

Exome Reanalysis Results in an 8% Reclassification Rate

Kelly Farwell Hagman, MS, CGC¹, Meghan C. Towne, MS, CGC¹, Kelly Radtke, PhD¹, Kirsten Blanco¹, Jennifer Huang, PhD¹

¹Ambry Genetics, Aliso Viejo, CA, USA

BACKGROUND

- Diagnostic exome sequencing (DES) has the potential to end expensive, invasive, time-consuming testing and lead to changes in patient care.¹⁻⁷
- Upon initial analysis, ~25% of patients with underlying Mendelian diseases receive a diagnosis via DES.^{1-2,8-13}
- A major advantage of DES is the ability to reanalyze the same data set and benefit from new gene-disease discoveries, new variant information, and changes in the patient's medical/family history.
- Reclassifications may result from a client request for reanalysis or proactively from the laboratory.

METHODS

- We analyzed a cohort of patients who underwent DES at a commercial lab between January 2016 and August 2018, and for whom a client-initiated exome reanalysis was subsequently requested.
- A reclassification was defined as any change to the overall results category among the following 4 groups:^{1,2}
 - Positive/likely positive
 - Uncertain findings within characterized genes
 - Candidate findings within uncharacterized genes
 - Negative
- Cases were categorized by the clinical information included in the reanalysis request.
 - No new clinical features reported
 - New organ system involvement
 - New feature(s) as denoted by one or more new HPO terms
- Reclassifications from candidate or uncertain to negative, or positive/likely positive to any other category were considered downgrades; all other changes were upgrades.

RESULTS

- From January 2016 through August 2018, a total of 436 patients had ≥1 client-initiated reanalysis request. A second request was received for some patients, bringing the total number of reanalysis/reclassification reports issued to 451.
- Overall, the rate of reclassification from client requested reanalysis was 8% (36/436) (FIGURE 1).**
- Among the 36 reclassified reports, there were 34 (94.4%) upgraded and 2 (5.6%) downgraded reports (FIGURE 2).**
- 20 reclassifications (46.5%) led to a change in clinical utility when a negative or uncertain result was upgraded to positive or likely positive.
- Among the 36 reclassified reports, 8 (22.2%) were due to variant reclassification, 13 (36.1%) were due to gene reclassification, and 15 (41.7%) were due to new clinical information allowing for an upgrade in clinical overlap (FIGURE 3).**
- All reports with an initial positive/likely positive conclusion were unchanged after reanalysis.
- No difference was seen in sex or age between the reanalysis requests that resulted in upgrades or those that remained unchanged.
- 64% (289/451) of client-driven reanalysis requests included updated clinical information. 9.3% of requests with new clinical information resulted in an upgrade, while only 4.9% of requests without new clinical information were upgraded (FIGURE 1).**
- Among the 34 upgraded reports following client-initiated reanalysis, **79.4% included new clinical information. Reanalysis requests that included additional family history and/or updated testing results were significantly more likely to result in an upgrade (p<0.05).** (FIGURE 4). Examples of changed testing or family history included new biochemical test results and updated affected status of a relative.

