New York Blood Center Enterprises

Unpacking relevance of race and ethnicity in transfusion medicine

HAABB – April 18th, 2025

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Objectives

1. Define race and ethnicity and explain guidance for reporting.

2. Describe the use of race and ethnicity in transfusion medicine with focus on blood group differences.

3. Discuss how expansion of cost effective and comprehensive genotyping methods can reduce reliance on race and ethnicity.

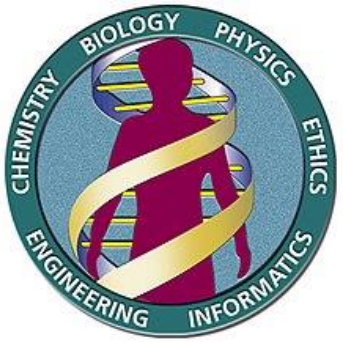
How is race and ethnicity generally defined?

- **Race** refers to a group sharing some outward physical characteristics and some commonalities of culture and history.
  - Unfortunately, used incorrectly to associate unfavorable characteristics such as unintelligent to certain groups
  - Socio-political construct

- **Ethnicity** refers to common cultural markers including language, nationality, religion, and customs
  - May suggest shared ancestor or geographic origin

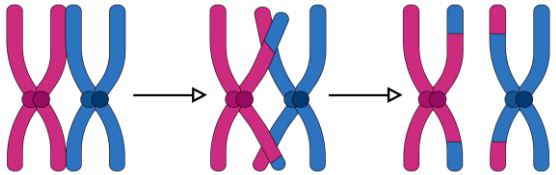
From a genomics perspective

- Revolutionary finding of the Human Genome Project completed in 2003 that all humans are >99% identical at DNA level
  - Highlighted that humans are all much more alike than different
  - “the concept of race has no scientific basis” - from genome pioneer J. Craig Venter
  - “no ‘race’ gene” that exists in all members of one group and none of another - from renowned evolutionary biologist Stephen J Gould

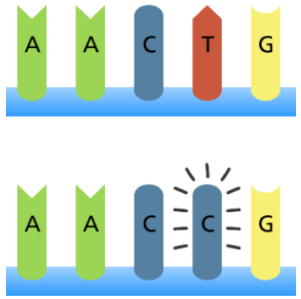


Some factors influencing genetic diversity

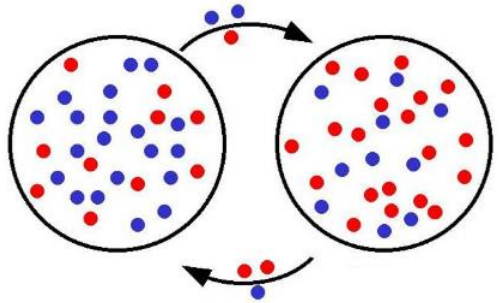
Gene recombination



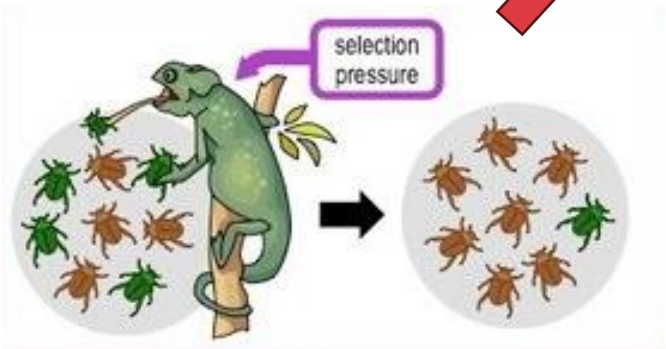
Mutation



Gene flow



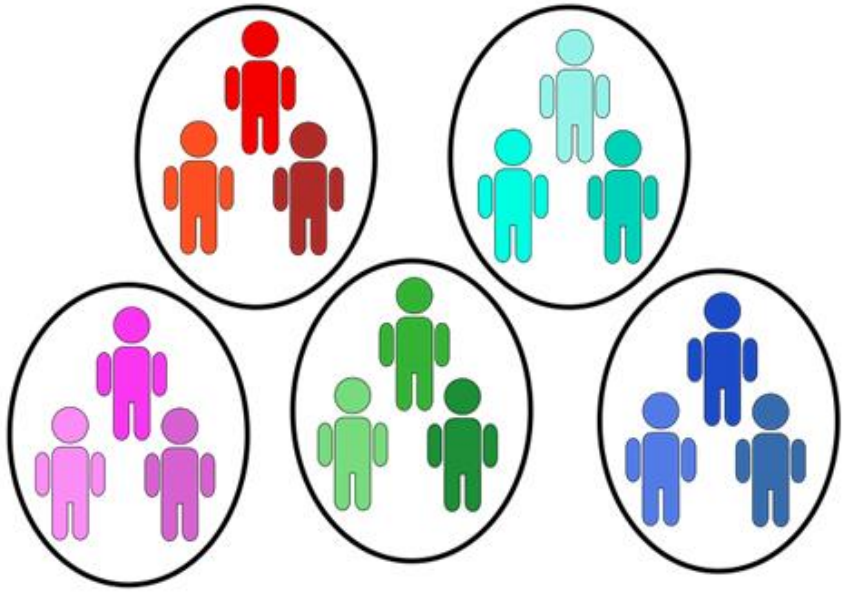
Genetic diversity



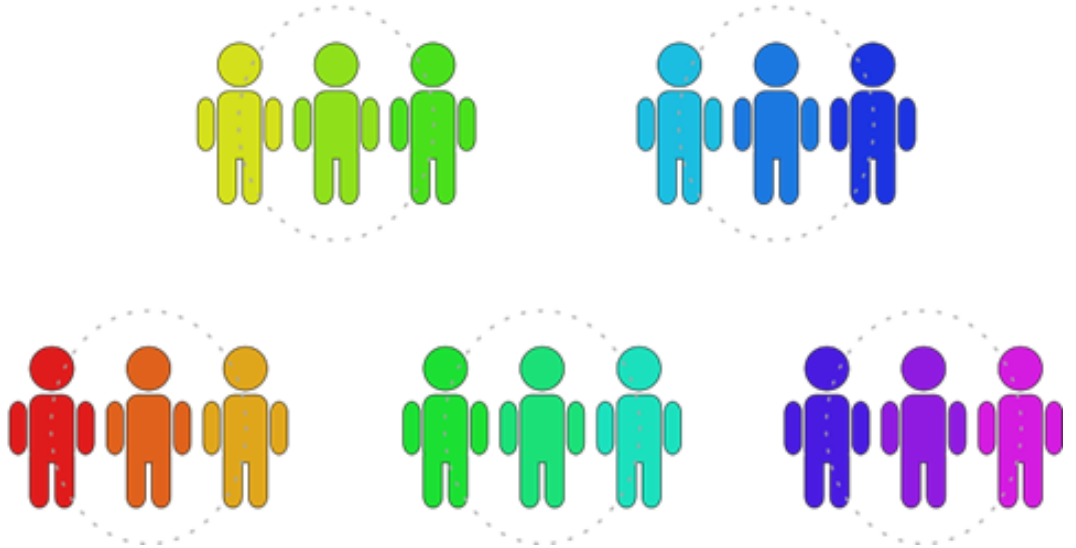
Selection pressures

Genetic drift

Clustering of groups is not distinct



Perception



Actual

https://sitn.hms.harvard.edu/flash/2017/science-genetics-reshaping-race-debate-21st-century/

Which is more favorable term?

- Population?
  - General: the total of individuals occupying an area or making up a whole
  - Biological: a group of interbreeding organisms
- Genetic ancestry?
  - Information about the people that an individual is biologically descended from, including their genetic relationships.
  - Often has geographic implications
- Of note:
  - gnomAD database that collates whole genome and exome sequences revised terms on their website:
    - Population → Genetic Ancestry Group

Guidance with race and ethnicity

JAMA
The Journal of the American Medical Association

- 2021 guidance from The Journal of the American Medical Association (JAMA) for reporting race and ethnicity in medical and science journals and does **not** address clinical reporting
- General recommendations:
  - Reduce language with unintentional bias in medical and science literature
  - Minorities → underserved or underrepresented populations
  - Race/ethnicity → race and ethnicity
  - Race and ethnic terms should not be used as nouns
    - Blacks, Whites → Black individuals, White patients, etc
  - Discouraged use of Caucasian unless person/group is from Caucasus region
  - The recommendations don't specify which race and ethnicity grouping to use and more encourage including geographic region when possible
  - Consider if race and ethnicity information should be included in publication

https://jamanetwork.com/journals/jama/fullarticle/2783090

Why ask for race or ethnicity information?

