

# *Welcome to today's* FDA/CDRH Webinar

*Thank you for your patience while we register all of today's participants.*

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# Next Generation Sequencing (NGS) Final Guidances

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# Agenda

- Background
- Final guidances
  - Design, development and analytical validation of NGS IVDs guidance
  - Use of human genetic variant databases guidance
- Summary
- Questions and answers

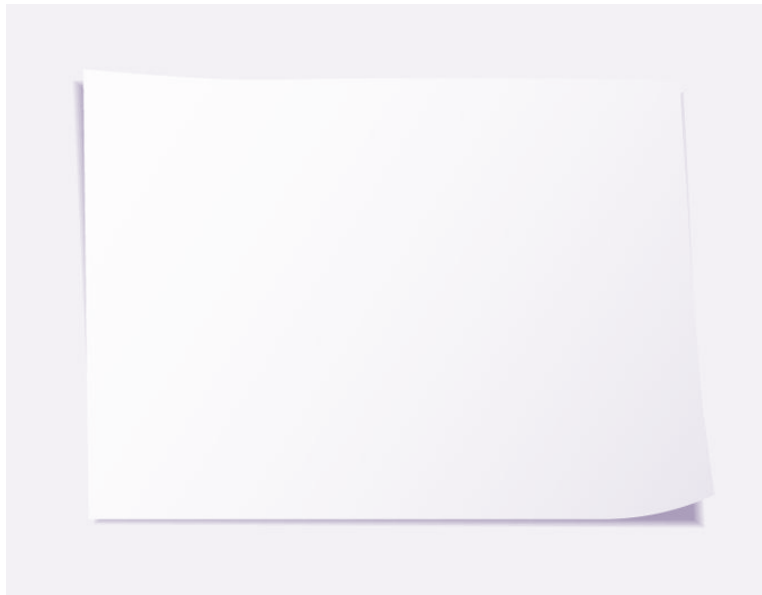
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# In Vitro Diagnostics in the Age of Precision Medicine



Traditional testing



Next generation sequencing



# Developing a Nimble Regulatory Approach for Genomic Tests



**Vision:** Implement new regulatory policies to promote research and accelerate the translation of precision medicine technologies into treatments that **benefit patients**.