FIGURE 1: Rates of Reanalysis-driven Reclassification

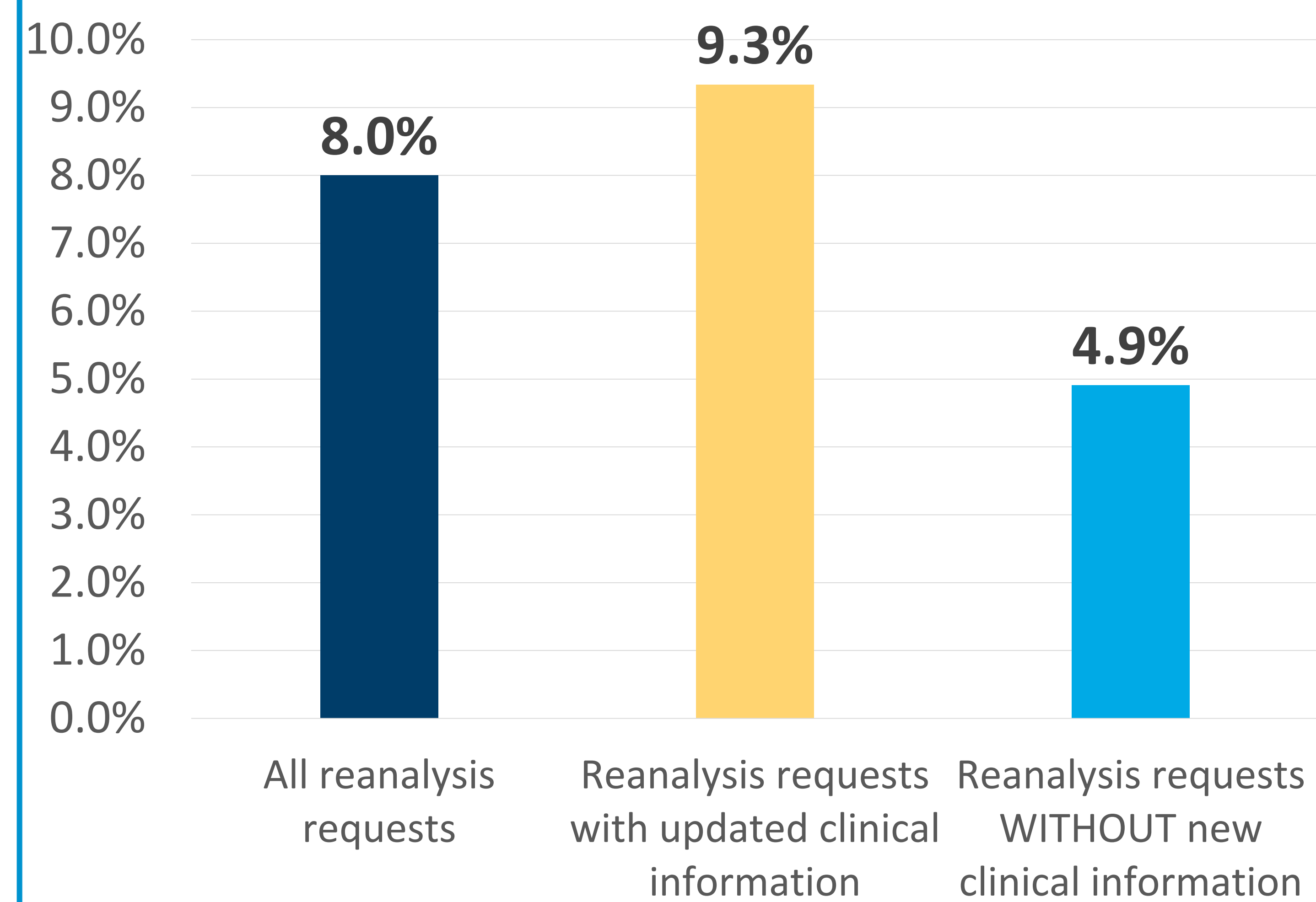


