Pre-Application Webinar for

PAR-19-104, Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)

January 18th, 2018

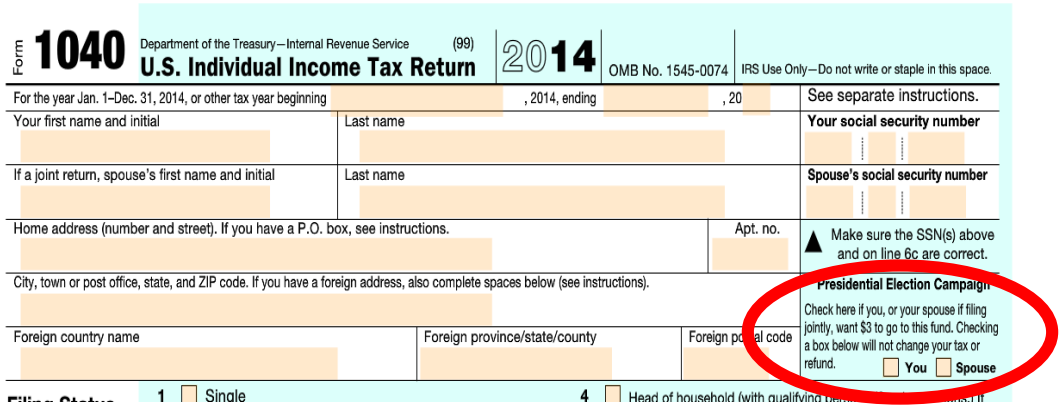
2:00 pm EST

Gabriella Miller Kids First

PEDIATRIC RESEARCH PROGRAM

Background

- Initiated in response to the [2014 Gabriella Miller Kids First Research Act]:
  - Signed into law on April 3, 2014
  - Ended taxpayer contribution to presidential nominating conventions
  - Transferred $126 million into the Pediatric Research Initiative Fund
  - Authorized appropriation of $12.6 million per year for 10 years to the NIH Common Fund for pediatric research; first appropriation was for FY2015


Form **1040** Department of the Treasury—Internal Revenue Service (99) **U.S. Individual Income Tax Return** 2014 OMB No. 1545-0074 IRS Use Only—Do not write or staple in this space.

For the year Jan. 1–Dec. 31, 2014, or other tax year beginning , 2014, ending , 20 See separate instructions.

Your first name and initial | Last name | Your social security number

If a joint return, spouse's first name and initial | Last name | Spouse's social security number

Home address (number and street). If you have a P.O. box, see instructions. | Apt. no. | Make sure the SSN(s) above and on line 6c are correct.

City, town or post office, state, and ZIP code. If you have a foreign address, also complete spaces below (see instructions). | **Presidential Election Campaign** Check here if you, or your spouse if filing jointly, want $3 to go to this fund. Checking a box below will not change your tax or refund. You Spouse

Foreign country name | Foreign province/state/county | Foreign postal code

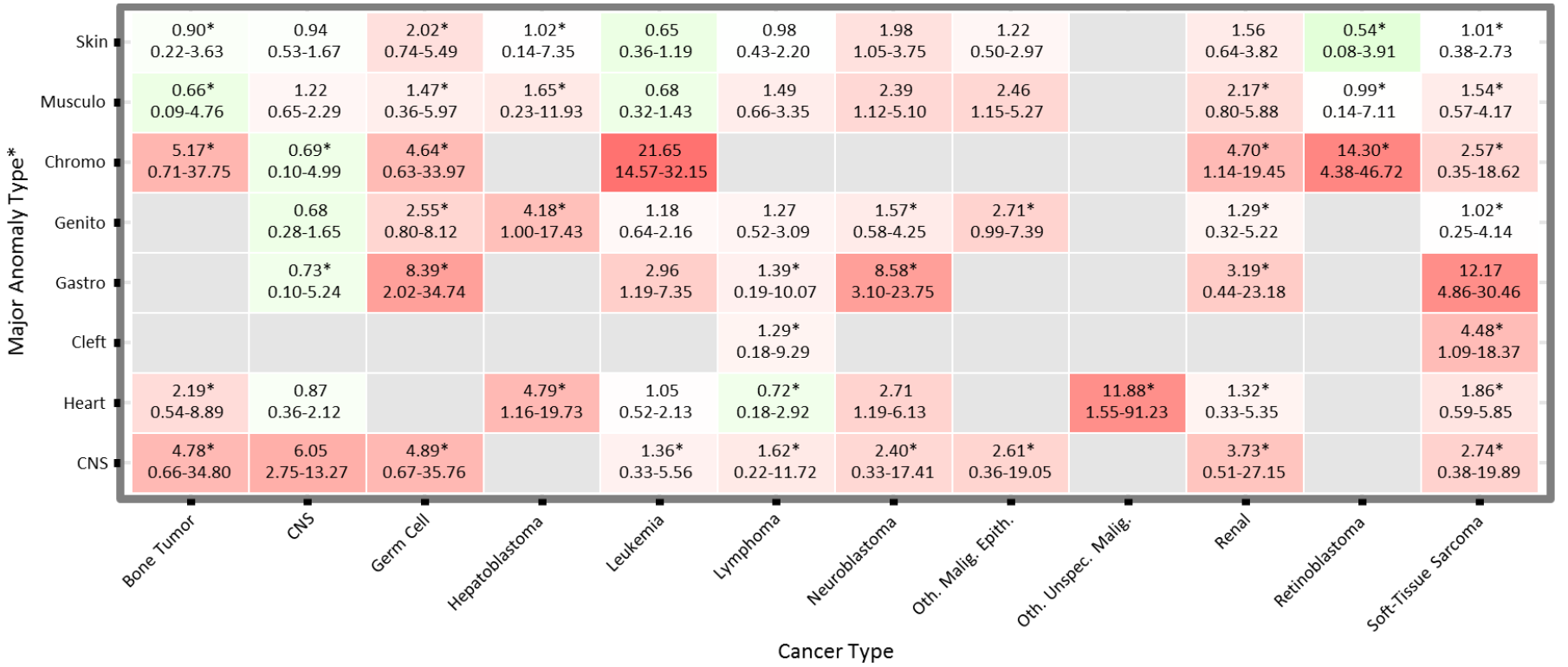
Filing Status 1 Single 4 Head of household (with qualifying

Vision

Alleviate suffering from childhood cancer and structural birth defects by fostering **collaborative research** to uncover the etiology of these diseases and supporting **data sharing** within the pediatric research community.

