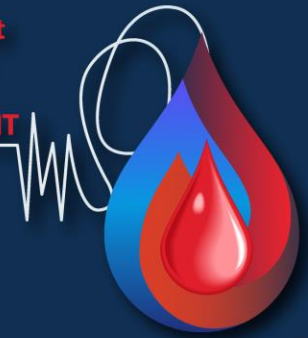


12

Congreso Colombiano **Acobasmet**
de Bancos de Sangre y Medicina
Transfusional
Congreso Iberoamericano **GCIAMT**

*Nuevamente juntos, innovando
para fortalecer capacidades*

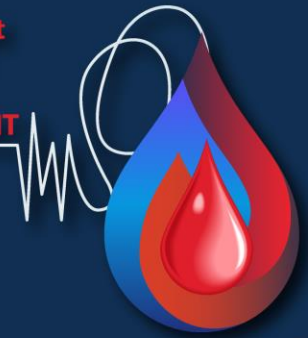


Nuevas tecnologías detección emergentes

12

Congreso Colombiano **Acobasmet**
de Bancos de Sangre y Medicina
Transfusional
Congreso Iberoamericano **GCIAMT**

*Nuevamente juntos, innovando
para fortalecer capacidades*

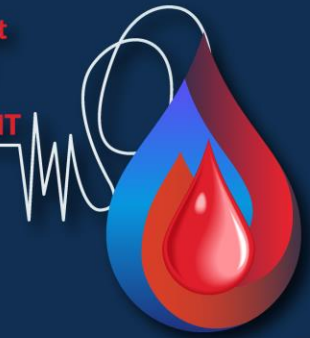


POTENCIAL CONFLICTO DE INTERESES:

En los últimos 2 años recibí honorarios por conferencias de las empresas Roche y Grifols.

12

Congreso Colombiano **Acobasmet**
de Bancos de Sangre y Medicina
Transfusional
Congreso Iberoamericano **GCIAMT**
*Nuevamente juntos, innovando
para fortalecer capacidades*



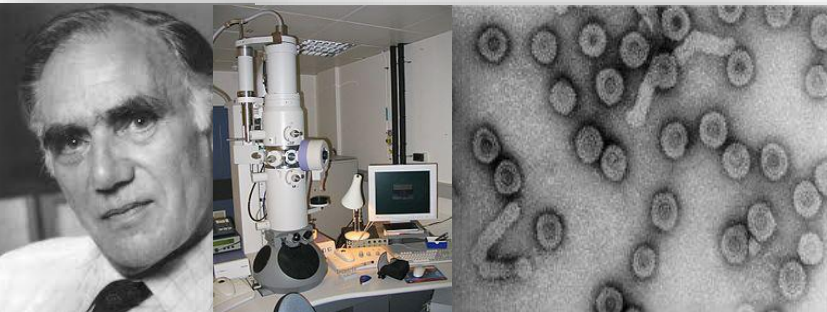
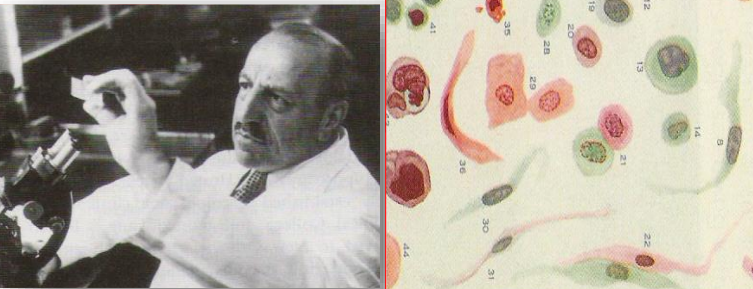
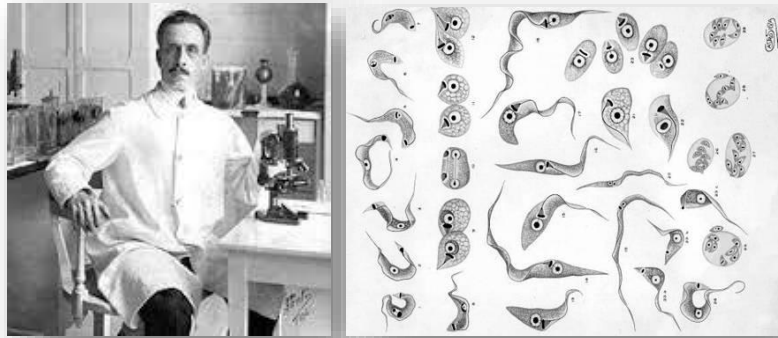
Ponente: José Eduardo Levi

- Biólogo
- Doctor en Virología
- Investigador del Instituto de Medicina Tropical de la Universidad de São Paulo, Brasil
- Superintendente de Investigación y Desarrollo de la red Dasa
- Director Regional América Latina, Sociedad Internacional de Transfusión Sanguínea (ISBT), 2022-2024

EVOLUCIÓN DE LAS PRUEBAS PARA ENFERMEDADES INFECCIOSAS

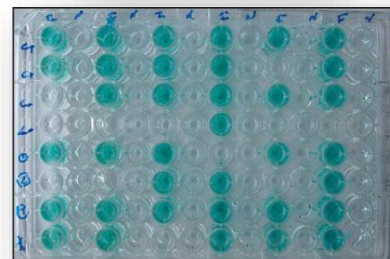
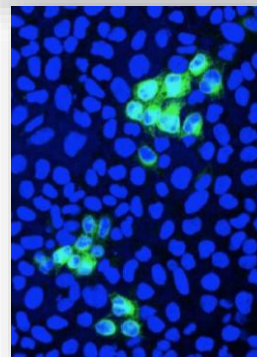
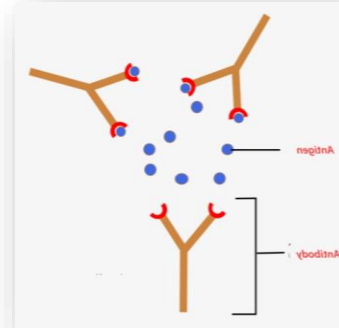
Hasta 1950

MICROSCOPIA



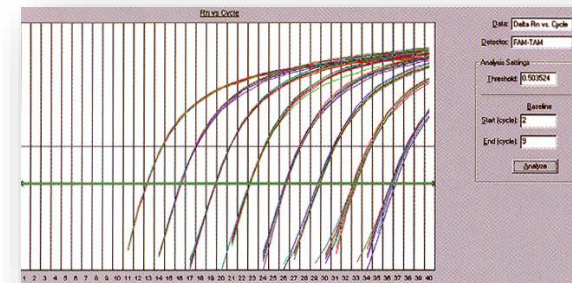
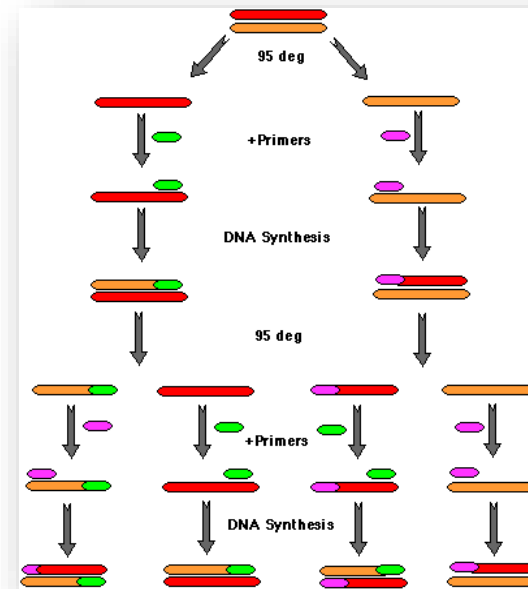
1960-2000

SEROLOGÍA



2001-2025

NAT



2025-?

NGS



Cost per Genome



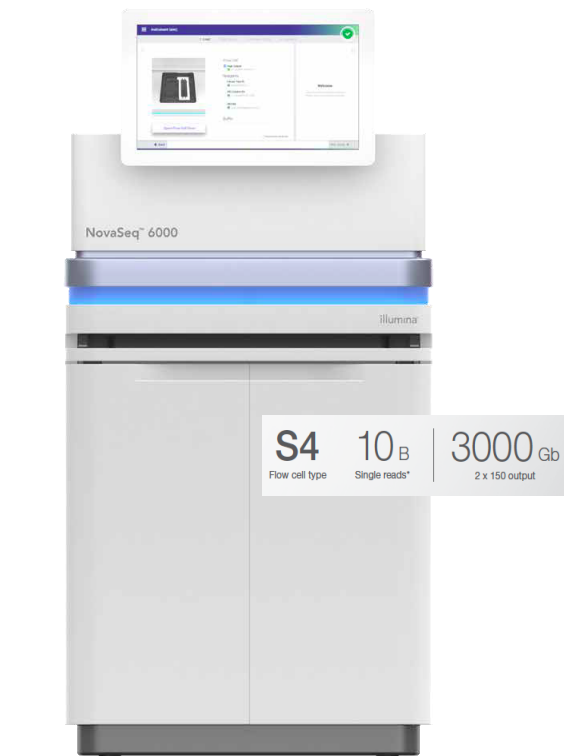
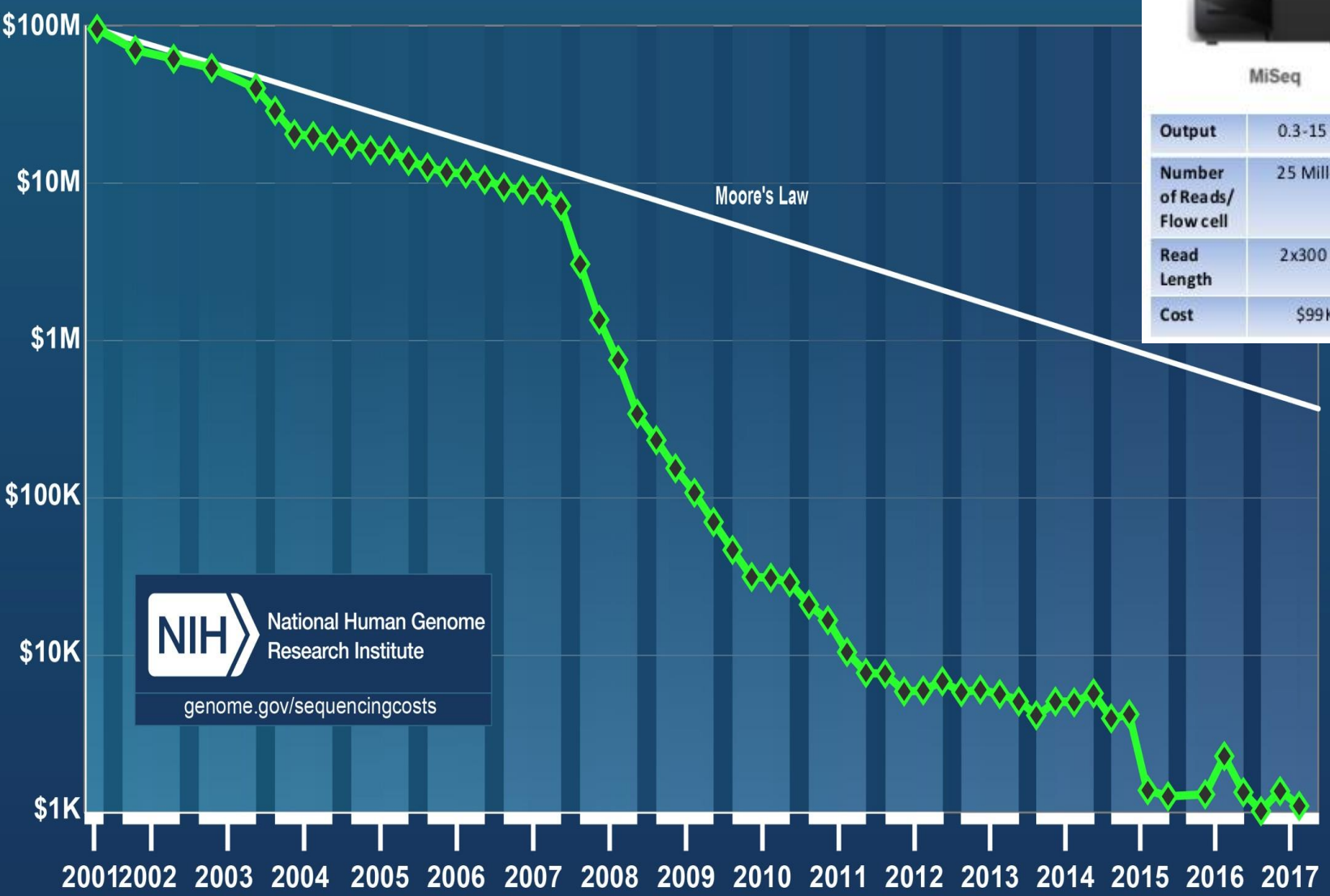
MiSeq