FIGURE 2: Direction of Reanalysis-driven Reclassifications

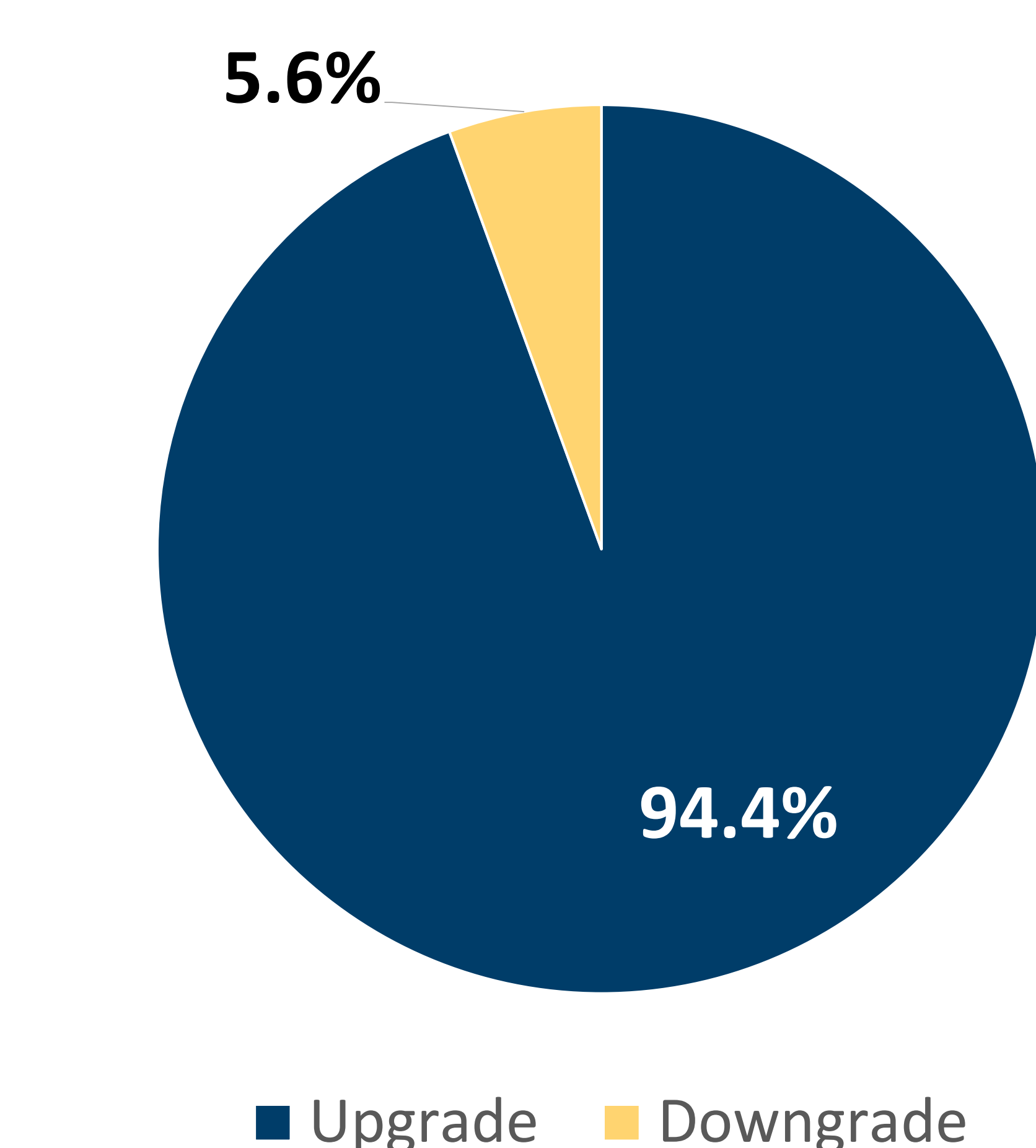


FIGURE 3: Reason for