Scientific Origin

Congenital anomalies associated with increased risk of childhood cancer



Norwood, *PLOS ONE*, 2017

Gabriella Miller Kids First Working Group

- Kids First is a trans-NIH effort supported by the NIH Common Fund
- Institutes that chair the Kids First Working Group: **NICHD, NHLBI, NCI, NHGRI**
- Other Working Group representation: NIDCR, NIDA, NIAAA, NINDS, NIDDK, NIEHS, NEI, NIAMS, NIAID, NCATS, ORIP, and the CDC

For full list of **50+** members:
https://commonfund.nih.gov/kidsfirst/members

Kids First WG Leadership Team

Program Officers

James Coulombe (NICHD)
Working Group Coordinator
Sequencing Centers Program Official

Danielle Daee (NCI)
Sequencing Center Project Scientist

Jaime Guidry Auvil (NCI)
Sequencing Center Project Scientist

Malcolm Smith (NCI)

Adam Felsenfeld (NHGRI)

Lu Wang (NIDCR)

Jonathan Kaltman (NHLBI)

Maarten Leerkes (NHLBI)
Data Resource Project Scientist

Charlene Schramm (NHLBI)
Data Resource Program Official

Point-of-Contact

Valerie Cotton (NICHD)
Program Manager

Common Fund trio, OD

Marie Nierras – Program Leader

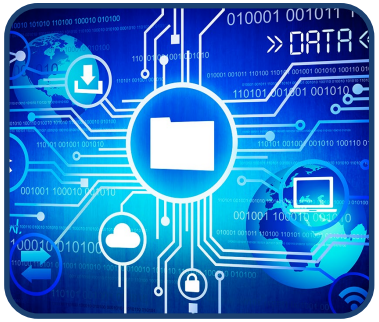
Danyelle Winchester – Policy, Planning, Evaluation, and Communications

Michael Steenstra – Operations and Budget

Kids First Major Initiatives

Cohort identification & DNA sequencing

- Identify children with cancer and/or structural birth defects, and their families (X01)
- Whole genome sequencing by the Kids First Sequencing Centers



Data Resource Center

- Develop a resource of well-curated clinical and genetic sequence data to facilitate and empower genomic discovery
- Provide computational infrastructure and analysis tools to interrogate large and complex datasets

Kids First Sequencing Centers

2019-2021 Sequencing Centers to be selected under RFA-RM-18-030

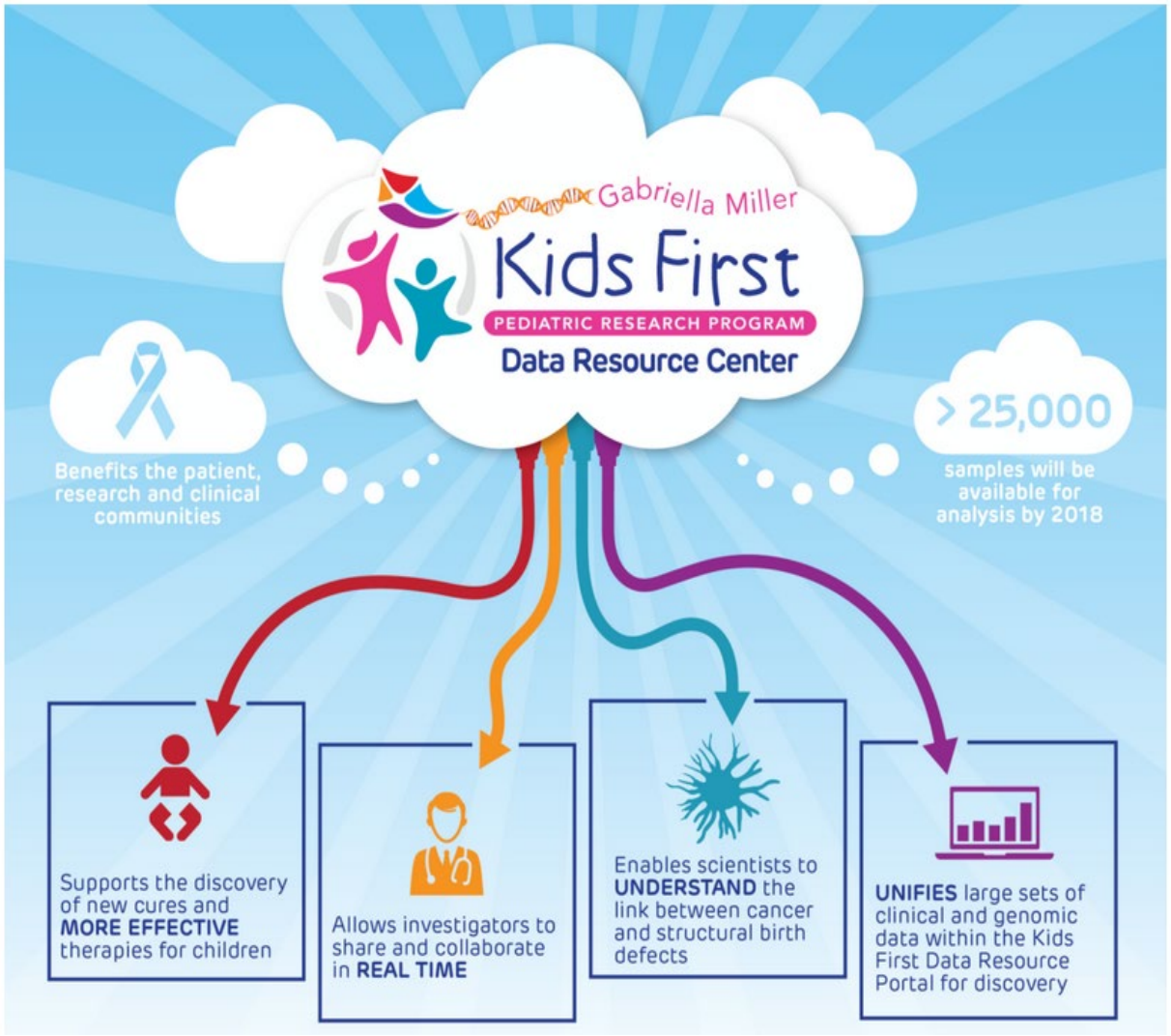
2016-2018 Sequencing Centers:

HudsonAlpha Institute for Biotechnology

Broad Institute

2015: Baylor College of Medicine & Washington University

Data Resource Center (DRC)



