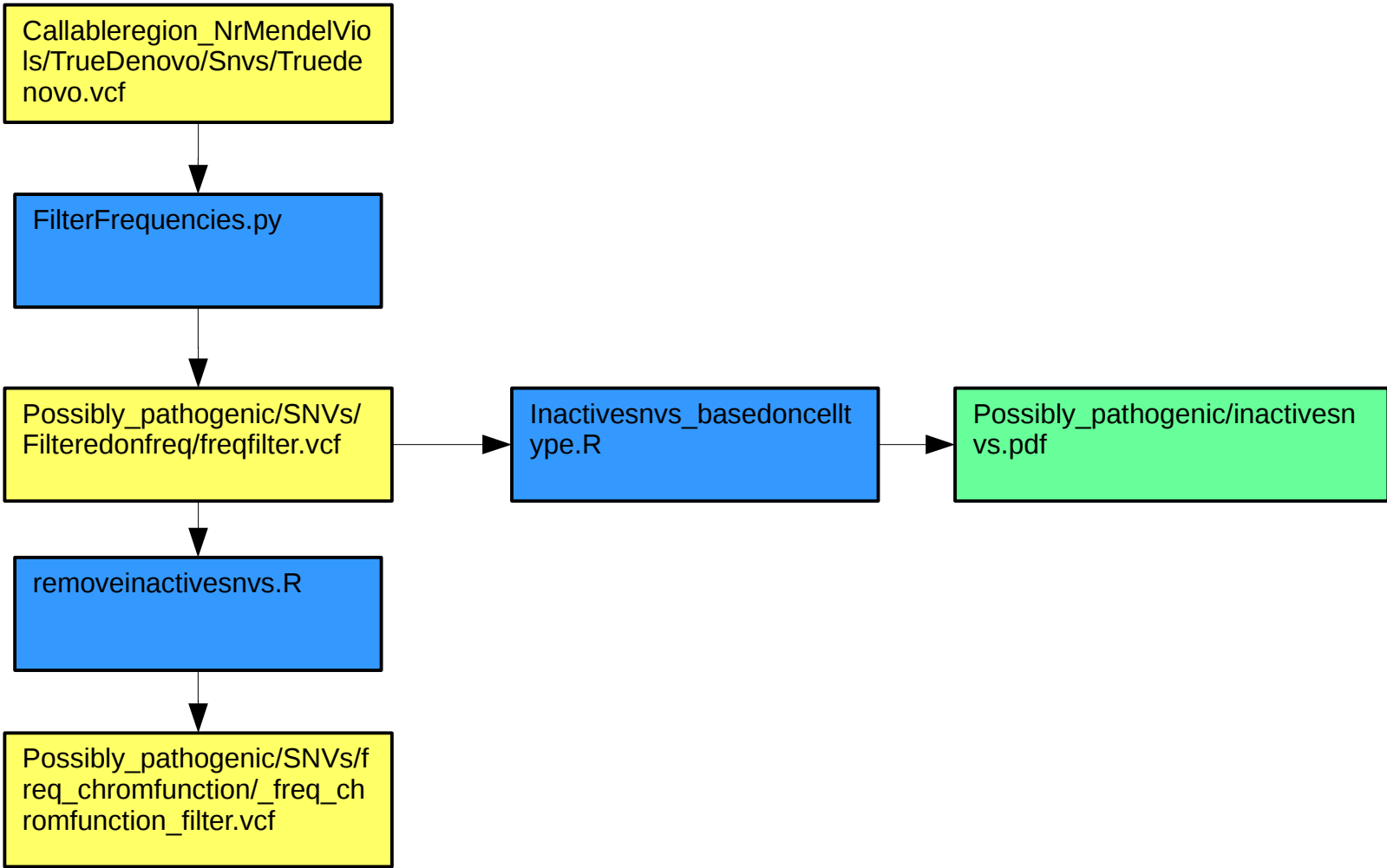
Annotations_characteristic
s.R



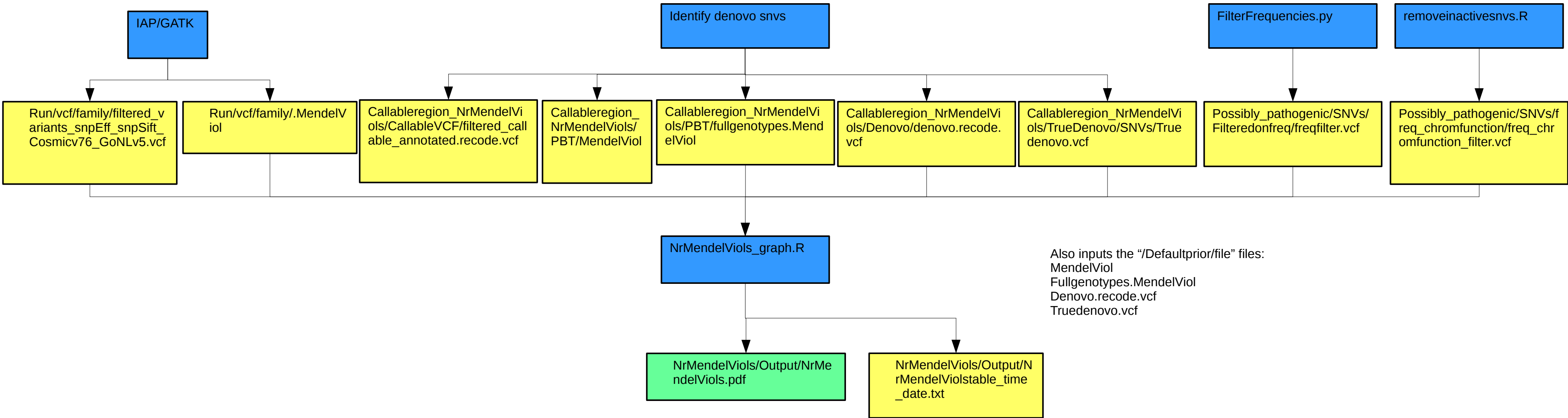
Mutational patterns



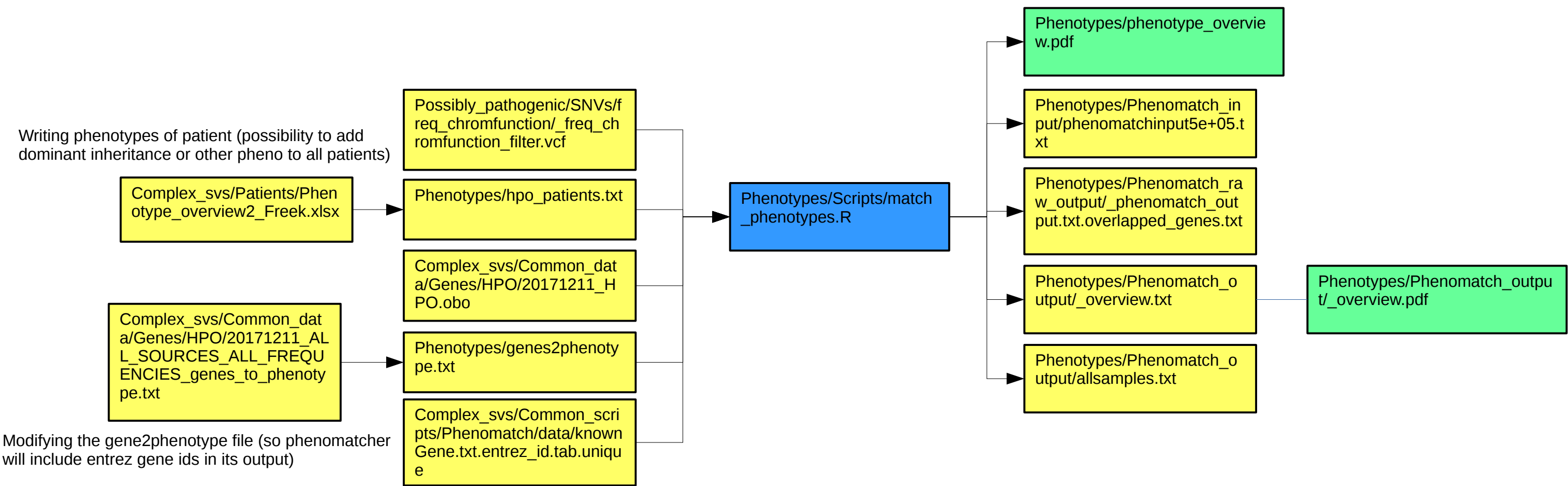
Filter out benign SNVs



Visualize: Identifying *de novo* SNVs +
Visualize: Filter out benign SNVs