Reanalysis-driven Reclassification

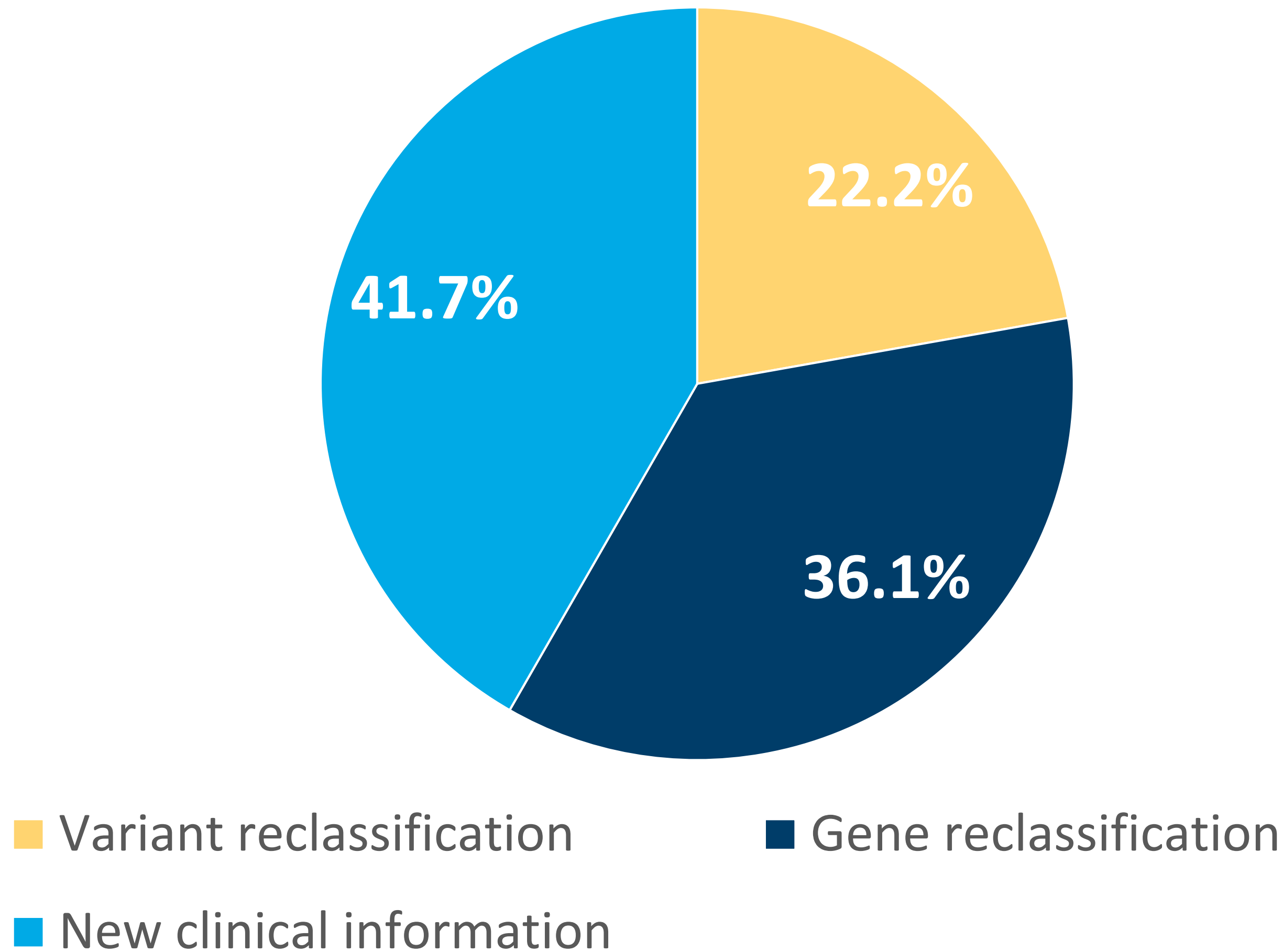
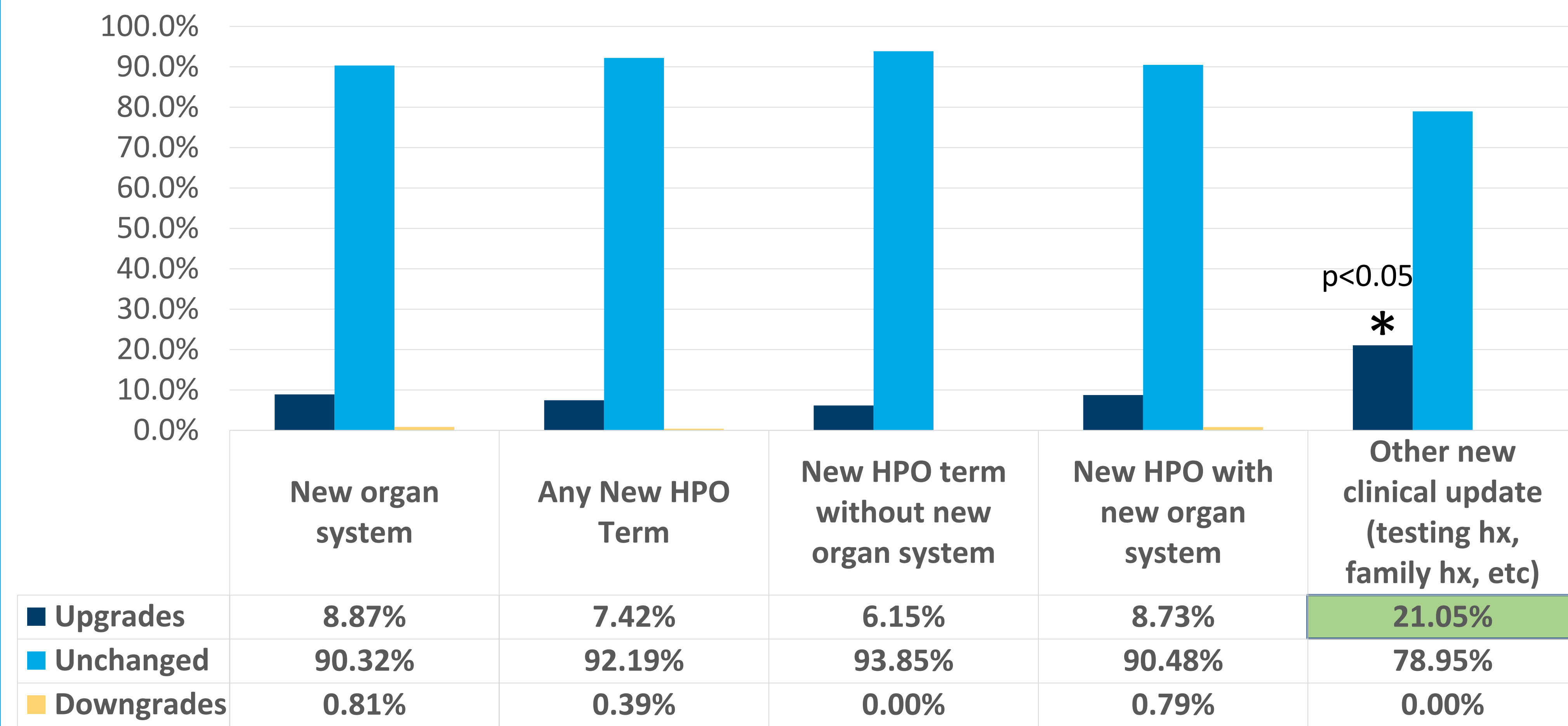