**Goal:** Improve regulatory efficiency; encourage and speed innovation

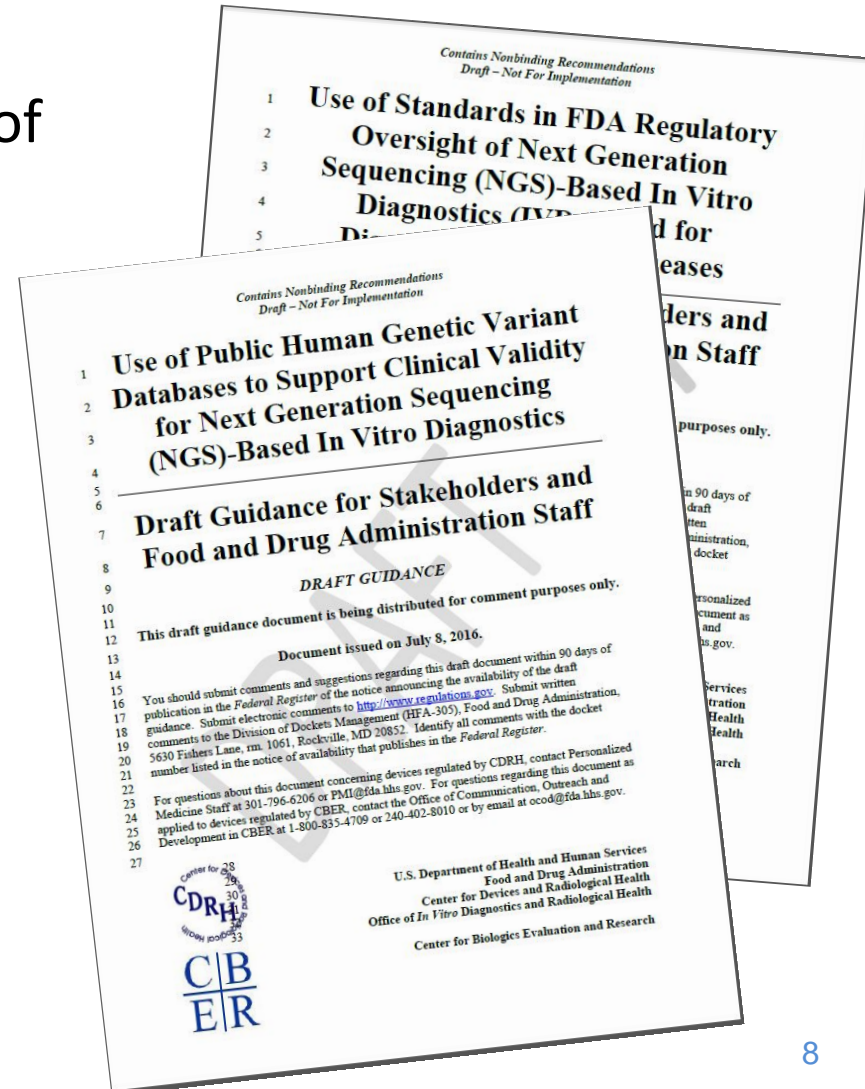
# Key Themes from Public Engagement



- Analytical standards should be a **combination of design process and performance standards**
- Need **clarity/transparency** about test performance and limitations
- Need to **incentivize data sharing**
- Need common nomenclature/standards for test results – *essential for providers and patients*
- Need for development of more reference materials

# NGS draft guidances (July 2016)

- Describe a regulatory pathway for NGS-based tests for certain uses
- Anticipate and support the needs of rapidly-evolving NGS technologies
- Intended to **ensure patient safety**, encourage **innovation**, and assure the **quality and reliability** of NGS-based tests and promote adoption of NGS-based tests into clinical practice
- NGS tests developed according to these guidances are anticipated to have an **efficient path to market**







# FDA's Concepts for Regulation of NGS-Based IVDs for Diagnosing Germline Diseases

- **Technical/analytical standards for NGS**
  - Test developers that meet these standards may not have to submit a premarket submission to the FDA.
  - Standards would be developed with the scientific community, and can be updated as science and technology advance.
- **Use of FDA-recognized databases to provide clinical evidence**
  - Use databases as information sources to support the link between genetic variation and health/disease.
  - Test developers may be able to use such databases in support or in lieu of traditional clinical studies.

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## *Guidance:*

Considerations for Design, Development,  
and Analytical Validation of Next  
Generation Sequencing (NGS)–Based In  
Vitro Diagnostics (IVDs) Intended to Aid in  
the Diagnosis of Suspected Germline  
Diseases



# 2016: Draft Guidance Use of Standards in FDA Regulatory Oversight of NGS-Based IVDs for Diagnosing Germline Diseases

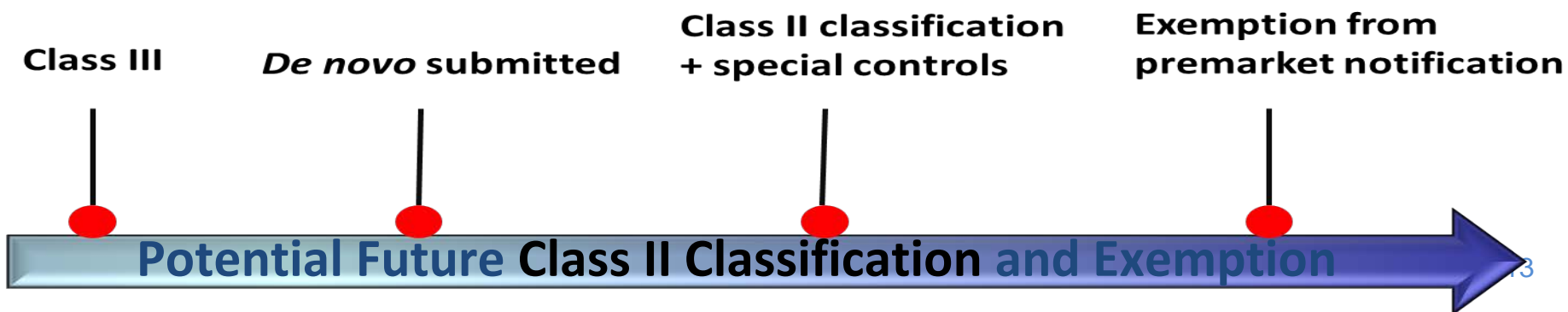
## ***Scope:***

The draft guidance applies only to targeted or Whole Exome Sequencing NGS-based tests intended to aid in the diagnosis of individuals with suspected germline diseases or other (germline) conditions