- Better allocation of resources
- Donors:
  - Limited resources to phenotype beyond ABO/RhD and genotype for extended red cell antigen profile
  - Therefore, considerations on which donors to test may depend on:
    - ABO group and RhD type
    - RhCE, K type
    - Frequency of donation
    - Self-identified race and ethnicity
  - Improve antigen negative inventory
  - Meet transfusion needs of patients, especially those on chronic or repeat transfusions
- Patients:
  - Aiding in serologic work-up

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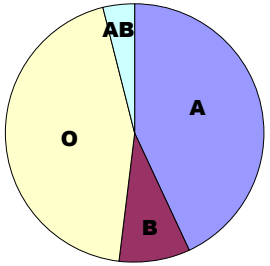
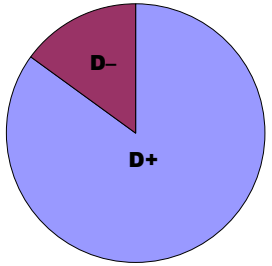
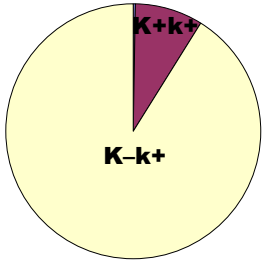
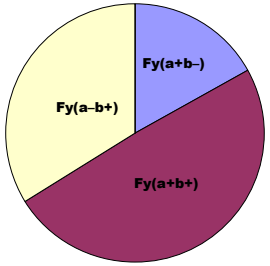
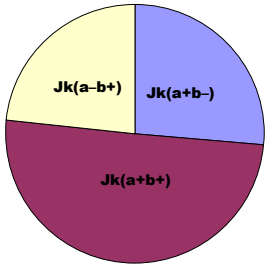
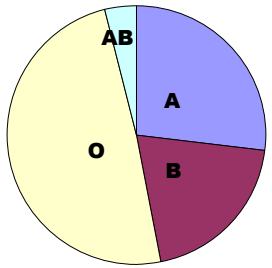
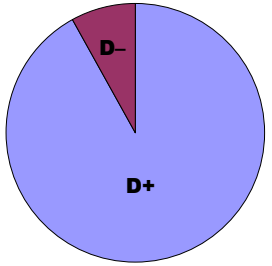
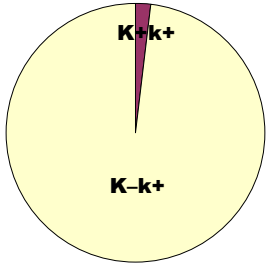
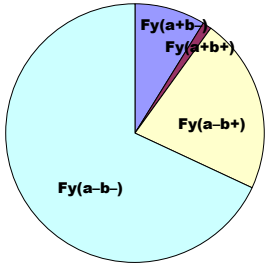
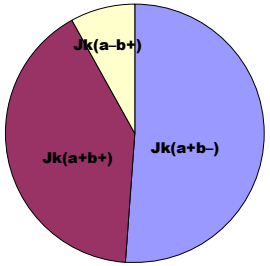
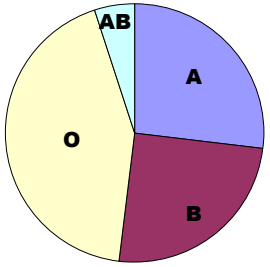
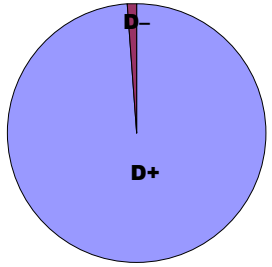
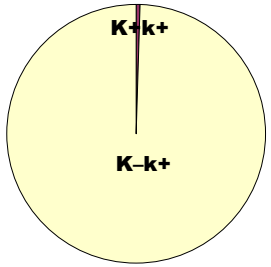
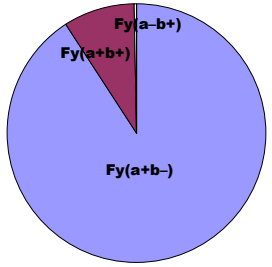
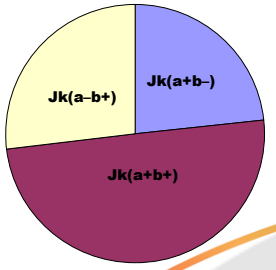
Blood groups and frequencies

- Currently 300+ antigens in 47 blood group systems known
- Blood group antigen distribution can vary greatly between ethnic groups
- The “uniqueness” of some blood groups has proved to be a useful tool for the study of global migration patterns
- Due to the “global community” a patient may be far from the population of their original ancestry, and this can result in delayed or lack of transfusion

Prevalence of “common” antigen combinations vary in different populations

Population	ABO	Rh	Kell	Duffy	Kidd	K–, Fy(a–), Jk(b–) prevalence
White						1:10
Black						1:2
Asian						1:100

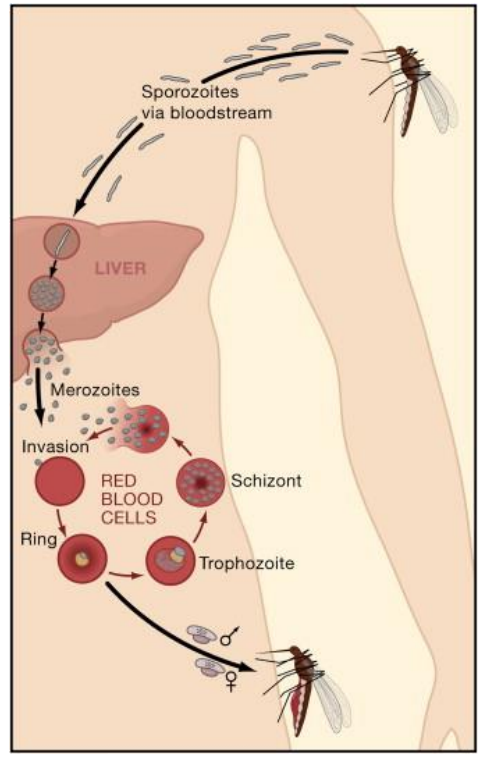
It can be tough to find blood when traveling

- Traveler: Group O, D– with anti-D and anti-Fy^a
- Traveling in South-East Asia
- Involved in a motor vehicle accident
- Transfusion required

- 1 in 20 donors with European ancestry will be D– Fy(a–)
- 1 in 10,000 donors in China, Taiwan and South-East Asia would be D– Fy(a–)

Selection pressures driving prevalence of phenotypes/alleles

- Some blood group antigens are receptors for malarial parasites
- RBCs with altered antigen or lacking antigen may resist invasion, offering selective advantage to phenotype and allele
- Fy(a–b–) phenotype due to GATA mutation
  - Lacks receptor for *P. vivax*, *P. knowlesi* malarial parasites.
  - Allele frequency: 0.85 African/African American and 0.21 Middle Eastern groups
- GE(–2,–3,4) phenotype ("Gerbich type):
  - Potential protection from *P. falciparum* invasion
  - 50% prevalence in people from Papua New Guinea and Melanesia
- Dantu+ phenotype (*GYP* variant)
  - Resistance to invasion by *P. falciparum*
  - This variant reduced risk for severe malaria by 40%
  - Uncommon variant – in East Africa with slightly higher prevalence in Kenya
  - lower prevalence may be due to being a recent evolutionary event or protection only against certain strains



(Leffler EM et al. Science. 2017 16;356(6343):eaam6393.)

https://www.sciencedirect.com/science/article/pii/S0092867406001814

Duffy (*FY*) – GATA mutation

- Absolute neutrophil count (ANC) range: 2,500 and 6,000 cells/ul
- Benign neutropenia
  - ANC <1500 cells/ul with no increased risk of infection
  - Primarily observed in individuals of African ancestry
  - Referred to as “Benign ethnic neutropenia” (BEN)
  - Recent association with *FY* GATA mutation
    - shift away from ethnicity and BEN especially since the *FY* GATA mutation occurs in other populations

Phenotype	Population (Any = may be found in any population; >=more prevalent than)
Fy(a–b–)	Blacks >> Arabs/Jews > Mediterraneans >> Caucasians

