Study of unrelated subjects by NGS KIR

Anthropological studies by NGS of full-length KIR genes to confirm and further characterize alleles and haplotypes identified in unrelated subjects from populations of interest.

We encourage participants to respond to the questionnaire, this will allow the component organizers more effectively coordinate exchange of samples and data.

NGS KIR Component questionnaire Link:
https://goo.gl/forms/zDQecX0X5SEpliUc2

A. Requirements Documentation:

Objective/Goals:
Characterize the nature and extent of KIR allelic diversity across human populations using Next Generation Sequencing (NGS). Haplotype distribution analysis will be performed on populations of interest.
This study is open to laboratories from all over the world and may include subjects of different ethnicities.

Samples type:
Samples from subjects belonging to a special interest anthropological unrelated group.

NOTE: Investigators may submit any of the following:

- Samples
- KIR NGS data
- Both samples and data

If samples are being submitted without KIR NGS data, contact the Component Chair to identify a collaborating laboratory who will perform the NGS testing. NGS could also be performed by a core laboratory if your group does not have a collaborating laboratory identified.

DNA requirements (if submitting samples only)

- **3µg DNA** is required. Minimum concentration is 5ng/µl (e.g., 20 µL of 150 ng/µL DNA)
- DNA must have > 10 kb fragments visible as a strong band when checked for quality.

Test Requirements:
There are no specific requirements for NGS platform/reagent combinations.
Samples tested by non- NGS methods may also be submitted

Proficiency testing:

- Labs performing NGS KIR testing are required to perform proficiency testing of 10 DNA samples. To request the samples, kindly contact:
  Cynthia Vierra-Green

Center for International Blood and Marrow Transplant Research, Minneapolis, Minnesota, USA
cvierra@NMDP.ORG

- Labs submitting NGS HLA typing are required to perform proficiency testing on a panel of 24 DNA. To order the panel, download the form from our website http://ihiws.org/wp-content/uploads/2016/01/Nonprofit-Order-Form-IHIW-Reference_panels.xlsx

Instructions to request panels:

Contact Cynthia Vierra-Green
cvierra@NMDP.ORG

Project Timelines:

January 2016:	Start registration for project online at http://ihiws.org
	Start ordering reference DNA panels
February 2016:	Start submitting study samples to NGS lab if not performing NGS testing
January 2017:	Start reference DNA panel distribution
	Start testing study subjects and reference DNA panel
March 2017:	Deadline for data submission proficiency and reference DNA panel(s) to IHIWS database.
May, 2017:	Deadline for all data submission of study samples.

IRB Requirements
Samples and data submitted must de-identified, it should not contain personally identifiable patient information and should not include "Protected Health Information" as defined under the United States Health Insurance Portability and Accountability Act (HIPAA), http://www.hhs.gov/hipaa/index.html.
An IRB submitted by Stanford University will cover de-identified samples and data from participating centers that contain no PHI or clinical data and samples were not collected specifically for this project.

Required NGS KIR loci: KIR2DL1, 2DL2/3, 2DL4, 2DL5, 3DL1, 3DL2, 3DL3, 2DS1-5
Optional NGS KIR Loci: KIR2DP1, 3DP1
MINIMUM NGS data to submit if performing NGS full length typing: unphased sequence sorted/filtered per locus, allele calls.

Data analysis and data entry:
Required fields

- LabCode: six character alphabetic code provided by the 17WS organizers
- SampleID: As labeled
- Inclusion Criteria
- Random
- Disease

- Transplant (donor/recipient)
- Case (patient/control)
- Collection Region
- Collection Country
- Sample Reference (Provide any primary bibliographic references which pertain to the collection of this sample.
- Birth Region
- Birth Country
- Ethnicity

Project Specific data:

- Race/ethnicity/country of origin of the subjects included in the study
- Closest allele in the IMGT database to novel alleles and differences from the closest allele, when applicable
- Inclusion: Reason for including the sample in this study (E.g., any characteristics of interest of the haplotypes identified or the population of the subject carrying these haplotypes)

Other data entry:

- Hardware related
  Instrument_Model_Number: the model number, or other identifier, defining the type of instrument used for the typing
  Instrument_name

- Software_related
  Software_Manufacturer: the manufacturer of the software
  Software_Name: the name of the software applied and version number used

- Alignment_Reference_DB: the IMGT/HLA Database release version (e.g., IMGT/HLA Database 3.18.0) or Genome Reference Consortium release version (GRCh37) used for aligning reads for consensus generation

- Locus_name: The locus for which the sequence data and metadata in a given Locus element are reported

- Optional: Consensus_Sequence: A nucleotide sequence representing a contiguous phased region of DNA. This can correspond to a single feature, or to multiple contiguous features. If a locus is absent, this is not reported.

B. Other Information that may be requested:
Raw (fastq) data