D3b Center for Data-Driven Discovery in Biomedicine

Children's Hospital of Philadelphia℠

SevenBridges genomics

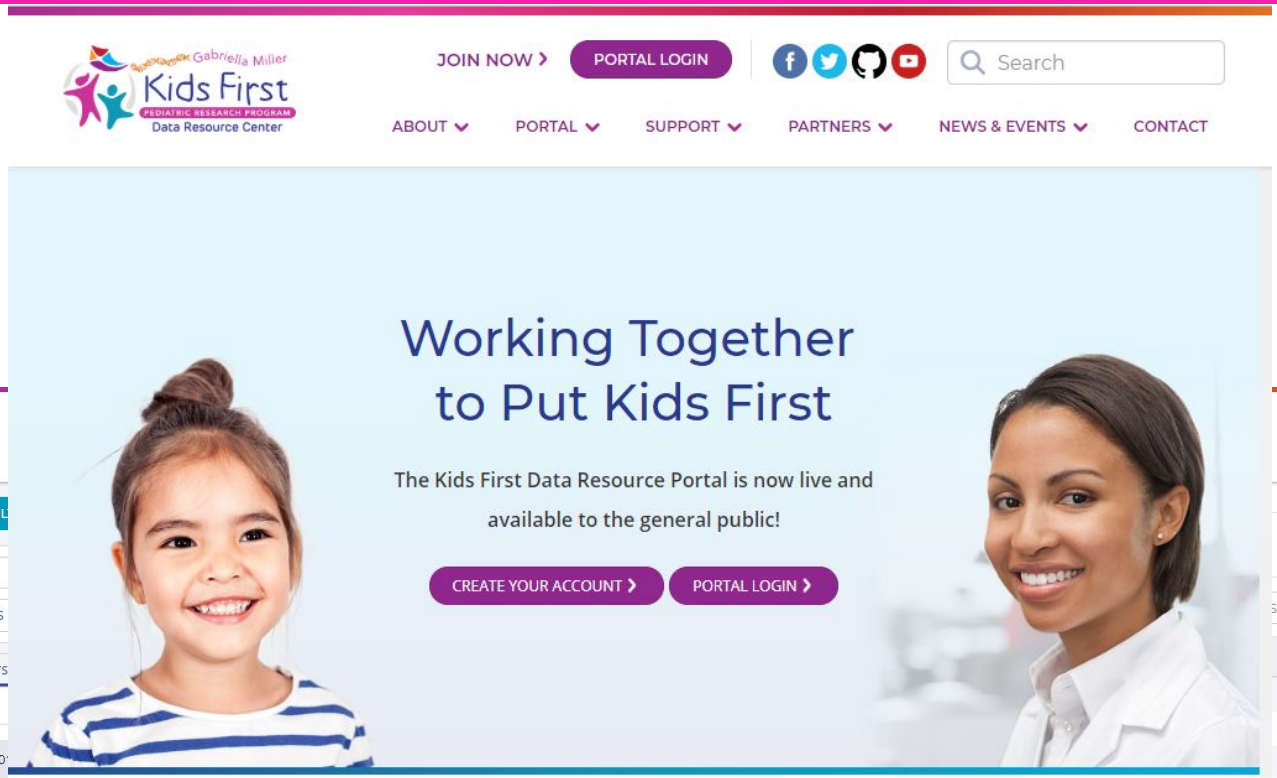
OICR Ontario Institute for Cancer Research | IORC Institut ontarien de recherche sur le cancer

THE UNIVERSITY OF CHICAGO

OHSU OREGON HEALTH & SCIENCE UNIVERSITY

Children's National Health System

Data Resource Center Website & Portal launched in 2018!



PAR-19-104

Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)

2019 X01: Fifth Cycle

Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)

1. FY 2015: PAR-15-259
   - 2 childhood cancer projects
   - 5 structural birth defects projects
2. FY 2016: PAR-16-150
   - 3 childhood cancer projects
   - 5 structural birth defects projects
3. FY 2017: PAR-17-063
   - 2 childhood cancer projects
   - 5 structural birth defects projects
   - 1 projects with overlap of structural birth defects and childhood cancer
4. FY 2018: PAR-18-583
   - 2 childhood cancer projects
   - 7 structural birth defects projects
   - 2 projects with overlap of structural birth defects and childhood cancer
5. **FY 2019: PAR-19-104**

X01 Mechanism

- Not an “award”; recipients are selected for the opportunity to have their cohort sequenced
- No Notice of Award; Kids First can provide a letter acknowledging and explaining that your project was selected for the X01 program
- Not listed in the NIH RePORTER
  - Abstracts and X01 information listed on Kids First website: https://commonfund.nih.gov/kidsfirst/x01projects
- No funds, but can apply for R01s or R03s to support analysis of X01 project:
  PAR-19-069: *Small Research Grants for Analyses of Data for the Gabriella Miller Kids First Data Resource (R03)*

X01 Selection Considerations

Following **scientific peer review**, Kids First program officers evaluate projects based on the following factors, and selections are finalized by Kids First Working Group Co-Chairs.

- Scientific and technical merit (determined by scientific peer review).
- Value of incorporating the dataset into the Data Resource to empower research among the pediatric research community.
- Balance of childhood cancers and birth defects; conditions not previously sequenced will be prioritized.
- Broad data sharing and use
- Informative study design and sufficient clinical and phenotypic data.
- Availability of samples in timely manner.
- Sample quality in terms of suitability for whole genome sequencing (as well as exome and RNASeq if applicable).

Kids First X01 Projects

Adolescent Idiopathic Scoliosis (FY16)
Cancer Susceptibility (FY16)
Congenital Diaphragmatic Hernia (FY15, 16, 17)
Craniofacial Microsomia (FY17)
Disorders of Sex Development (FY15)
Enchondromatoses (FY17)
Ewing Sarcoma (FY15, 17)
Familial Leukemia (FY16)
Hearing Loss (FY16)
Infantile Hemangiomas & Vascular Anomalies, Overgrowth (FY17, 18)
Neuroblastomas (FY16)
Nonsyndromic Craniosynostosis (FY17)
Orofacial Clefts; Caucasian (FY15), Latin American (FY16), Asian & African (FY17)
Osteosarcoma (FY15)
Patients with both childhood cancer and birth defects (FY17)
Structural Heart & Other Defects (FY15, 16, 18)
Syndromic Cranial Dysinnervation Disorders (FY15)
BEEC (Bladder extrophy, Epispadias, Complex) (FY18)
Congenital Heart Defects and Acute Lymphoblastic Leukemia in Children with Down Syndrome** (FY18)
Cornelia de Lange Syndrome (FY18)
Esophageal Atresia and Tracheoesophageal Fistulas (FY18)
Fetal Alcohol Spectrum Disorders* (FY18)
Intracranial Germ Cell Tumors (FY18)
Kidney and Urinary Tract Defects (FY18)
Microtia (FY18)
Myeloid Malignancies + overlap with Down syndrome** (FY18)

> 26,000 genomes

26 projects

Kids First Data Resource Center

Goal: Accelerate discovery of genetic etiology and shared biologic pathways by building a collection of curated genomic and phenotypic data from Kids First X01 projects and providing a central portal where these data and analysis tools will be readily accessible to the research community

- Charged with re-processing and "harmonizing" data generated by the sequencing centers to facilitate analyses across all Kids First datasets

Phenotypic data →
Sequence data →

→

X01 Recipients

Pediatric Research Community

X01 investigators are encouraged to utilize and work collaboratively with the Kids First Data Resource Center to pursue specific analyses. Visit: kidsfirstdrc.org

dbGaP & the DRC

Data is made accessible through dbGaP & Kids First Data Resource Center (DRC)

- While the DRC is the NIH designated repository for Kids First data, all Kids First projects are registered, authenticated, and approved through dbGaP
- All dbGaP Data Access Requests (DARs) will be processed by **the Kids First Data Access Committee** run by the NCI Office of Data Sharing

Kids First
Data Access Committee
(NIH)

PAR-19-104
Goals & Expectations

Overall Goal

Identify a diversity of childhood cancer and structural birth defects cohorts to generate high quality and broadly shareable and usable genomic datasets that will be of high value to the pediatric research community.

Sequencing

<u>Goal</u>: Generate high quality whole genome sequence and variant data from childhood cancer and structural birth defects cohorts.

WGS, whole exome sequencing (WES), and RNA sequencing may be available for tumor or affected tissue, when justified.