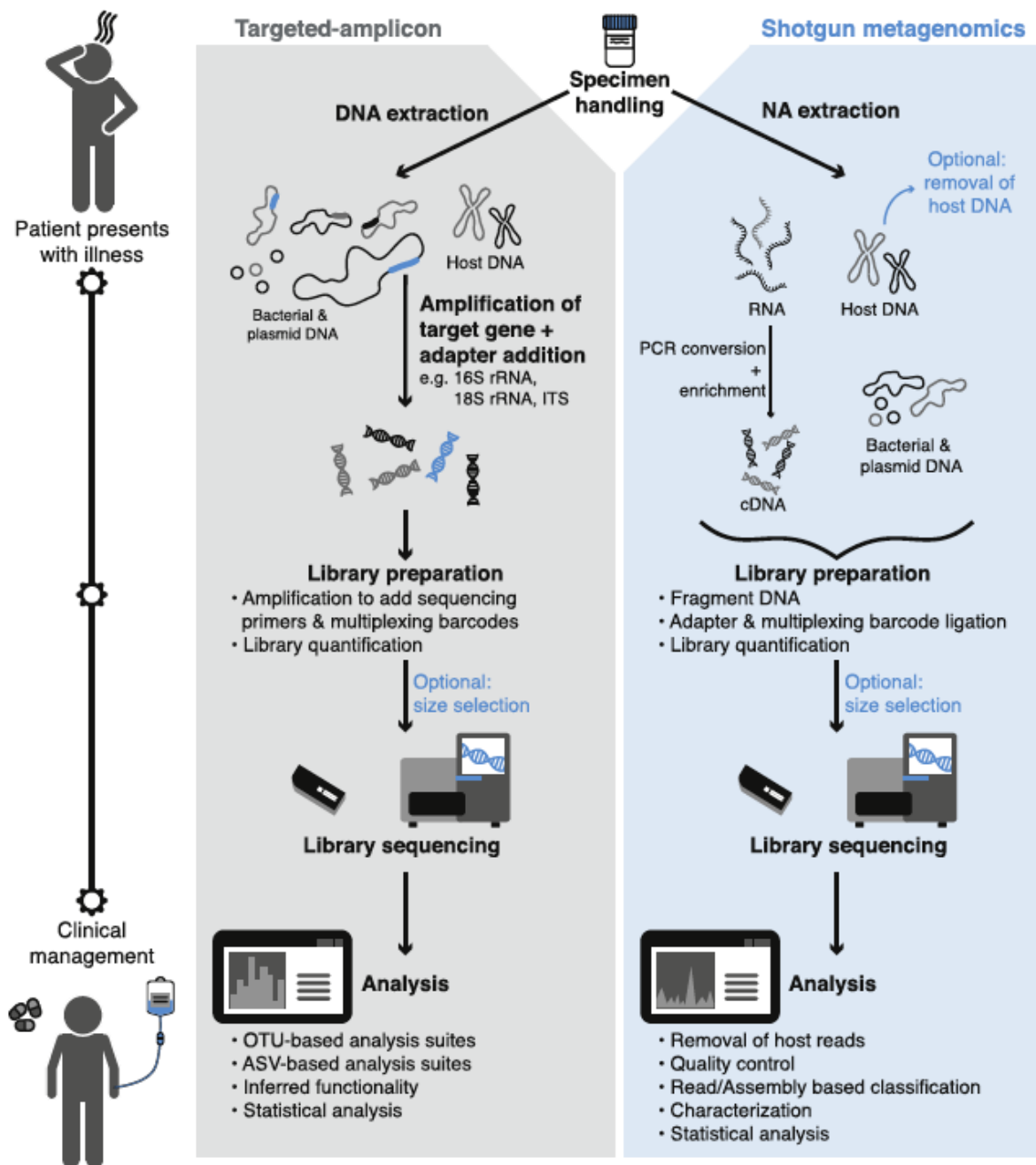
NextSeq 500

2500
HiSeq 3000
4000

HiSeq X Ten

Output	0.3-15 Gb	20-120 GB	10-1500 GB	900-1800 GB
Number of Reads/ Flow cell	25 Million	130-400 Million	300 million – 2.5 Billion	3 Billion
Read Length	2x300 bp	2x150 bp	2x250 - 2x125 bp	2x150 bp
Cost	\$99K	\$250K	\$740K	\$10M (10 units)

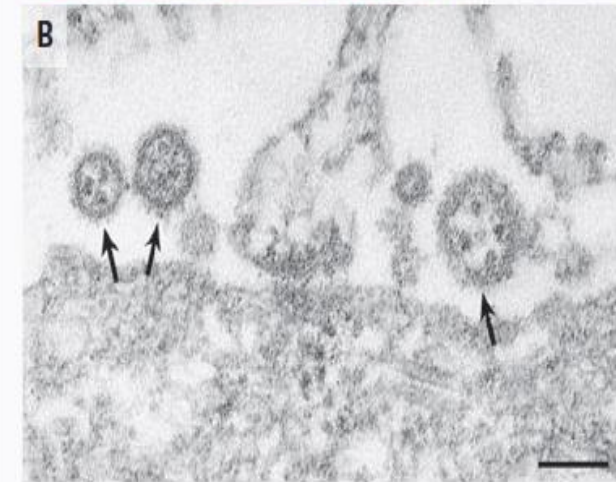
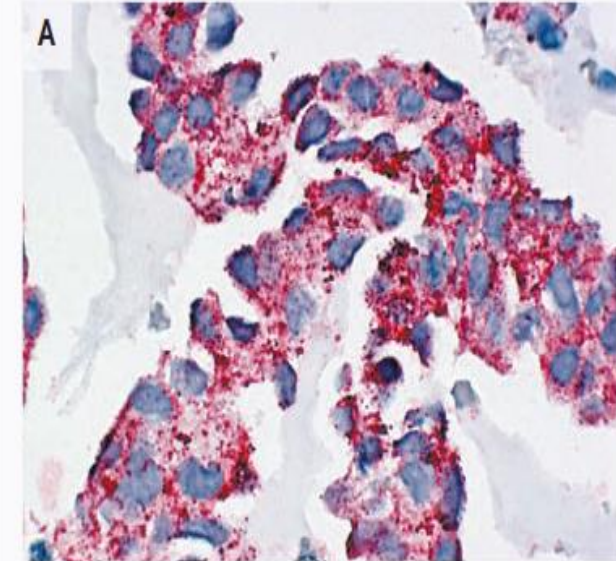
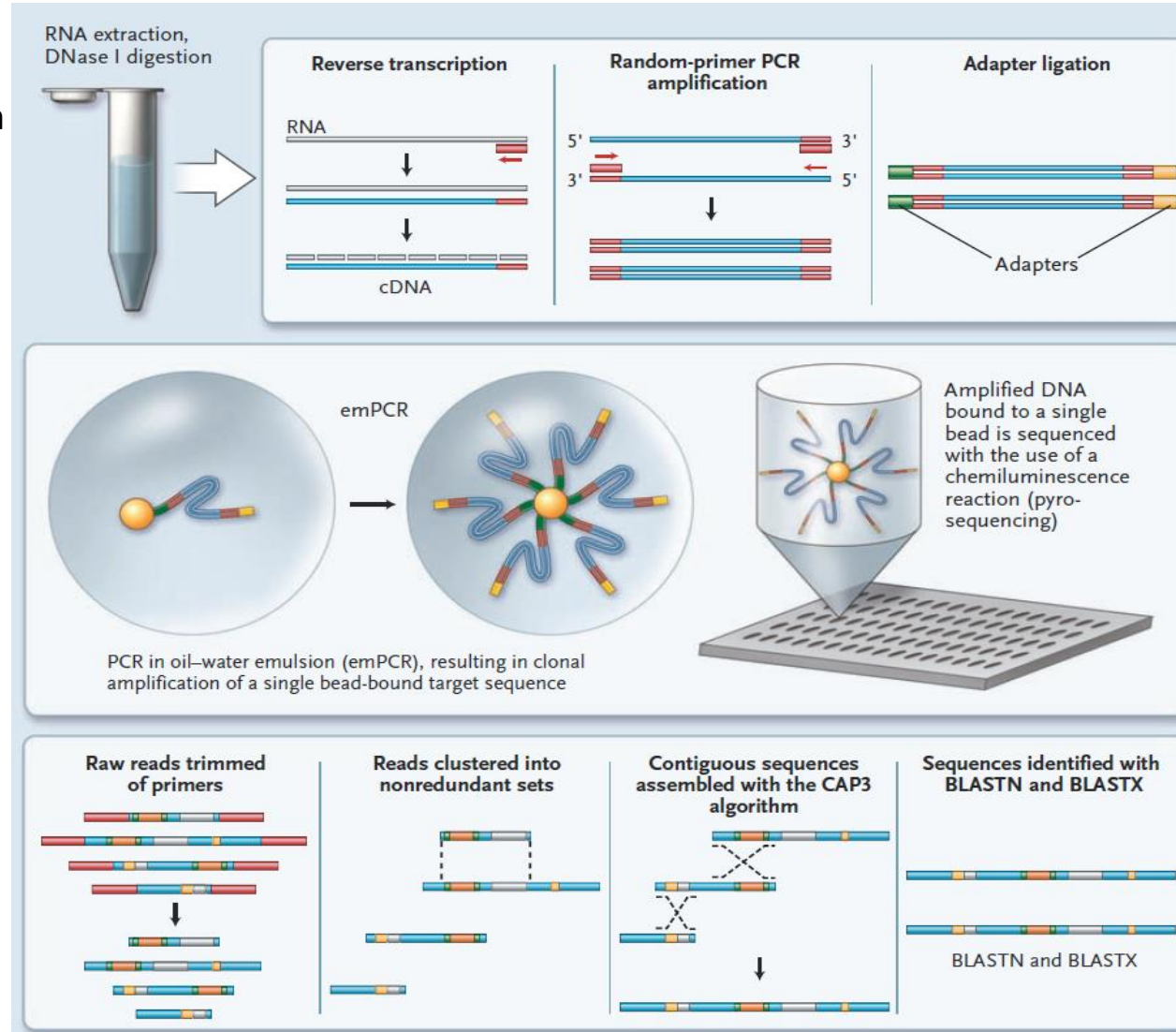




A New Arenavirus in a Cluster of Fatal Transplant-Associated Diseases

N Engl J Med 2008;358:991-8.