- Can form the basis for future **FDA-recognized standard(s) and/or special controls.**

# Regulatory Considerations

- All novel tests, including those with the intended use described in the guidance, are Class III *by default*
- The FDA believes it may be possible to classify tests that fall within the scope of the guidance as Class II devices; the guidance outlines what FDA believes is needed to support this classification
- As we gain more experience with these devices, the FDA believes that it may be possible, in the future, to develop special controls that could provide a reasonable assurance of the safety and effectiveness of NGS-based tests intended to aid in the diagnosis of suspected germline disease, possibly under certain conditions of exemption, without the need for 510(k) premarket review



# Comments on the Draft Guidance



- Public comments received from 38 organizations and individuals
- Commenters were generally supportive of the proposed regulatory approach
- Requests for clarification of the background, scope, and certain technical recommendations

# April 2018 Final Guidance: *Changes from Draft to Final*



- Title Revised
  - To better reflect scope and content
  - To acknowledge that currently there are no applicable standards that FDA can recognize
  - To support community engaging in developing standards by SDOs
- Scope Revised
  - Clarify that the document only specifically applies to NGS-based tests intended to aid clinicians in the diagnosis of symptomatic individuals with suspected germline diseases
- Thresholds Removed
  - Guidance recommends that test developers predefine, justify, and report minimum acceptable overall and target threshold metrics such as accuracy, precision, and coverage
- Revised Recommendations for Design, Development, and Validation
  - Clarifications to accuracy metrics, performance evaluation studies, and other technical recommendations



# Recommendations for Design, Development, and Validation

- Test **design** considerations:
  - Approach to test design
  - Recommendations are flexible, to accommodate different test designs, components, indications, etc.
- Test **performance characteristics**
  - Accuracy, precision, limit of detection, analytical specificity
- Test **run quality** metrics
  - Including read depth, completeness
- General recommendations for performance **evaluation studies**

*Can form the basis for future FDA-recognized consensus standard(s) and/or special controls*



- Thresholds would be defined in upcoming consensus standards or special controls
  - Will depend on the specific tests and indications for use, and variables such as types of variants detected and reported
- Accuracy
  - Definitions of positive percent agreement (PPA), negative percent agreement (NPA), and technical positive predictive value (TPPV)
  - Calculating accuracy
    - Appendix with a simplified example of calculations
- Performance evaluation studies
  - Describing types of samples and studies for different indications and variant types
  - Evaluate end-to-end performance
  - Break down accuracy evaluation results by variant, sequence context, specimen type, etc.

# Accuracy Evaluation Studies



- **Comparator method**
  - Appropriate comparator, and/or consensus sequence of agreed-upon well-characterized samples, as appropriate
- **Study samples** (reflecting test specimen types)
  - Well characterized reference samples
  - Clinical samples relevant for the test
  - Appropriate surrogate samples
- Include what can test detect (what is **relevant for indication**)
  - Representative genomic regions, variant types, sequence contexts
  - Clinically meaningful regions
  - Appropriately sized increments
- Number of specimens based on test performance, point estimate and **statistical confidence intervals**

# Additionally, guidance includes:



- Discussion on **supplemental procedures** such as trio testing or orthogonal confirmation
- Variant **annotation and filtering** considerations
- Recommendations for **presentation of test performance / labeling** such as:
  - Identify regions of the genome in which sequence **meeting pre-specified performance specifications** can be generated by the NGS-based test
  - Types of sequence **detected and reported** by the test
  - Types of sequence **variants test cannot detect** with adequate accuracy and precision
  - **Performance summary**
  - The relationship between reported variants and the clinical presentation, as applicable
- How to address NGS test modifications

# Significance

- Provides **key considerations** for designing, developing, and establishing analytical validity of NGS-based tests for suspected germline diseases
- Informs the development of **consensus standards** by experts in the community
  - Consensus standards developed by accredited consensus standards bodies (SDO) and recognized by FDA could help streamline review process
- Recommendations in this guidance and/or standards that address these recommendations may form the basis of **special controls**, allowing these tests to be candidates for down-classification
  - Could be considered for exemption from premarket notification if they meet certain criteria

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## *Guidance:*

Use of Public Human Genetic Variant Databases to Support Clinical Validity for Genetic and Genomic-Based In Vitro Diagnostics

# What do we mean by human genetic variant database?

- For the purpose of this guidance, a human genetic database is:
  - A collection of assertions about a link between a genetic variant and a disease or condition.
  - Publicly accessible – meaning that those assertions, and any underlying data, are transparent and available to all users.