<u>Expectations</u>:

- DNA extractions must be of sufficient quality and concentration for WGS (and/or WES).
- RNA extractions (for tumor/affected tissue) must be of sufficient quality and concentration for RNASeq.
- Extractions will be ready to ship shortly after selection

Sequencing

Sequencing Centers perform sequencing & variant calling
Generate CRAM/BAM & VCF files

- **Germline/Normal**: WGS at 30X coverage
- **Tumor or Affected tissue** (when available)

- *You may propose other approaches (e.g., higher coverage or complementary exome sequencing).*
- *Project design will be finalized in discussions among the X01 investigators, the sequencing centers, and NIH program staff*

Volume/Concentration Recommendations

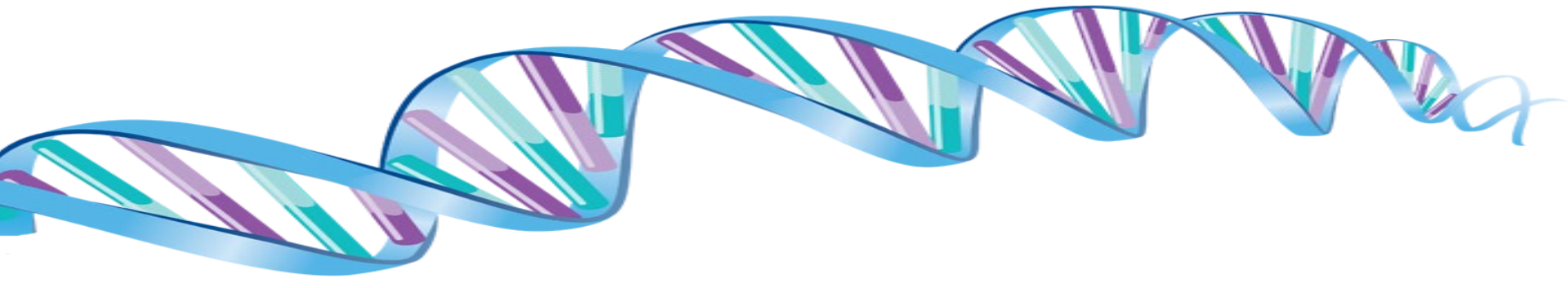
Can be found on our FAQ page: https://commonfund.nih.gov/kidsfirst/FAQ

Amount of DNA/RNA and coverage

	Amount DNA or RNA required/recommended	Concentration	Coverage	Additional info.
WGS	~2ug DNA	20-50 ng/ul preferred	30X	paired end reads
WES	275 ng DNA (minimum); 1 ug recommended	20 ng/ul (minimum)	100X, greater than 80% coding exons covered at 20X	paired end reads
RNA-Seq	750 ng total RNA (minimum); 1 ug recommended	20 ng/ul (minimum)	100X, greater than 40% coding exons covered at 20X	paired end reads

Pilot: **Long Read Sequencing?**

- Kids First is interested in running a pilot on the value of using “true” long read sequencing approaches for childhood cancer & structural birth defects research
- Tip: If you are interested in proposing long read sequencing for a **subset** of your cohort, you must:
  - justify how such data would inform your analysis
  - confirm the DNA is of sufficient quality for long-reads



Data Sharing

Goals:

1. **Make data generated by Kids First as accessible and usable as possible to the research community.**
2. **Enable researchers to easily combine/compare datasets for cross-disease analyses.**

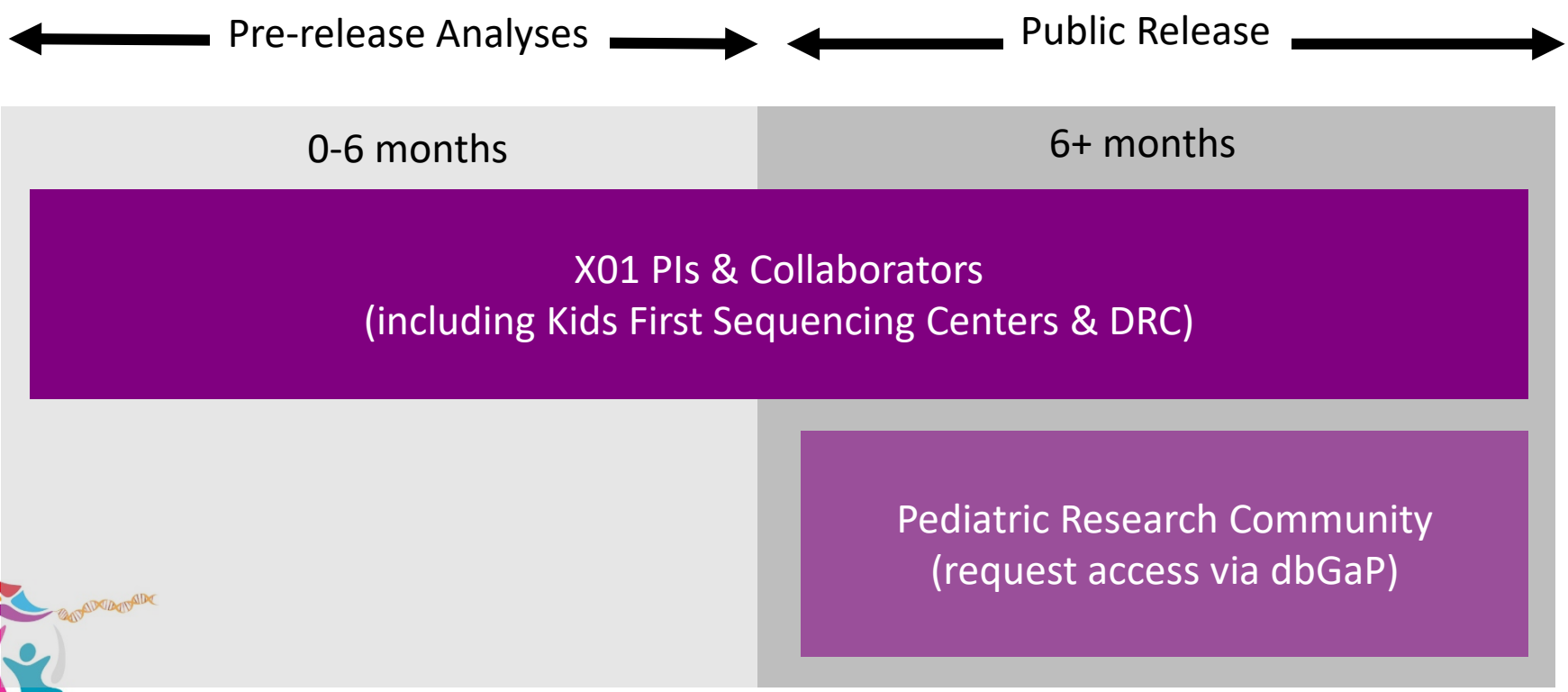
Expectations:

- Individual-level sequence and relevant phenotypic data are approved for deposition in a NIH-approved repository (e.g. dbGaP)
- Samples that are consented in a way that allows broad access and use, including combining and cross-analyzing datasets (General Research Use, Health/Medical/Biomedical), will be prioritized

See below and visit Kids First Data Sharing FAQs for more information

Six Month Pre-Release Period

- X01 investigators have six (6) months of proprietary access to the dataset before it is made available to the public.
- Pre-release period starts when the X01 team has access to all individual level sequence data (BAM/CRAM, VCFs)



Clinical/Phenotypic Data

Goal: **Well-phenotyped data empowers analyses and informs how pathways/conditions overlap.**
The DRC will leverage existing community standards to harmonize clinical/phenotypic data which facilitates searching, analysis, and interoperability with other data efforts.