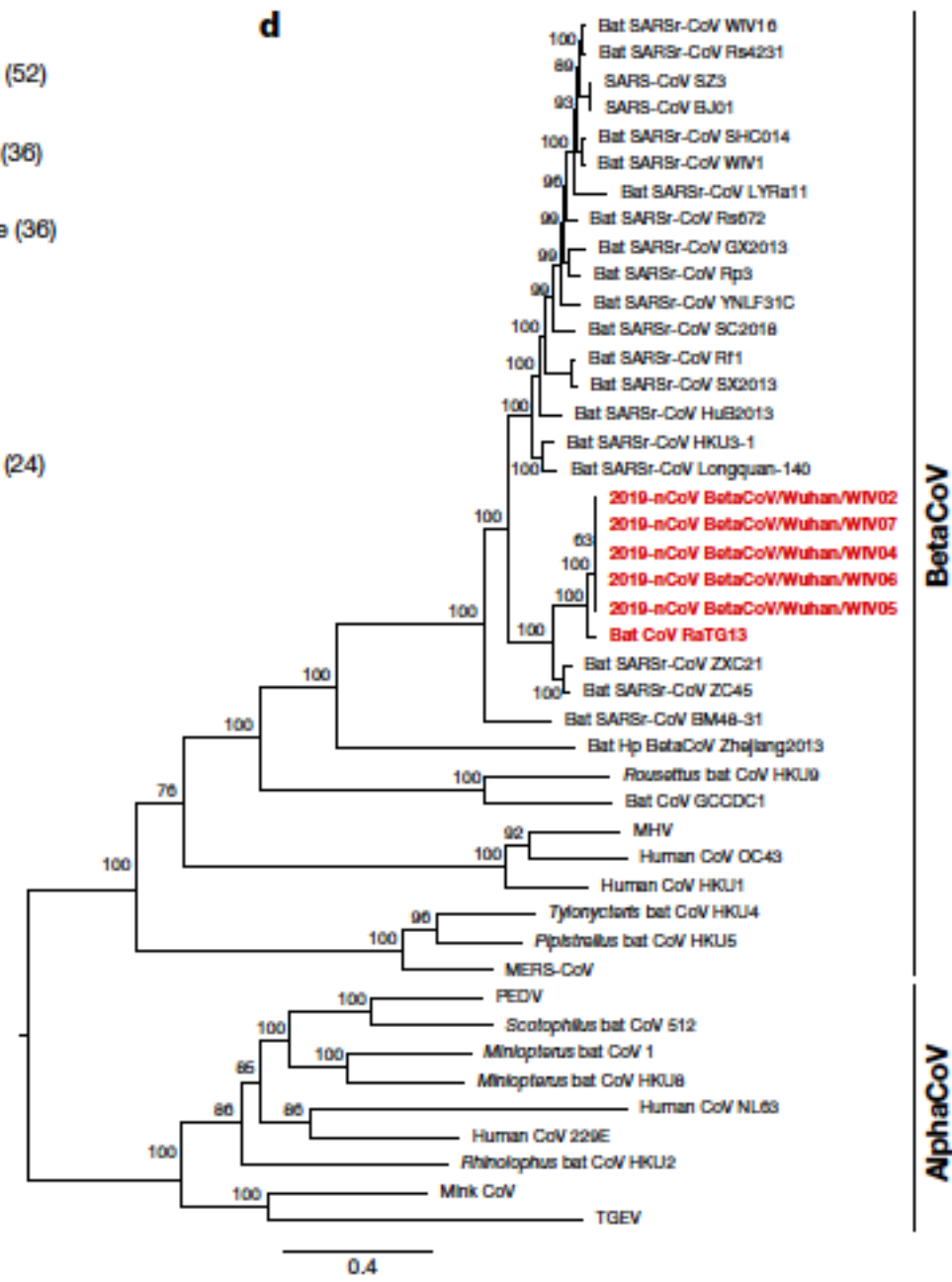
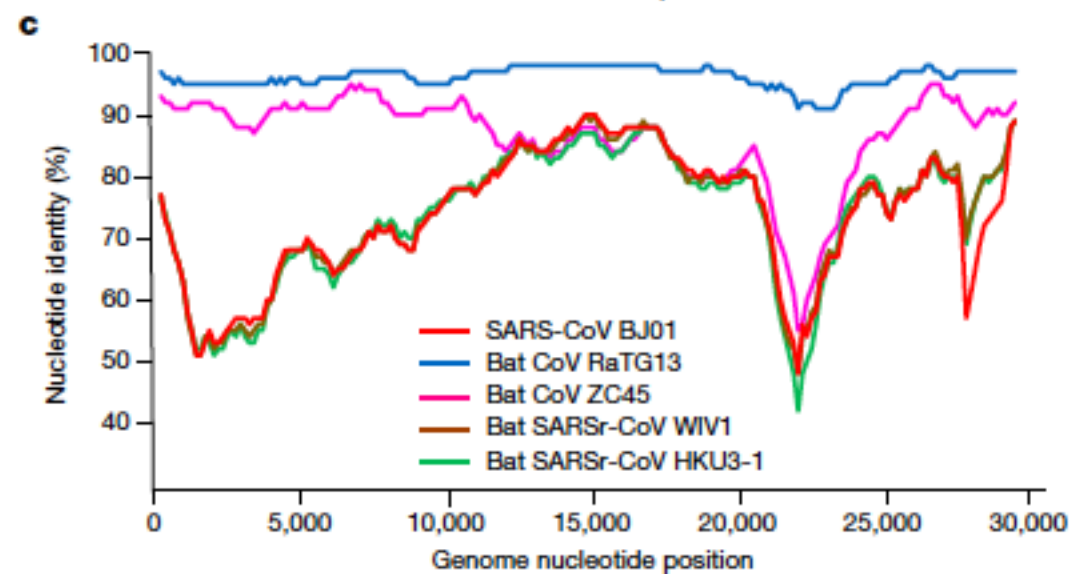
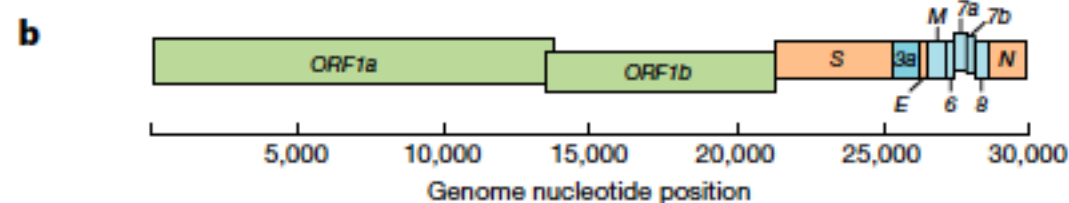
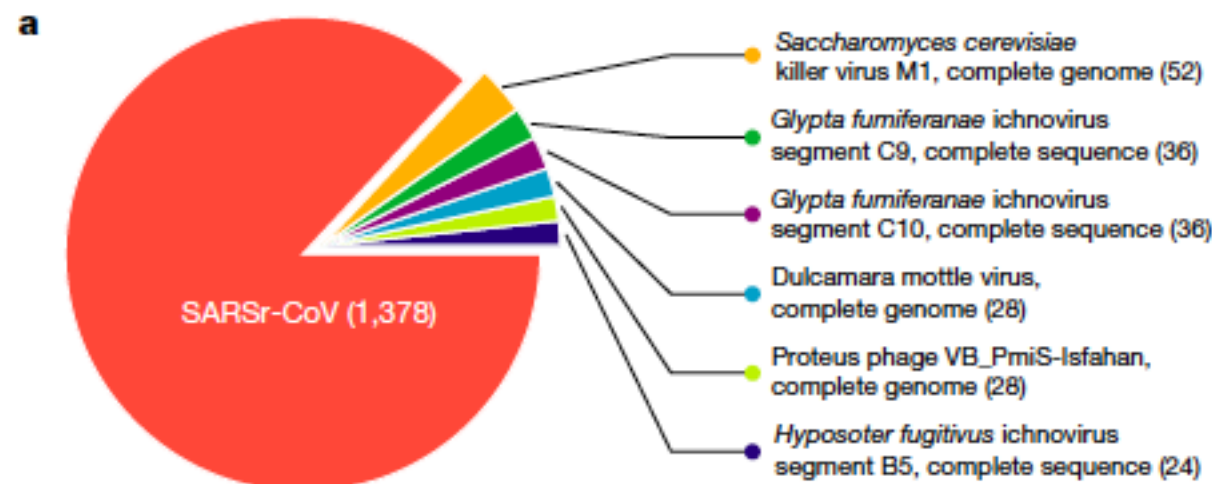
Bacterial and viral cultures; polymerase-chain-reaction (PCR) assays for herpesviruses 1 through 8, lyssavirus, influenza A and B viruses, respiratory syncytial virus, picornavirus, adenovirus, human parainfluenzavirus, flavivirus, alphavirus, hantavirus, polyomavirus, Crimean–Congo hemorrhagic fever virus, Rift Valley fever virus, toxoplasma, Mycobacterium tuberculosis, and Mycoplasma pneumoniae; and viral and panmicrobial oligonucleotide microarray analysis revealed no candidate pathogens



High-throughput sequencing yielded 103,632 sequences, of which 14 represented an Old World arenavirus.

A pneumonia outbreak associated with a new coronavirus of probable bat origin

Nature | Vol 579 | 12 March 2020



Shotgun metagenomic sequencing of the first case of monkeypox virus in Brazil, 2022

Ingra Morales Claro^{1,2}, Camila Malta Romano¹, Darlan da Silva Candido^{1,2,3}, Evelyn Lepka de Lima⁴, José Angelo Lauletta Lindoso^{1,4,5}, Mariana Severo Ramundo¹, Filipe Romero Rebello Moreira^{2,6}, Luiz Alberto Costa Barra⁴, Luciana Marques Sansão Borges⁴, Lucas Alberto Medeiros⁴, Marcia Y. S. Tomishige⁴, Tomas Moutinho⁵, Anderson José Dias da Silva⁴, Camila Cristina Martini Rodrigues⁴, Luiz Cesar Fernandes de Azevedo⁴, Lucy Santos Villas-Boas¹, Camila Alves Maia da Silva¹, Thaís Moura Coletti¹, Erika R. Manuli¹, Aine O'Toole⁷, Joshua Quick⁸, Nicholas Loman⁸, Andrew Rambaut⁷, Nuno R. Faria^{1,2,3}, Claudia Figueiredo-Mello⁴, Ester Cerdeira Sabino¹

REVISTA
DO
INSTITUTO
DE
MEDICINA
TROPICAL
DE
SÃO PAULO
JOURNAL OF THE SÃO PAULO
INSTITUTE OF TROPICAL MEDICINE



PLASMA= ORO LIQUIDO

PETRÓLEO

- **Fracionado em diversos subprodutos**
- **Produção anual: 16 bilhões de barris (1 barril ~ 200 litros)**
- **Maior Produtor: OPEP**
- **Mercado Anual: US 500 bilhões**
- **Preço do Barril de Petróleo Bruto: US 25**
- **Valor dos Derivados contidos em um barril de petróleo: US 45**

