Analyte	Subanalyte	Data Collection	Status	Estimated Availability	Notes
Dietary Biomarkers	Ascorbic Acid	Result file	Available, Final	December 2015	 Samples that did not pass the lab's QC were excluded from the final dataset. These data are considered the TEDDY standard for Ascorbic Acid.
Dietary Biomarkers	Carotenoids	Result file	Available, Final	December 2015	Samples that did not pass the lab's QC were excluded from the final dataset. These data are considered the TEDDY standard for Carotenoids.
Dietary Biomarkers	Cholesterol	Result file	Available, Final	December 2015	 Samples that did not pass the lab's QC were excluded from the final dataset. These data are considered the TEDDY standard for Cholesterol.
Dietary Biomarkers	RBC Fatty Acids	Result file	Available, Final	December 2015	 Samples that did not pass the lab's QC were excluded from the final dataset. These data are considered the TEDDY standard for Fatty Acids.
Dietary Biomarkers	Retinol	Result file	Available, Final	April 2018	 Samples that did not pass the lab's QC were excluded from the final dataset. These data are considered the TEDDY standard for Retinol.
Dietary Biomarkers	Tocopherols	Result file	Available, Final	December 2015	Samples that did not pass the lab's QC were excluded from the final dataset These data are considered the TEDDY standard for Tocopherols.
Dietary Biomarkers	Vitamin D	Result file	Available, Final	December 2015	 Samples that did not pass the lab's QC were excluded from the final dataset. These data are considered the TEDDY standard for Vitamin D.
Exome	TEDDY-T1DExome chip	Raw intensity files	Pending Lab Processing	Quarter 1 of 2019	1) Genotyping is underway.
Exome	TEDDY-T1DExome chip	Plink files	Pending Lab Processing	Quarter 1 of 2019	1) Genotyping is underway.
Gene Expression	Gene Expression	Raw instrumentation files	Available, Final	March 2016	1) Samples that did not pass the lab's QC will be excluded by the DCC from the final file collection.
Gene Expression	Gene Expression	Normalized results	Available, Final	March 2016	 Samples that did not pass the DCC's QC were excluded from the final dataset. This dataset is considered the TEDDY standard for gene expression.

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Gene Expression	Gene Expression	Inverse VST results	Available, Final	March 2016	1) Samples that did not pass QC at the DCC were excluded from the final dataset.
Metabolomics	Lipidomics (CSH-QTOF)	Raw instrumentation files	Available, Preliminary	August 2018	1) The vast majority of raw instrument files are available; raw data for some samples was not transmitted to the DCC. The lab is trying to locate files.
Metabolomics	Lipidomics (CSH-QTOF)	Result files	Available, Final	May 2016	1) Lipidomics result files are pre-normalized.
Metabolomics	Lipidomics (CSH-QTOF)	Normalized results	Pending Lab Processing	Quarter 4 of 2018	Samples that did not pass the lab's QC were excluded from the final dataset. The DCC is planning to renormalize the primary metabolomics (GCTOF) dataset with the Metabolomics Lab's new random forest normalization algorithm to reduce the variation seen across batches.
Metabolomics	Primary Metabolites (GCTOF)	Raw instrumentation files	Available, Preliminary	August 2018	1) The vast majority of raw instrument files are available; raw data for some samples was not transmitted to the DCC. The lab is trying to locate files.
Metabolomics	Primary Metabolites (GCTOF)	Result files	Available, Final	June 2016	1) Primary metabolites result files are pre-normalization.
Metabolomics	Primary Metabolites (GCTOF)	Normalized results	Pending DCC Processing	Quarter 4 of 2018	Samples that did not pass the lab's QC were excluded from the final dataset. The DCC is planning to renormalize the primary metabolomics (GCTOF) dataset with the Metabolomics Lab's new random forest normalization algorithm to reduce the variation seen across batches.
Microbiome	Nasal Swab 16S	Sequence files	Available, Final	April 2017	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Nasal Swab CV	Sequence files	Available, Final	April 2017	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Nasal Swab CV	VirMap results	Pending DCC processing	Quarter 4 of 2018	 Data that did not pass Baylor's QC were excluded from the final dataset. Pending the DCC's review of the data and determination on whether the dataset will be considered the TEDDY standard for nasal cultured virome.
Microbiome	Nasal Swab ITS	Sequence files	Available, Final	April 2017	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Nasal Swab PV	Sequence files	Available, Final	April 2017	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.