The Blood Group Antigen FactsBook

Solving complex immunohematology cases

- Race and ethnicity information can help focus testing for quick resolution for problems involving antibodies to high prevalence antigens and for identifying the appropriate donor population if rare blood needed
- JK:–3 [Jk(a–b–)]: higher occurrence in Polynesians, and SE Asians individuals
- Yt(a–) higher occurrence in Arabs and Jews
- SC:–1,–2,–3 mostly in people from Marshall Islands or other Pacific Islands
- O_h (Bombay phenotype) greater prevalence in Indians and Pakistanis but not restricted to those populations
- Kp(b–) found almost exclusively in White individuals
- Blood negative for U, Js^b, Hy, Jo^a, Cr^a, Tc^a, At^a, hr^S, hr^B, RH46 is found in people with African ancestry

Case 1

- Female patient
- No recent transfusion (> 3 months prior)
- Plasma was reactive with all screening cells

Initial Antibody Screen																	
		Rh					Kell		Duffy		Kidd		MNS				Results
		D	C	E	c	e	K	k	Fy^a	Fy^b	Jk^a	Jk^b	M	N	S	s	PEG IAT
I	R_1R_1	+	+	0	0	+	0	+	+	+	0	+	0	+	+	0	3+
II	R_2R_2	+	0	+	+	0	0	+	+	0	+	+	+	0	0	+	3+
III	rr	0	0	0	+	+	+	+	0	+	+	0	+	0	+	+	3+

- Referred to Immunohematology laboratory

Initial antibody results

Panel																	
		Rh					Kell		Duffy		Kidd		MNS				Results
		D	C	E	c	e	K	k	Fy^a	Fy^b	Jk^a	Jk^b	M	N	S	s	PEG IAT
1	R_1R_1	+	+	0	0	+	0	+	+	+	+	+	+	+	+	+	3+
2	R_1R_1	+	+	0	0	+	+	+	0	+	0	+	0	+	0	+	3+
3	R_2R_2	+	0	+	+	0	0	+	+	0	+	+	+	0	+	+	3+
4	R_0r	+	0	0	+	+	0	+	0	0	+	0	+	+	0	+	3+
5	r'r	0	+	0	+	+	0	+	+	0	+	0	+	+	0	0	3+
6	r"r	0	0	+	+	+	0	+	0	+	+	+	0	+	0	+	3+
7	rr	0	0	0	+	+	+	+	0	+	+	0	+	0	+	+	3+
8	rr	0	0	0	+	+	0	+	+	+	0	+	0	+	+	+	3+
9	rr	0	0	0	+	+	0	+	+	+	0	+	+	0	0	+	3+
10	R_1R_1	+	+	0	0	+	0	+	+	0	+	+	+	+	+	0	3+
11	R_0r	+	0	0	+	+	+	+	0	0	+	+	0	+	+	+	3+
Auto		+	+	0	+	+	0		0	+	+	+			0	+	0√

- 3+ reactivity throughout, auto control negative
- Suggest antibody to high prevalence antigen

Additional serology testing

Testing Phenotype Matched RBCs																	
		Rh					Kell		Duffy		Kidd		MNS				Results
		D	C	E	c	e	K	k	Fy^a	Fy^b	Jk^a	Jk^b	M	N	S	s	PEG IAT
1	R_1R_1	+	+	0	0	+	0	+	0	+	+	+	+	+	0	+	3+
2	R_1r	+	+	0	+	+	0	+	0	+	0	+	0	+	0	+	3+
3	R_0	+	0	0	+	+	0	+	0	0	+	0	0	+	0	+	3+

Testing Treated RBCs																		
		Rh					Kell		Duffy		Kidd		MNS				Results	
		D	C	E	c	e	K	k	Fy^a	Fy^b	Jk^a	Jk^b	M	N	S	s	Ficin IAT	Trypsin IAT	DTT IAT
1	R_1R_1	+	+	0	0	+	0	+	+	+	+	+	+	+	+	+	3+	3+	0√
2	R_1R_1	+	+	0	0	+	+	+	0	+	0	+	0	+	0	+	3+	3+	0√
3	R_2R_2	+	0	+	+	0	0	+	+	0	+	+	+	0	+	+	3+	3+	0√
4	R_0r	+	0	0	+	+	0	+	0	0	+	0	+	+	0	+	3+	3+	0√
5	rr	0	0	0	+	+	+	+	0	+	+	0	+	0	+	+	3+	3+	0√
6	rr	0	0	0	+	+	0	+	+	+	0	+	0	+	+	+	3+	3+	0√

RBC treatment pattern of reactivity to aid in antibody identification

Ficin/Papain	Trypsin	α-chymotrypsin	DTT (200mM)	Possible specificity
Neg	Neg	Neg	Pos	Bp^a; Ch/Rg; Xg
Neg	Neg	Neg	Neg	Indian; JMH
Neg	Neg	Pos	Pos	M, N, En^aTS; Ge2, Ge4
Neg/Variable	Pos	Neg	Pos	'N', S, s; Fy^a, Fy^b, Fy6
Variable	Pos	Neg	Neg	Yt^a
Neg	Pos	Pos	Pos	En^aFS
Pos	Neg	Neg	Weak	Lutheran; MER2
Pos - Papain Weak or neg - Ficin	Neg	Neg	Weak	Knops
Pos	Pos	Pos	Neg	Kell (except KALT); Scianna
Pos	Neg	Pos/Weak	Neg	Dombrock
Pos	Pos	Neg	Neg	Some DI antigens; Cromer
Pos	Pos	Pos/Weak	Neg	LW
Pos	Pos	Pos	Enhanced	Kx
Pos	Pos	Pos	Pos	A,B; H; P1; Lewis; Rh; Kidd; En^aFR, U; Fy3; Di^a, Di^b, Wr^a, Wr^b, some DI antigens; Colton; Ok^a; RAPH, I, i; P, $PP1P^k$, LKE; AnWj; At^a; Cs^a; Emm; Er; Jr^a; Lan; Vel; Sd^a; PEL; MAM; ABTI

Testing select rare cells

Selected Rare RBCs																	
		Rh					Kell		Duffy		Kidd		MNS				Results
		D	C	E	c	e	K	k	Fy^a	Fy^b	Jk^a	Jk^b	M	N	S	s	LISS IAT
1	Yt(a–)	+	+	0	+	+	0	+	+	+	+	+	+	+	+	+	3+
2	K_0	+	+	0	0	+	0	0	0	+	0	+	0	+	0	+	0√

➢ antibody directed against high prevalence antigen in Kell system

- How might race and ethnicity help in this case?
  - Patient race and ethnicity:
    - White → Test k– RBCs, test Kp(b–) RBCs
    - Black → Test Js(b–) RBCs
- Patient had been seen previously and records indicated ethnicity as White
- Plasma was found non-reactive with two Kp(b–) cells and they confirmed her RBCs typed Kp(b–) → patient has anti-Kp^b

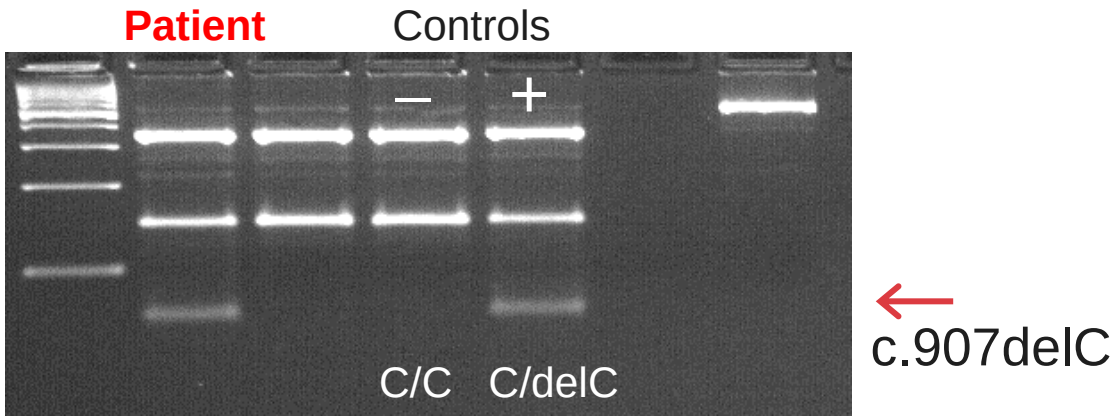
Case 2

- Hispanic female patient
- Multiple transfusions and therefore, unable to type the patient's RBCs
- A DNA BeadChip for common blood groups was preformed and predicted C–**E+**c+e+ but **anti-E** was detected in the patient's plasma