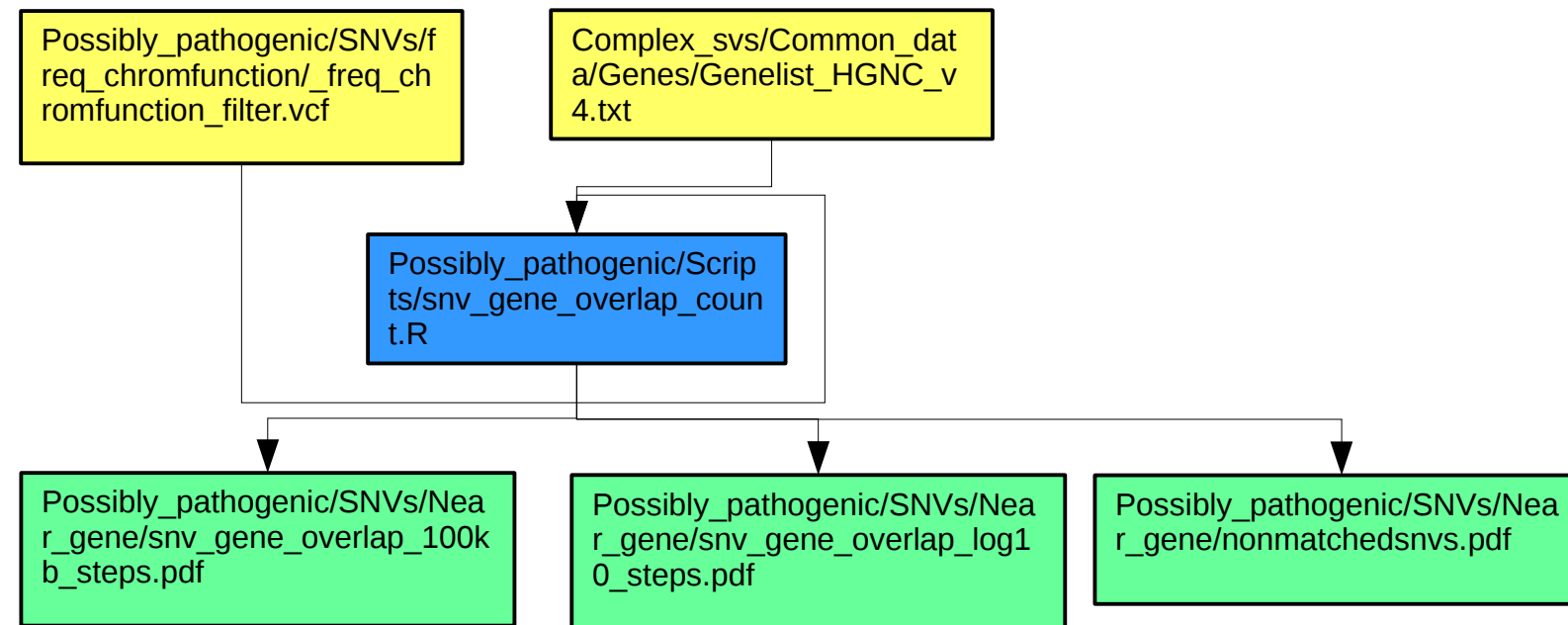
Match genes to phenotypes



Modifying the gene2phenotype file (so phenomatcher will include entrez gene ids in its output)

Watch out: If you change the genes_to_phenotype and the .obo file to a newer version. You should also do this for the Genelist_HGNC_v4.txt file, as this file also contains hpo terms. If you don't update this file, then the snv-gene overlap by phenomatcher will use different genes then the snv-gene overlap performed in !!!

Effect of distance on linking SNVs to genes



Linking SNVs to genes +
Classifying SNVs as possibly pathogenic