PLASMA

- **Fracionado em diversos subprodutos**
- **Produção anual: 61 milhões de litros**
- **Maior Produtor: EUA**
- **Mercado Anual: US 20 bilhões**
- **“Preço” do Barril de Plasma “Bruto”: US 16.000**
- **Valor dos hemoderivados contidos em um barril de plasma: US 70.000**

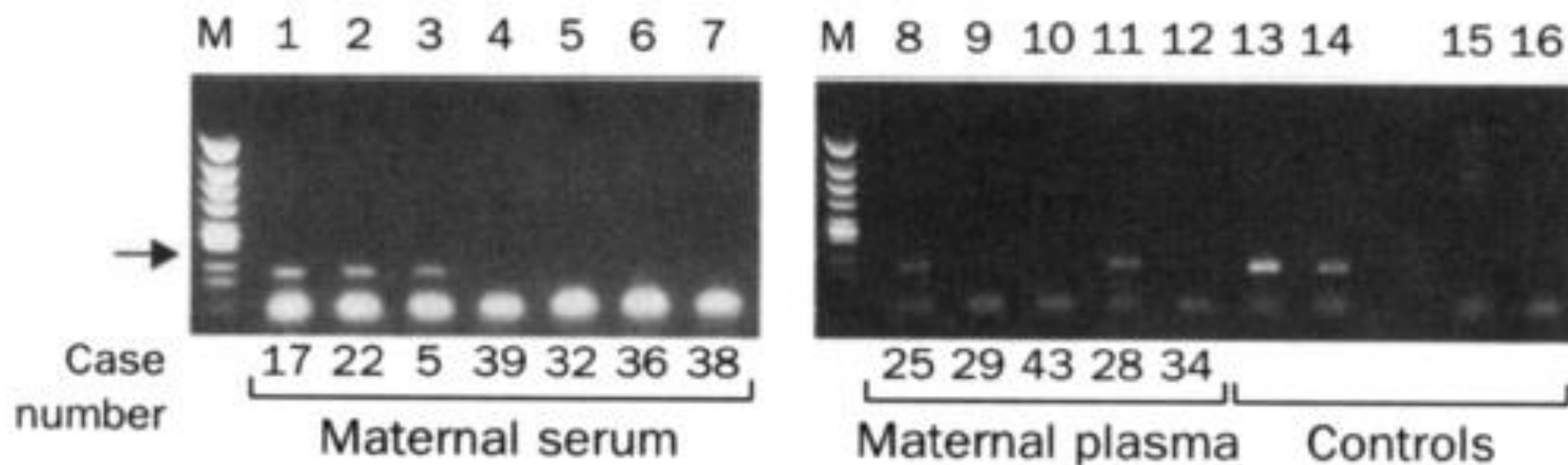


MINISTERIO DA SALUD BRASIL, GASTOS COM HEMODERIVADOS

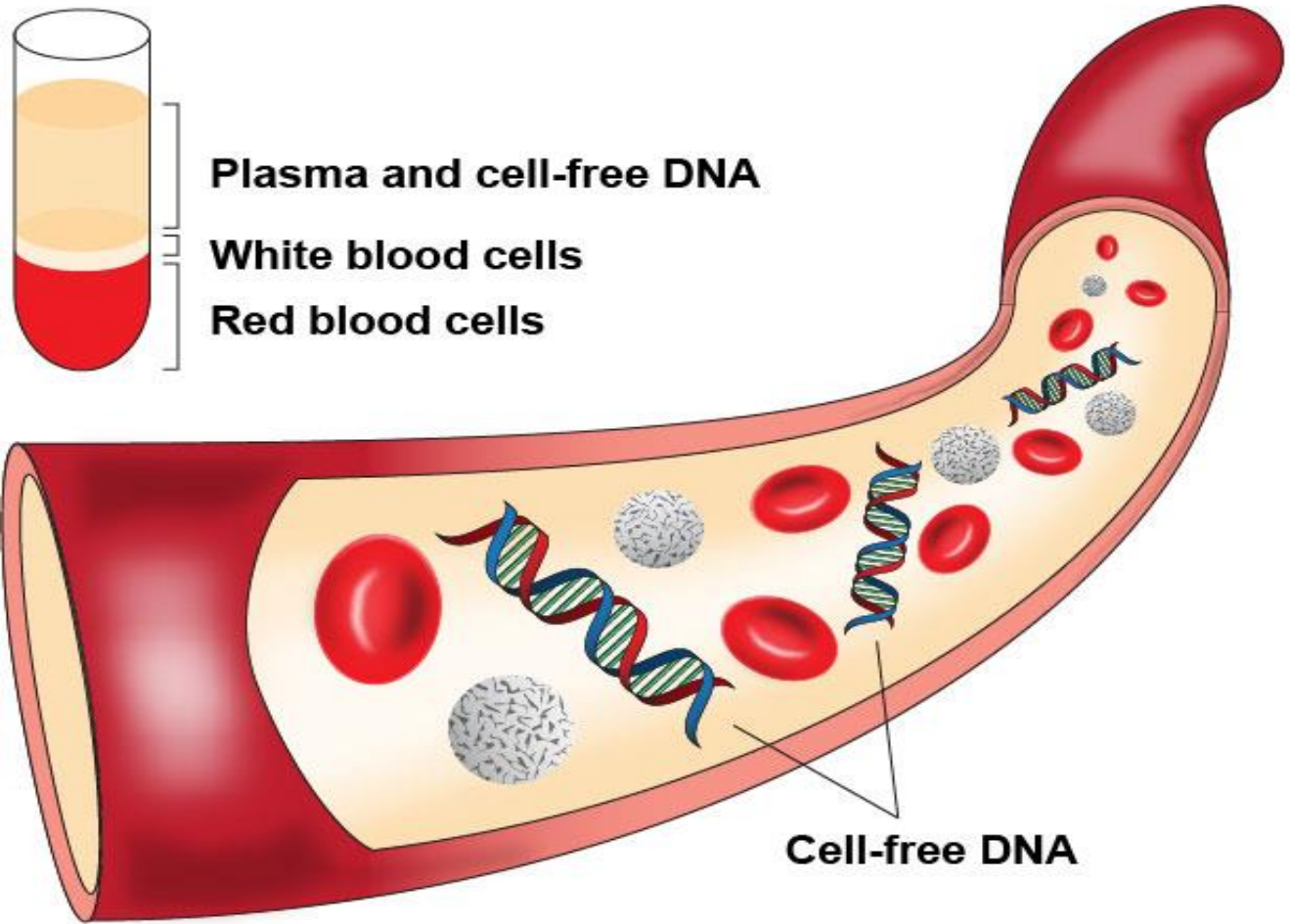
Produto	Valores (R\$)	Quantidades	Valor por unidade
Albumina			
Imunoglobulina	310.408.110,00	679.230	R\$ 457,00
Fator VIII Recomb	441.000.000,00	525.000.000	R\$ 0,84
Complexo protrombinico humano parc.ativ.	253.219.920,00	121.000.000	R\$ 2,09
Fator VII Recombi	142.543.980,00	3.400.000	R\$ 41,92
Fator VIII Plasmatico	62.085.000,00	195.000.000	R\$ 0,32
Fator VIII associado a Von Willebrand	35.032.500,00	75.000.000	R\$ 0,47
Fator IX	56.922.325,00	110.750.000	R\$ 0,51
Fator VIII para doença Von Willebrand	23.250.000,00	37.500.000	R\$ 0,62
Complexo protrombinico humano	1.690.875,00	3.750.000	R\$ 0,45
Concentrado de Fator I	640.637,00	618	R\$ 1.036,63
Fator VIII 250 UI	287.000,00	350.000	R\$ 0,82
TOTAL	1.327.080.347,00		

APROX. 250 MILLONES DE US DÓLARES/AÑO

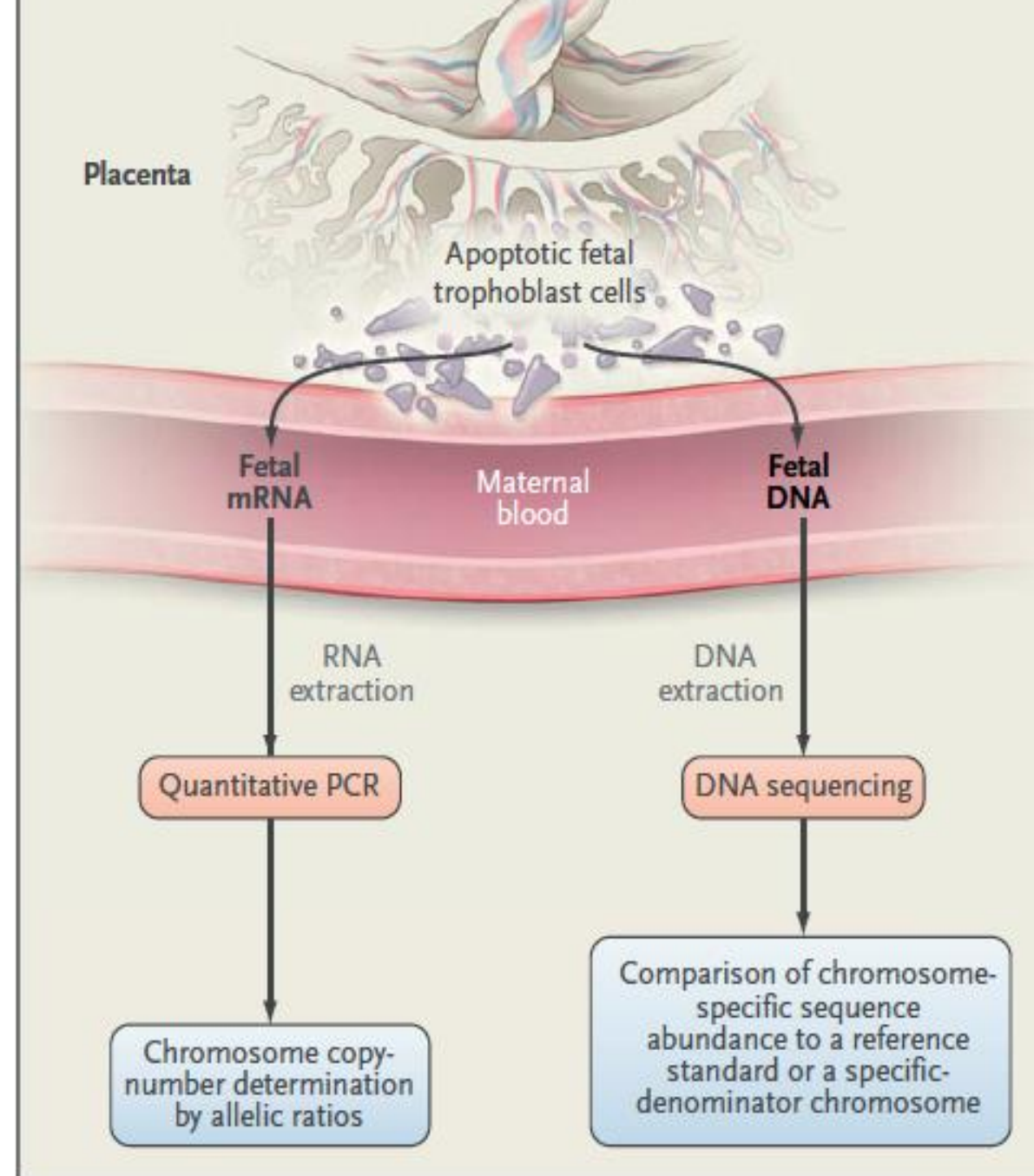
Early report

Lancet 1997; 350: 485–87**Presence of fetal DNA in maternal plasma and serum***Y M Dennis Lo, Noemi Corbetta, Paul F Chamberlain, Vik Rai, Ian L Sargent, Christopher W G Redman, James S Wainscoat***Amplification of fetal Y-chromosomal sequences from maternal plasma and serum**

FETAL CELL FREE DNA (cfDNA)



N Engl J Med 2012;366:64-73.