# Benefits of Using Data from Publicly Accessible Genetic Databases

- Evidence generated by multiple parties
- Aggregated data provide a stronger evidence base (i.e., current state of scientific knowledge)
- As clinical evidence improves, new assertions could be supported





# Use of Genetic Variant Databases to Support Regulatory Decisions



- CFTR2 database accepted as valid scientific evidence to demonstrate clinical validity for the Illumina MiSeq CF 139 Variant Assay
  - Data regarding variants sufficient to provide assurance of the clinical validity of the variants reported by the test
  - Acceptance specific to this single intended use
- Myriad proprietary database and interpretation processes accepted as valid scientific evidence for BRACAnalysis CDx
  - Data and evidence evaluation process sufficient to provide assurance of clinical validity of the variants reported by the test
  - Myriad allowed to report novel variants to physicians and patients



# July 2016 Draft Guidance



*Title:* Use of Public Human Genetic Variant Databases to Support Clinical Validity for Next Generation Sequencing (NGS)-Based In Vitro Diagnostics

- Outlined recommendations for administrators of publicly accessible genetic variant databases to demonstrate that the database can be considered a source of “valid scientific evidence”
- Evidence from such databases could support the clinical validity of NGS-based tests
- Defined a **voluntary** database recognition pathway (similar to standards recognition)



# Comments on the Draft Guidance

- Public comments from 38 organizations and individuals.
- Commenters were generally supportive
- Requests to expand the scope:
  - Somatic Genetic Databases
  - For genetic and genomic based test that use technology other than NGS
- Clarify what is meant by “publicly accessible”
- Discuss how proprietary databases can leverage this guidance document
- Requests for clarity on or technical corrections to other aspects of the draft guidance

# April 2018 Final Guidance: *Changes from Draft to Final*

*Title:* Use of Public Human Genetic Variant Databases to Support Clinical Validity for Genetic and Genomic-Based In Vitro Diagnostics

- Evidence from such databases could support the clinical validity of **genetic and genomic-based** tests
- Clarified what is meant by **publicly accessible**
- Noted that aspects of guidance could be useful for proprietary models
- Clarified recommendations are applicable to germline and **somatic variant databases**
- Expanded details about the **voluntary** database recognition pathway





Outlines recommendations for administrators of publicly accessible genetic variant databases to demonstrate that the database can be considered a source of “valid scientific evidence”

- **Transparency** of database operations: documentation, versioning, SOPs, standard formats
- Data **quality**: information about data and its sources (nomenclature and metadata)
- SOPs for the evaluation of variants with **validation studies** supporting their use
- Relies upon **expert curation**: training and disclosure of conflicts of interest
- Database **hygiene**: privacy, security, data preservation

# April 2018 Final Guidance

## *Recognition Pathway*



- **Voluntary** request for database recognition
  - Cover Letter detailing scope of recognition application
  - Application
    - SOPs, policies or other documents related to the recommendations in the guidance
    - Validation studies for evaluation SOPs
    - Documentation of the qualifications of the individuals evaluating variants and policies for approving those individuals
    - Data preservation plan
    - Conflict of interest policies and disclosures of conflicts of interest
    - A commitment to make all recommended documents publicly accessible via weblinks
- **Maintenance of FDA recognition**
  - Periodic review to maintain recognition