Expectations:

- Basic data elements are expected and deep phenotyping is preferred.
- Describe what clinical/phenotypic information is available and how these data will:
    1) support your proposed analysis
    2) contribute to the DRC to empower collaborative research

Study Design

Goal: Study design, sample size, and family structures are sufficient to lead to genetic discovery

Expectations:

- Large sample sizes preferred
  - Consider collaborating with other investigators to pool samples together
- Non-trio family designs: describe the number of probands and affected/unaffected family members proposed for sequencing

Analysis Plans

Goal: Have investigators demonstrate that the proposed project has an adequate research design for genetic discovery, and that the X01 applicants are prepared to perform these analyses

Expectations:

- While Kids First recognizes that analytical power will increase when the data from each individual study is incorporated with other data that will be part of the Data Resource, it is important to demonstrate that the data will be useable on its own
- Consider partnering with other research teams with relevant expertise to develop the analysis plan

Program Balance

Goal: Broaden the diversity of both childhood cancer and structural birth defects datasets that are represented in the Data Resource

Expectation: Priority may be given to cohorts with conditions not previously sequenced under Kids First (if many applications score well and meet other criteria)

Other Attachments

1) Institutional Certification (or provisional certification with data use limitations designations)
2) Sample Information
3) Clinical/Phenotypic Data
4) Family Structure (Optional)

fillable tables (optional)

Institutional Certification: Steps

1) Download the current NIH Institutional (or Provisional) Certification template: *https://osp.od.nih.gov/scientific-sharing/institutional-certifications/*
   template was updated on November 1, 2018
2) Fill out the first page, include all sites contributing samples for sequencing.
3) Provide the Institutional Certification to the IRB along with the participant consent forms for each site and any other pertinent information.
4) The IRB reviews the consent form(s) to determine the data use limitations (DULs) and/or DUL modifiers for each consent form.
   - **"General Research Use" with no modifiers is expected for individual-level data, unless specific uses are clearly prohibited in the participant consent**
   - **"Unrestricted" access is expected for genomic summary results unless the IRB provides a justification for designating the dataset as "sensitive"**
5) After IRB review, the Institutional Certification is signed by the appropriate officials and submitted to NIH.

Download a letter that explains these steps

Institutional Certification: Page 1

Date: [MM/DD/YYYY] 12/03/2018
Name of GPA: Jaime Guidry Auvil
Genomic Program Administrator
NCI, NIH, HHS
9000 Rockville Pike
Bethesda, MD 20892-7395

Re: Institutional Certification of _____ [NAME OF INSTITUTION] to Accompany Submission of the Dataset from _____ [ORIGINAL STUDY NAME[1]] for _____ [PROJECT TITLE FOR DATA TO BE SUBMITTED] to an NIH-designated data repository.

Dear Jaime Guidry Auvil,

The submission of data to the NIH-designated data repository is being made with institutional approval from _____, along with appropriate institutional approvals from collaborating sites, as listed here:

[IF APPLICABLE ENTER COLLABORATING SITE NAMES HERE AND CLICK 'ADD TO LIST'] _____ LIST OF COLLABORATING SITES

Add to list >> Clear list

The _____ hereby assures that submission of data from the study entitled _____ to an NIH-designated data repository meets the following expectations, as defined in the NIH Genomic Data Sharing Policy:

- The data submission is consistent, as appropriate, with applicable national, tribal, and state laws and regulations as well as relevant institutional policies.
- Any limitations on the research use of the data, as expressed in the informed consent documents, are delineated in the table on page 3.
- The identities of research participants will not be disclosed to NIH-designated data repositories.
- An Institutional Review Board (IRB), and/or Privacy Board, and/or equivalent body, as applicable, has reviewed the investigator's proposal for data submission and assures that:
  - The protocol for the collection of genomic and phenotypic data is consistent with 45 CFR Part 46;[2]
  - Data submission and subsequent data sharing for research purposes are consistent with the informed consent of study participants from whom the data were obtained;
  - Consideration was given to risks to individual participants and their families associated with data submitted to NIH-designated data repositories and subsequent sharing, including unrestricted access to genomic summary results;
  - To the extent relevant and possible, consideration was given to risks to groups or populations associated with submitting data to NIH-designated data repositories and subsequent sharing, including unrestricted access to genomic summary results; and
  - The investigator`s plan for de-identifying datasets is consistent with the standards outlined in the NIH Genomic Data Sharing Policy (See section IV.C.1).

* Certification must be provided for all sites contributing samples. If more than one site is contributing samples, the primary site may submit one Institutional Certification indicating that they are providing certification on behalf of all collaborating sites. Alternatively, each site providing samples may provide its own Institutional Certification.

GPA: Jaime Guidry Auvil, NCI

List all sites contributing samples

Institutional Certification: Page 2

The individual-level data are to be made available through (check one)

- (•) **controlled-access** [3]
- ( ) **unrestricted access** [4]

individual-level sequence data are expected to be "controlled-access", unless consent allows for unrestricted access

If **unrestricted access** is marked, the data use limitations table on the following page(s) does not need to be completed.

NIH provides genomic summary results[5] (GSR) from most studies submitted to NIH-designated data repositories through unrestricted access. However, data from data sets considered to have particular 'sensitivities' related to individual privacy or potential for group harm (e.g., those with populations from isolated geographic regions, or with rare or potentially stigmatizing traits) may be designated as "sensitive" by

In such cases, "controlled-access" should be checked below and a brief explanation for the sensitive designation should be provided. GSR from any such data sets will only be available through controlled-access.

The genomic summary results (GSR) from this study are only to be made available through
☐ **controlled-access.**

Explanation if controlled-access was selected for GSR.

Keep unchecked for "unrestricted" access to **genomic summary results** unless the IRB provides a justification for designating the dataset as "sensitive"

Institutional Certification: Page 3

NIH expects the submitting institution(s) to select one of the three standard Data Use Limitations (DULs) for appropriate secondary use, or, if necessary, create a customized DUL. DULs are developed based on the original informed consent of the participant(s).

Data Use Limitations

General Research Use	GRU	Use of the data is limited only by the terms of the Data Use Certification: these data will be added to the dbGaP Collection.
Health/Medical/Biomedical	HMB	Use of the data is limited to health/medical/biomedical purposes, does not include the study of population origins or ancestry.
Disease-specific [list disease]	DS	Use of the data must be related to the specified disease.
Other		[ENTER CUSTOMIZED TEXT, IF APPLICABLE]

Additional modifiers to the standard DULs (e.g., Not-for-profit Use On
basis in the informed consent from the participants or in special knowle

"General Research Use" with no modifiers is expected for individual-level data, unless specific uses are clearly prohibited

Data Use Limitation Modifiers (Optional)

IRB Approval Required	IRB	Requestor must provide documentation of local IRB approval.
Publication Required	PUB	Requestor agrees to make results of studies using the data available to the larger scientific community.
Collaboration Required	COL	Requestor must provide a letter of collaboration with the primary study investigator(s).
Not-for-profit Use Only	NPU	Use of the data is limited to not-for-profit organizations.
Methods	MDS	Use of the data includes methods development research (e.g., development and testing of software or algorithms).
Genetic Studies Only	GSO	Use of the data is limited to genetic studies only.