Maternal Plasma DNA Sequencing Reveals the Genome-Wide Genetic and Mutational Profile of the Fetus

www.ScienceTranslationalMedicine.org 8 December 2010 Vol 2 Issue 61 61ra91

Y. M. Dennis Lo,^{1,2*} K. C. Allen Chan,^{1,2} Hao Sun,^{1,2} Eric Z. Chen,^{1,2} Peiyong Jiang,^{1,2} Fiona M. F. Lun,^{1,2} Yama W. Zheng,^{1,2} Tak Y. Leung,³ Tze K. Lau,³ Charles R. Cantor,⁴ Rossa W. K. Chiu^{1,2}

FETAL CELL FREE DNA (cfDNA)

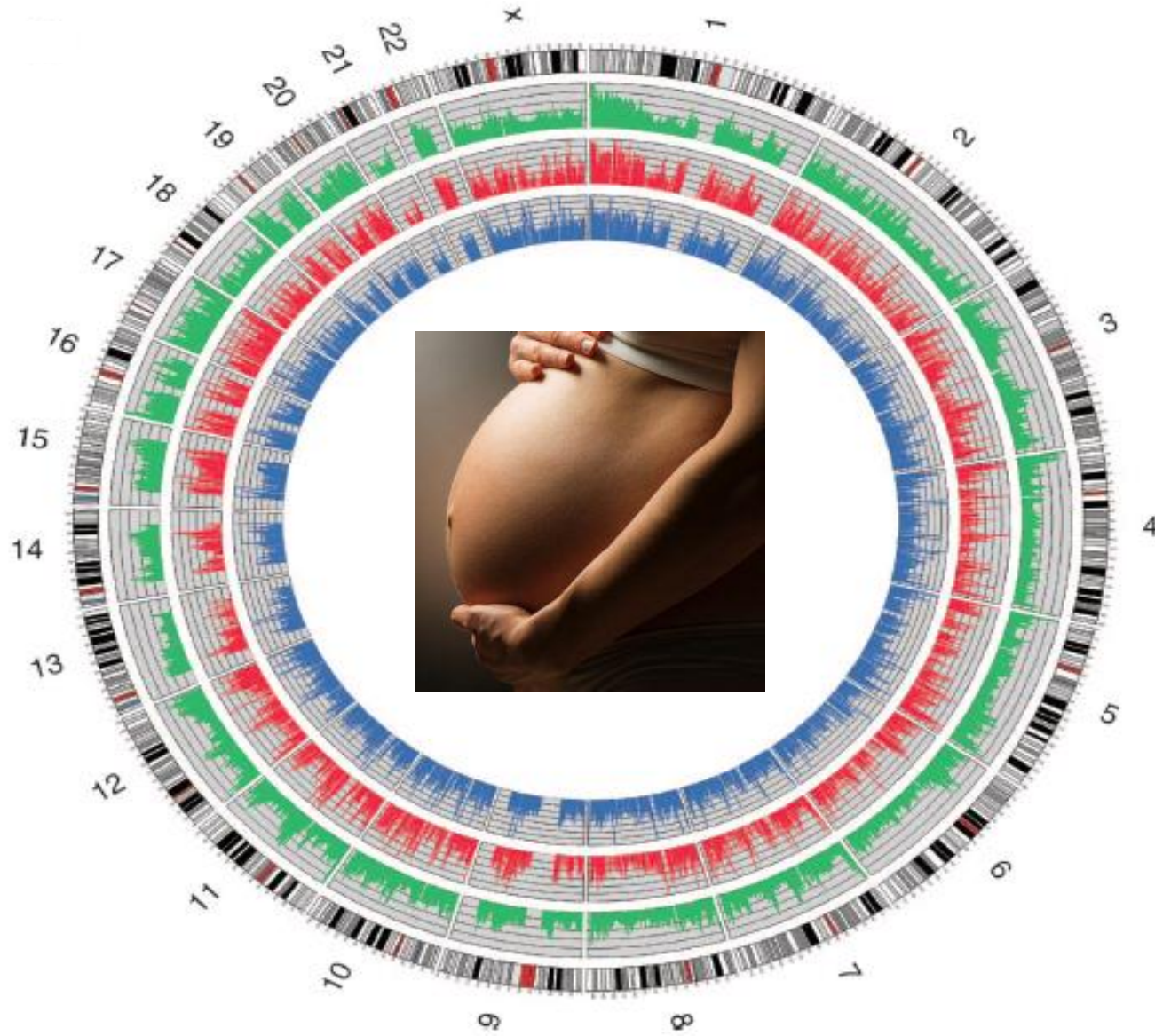


Table 1. Fractional concentrations of fetal DNA calculated based on the analysis of category 1 SNPs for different chromosomes.

Chromosome	Fetal DNA concentration (%)
1	11.57
2	11.57
3	11.59
4	11.49
5	11.66
6	11.43
7	11.49
8	11.53
9	11.51
10	11.36
11	11.51
12	11.41
13	11.47
14	11.38
15	11.07
16	11.08
17	11.17
18	11.60
19	11.55
20	11.33
21	10.87
22	11.19
X	11.10
Whole genome	11.43



Cell-free DNA Analysis for Noninvasive Examination of Trisomy

N Engl J Med 2015;372:1589-97.

DOI: 10.1056/NEJMoa1407349

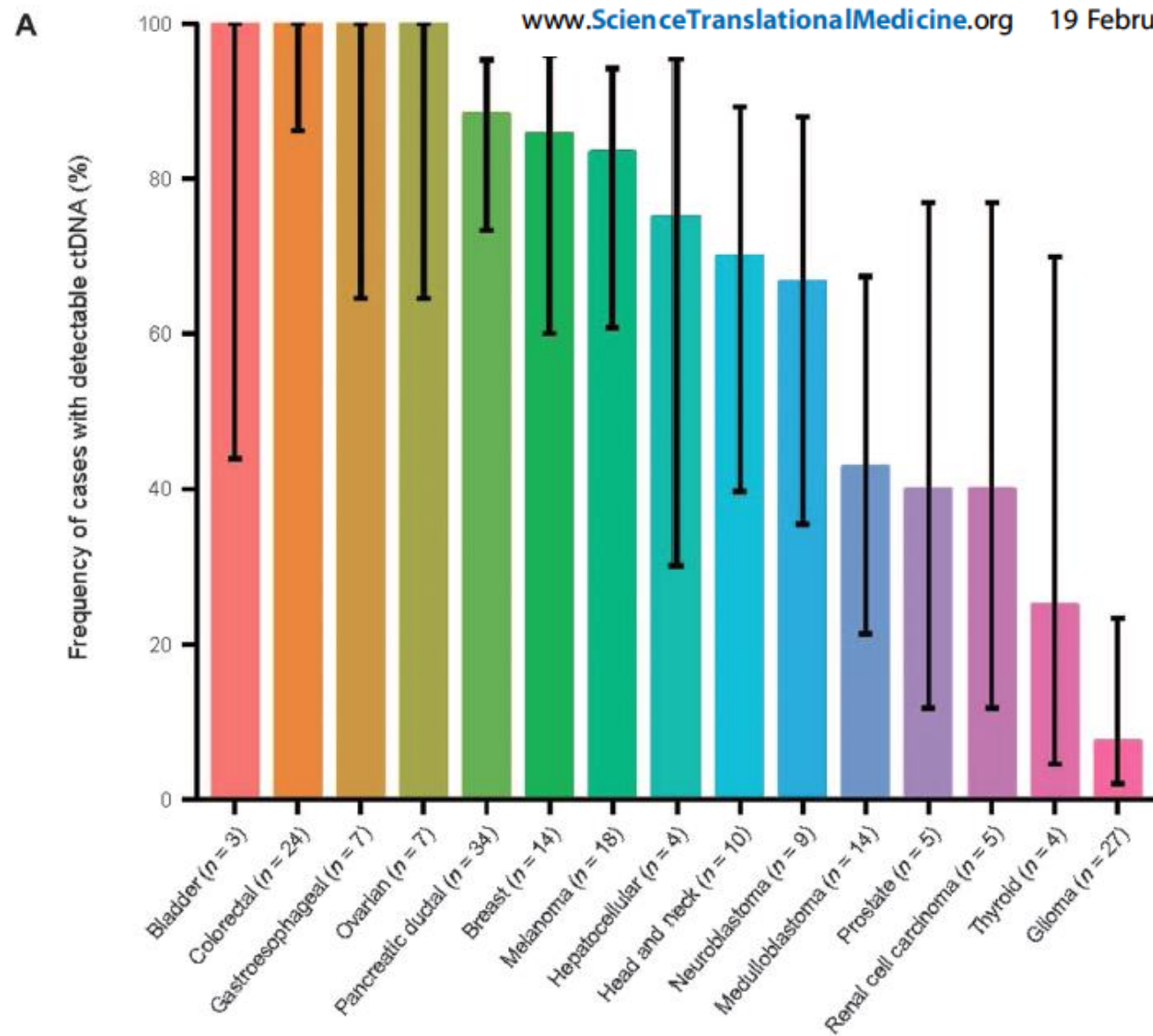
Mary E. Norton, M.D., Bo Jacobsson, M.D., Ph.D., Geeta K. Swamy, M.D., Louise C. Laurent, M.D., Ph.D., Angela C. Ranzini, M.D., Herb Brar, M.D., Mark W. Tomlinson, M.D., Leonardo Pereira, M.D., M.C.R., Jean L. Spitz, M.P.H., Desiree Hollemon, M.S.N., M.P.H., Howard Cuckle, D.Phil., M.B.A., Thomas J. Musci, M.D., and Ronald J. Wapner, M.D.