- Referred for E investigation

RHCE variant testing

- Currently on ISBT *RHCE* allele table, >40 variant *RHCE*cE* are listed associated with E weak, partial, or negative phenotype
- RHCE BeadChip (Werfen/Immucor):
  - *RHCE*ce / cE,* no variants detects
- In-house assay for silenced allele, *RHCE*cEN.02*, c.907delC associated with no expression of E (or c) antigen



← c.907delC

- Patient has the c.907delC
- RBCS are predicted to type E–
- Consistent with production of anti-E

- This allele was first reported in Hispanic individual
- Screening of donors found allele frequency of 0.005.
- At NYBC, >50% of E serology-DNA discrepancies are due to this allele

Westhoff CM *et al*. *Transfusion*. 2011 51(10):2142-7.

https://www.isbtweb.org/isbt-working-parties/rcibgt.html

Case 3

- Black female; prenatal evaluation
- Currently, typing as D– by automation
- **However**, the patient said they were D+ at another hospital
- Referred for investigation of D
- Testing with multiple Anti-D reagents:

	Anti-D (IS/IAT)		
	Reagent 1	Reagent 2	Reagent 3
Sample	0/3+	+w/4+	+w/3+

RHD genotyping

- RHD BeadChip assay and in-house assay for *RHD* zygosity:
  - ***RHD*Weak D type 2* hemizygote**
- Few days later, hospital called asking if possible sample switch as patient ethnicity is listed as ‘Black’ and *weak D type 2* is common in White individuals
- Verified no sample switch on DNA extraction or testing
- Physician wanted to ensure no ‘wrong blood in tube’ (WBIT) and new sample was submitted
- Repeat testing confirmed:
  - ***RHD*Weak D type 2* hemizygote**
- Patient is not candidate for RhIG!

➢ Ethnicity information can be useful but shouldn’t limit possibilities

RH genetic diversity

- *RH* variants more prevalent in individuals of African and Hispanic ancestry
  - Many variant *RHD* in *cis* with variant *RHCE*
  - Some genotypes put patient at risk for allo anti-D, -C, -E, -c, and -e
  - Some variant *RHCE* alleles encode a protein that lacks high prevalence antigen(s) (ex. hr^B, hr^S, Hr^B, Hr)
    - Additional alloimmunization risk
- Alloimmunization prevalences vary:
  - 7 - 47% in patients with sickle cell disease (SCD)
  - 3 - 42% in patients with thalassemia

Transfusion challenges

- Numerous studies have shown that despite prophylactic matching for Rh antigens, patients with SCD still made Rh antibodies
  - Similar with patients with β-thalassemia though studies not as extensive
- Some Rh antibodies attributed to patients with partial Rh antigens
  - Not detected by commercial antisera
  - Partial antigen status often identified AFTER patient makes corresponding antibody
- Some unexpected Rh antibodies in patients with apparently conventional *RH* alleles may be directed against DONOR partial/altered Rh antigens

Chou et al, 2018, *Blood* 132 and 2013, *Blood* 122; Waldis et al, 2021, *Blood Adv 5;* Noizat-Pirenne 2012, *Transfus Clin Biol* 19; Silvy et al, 2014, *Haematologica* 99; Gaspardi et al. 2014, *Blood Transfus Trasfus Sangue* 14, Sippert et al. 2015, *Blood Transfus Trasfus Sangue* 14 13.

RH variants in donors

- Kirkegaard *et al* (2023, *Transfusion*) investigated C– patient receiving C– units but made anti-C
  - Patient's genotype: *RHD ce / DAU0 ce(48C)*
  - 10 units transfused over prior 6 months were confirmed C– by serology and DNA
- Why did the patient make anti-C?
  - *RH* genotyping found 1 unit transfused 5 weeks prior to anti-C had variant alleles:
    - *DIIIa ceVS.03 / weak partial 4.0 ceVS.02* → **C–**
      - Encoded altered RhD protein may express an epitope similar to C and may have stimulated "anti-C"
    - Patient's plasma reacted stronger with RBCs with same *RH* genotype as donor
  - Clinical significance of the anti-C is unknown

Where do we go from here?

- Patients with partial Rh antigens can make corresponding antibody
- Patients with **no** partial Rh antigens *may* produce antibody to partial Rh antigens in donors
- High-throughout donor testing for *RH* using multiple commercial kits and in-house assays to cover relevant variants is costly and labor and time intensive
  - Therefore, testing is often driven by initial DNA tests that indicate an *RH* variant (i.e., possible homozygous r'^{S}) and focused primarily to donors self-identified as Black that have *RH* diversity similar to that observed in patients with sickle cell disease

Objectives

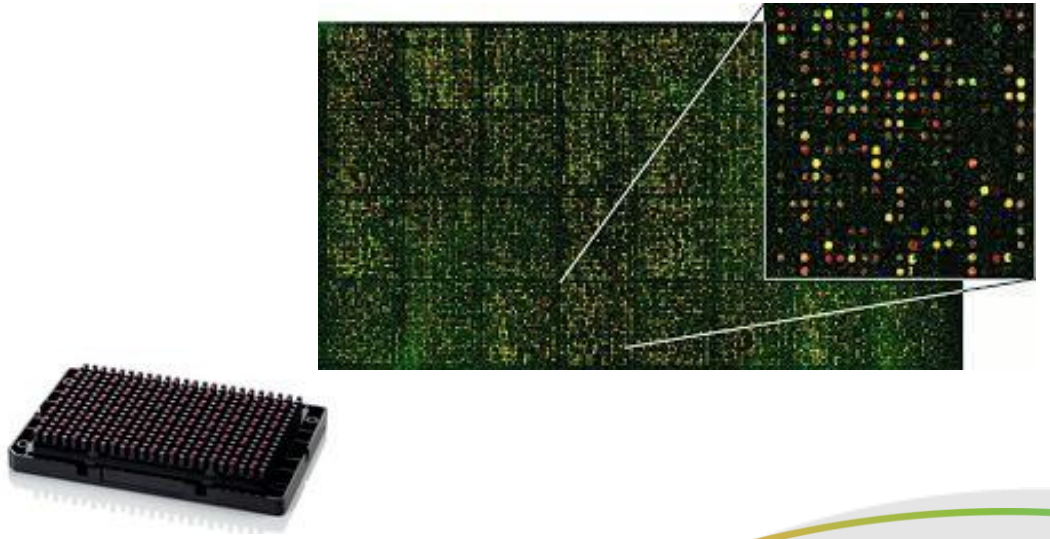
1. Define race and ethnicity and explain guidance for reporting.

2. Describe the use of race and ethnicity in transfusion medicine with focus on blood group differences.

3. **Discuss how expansion of cost effective and comprehensive genotyping methods can reduce reliance on race and ethnicity.**