Using the tables above, please indicate in the table below the consent group(s) for each collaborating study site. Use one row per consent group.

Collaborating Site Name	Data Use Limitation	Data Use Limitation Modifiers (optional)
Eg: Cold Cohort Study	*Health/Medical/Biomedical*	IRB ☐ PUB ☐ COL ☐ NPU ☐ MDS ☐ GSO ☐
Eg: Cold Cohort Study	*Disease Specific Research [Lung Cancer]*	IRB ☐ PUB ☐ COL ☐ NPU ☒ MDS ☐ GSO ☐
	General Research Use	IRB ☐ PUB ☐ COL ☐ NPU ☐ MDS GSO
	Select consent group title	IRB ☐ PUB ☐ COL ☐ NPU ☐ MDS GSO
	Select consent group title	IRB ☐ PUB ☐ COL ☐ NPU ☐ MDS GSO

The following data use limitations and modifiers limit broad data access and impede the ability of the Kids First program to accomplish its goals

- **Disease Specific Consent Group:** When data use is restricted to a specific disease area, the data cannot be combined with a dataset with a different disease specific data use limitation. Combining and cross-analyzing datasets are a primary goal of Kids First and therefore datasets that are consented for General Research Use and/or Health/Medical/Biomedical purposes will be prioritized over datasets restricted to Disease Specific use.
- **IRB modifier:** With this box checked, the Requester must provide documentation of a their local IRB's approval for the proposed research. We find that it is rare for consent language to include such a requirement and that this modifier is often included in error. As a reminder, every requester and their institution must agree to the terms of the Data Use Certification (DUC), which verifies that the requesting PI is accredited within the institution, the institution is aware of the project for which the PI is proposing to use the data, and that the Institution has all appropriate security measures in place to manage and maintain the controlled-access dataset(s) being retrieved. For a sample DUC, see: https://osp.od.nih.gov/wp-content/uploads/Model_DUC.pdf
- **COL modifier**: This box is checked when the consent form states that collaboration with the original/submitting investigator is required in order to use the dataset; therefore, the Requestor must provide a collaboration agreement document in order to be approved for access the dataset. This can limit the number of end-users who are able to use the dataset.

For more detail on DUL definitions:

https://osp.od.nih.gov/wp-content/uploads/NIH_PTC_in_Developing_DUL_Statements.pdf

Genomic Data Sharing Contacts

Jaime M. Guidry Auvil, Ph.D.
Genomic Program Administrator (GPA)
Director, NCI Office of Data Sharing
NCIOfficeofDataSharing@mail.nih.gov

Vivian Ota Wang, Ph.D.
Kids First Data Access Committee (DAC) Chair
Deputy Director, NCI Office of Data Sharing
KidsFirstDAC@nih.gov

General NIH Genomic Data Sharing questions: GDS@mail.nih.gov

dbGaP (NCBI) helpdesk: dbgap-sp-help@ncbi.nlm.nih.gov

Other Attachments

1) Institutional Certification (or provisional certification with description of data use limitations)
2) Sample Information
3) Clinical/Phenotypic Data
4) Family Structure (Optional)

fillable tables (optional)

Other Attachments: Fillable Table

Provisional Certification

1) Provisional Certification: Data Sharing and Data Use Limitations

If you provided a Provisional Institutional Certification, because you are unable to provide a full Institutional Certification, please describe the anticipated data use limitations based on the language of the consent form(s) signed by the participants in the proposed cohort. For a list of standard DULs and modifiers, please review the Institutional Certification template: https://osp.od.nih.gov/scientific-sharing/institutional-certifications or https://osp.od.nih.gov/wp-content/uploads/standard_data_use_limitations.pdf.

Site	**Data Use Limitation** (GRU, HMB, DS)	**Data Use Limitation Modifiers** (IRB, PUB, COL, NPU, MDS, GSO)

Other Attachments: Fillable Table

Sample Information

DNA (and RNA) tissue of origin	**Number of Samples**	**Extraction Method**	**Concentration**	**Quality (Metric used:** *[edit here to specify])*	**Method of Quantitation**	**Number of Samples Ready to Ship by August 2019**	**Number of Samples Ready to Ship by January 2020**
Blood							
Saliva or Buccal swab							
[other tissue, edit here to describe]. **Note: cell lines will not be accepted**							
Tumors or Affected Somatic Tissue							
DNA – Frozen Tissue							
RNA – Frozen Tissue							
DNA – Embedded Tissue							
RNA – Embedded Tissue							
Total							

*For tumor specimens or affected tissue samples, please also describe the fixation methods and the pathology review to which the specimens were subjected, separate from the table. For tumors, describe the percentage of tumor cells within the specimen used for DNA and/or RNA isolation and % necrosis.

Other Attachments: Fillable Table

Clinical/Phenotypic Data & Demographics

Available Phenotype or Clinical Information (for #3 Clinical, Phenotypic, and Demographic Data). Please edit or add to the table below to indicate what phenotype information is available for the case/proband, parents, and/or other family members. The information you list is intended to be shared through the Kids First Data Resource.

