

Laboratory-driven Exome Reanalysis Increases Diagnostic Yield and Decreases Burden on Clinicians

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BACKGROUND

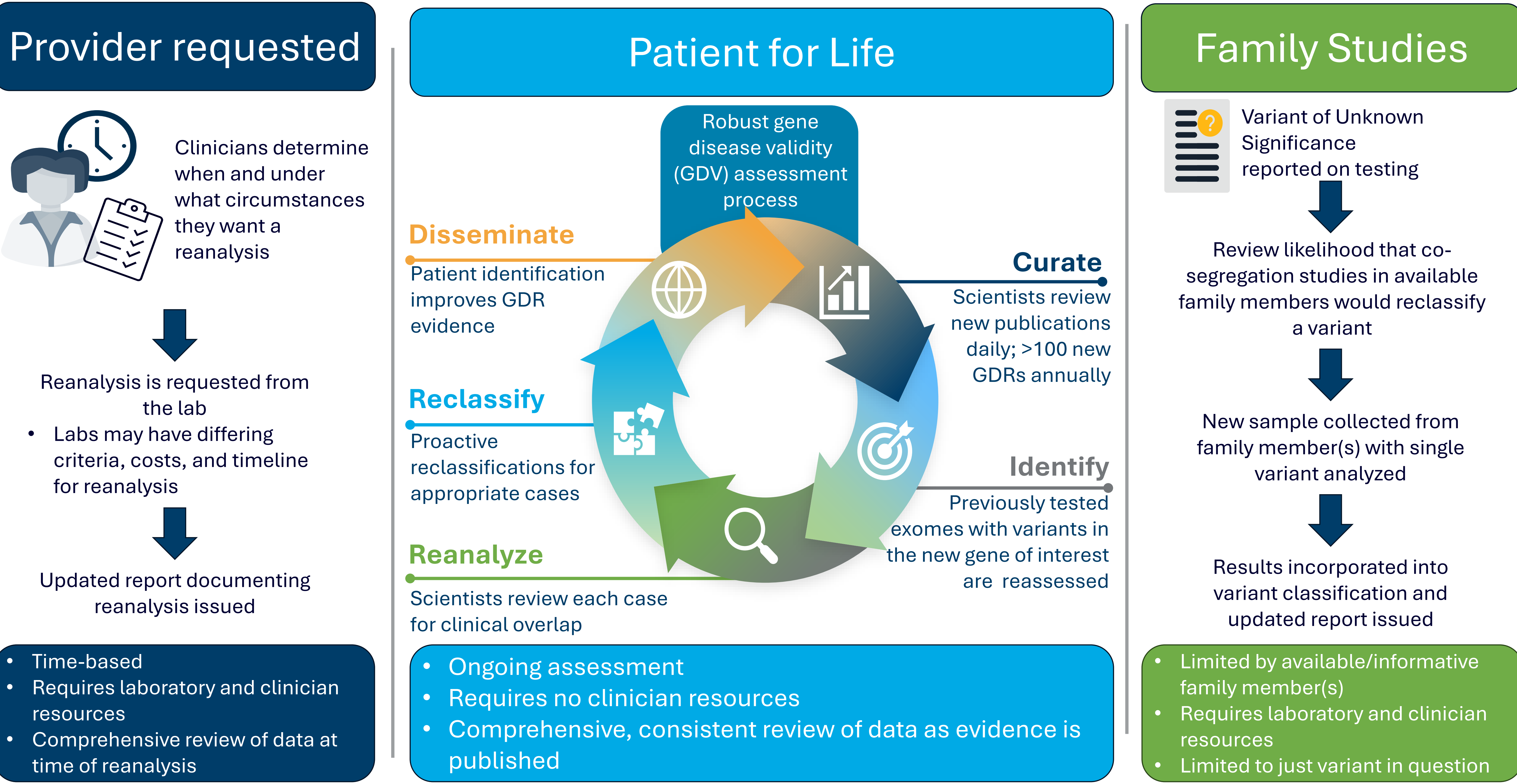
- Exome sequencing (ES) data can be reanalyzed as understanding of genetic contributions to disease grows
- Reanalysis increases ES diagnostic yield over time
 - Mostly due to gene-disease relationships (GDR)