Table 2. Test Performance for Trisomy 21 in the Primary Analysis Cohort, According to Maternal Age and Risk.*

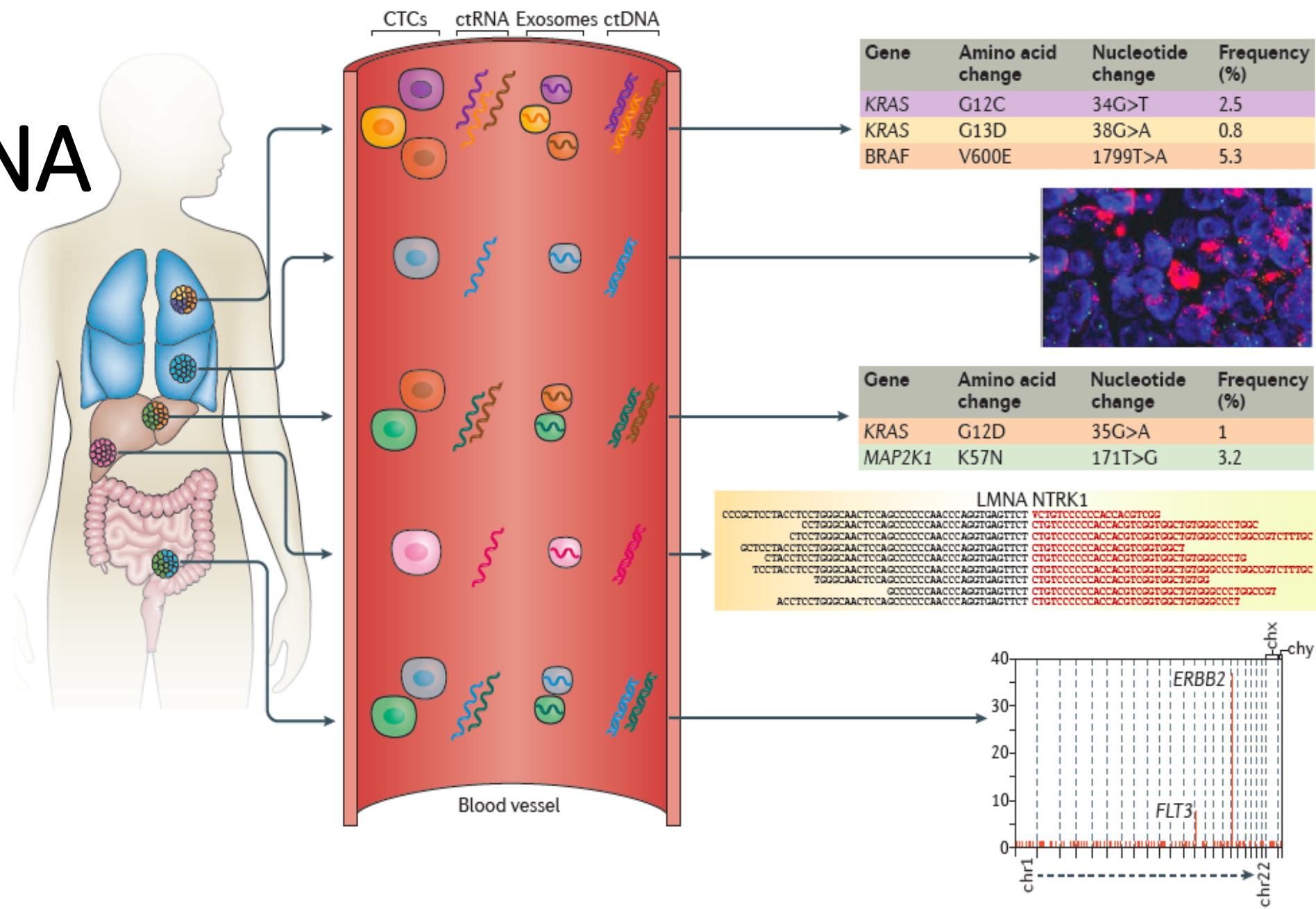
Variable	Standard Screening		Cell-free DNA Testing	
	All Patients (N = 15,841)	All Patients (N = 15,841)	Maternal Age <35 Yr (N = 11,994)	Low Risk (N = 14,957)†
True positive — no.	30	38	19	8
True negative — no.	14,949	15,794	11,969	14,941
False positive — no.	854	9	6	8
False negative — no.	8	0	0	0
Sensitivity (95% CI) — %	78.9 (62.7–90.4)	100 (90.7–100)‡	100 (82.4–100)	100 (63.1–100)
Specificity (95% CI) — %	94.6 (94.2–94.9)	99.9 (99.9–100)§	99.9 (99.9–100)	99.9 (99.9–100)
Positive predictive value (95% CI) — %	3.4 (2.3–4.8)	80.9 (66.7–90.9)§	76.0 (54.9–90.6)	50.0 (24.7–75.3)
Negative predictive value (95% CI) — %	99.9 (99.9–100)	100 (99.9–100)¶	100 (99.9–100)	100 (99.9–100)

Detection of Circulating Tumor DNA in Early- and Late-Stage Human Malignancies

CELL FREE
TUMOR DNA
(cfT DNA)



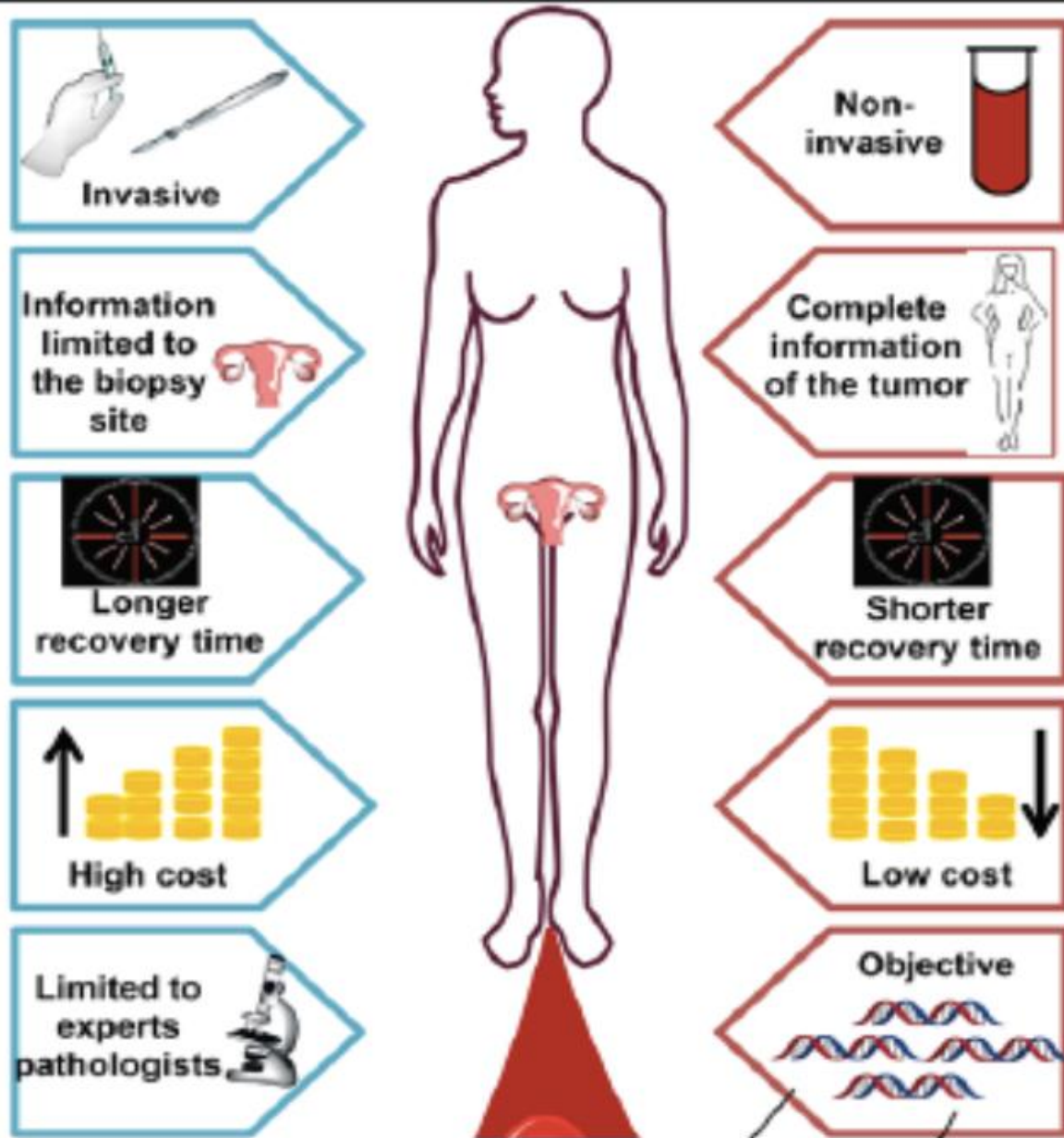
CELL FREE TUMOR DNA (cfT DNA)



Surgical Biopsy vs. Liquid Biopsy

The dawn of the liquid biopsy in the fight against cancer

Irma G. Domínguez-Vigil¹, Ana K. Moreno-Martínez^{1,2}, Julia Y. Wang³, Michael H. A. Roehrl⁴ and Hugo A. Barrera-Saldaña^{1,5}



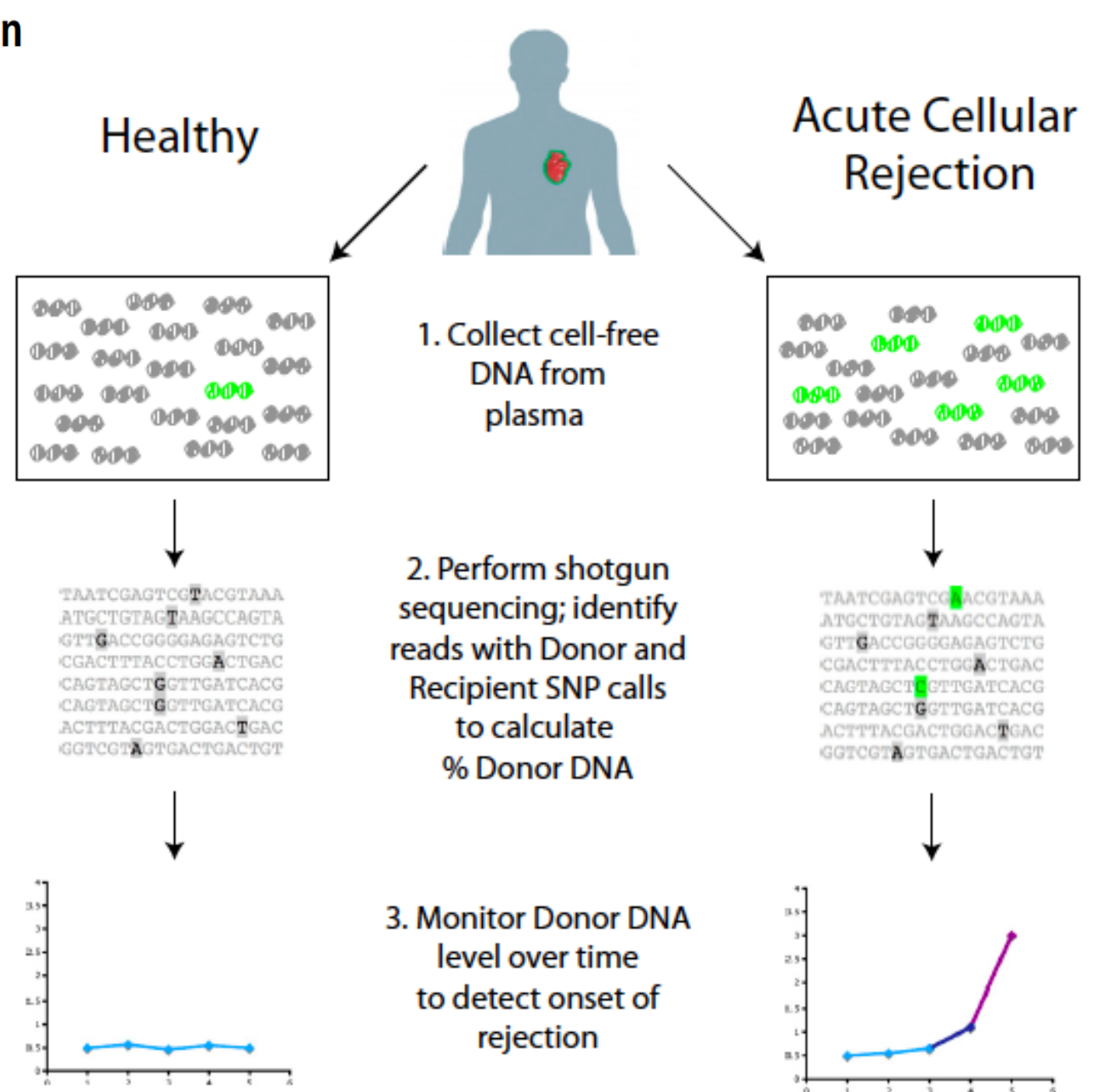
CELL FREE TUMOR DNA (cfTDNA)