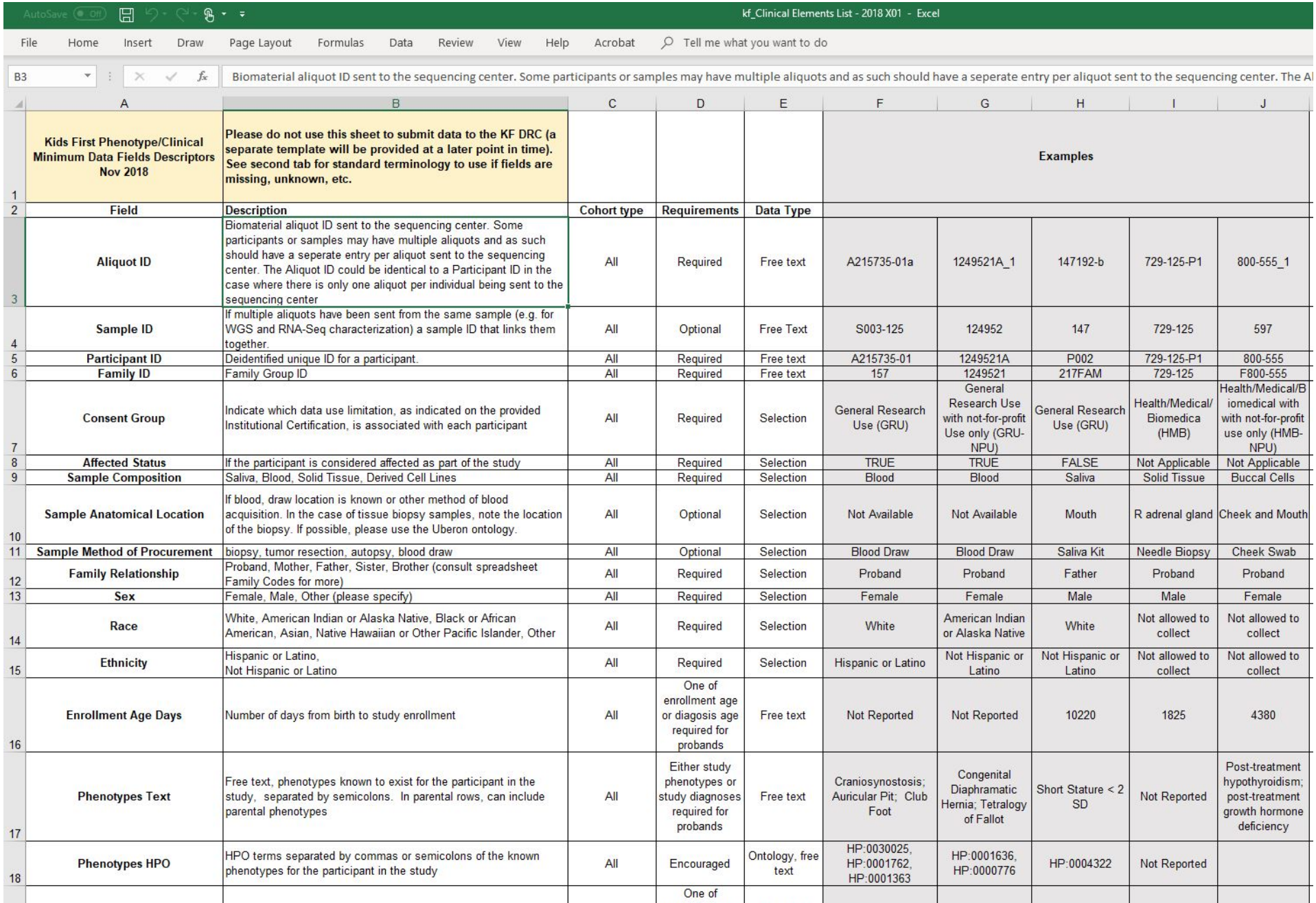
Demographics	Case/Proband/Affected	Unaffected family members/parents
o Age at enrollment or age at diagnosis		
o Other age information (age at specimen collection, age at death etc.…)		
o Sex		
o Race		
o Hispanic ethnicity		
o List any other demographic information:		

Clinical information (e.g., diagnoses, type of birth defect, primary tumor type, vital status, age at last know vital status, treatment information).		
	Case/Proband/Affected	Unaffected family members/parents
List the variables:		
Are electronic health records available?		

Other phenotypic information (e.g., other phenotypic measurements that may be related to the primary outcome)		
	Case/Proband/Affected	Unaffected family members/parents
List the variables		

Family medical history (e.g., family history of birth defects, family history of cancer)		
	Case/Proband/Affected	Unaffected family members/parents
List the variables:		

Biospecimen & Phenotypic Data Elements



kf_Clinical Elements List - 2018 X01 - Excel

File Home Insert Draw Page Layout Formulas Data Review View Help Acrobat Tell me what you want to do

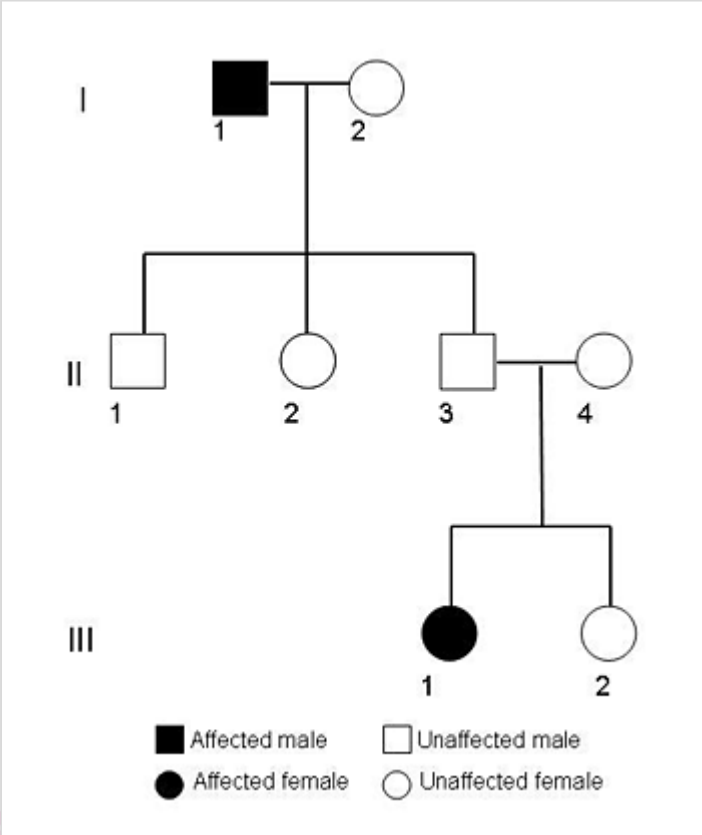
B3: Biomaterial aliquot ID sent to the sequencing center. Some participants or samples may have multiple aliquots and as such should have a seperate entry per aliquot sent to the sequencing center. The Al

	A	B	C	D	E	F	G	H	I	J
1	**Kids First Phenotype/Clinical Minimum Data Fields Descriptors Nov 2018**	**Please do not use this sheet to submit data to the KF DRC (a separate template will be provided at a later point in time). See second tab for standard terminology to use if fields are missing, unknown, etc.**				**Examples**				
2	**Field**	**Description**	**Cohort type**	**Requirements**	**Data Type**					
3	**Aliquot ID**	Biomaterial aliquot ID sent to the sequencing center. Some participants or samples may have multiple aliquots and as such should have a seperate entry per aliquot sent to the sequencing center. The Aliquot ID could be identical to a Participant ID in the case where there is only one aliquot per individual being sent to the sequencing center	All	Required	Free text	A215735-01a	1249521A_1	147192-b	729-125-P1	800-555_1
4	**Sample ID**	If multiple aliquots have been sent from the same sample (e.g. for WGS and RNA-Seq characterization) a sample ID that links them together.	All	Optional	Free Text	S003-125	124952	147	729-125	597
5	**Participant ID**	Deidentified unique ID for a participant.	All	Required	Free text	A215735-01	1249521A	P002	729-125-P1	800-555
6	**Family ID**	Family Group ID	All	Required	Free text	157	1249521	217FAM	729-125	F800-555
7	**Consent Group**	Indicate which data use limitation, as indicated on the provided Institutional Certification, is associated with each participant	All	Required	Selection	General Research Use (GRU)	General Research Use with not-for-profit Use only (GRU-NPU)	General Research Use (GRU)	Health/Medical/ Biomedica (HMB)	Health/Medical/Biomedical with with not-for-profit use only (HMB-NPU)
8	**Affected Status**	If the participant is considered affected as part of the study	All	Required	Selection	TRUE	TRUE	FALSE	Not Applicable	Not Applicable
9	**Sample Composition**	Saliva, Blood, Solid Tissue, Derived Cell Lines	All	Required	Selection	Blood	Blood	Saliva	Solid Tissue	Buccal Cells
10	**Sample Anatomical Location**	If blood, draw location is known or other method of blood acquisition. In the case of tissue biopsy samples, note the location of the biopsy. If possible, please use the Uberon ontology.	All	Optional	Selection	Not Available	Not Available	Mouth	R adrenal gland	Cheek and Mouth
11	**Sample Method of Procurement**	biopsy, tumor resection, autopsy, blood draw	All	Optional	Selection	Blood Draw	Blood Draw	Saliva Kit	Needle Biopsy	Cheek Swab
12	**Family Relationship**	Proband, Mother, Father, Sister, Brother (consult spreadsheet Family Codes for more)	All	Required	Selection	Proband	Proband	Father	Proband	Proband
13	**Sex**	Female, Male, Other (please specify)	All	Required	Selection	Female	Female	Male	Male	Female
14	**Race**	White, American Indian or Alaska Native, Black or African American, Asian, Native Hawaiian or Other Pacific Islander, Other	All	Required	Selection	White	American Indian or Alaska Native	White	Not allowed to collect	Not allowed to collect
15	**Ethnicity**	Hispanic or Latino, Not Hispanic or Latino	All	Required	Selection	Hispanic or Latino	Not Hispanic or Latino	Not Hispanic or Latino	Not allowed to collect	Not allowed to collect
16	**Enrollment Age Days**	Number of days from birth to study enrollment	All	One of enrollment age or diagosis age required for probands	Free text	Not Reported	Not Reported	10220	1825	4380
17	**Phenotypes Text**	Free text, phenotypes known to exist for the participant in the study, separated by semicolons. In parental rows, can include parental phenotypes	All	Either study phenotypes or study diagnoses required for probands	Free text	Craniosynostosis; Auricular Pit; Club Foot	Congenital Diaphramatic Hernia; Tetralogy of Fallot	Short Stature < 2 SD	Not Reported	Post-treatment hypothyroidism; post-treatment growth hormone deficiency
18	**Phenotypes HPO**	HPO terms separated by commas or semicolons of the known phenotypes for the participant in the study	All	Encouraged	Ontology, free text	HP:0030025, HP:0001762, HP:0001363	HP:0001636, HP:0000776	HP:0004322	Not Reported	
				One of						