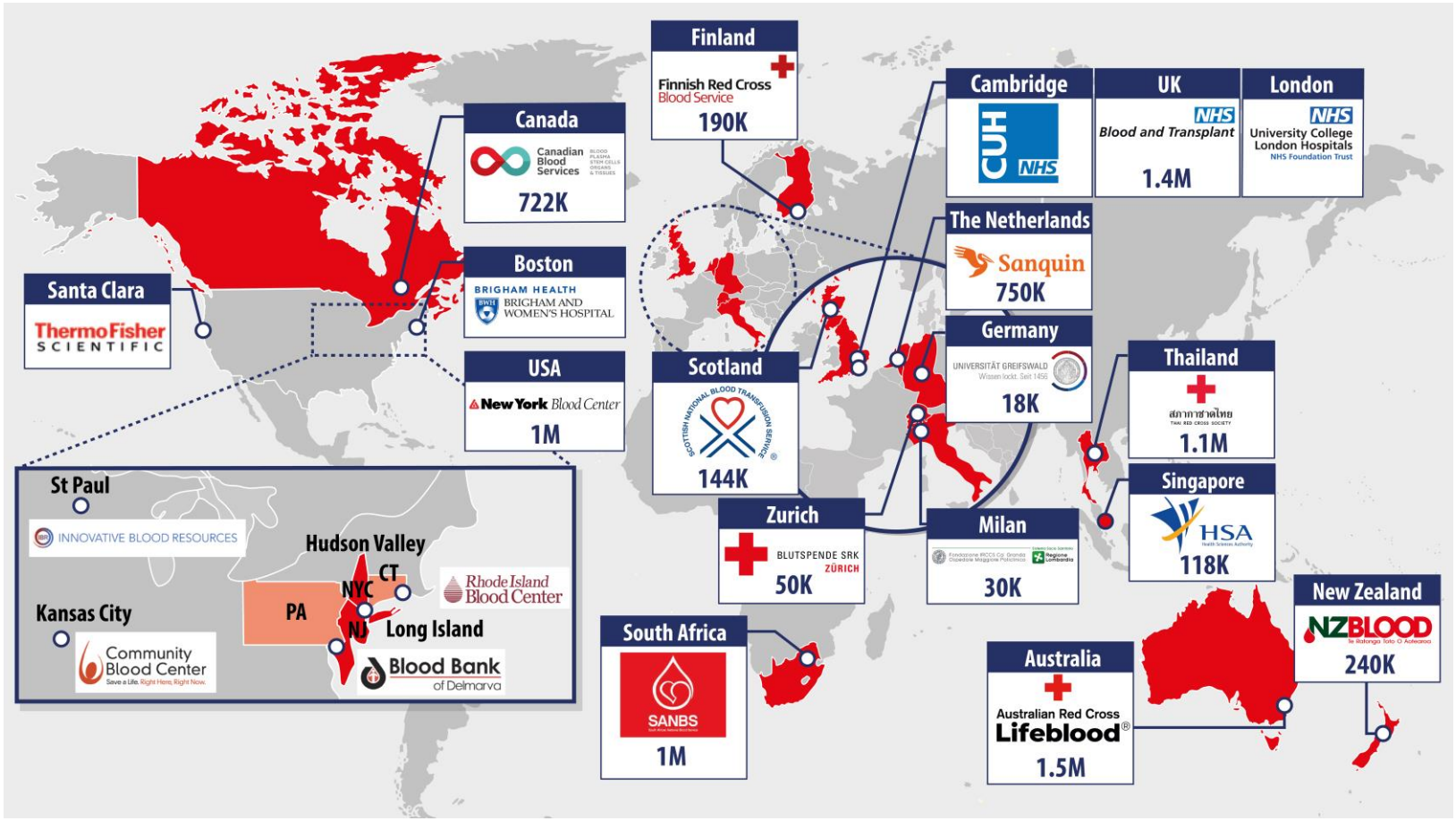
High Density DNA microarray

- Arrays can have few thousand to 1 million probes for variants
- In comparison, only ~25-35 SNVs on most commercial red cell genotyping assays (such as the FDA licensed genotyping platforms).



The Blood transfusion Genomics Consortium (BGC)

brings together a range of skills and expertise to deliver the future of precision transfusion medicine



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Maja Mattle-Greminger	Zurich
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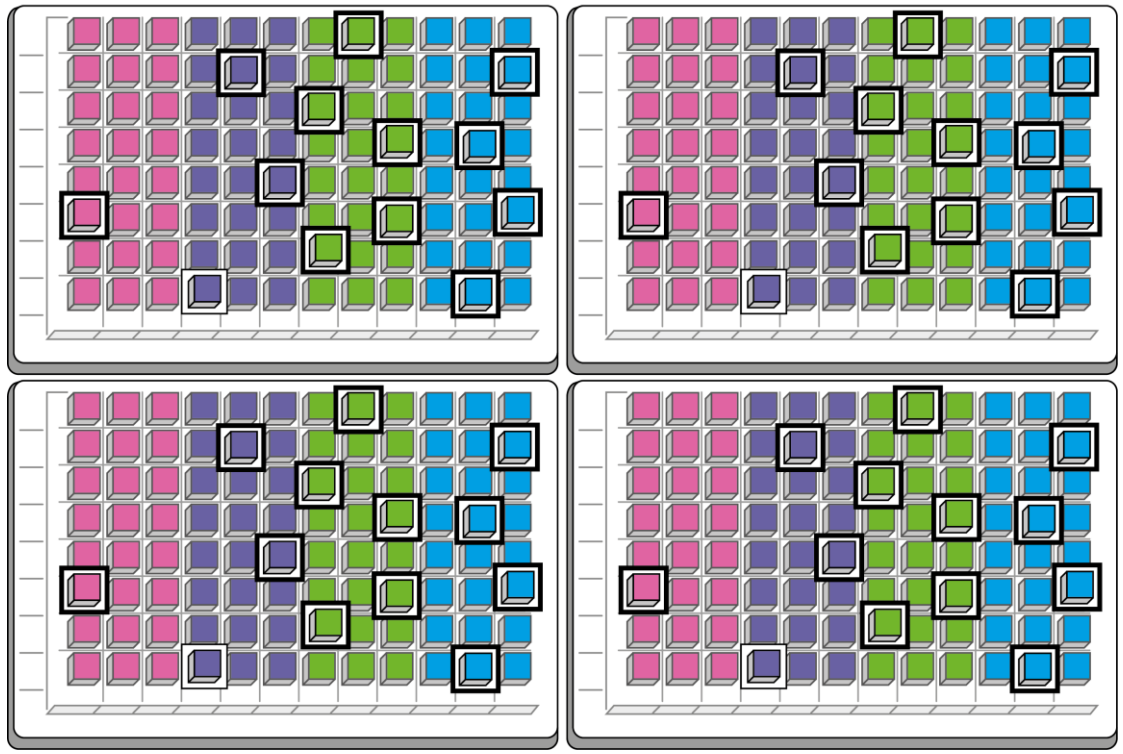
Pawinee Kupatawintu	National Blood Centre of Thailand
Luca Valenti	Milan
Jennifer Laird	Scotland
Ai Leen Ang	Singapore
Founding members: bold; Chair/Dep. Chair: italics	

Custom-designed Axiom™ Array

50,000 DNA variants - 384 samples



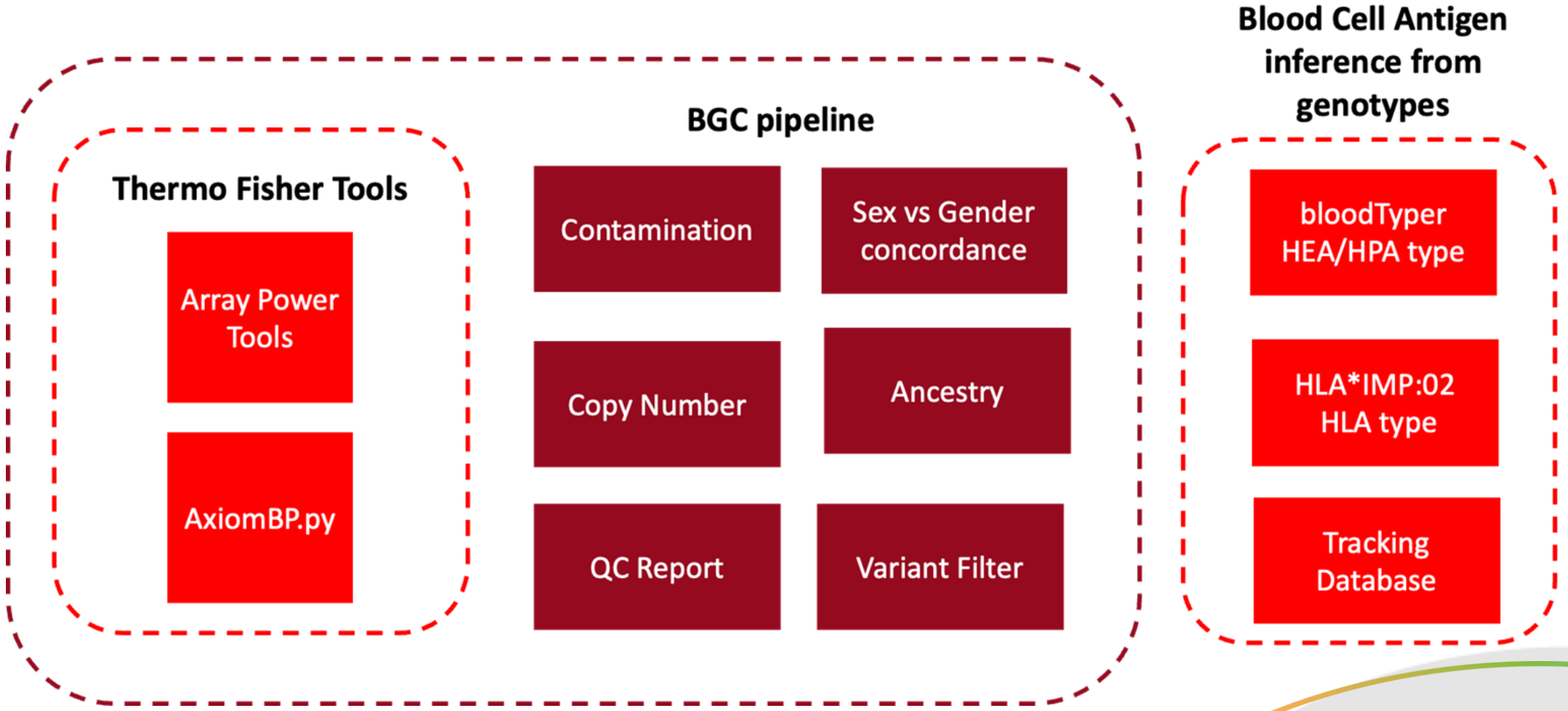
Array Characteristics

- Content enhanced for samples of African ethnicity
- Probes for DNA variants relevant for Transfusion Practice including blood storage and donor health
- The array generates:
  - Blood group typing
  - HLA, HPA and HNA types
  - Product use such as HbS carriers, G6PD