OBJECTIVE: Assess the outcomes of proactive vs. reactive ES reanalysis processes

STUDY METHODS

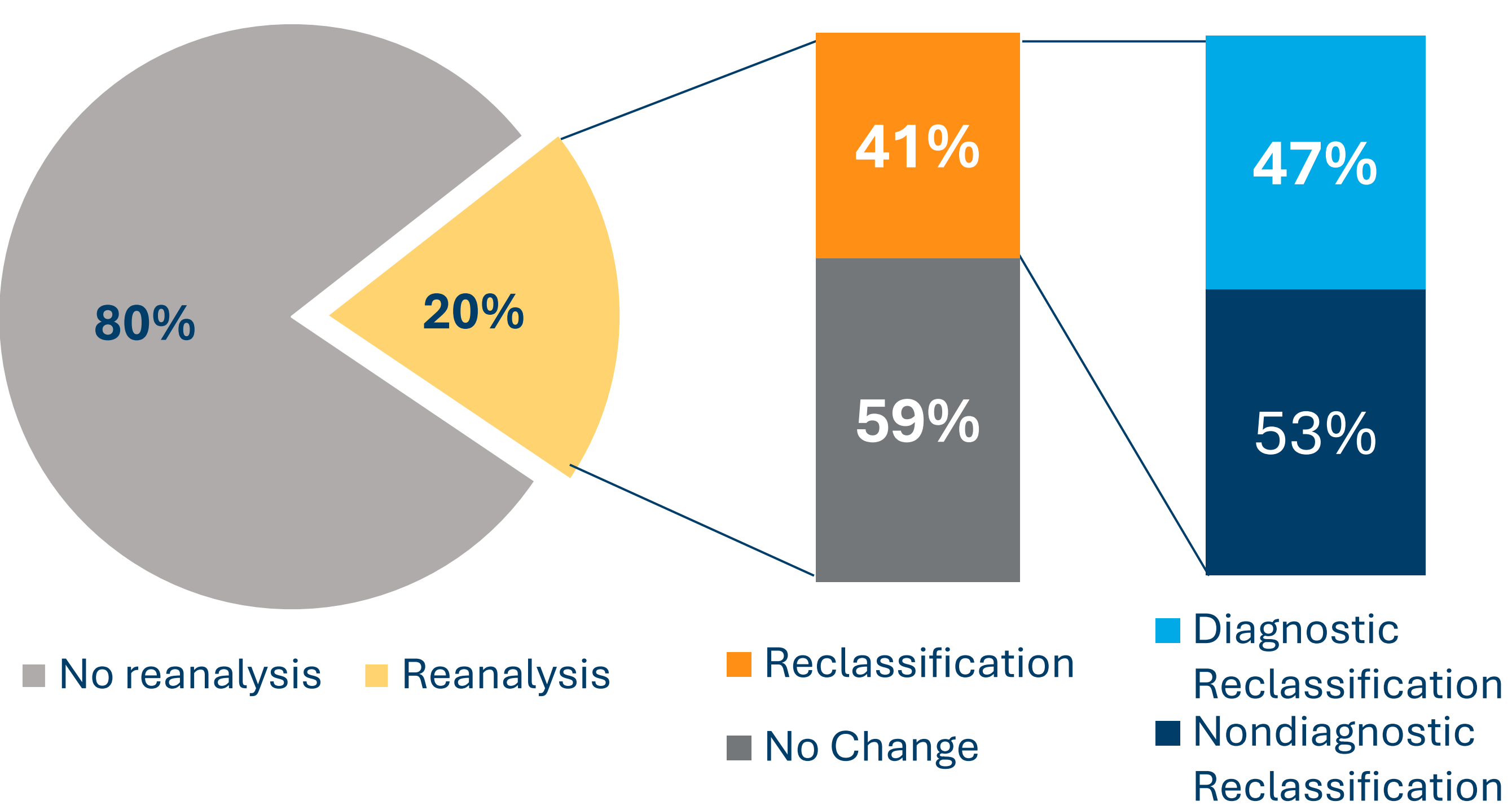
- Reviewed 10 years of ES for neurological indications (n=8539)
 -  **Neurodevelopmental** 74% of cohort
 -  **Epilepsy** 9% of cohort
 -  **Neuromuscular** 17% of cohort
- Compared reanalysis outcomes and evidence used for reclassifications based on the reanalysis initiation factor

METHODS FOR EXOME REANALYSIS



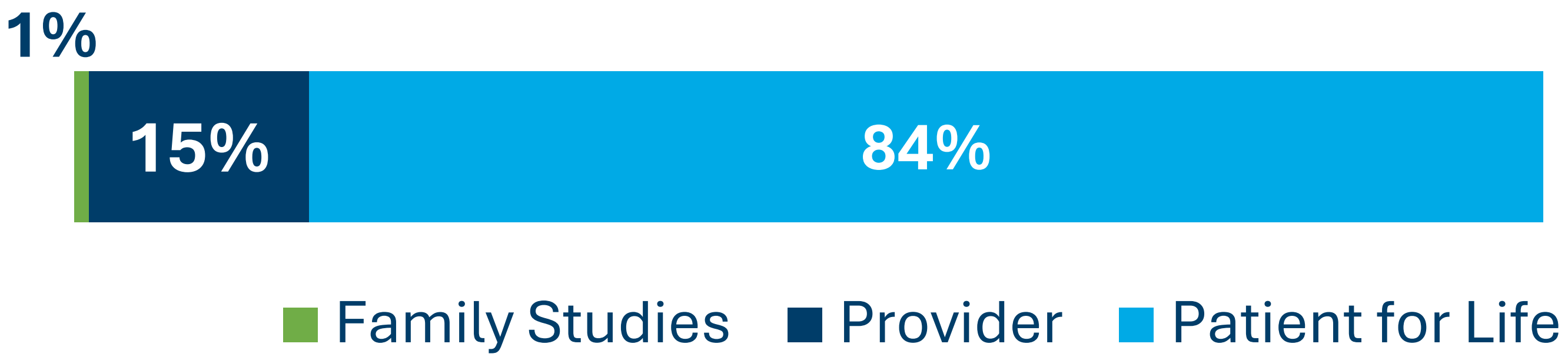
RESULTS

FIGURE 1: COHORT REANALYSIS AND RECLASSIFICATION



- 20% of cases (n= 1685) underwent at least one reanalysis during the study period [Figure 1]
 - Of these, 41% (n=694) received a reclassification report
- Increase in overall diagnostic yield (21% vs 25%)
 - **5% of all originally unsolved ES received a diagnostic finding**

FIGURE 2: DIAGNOSTIC RECLASSIFICATIONS BY INITIATING FACTOR



- 327 total diagnostic reclassifications (4% of all cases)
- 84% of diagnostic upgrades were through PFL, compared to 15% provider-requested reanalyses, and 1% family studies [Figure 2]

TAKE HOME POINTS

- ES reanalysis increases the diagnostic yield over time
- Patient for Life resulted in higher rates of diagnostic reclassification and initiates when new relevant data is available
- Majority of provider-requested reanalyses resulted in a ‘no change’ notification, adding work for the provider and laboratory with no clinical benefit