Universal noninvasive detection of solid organ transplant rejection

Thomas M. Snyder^{a,b}, Kiran K. Khush^c, Hannah A. Valentine^{c,1}, and Stephen R. Quake^{a,b,1}

PNAS | April 12, 2011 | vol. 108 | no. 15 | 6229–6234

DONOR-DERIVED CELL FREE DNA (**dd**-cfDNA)

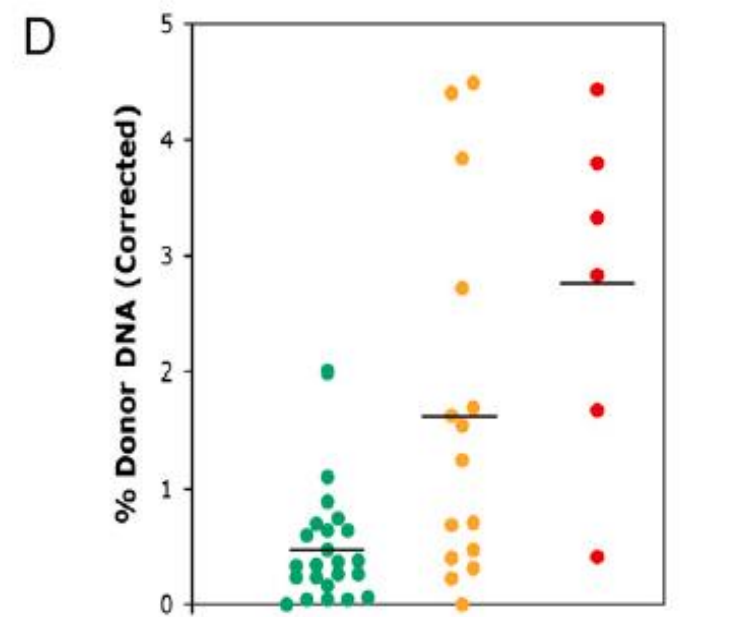
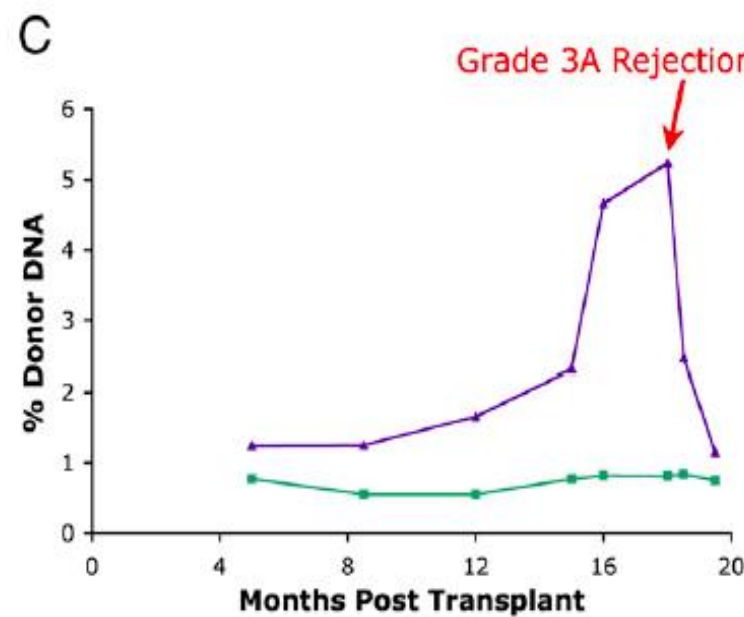
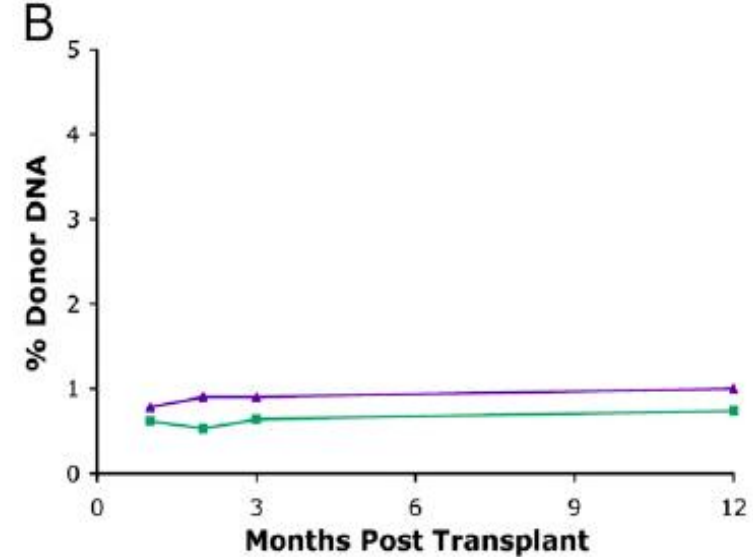
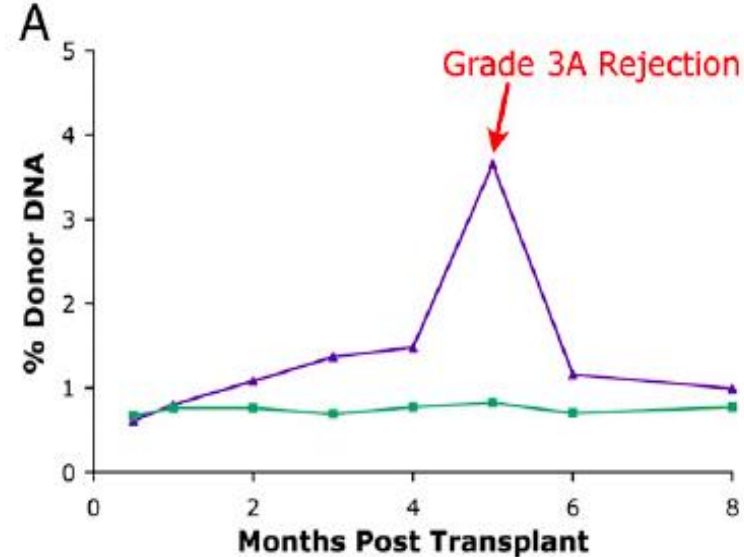


Universal noninvasive detection of solid organ transplant rejection

Thomas M. Snyder^{a,b}, Kiran K. Khush^c, Hannah A. Valentine^{c,1}, and Stephen R. Quake^{a,b,1}

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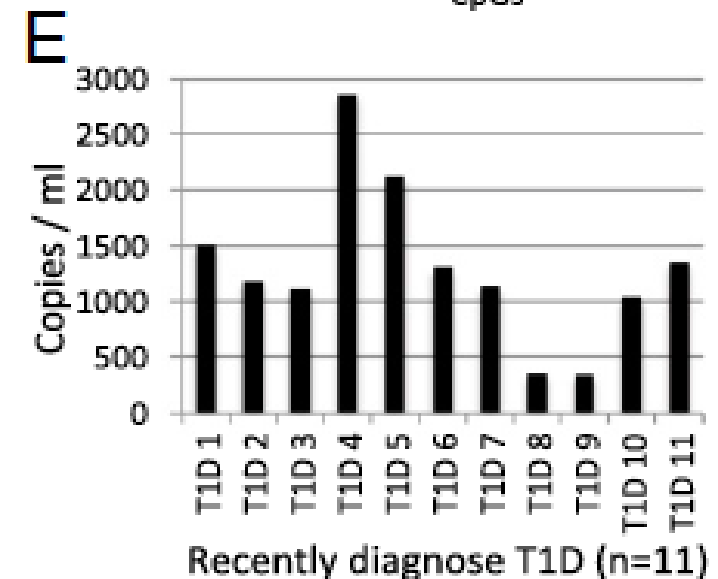
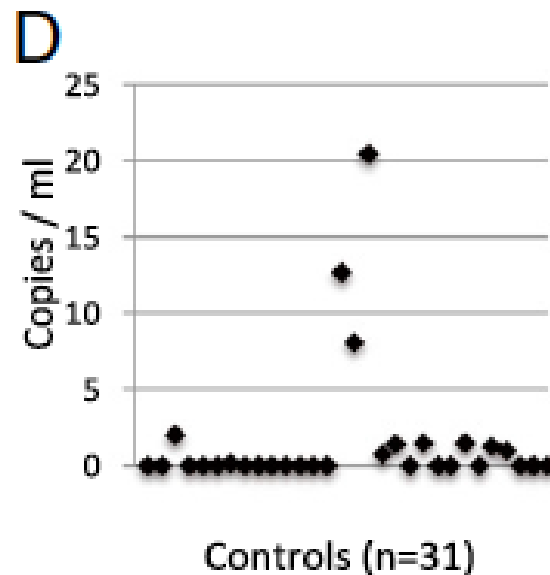
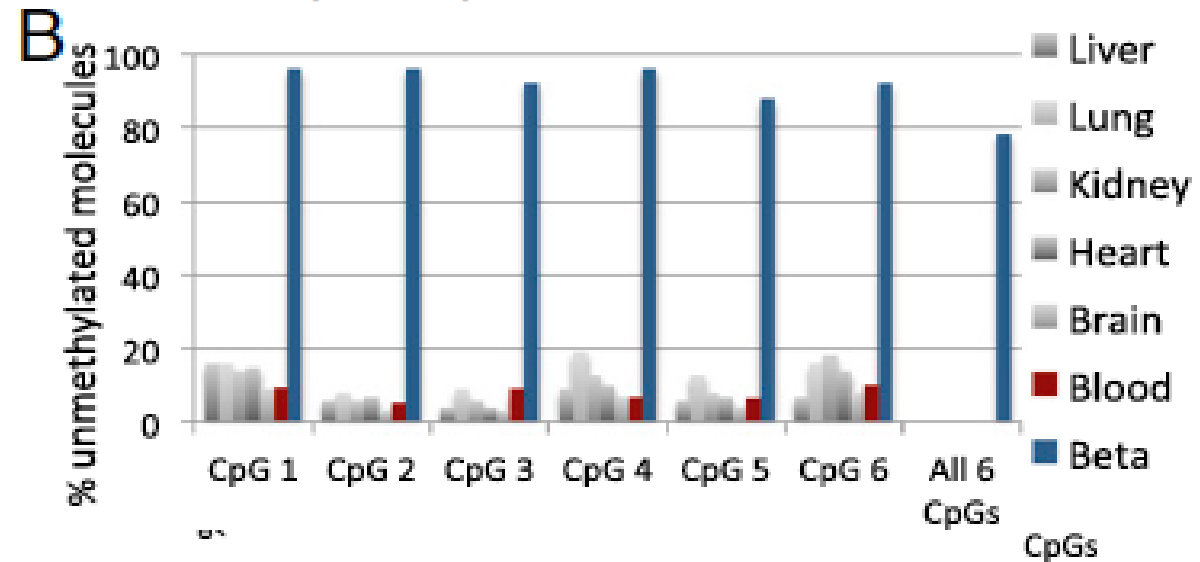
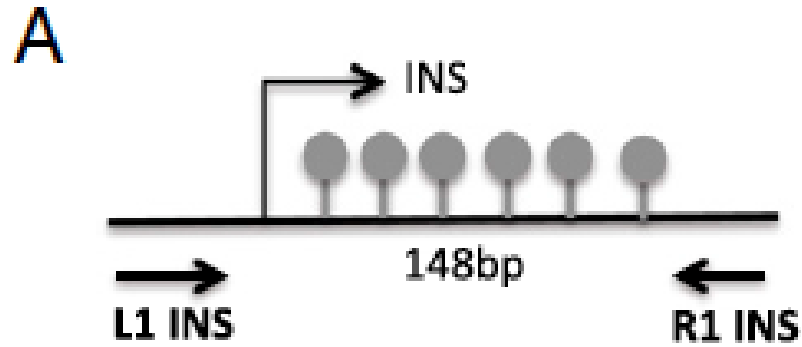