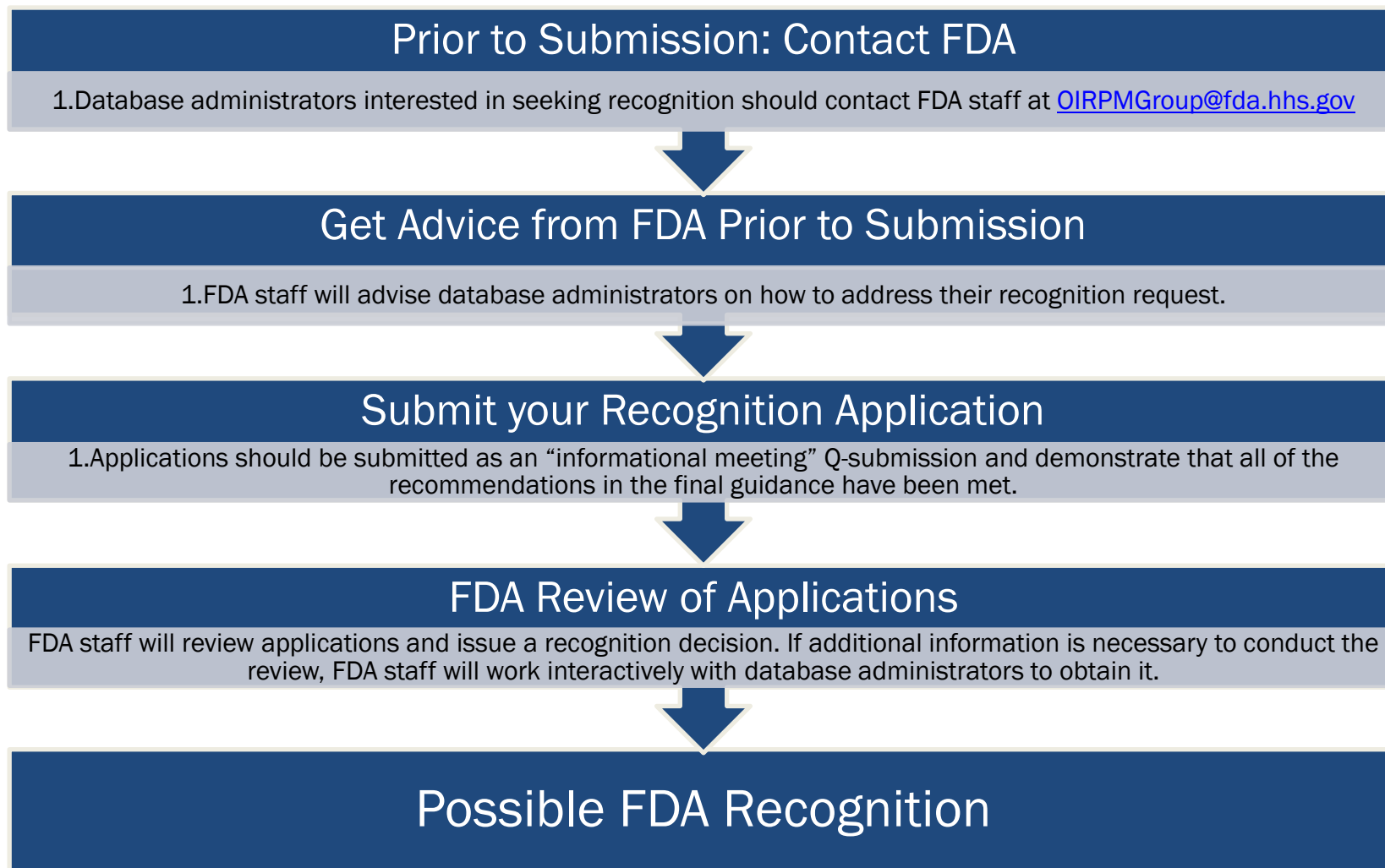
# April 2018 Final Guidance

## *Use of Recognized Databases*



- Assertions in FDA-recognized databases can include a variety of variant types and descriptive language (e.g., clinically significant, pathogenic, variant of uncertain significance), but must be supported by the evidence.
- Assertions from FDA-recognized databases would generally constitute valid scientific evidence
- Can be used to support the clinical validity of genetic and genomic tests

# Recognition Process





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# Key Take Aways

- These two final guidances represent part of FDA’s approach to reviewing innovative and rapidly evolving technologies in a least burdensome manner.
- The analytical guidance arms developers with insight on ways to validate their tests and provides a potential expedited path to market.
- The database guidance enables test developers to harness crowd-sourced data to support the clinical validity of their tests.



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# Questions?

Personalized Medicine Staff: [OIRPMGroup@fda.hhs.gov](mailto:OIRPMGroup@fda.hhs.gov)

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<http://www.fda.gov/training/cdrhlearn>

Under Heading: In Vitro Diagnostics

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# Accuracy calculations

PPA –  $TP/TP+FN$  (number of known variants detected by the test (TP) divided by the number of known variants tested (TP + FN) for each variant type that is being reported)

NPA -  $TN/TN+FP$  (number of TN results divided by the number of wild type results for variants tested (TN + FP) for each variant type that is being reported)

TPPV –  $TP/TP+FP$  (number of TPs from the test divided by the total number of positive results (TP + FP) obtained by the test)