The 384-format: One GeneTitan-MC instrument processes **8 plates/week** generating typing results for **3,008 samples** and 64 QC samples

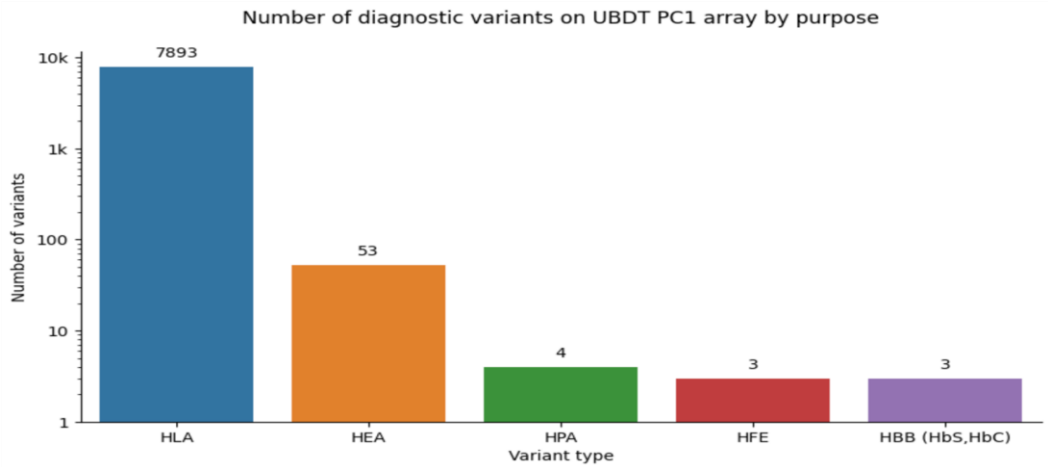
Integrated Analysis Package

used for analysis of GeneTitan CEL files at the BGC-SRCP using a high-performance compute environment



Diagnostic antigens: 53 HEA in 15 blood group systems, HPA1,2,5,15 and HLA

System	Gene	No. variants	Antigens / variants
MNS	*GYPA*	3	M, N
	GYPB	8	S, s, U, Uvar, He
RH	*RHD*	7	D- (Dps/r's), Weak D type 1/2/3, D^{el} (c.1227G>A)
	RHCE	8	C, c, E, e, Cw, Cx, V, VS
LU	*BCAM*	1	Lu(a), Lu(b)
KEL	*KEL*	4	K, k, Kp(a), Kp(b), Kp(c), Js(a), Js(b)
FY	*ACKR1*	3	Fy(a), Fy(b), Fynull, Fyweak
JK	*SLC14A1*	4	Jk(a), Jk(b), Jknull, Jkweak
DI	*SLC4A1*	2	Di(a), Di(b), Wr(a), Wr(b)
YT	*ACHE*	1	Yt(a), Yt(b)
SC	*ERMAP*	1	Sc1, Sc2
DO	*ART4*	3	Do(a), Do(b), Jo(a), Hy
CO	*CO*	1	Co(a), Co(b)
LW	*ICAM4*	1	Lw(a), Lw(b)
CROM	*CD55*	1	CROM1
KN	*CR1*	4	Kn(a), Kn(b), McC(a), McC(b), Yk(a), KCAM, KDAS
VEL	*SMIM1*	1	Vel
		53	



DNA samples and antigen typing data from 13,908 blood donors:

- 74.1% European, 11.4% African, 8.6% Admixed American, 3% South Asian, 1.1% East Asian, 1.9% Other

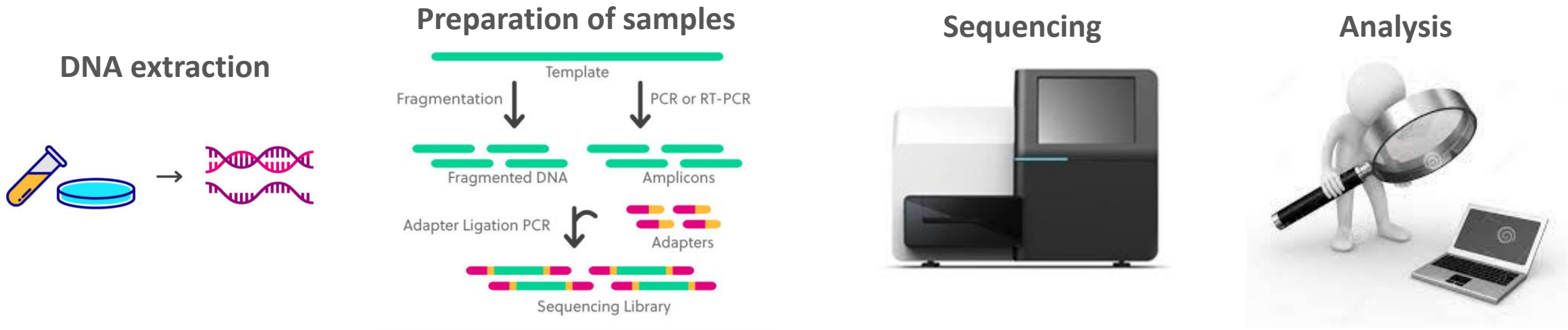
- >99.8% concordance for ~100,000 comparisons between HEA antigen types and array results
  - High accuracy for European and non-European samples

Important to evaluate screening probes:

- Expand variants, including *RH*, that can be detected by array

Targeted next generation sequencing (NGS)

- Similar concept to whole genome and exome next generation sequencing



- Rather than entire genome or exome, focus on *RH*
  - Unlike previously described testing with *RHD* and *RHCE* analysis done separately, target *RHD* and *RHCE* **simultaneously**
  - Cost is significantly less than whole genome or exome sequencing
  - Advantage:
    - interrogates all positions of *RH* regions of interest
    - determine gene/exon copy # helping resolves complex *RH* alleles (ie. hybrids)
  - Useful for genotyping donors **and** patients

High Throughput Genotyping using HemoSelect

- Complete biochemistry panel and bioinformatics workflow to be used for extended red blood cell antigen typing by DNA Analysis for **donor** samples
- Utilizes a novel biochemistry to detect and quantify presence or absence of hundreds of polymorphisms via an amplicon sequencing reaction.