Other Attachments: Pedigree or Table

Describe Family structures (proband-parent dyads, proband-parent-sibling quads, multiplex families, consanguineous families)

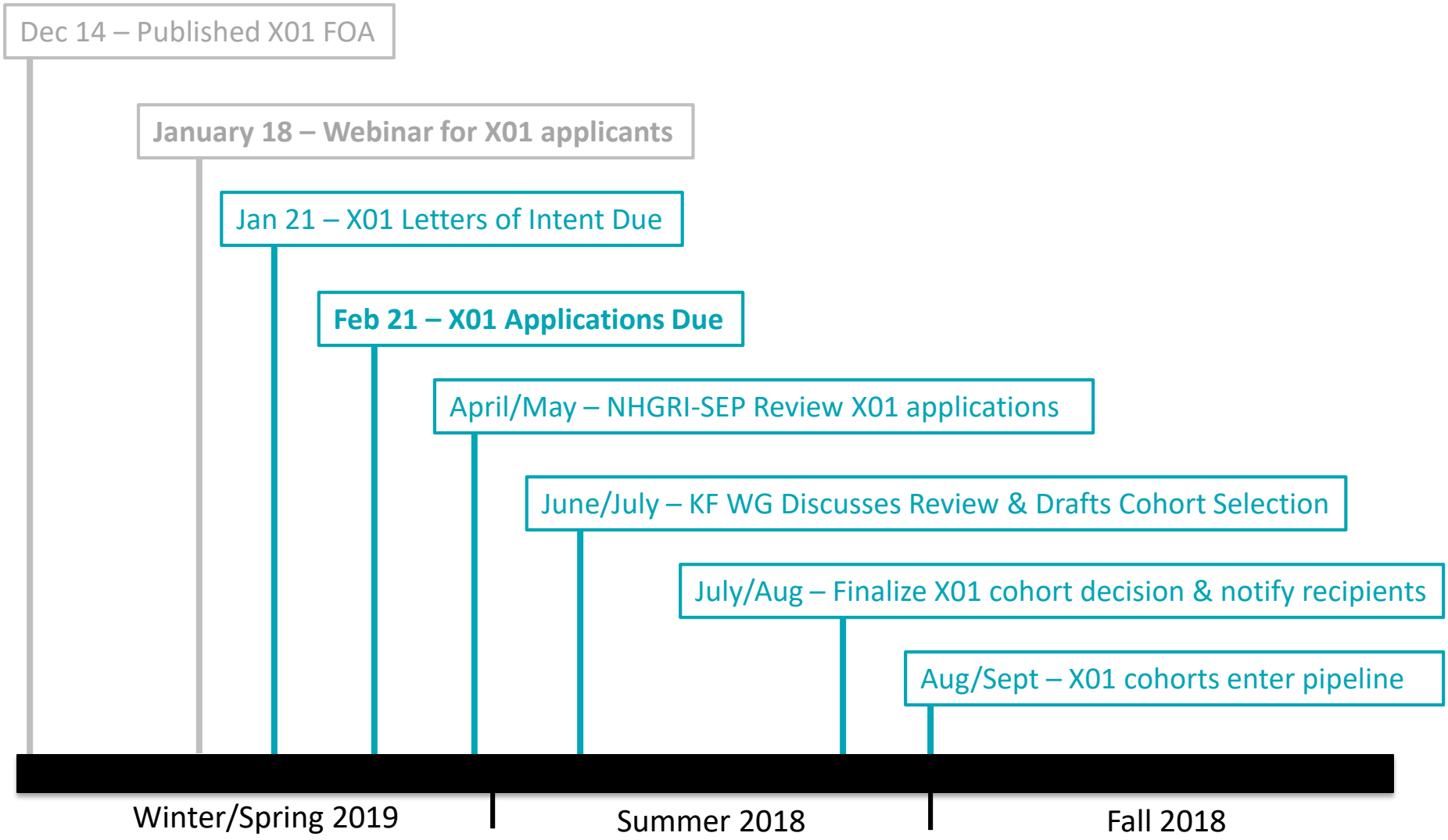
- How many samples per family? How many are affected/unaffected?



Family type	Number of families	Total Germline Samples
Proband/Child + Parents (unaffected) Trios	XX	XX affected XX unaffected
Proband + 1 affected FDR + [Unaffected FDRs]	XX	XX affected XX unaffected
Proband + 2 affected FDR + [Unaffected FDRs]	XX	XX affected XX unaffected
Total	XXX	XXX

FDR= First Degree Relative

2019 X01 Timeline



Helpful Links

- https://grants.nih.gov/grants/guide/pa-files/PAR-19-104.html
- https://commonfund.nih.gov/kidsfirst/faq
- https://kidsfirstdrc.org/
- https://portal.kidsfirstdrc.org
- https://osp.od.nih.gov/scientific-sharing/institutional-certifications/

Questions?

- Un-mute yourself by selecting *6 on your telephone or clicking on the mic symbol under “Audio Connection”,
  or
- Message us via the WebEx chat function

Thank You!

Email Additional Questions and Comments to the Kids First Mailbox: **kidsfirst@od.nih.gov**