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Microbiome	Nasal Swab PV	VirMap results	Pending DCC processing	Quarter 4 of 2018	 Data that did not pass Baylor's QC were excluded from the final dataset. Pending the DCC's review of the data and determination on whether the dataset will be considered the TEDDY standard for nasal primary virome.
Microbiome	Nasal Swab WGS	Sequence files	Available, Final	April 2017	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Plasma CV	Sequence files	Available, Final	February 2016	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Plasma CV	VirMap results	Pending DCC processing	Quarter 4 of 2018	 Data that did not pass Baylor's QC were excluded from the final dataset. Pending the DCC's review of the data and determination on whether the dataset will be considered the TEDDY standard for plasma cultured virome.
Microbiome	Plasma WGS-PV	Sequence files	Available, Final	February 2016	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Plasma WGS-PV	VirMap results	Pending DCC processing	Quarter 4 of 2018	Data that did not pass Baylor's QC were excluded from the final dataset. Pending the DCC's review of the data and determination on whether the dataset will be considered the TEDDY standard for plasma primary virome.
Microbiome	Stool 16S	Abundance table	Available, Preliminary	Quarter 4 of 2018	Data that did not pass Baylor's QC were excluded from the final dataset. Pending the DCC's review of the data and determination as to which dataset will be considered the TEDDY standard for Stool 16S.
Microbiome	Stool 16S	Sequence files	Available, Final	September 2015	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Stool CV	Sequence files	Available, Final	January 2016	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Stool CV	VirMap results	Pending DCC processing	Quarter 4 of 2018	 Data that did not pass Baylor's QC were excluded from the final dataset. Pending the DCC's review of the data and determination on whether the dataset will be considered the TEDDY standard for stool cultured virome.

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Microbiome	Stool ITS	Sequence files	Available, Final	January 2016	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Stool PV	Sequence files	Available, Final	May 2017	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Stool PV	VirMap results	Pending DCC processing	Quarter 4 of 2018	Data that did not pass Baylor's QC were excluded from the final dataset. Pending the DCC's review of the data and determination on whether the dataset will be considered the TEDDY standard for stool primary virome.
Microbiome	Deep Stool WGS	Sequence files	Available, Final	September 2015	Samples were selected for deep WGS sequencing with guidance from the Infectious Agents Committee based on the lowest time-to-onset to IA cases and matched control pair samples. Sequence files have been trimmed, quality filtered, and dehumanized by the lab.
Microbiome	Stool WGS	Abundance table	Pending DCC processing	Quarter 4 of 2018	Data that did not pass Baylor's QC were excluded from the final dataset. Pending the DCC's review of the data and determination as to which dataset will be considered the TEDDY standard for Stool WGS.
Microbiome	Stool WGS	HUMAnN2 output	Pending DCC processing	Quarter 4 of 2018	Data that did not pass Broad's QC were excluded from the final dataset. Pending the DCC's review of the data and determination as to which dataset will be considered the TEDDY standard for Stool WGS.
Microbiome	Stool WGS	MetaPhlAn2 output	Pending DCC processing	Quarter 4 of 2018	Data that did not pass Broad's QC were excluded from the final dataset. Pending the DCC's review of the data and determination as to which dataset will be considered the TEDDY standard for Stool WGS.
Microbiome	Stool WGS	PUMA output	Pending DCC processing	Quarter 4 of 2018	 Data that did not pass Baylor's QC were excluded from the final dataset. Pending the DCC's review of the data and determination as to which dataset will be considered the TEDDY standard for Stool WGS.
Microbiome	Stool WGS	Sequence files	Available, Final	September 2015	1) Sequence files have been trimmed, quality filtered, and dehumanized by the lab.