Total assay time: < 1day

1. DNA extraction

2. Assay set up & PCR

3. Sample Indexing

4. Multiplexing and Clean Up

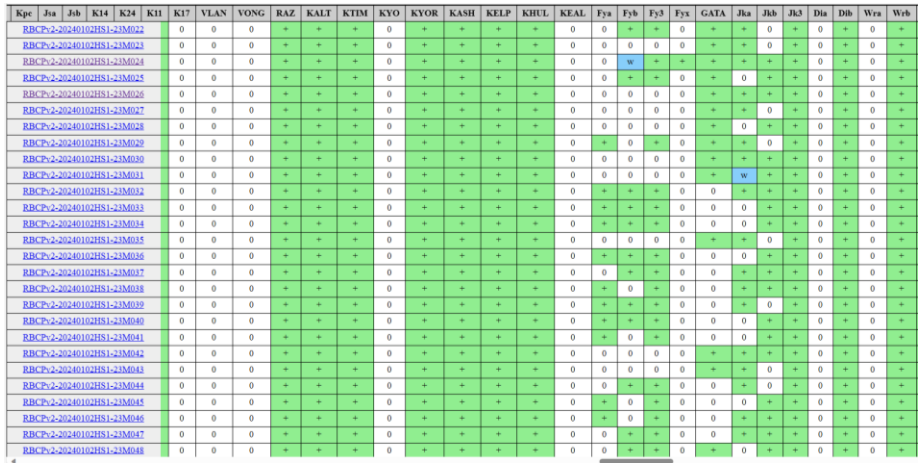
5. Sequencing

6. Analysis

High Throughput Genotyping using HemoSelect

- Interactive html-based visualization

Summary view

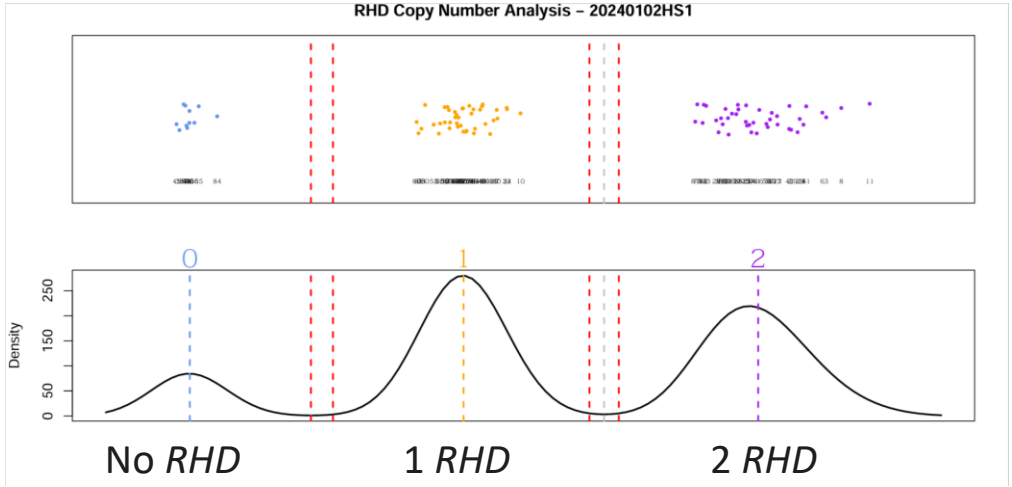


Sample view

RBCPv2-20240102HS1-[redacted]

Group	Genotypes	Phenotypes
ABO	ABO*O.01.01 / ABO*O.01.01	A1:0 A2:0 A3:0 Am:0 Ael:0 cisAB:0 A:0 BA:0 B1:0 B2:0 B3:0 Bel:0 B:0 O1:+ O2:0 O3:0 O5:0 O
MN	GYPA*01 / GYPA*02	M:+ N:+ Mg:0 Mc:0
GypAvar	WildType / WildType	Vw:0 Vr:0 Mta:0 Ria:0 Nya:0 Hut:0 Or:0 ERIK:0 Osa:0 HAG:0 MARS:0 ENEV:+ MNTD:0 SARA:0
SsU	GYPB*04 / GYPB*04	S:0 s:+ U:+ sD:0 Mit:0
GypBvar	NEGATIVE / NEGATIVE	He:0 Mv:0
Mia	NEGATIVE / NEGATIVE	Mia:0
Cc	*	C:* c:+
Ee	RHCE*01 / RHCE*01	E:0 e:+
nt48	RHCE*01 / RHCE*01.01	nt48:+
CENull	Negative / Negative	CENull:0
CEvar1	Negative / Negative	V:0 VS:0 hrB:+ hrS:+ Crawford:0
CEAG	Negative / Negative	CEAG:+
CEvar2	Negative / Negative	STEM:0 CELO:+ Bea:0 LOCR:0 JAL:0 CEST:+ ceHAR:0 CW:0 CX:0 MAR:+ PARG:0 Sec:+ DAK:0
DnegExon1	RHD*01 / RHD*01	DnegExon1:0
DnegExon2	RHD*01 / RHD*01	DnegExon2:0
DnegExon3	RHD*01 / RHD*01	DnegExon3:0
DnegExon4	RHD*01 / RHD*08N.01	DnegExon4:+
DnegExon5	RHD*01 / RHD*01	DnegExon5:0
DnegExon6	RHD*01 / RHD*01N.18	DnegExon6:+
DnegExon7	RHD*01 / RHD*01	DnegExon7:0
DnegExon8	RHD*01 / RHD*01	DnegExon8:0
DnegExon9	RHD*01 / RHD*01	DnegExon9:0

- Quantitative analysis such as for *RH*



Allele view

RBCPv2-20240102HS1-[redacted]

Gene Symbol	ACKR1
Transcript ID	NM_002036.4
Protein ID	NP_002027.2

Antigen Group	Fy

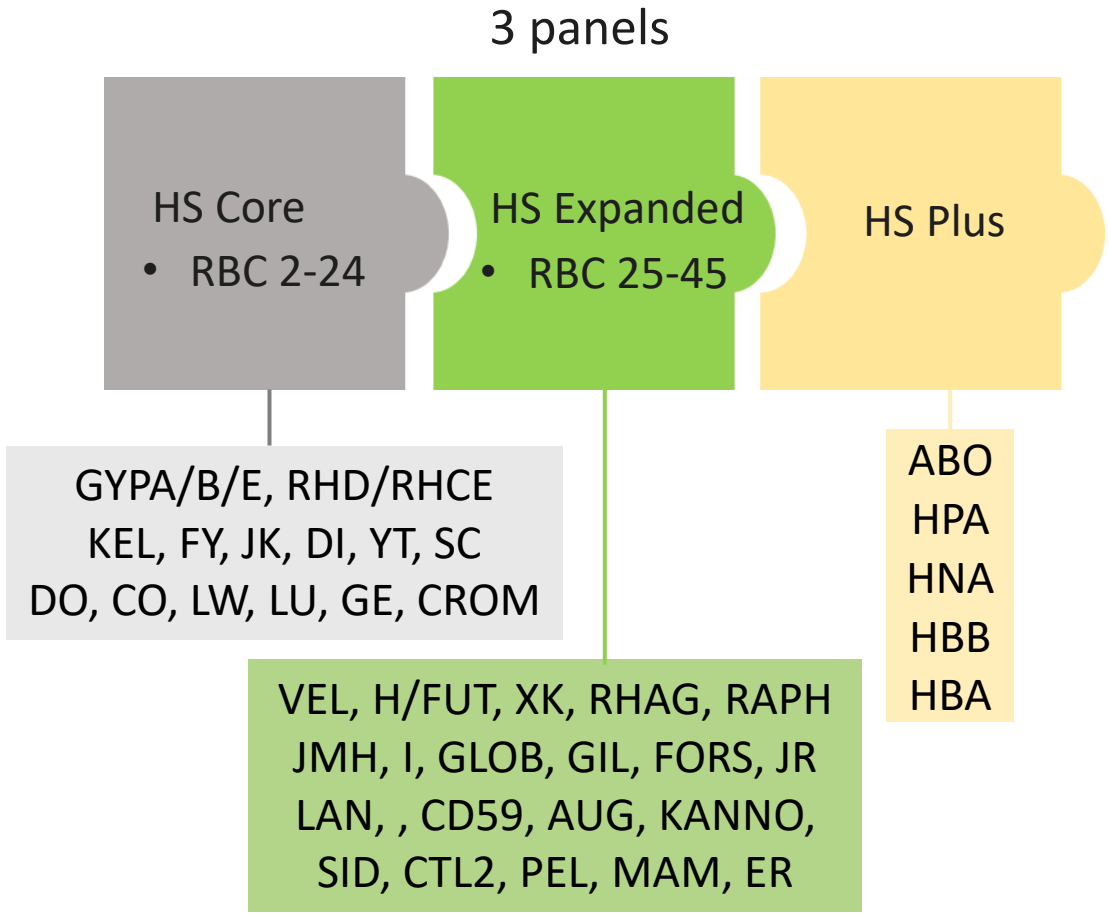
Amplicon	ACKR1ex1		ACKR1ex2																						
cDNA	1-67	1-69	124	125	126	145	151	179	180	214	265	266	327	395	400	407	408								
cDNA (DETECTED)								177	178																
REFERENCE	**T**	**T**	**G**	**G**	**T**	**G**	**T**	**C**	**T**	**G**	**C**	**G**	**C**	**G**	**T**	**G**	**G**	**ISBT**	**Fya**	**Fyb**	**Fy3**	**Fyx**	**GATA**
ALLELE 1	C	T	G	A	T	G	T	C	T	G	C	G	C	G	T	G	G	FY*02N.01	0	0	0	0	+
ALLELE 2	T	T	G	A	T	G	T	C	T	G	T	G	C	G	T	G	G	FY*02W.01	0	w	+	+	0
Predicted Phenotype																			**0**	**w**	**+**	**+**	**+**