FIGURE 4: Reanalysis Requests with Additional Family History or Updated Test Results Increase the Likelihood for a Reclassification



TAKE-HOME POINTS

- Overall, 8% of clients ordering a reanalysis received a reclassified report.
- New test results or new family history details resulted in a significantly higher likelihood of a reclassification.
- These data highlight the utility of DES in providing a comprehensive and timely molecular diagnosis with the ability to continually assimilate new information.
- The ability to continually reanalyze exome data adds to the economic value of the test compared to traditional testing methods.
- The data emphasize the importance of counseling patients about the likelihood of a result reclassification in the future.

REFERENCES

- Srivastava S, Cohen JS, Vernon H, et al. Clinical whole exome sequencing in child neurology practice. *Annals of neurology*. 2014;76(4):473-483.
- Iglesias A, Anyane-Yeboah K, Wynn J, et al. The usefulness of whole-exome sequencing in routine clinical practice. *Genetics in medicine : official journal of the American College of Medical Genetics*. 2014.
- Worthington EA, Mayer AN, Spiverson GD, et al. Making a definitive diagnosis: successful clinical application of whole exome sequencing in a child with intractable inflammatory bowel disease. *Genetics in medicine : official journal of the American College of Medical Genetics*. 2011;13(3):255-262.
- Fogel BL, Lee H, Deignan JL, et al. Exome sequencing in the clinical diagnosis of sporadic or familial cerebellar ataxia. *JAMA Neurol*. 2014;71(10):1237-1246.
- Hanchard NA, Murdoch DR, Magoulas PL, et al. Exploring the utility of whole-exome sequencing as a diagnostic tool in a child with atypical episodic muscle weakness. *Clinical genetics*. 2013;83(5):457-461.
- Fan Z, Greenwood R, Felix AC, et al. GCH1 heterozygous mutation identified by whole-exome sequencing as a treatable condition in a patient presenting with progressive spastic paraplegia. *J Neurol*. 2014;261(3):622-624.
- Sawyer SL, Hartley T, Dymont DA, et al. Utility of whole-exome sequencing for those near the end of the diagnostic odyssey: time to address gaps in care. *Clinical genetics*. 2016;89(3):275-284.
- Farwell KD, Shahmirzadi L, El-khechen D, et al. Enhanced utility of family-centered diagnostic exome sequencing with inheritance model-based analysis: results from 500 unselected families with undiagnosed genetic conditions. *Genetics in medicine : official journal of the American College of Medical Genetics*. 2015;17(7):578-586.
- Farwell Hagman KD, Shinde DN, Mroske C, et al. Candidate-gene criteria for clinical reporting: diagnostic exome sequencing identifies altered candidate genes among 8% of patients with undiagnosed diseases. *Genetics in medicine : official journal of the American College of Medical Genetics*. 2016.
- Yang Y, Muzny DM, Reid JG, et al. Clinical whole-exome sequencing for the diagnosis of mendelian disorders. *The New England journal of medicine*. 2013;369(16):1502-1511.
- Yang Y, Muzny DM, Xia F, et al. Molecular findings among patients referred for clinical whole-exome sequencing. *Jama*. 2014;312(18):1870-1879.
- Lee H, Deignan JL, Dorrani N, et al. Clinical exome sequencing for genetic identification of rare Mendelian disorders. *Jama*. 2014;312(18):1880-1887.
- Retterer K, Juusola J, Cho MT, et al. Clinical application of whole-exome sequencing across clinical indications. *Genetics in medicine : official journal of the American College of Medical Genetics*. 2016;18(7):696-704.