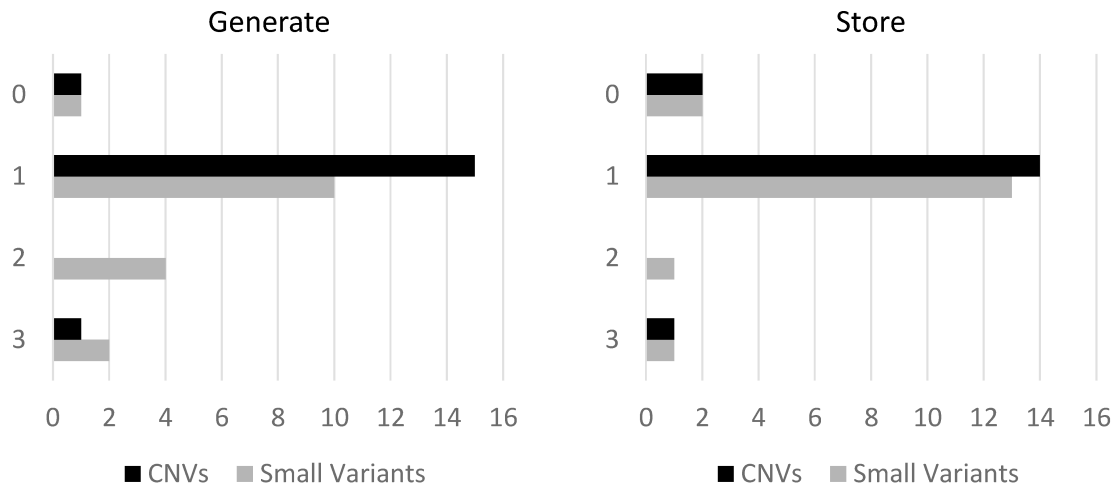
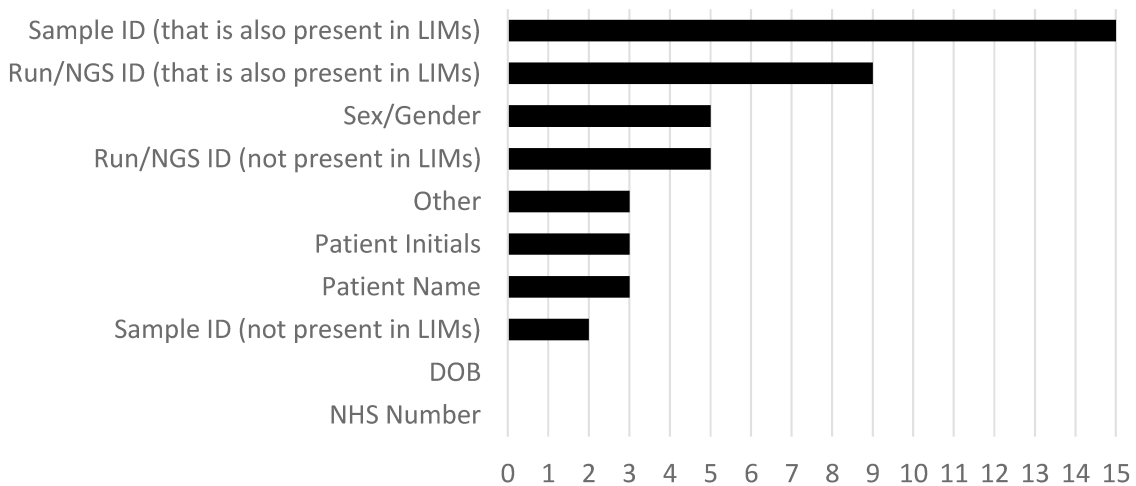


A) How many types/tiers of VCF-derived files do you generate and store?

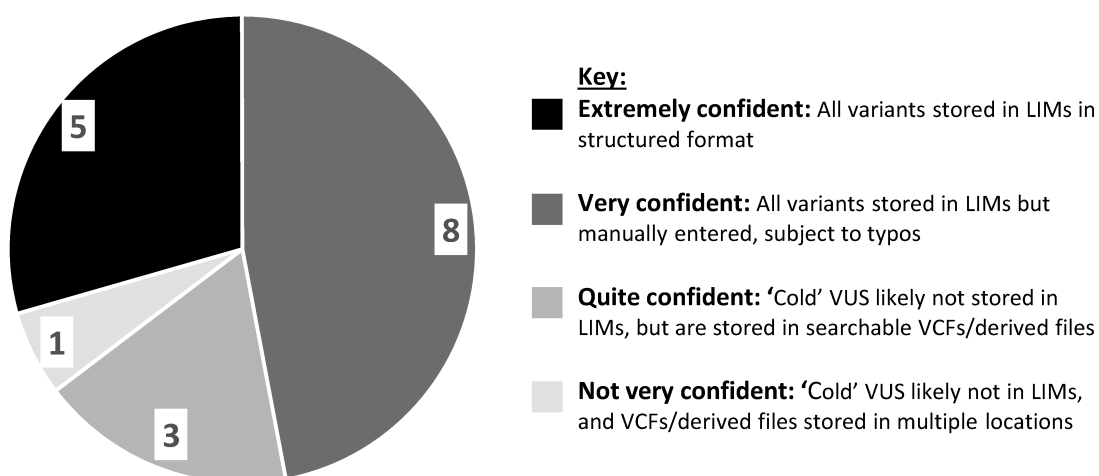


B) Which of the following identifiers are present against a detected variant in the output of your NGS pipeline (VCF file and derived files)?



Supplementary Figure 1: Additional questions pertaining to variant workflows. A: Approaches to storing intermediary files generated as part of the workflow. B: The range of patient identifiers available within the workflow upstream of entry in the LIMs.

In the event a 'Cold' VUS is re-classified, how confidently/readily could you identify all patients in whom that variant had been identified?



Supplementary Figure 2: Confidence of responding laboratories in ability to reliably retrieve 'cold' VUS variant information in the event of reclassification.