Provided by HaploGNX 2024

High Throughput Genotyping using HemoSelect

- Currently, three panels that together provide variants for 45 RBC, platelet and neutrophil systems
  - Some genes: only target exons with known variants

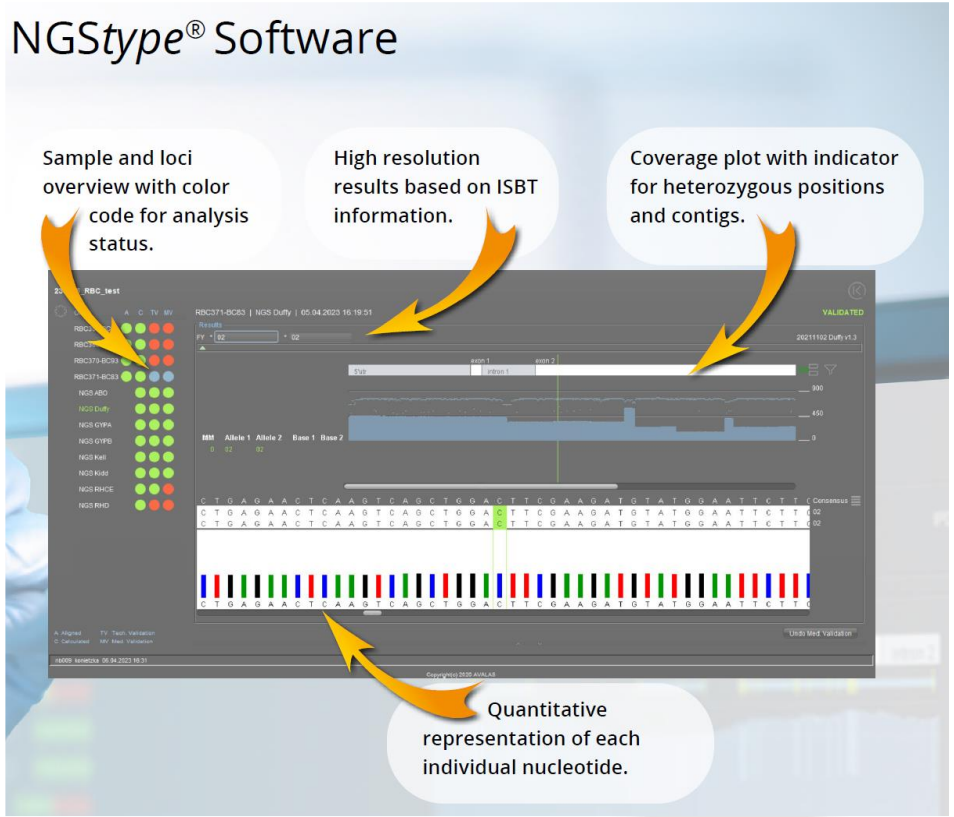
- Interactive html-based visualization by summary view, sample view, and allele view



RBC-NGS*type*® from inno-train

- Currently lists:

	RBC-NGS*type*® CORE	RBC-NGS*type*® enCORE	RBC-NGS*type*® enCORE+
Article No.:	001 110 024	001 120 024	001 130 024
Multiplexes	4	2	2
Available	Yes	Yes	Coming soon
Blood Group Systems	ABO	Lutheran	P1PK
	Rh	Yt	Diego
	MNS	Dombrock	Scianna
	Kell	Colton	Chido/Rodgers
	Kidd	Landsteiner-Wiener	Gerbich
	Duffy	Knops	Cromer
			Indian
			John Milton Hagen
	All exons and relevant non-coding region amplified		Rh-asso. glycoprotein
	Key exons and relevant non-coding region amplified		JR
			LAN



Benefit of High-density Arrays and Targeted NGS

- Obtain a broader and more comprehensive genotype with cost-effective high-density (HS) array and targeted next generation sequencing (NGS) testing
  - Require management of the ‘big’ data
- Provide more precise match of donor products to patients to minimize alloimmunization stimulated by transfusion, particularly chronically transfused patients such as those with sickle cell disease
- Identify uncommon and rare phenotypes and uncommon antigen combinations to:
  - improve inventory of panel cells to aid in serologic antibody identification
  - potentially have liquid units available without resorting to frozen units

In closing

- Lower costs of these NGS and HS arrays will hopefully lessen the reliance on self-identified race and ethnicity as factor in determining which donors to further genotype and when investigating typing discrepancies or identifying antibodies to high prevalence antigens.

- Race and ethnicity information is still useful and improves our understanding of the diversity of populations and factors impacting alloimmunization risk

- Mindful that race and ethnicity are imperfect indicators of genetic composition

Acknowledge

NYBC Genomics Lab:

Kim Hue-Roye

June Fuertes

Mohammad Alam

Anthony Huang

Emily Mapes

Shaimaa Makrm

Nyya Waring-Yaoda

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NYBCe NCBGG Genomics Lab:

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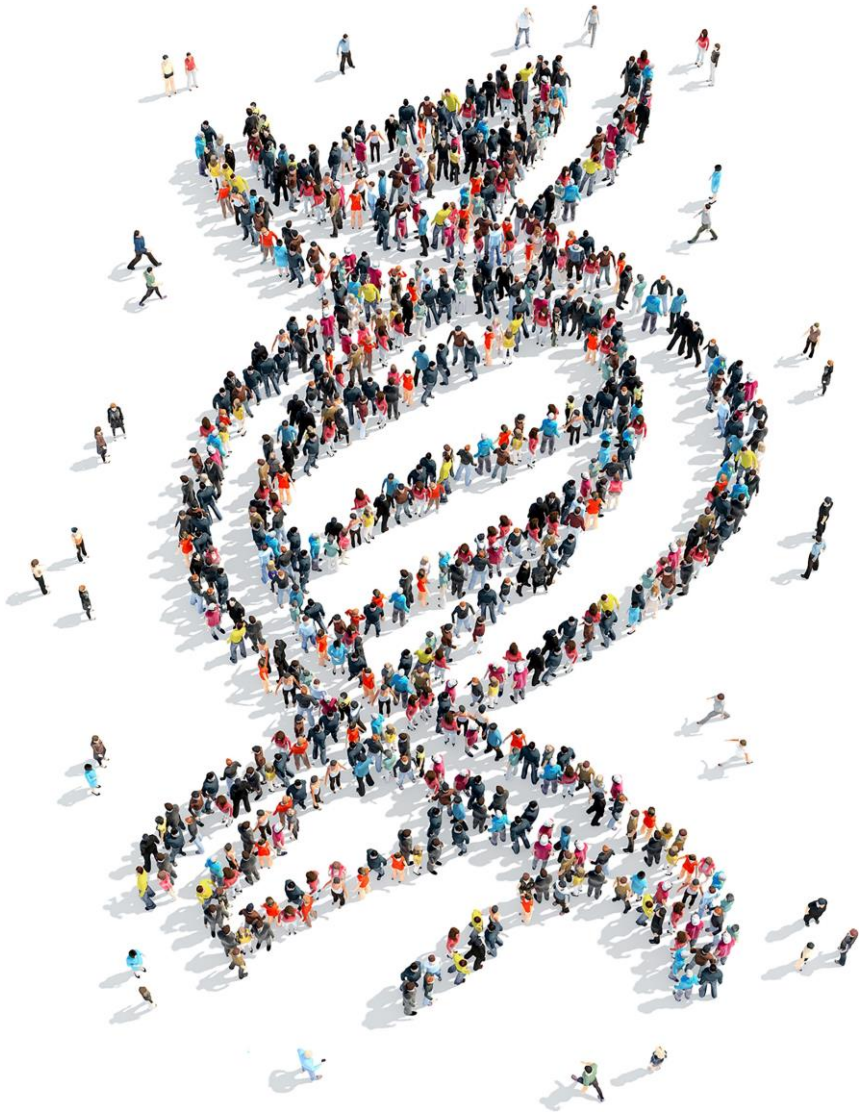
All the NYBCe Immunohematology Reference Labs

Thank you!



https://www.pnas.org/doi/full/10.1073/pnas.2203033119