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Proteomics	Discovery Phase	BCA results	Available, Preliminary	July 2015	1) 92 case-control pairs were selected for the discovery phase. 2) Samples were pooled prior to the case's seroconversion and at/after seroconversion. 3) Includes pre and post-enzymatic digestion protein and peptide abundance and percent (%) recovery measurements via the BCA (bicinchoninic acid) assay
Proteomics	Discovery Phase	Raw instrumentation files	Available, Preliminary	August 2016	 92 case-control pairs were selected for the discovery phase. Samples were pooled prior to the case's seroconversion and at/after seroconversion.
Proteomics	Discovery Phase	MASIC results	Available, Preliminary	August 2016	1) 92 case-control pairs were selected for the discovery phase. 2) Samples were pooled prior to the case's seroconversion and at/after seroconversion. 3) MASIC (MS/MS Automated Selected Ion Chromatogram generator) results contain intensity values of the iTRAQ reporter ions, which is used for the quantification.
Proteomics	Discovery Phase	MSGF+ results	Available, Preliminary	August 2016	1) 92 case-control pairs were selected for the discovery phase. 2) Samples were pooled prior to the case's seroconversion and at/after seroconversion. 3) MSGF+ results contain all of the unfiltered peptide identifications by scoring MS/MS spectra against peptides derived from a protein sequence database.
Proteomics	Discovery Phase	Filtered peptide reporter ion results	Available, Preliminary	August 2016	 1) 92 case-control pairs were selected for the discovery phase. 2) Samples were pooled prior to the case's seroconversion and at/after seroconversion. 3) Filtered peptide reporter ion result files contain the iTRAQ reporter ion intensity values of the confidently identified peptides and a protein-peptide map file.
Proteomics	Validation Phase	BCA results	Pending Lab Processing	Quarter 1 of 2019	1) Sample processing is underway.
Proteomics	Validation Phase	Raw instrumentation files	Pending Lab Processing	Quarter 3 of 2020	1) Sample processing is underway.
Proteomics	Validation Phase	MASIC results	Pending Lab Processing	Quarter 3 of 2020	1) Sample processing is underway.

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Proteomics	Validation Phase	MSGF+ results	Pending Lab Processing	Quarter 3 of 2020	1) Sample processing is underway.
Proteomics	Validation Phase	Filtered peptide reporter ion results	Pending Lab Processing	Quarter 3 of 2020	1) Sample processing is underway.
RNA Sequencing	RNA-Seq	Sequence files	Pending Lab Processing	Quarter 4 of 2018	1) Data has been received for around half of the samples selected.
RNA Sequencing	RNA-Seq	Result file	Pending DCC processing	Quarter 1 of 2019	1) After all data are received, the DCC will generate an analysis-ready result file that can be used as the TEDDY standard for RNA-Seq. 2) Samples that do not pass the DCC's QC will be excluded from the final dataset.
SNP	Immunochip	Raw intensity files	Available, Final	May 2017	1) Samples that did not pass the lab's QC will be excluded by the DCC from the final file collection.
SNP	Immunochip	Plink files	Available, Final	July 2018	1) Samples that did not pass the lab's QC were excluded from the final dataset. 2) Some of the SNPs in the original dataset were not mapped to the correct positions. This mapping issue was related to multiple groups contributing to the design of the chip, which resulted in physical positions mapping to multiple genome builds in the Illumina ImmunoChip Manifest B file. The rs IDs and positions have been corrected in the June 2018 updated dataset. 3) This dataset is considered the TEDDY standard for SNP (Immunochip).
Whole Genome Sequencing	Human WGS	Sequence files	Pending DCC processing	Quarter 4 of 2018	Data has been generated on the vast majority of NCC1 subjects. DCC QC, alignment, and variant calling is underway.
Whole Genome Sequencing	Human WGS	Result file	Pending DCC processing	Quarter 4 of 2018	After all NCC1 data are received, variant calling will be performed by the University of Michigan (UM) in collaboration with the DCC. Samples that do not pass the DCC's QC will be excluded from the final dataset.

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