▲ Donor SNP Signal
■ Matched SNP Background

● Healthy
● Close to Rejection
● At Rejection

Identification of tissue-specific cell death using methylation patterns of circulating DNA

E1826–E1834 | PNAS | Published online March 14, 2016



cfmetDN

A

Prueba Pre-Natal No Invasiva
(NIPT)

7-10%

Rechazo de Trasplante

3-12%

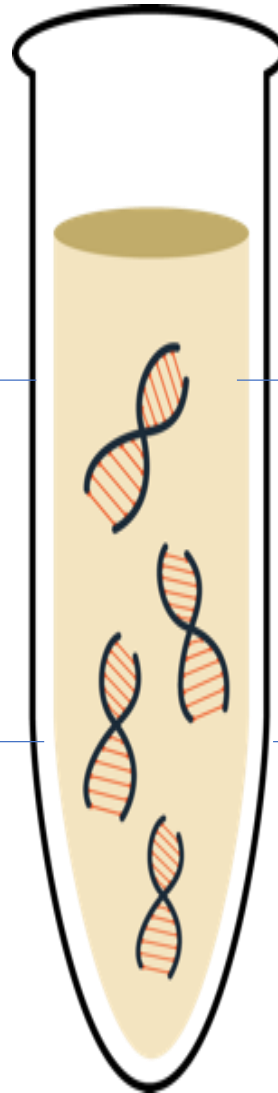
PLASMA= ORO LIQUIDO

Cancer ctDNA
("Biopsia Liquida")

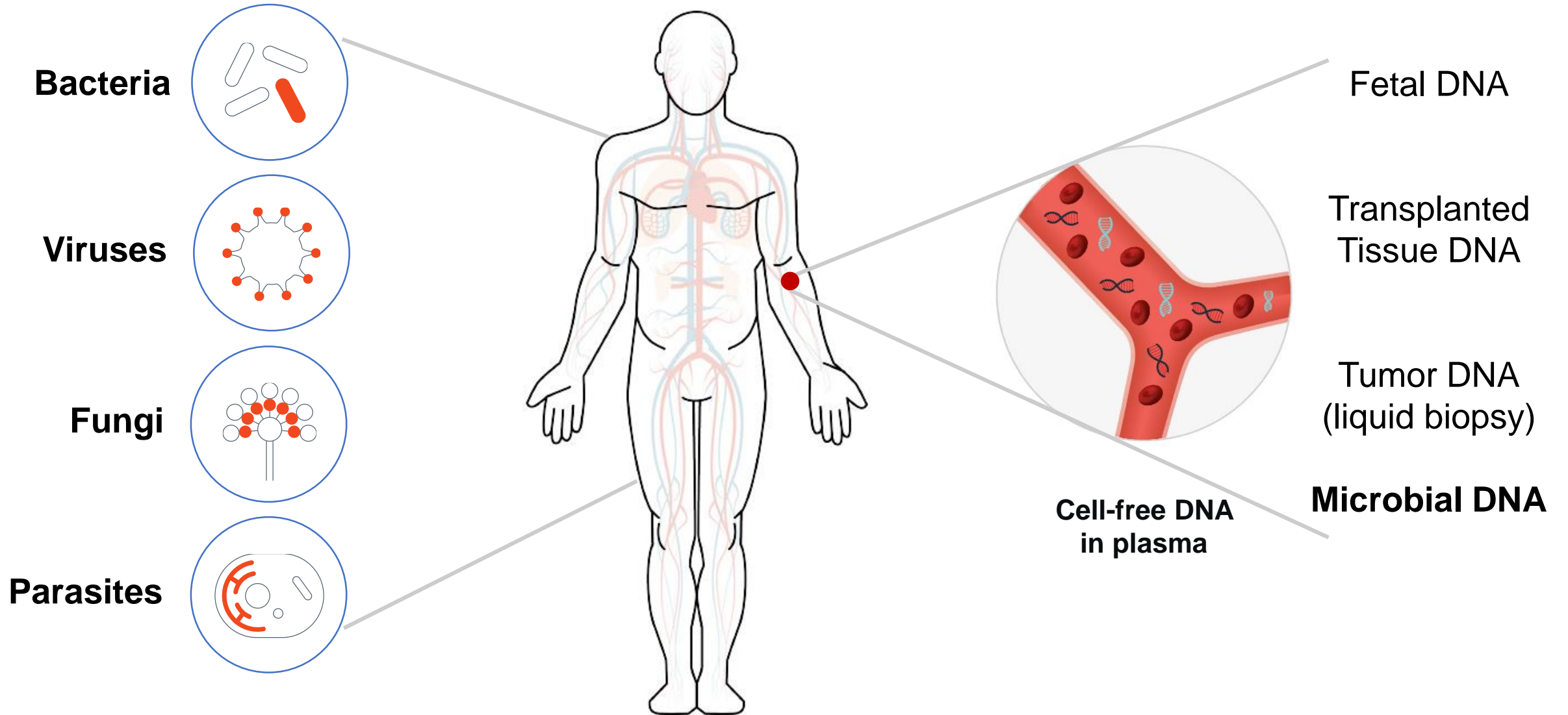
0.1%

Detección de Patógenos

0.001%



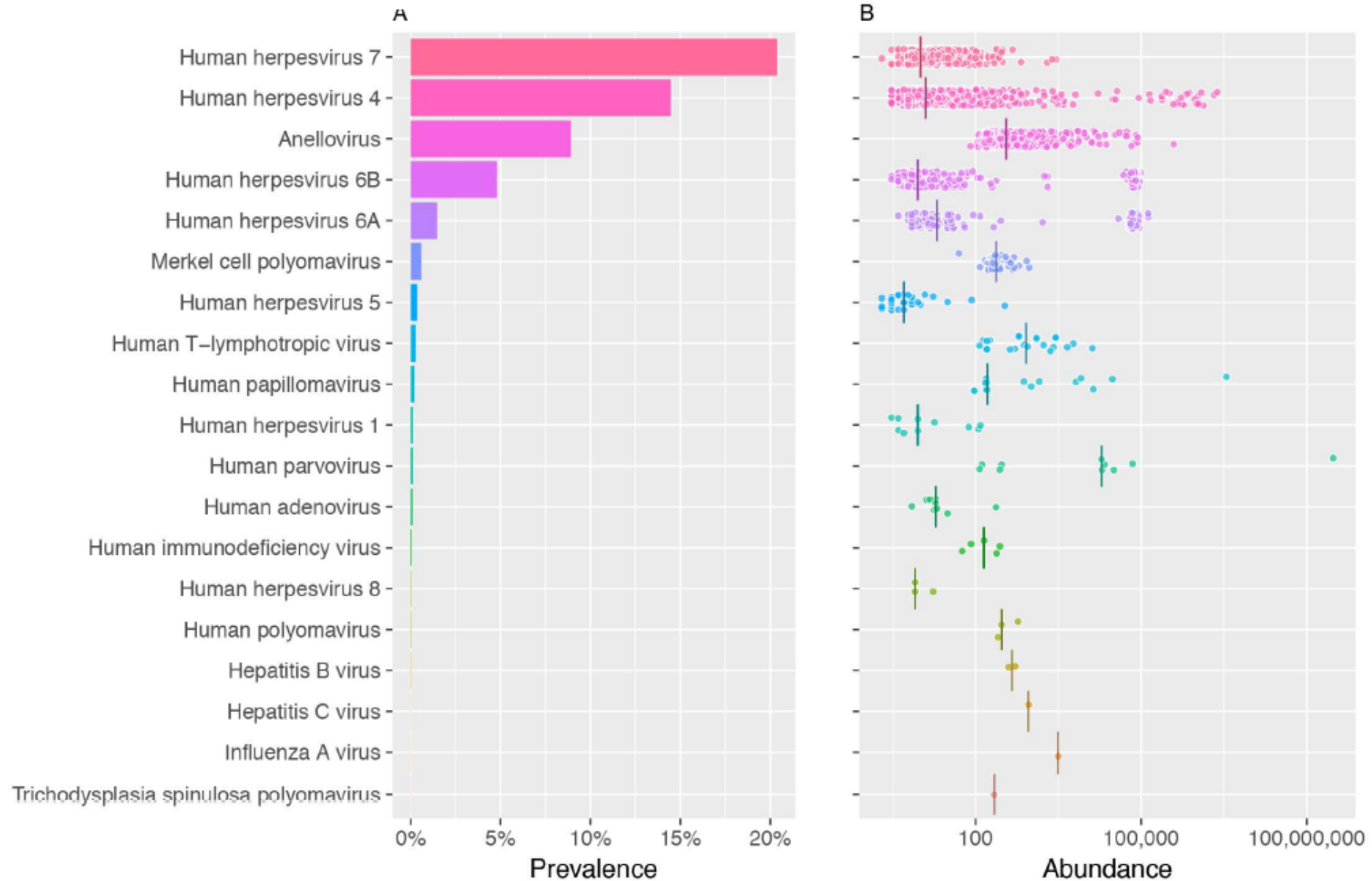
MICROBIAL CELL FREE DNA (McfDNA)



The blood DNA virome in 8,000 humans

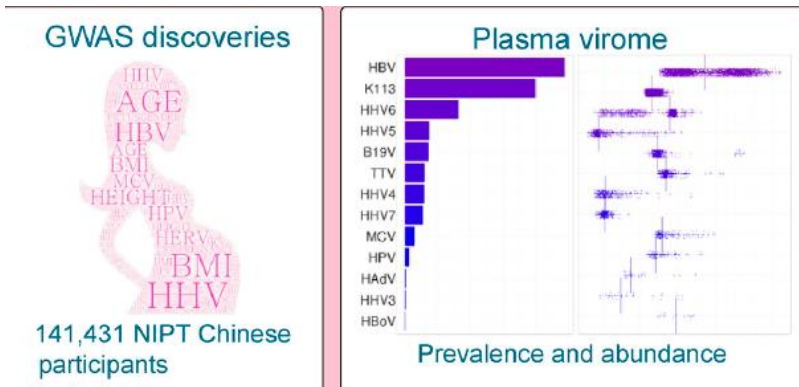
PLOS Pathogens | <https://doi.org/10.1371/journal.ppat.1006292> March 22, 2017

Ahmed Moustafa¹, Chao Xie², Ewen Kirkness¹, William Biggs¹, Emily Wong¹, Yaron Turpaz², Kenneth Bloom¹, Eric Delwart³, Karen E. Nelson⁴, J. Craig Venter^{1,4*}, Amalio Telenti^{1,4*}

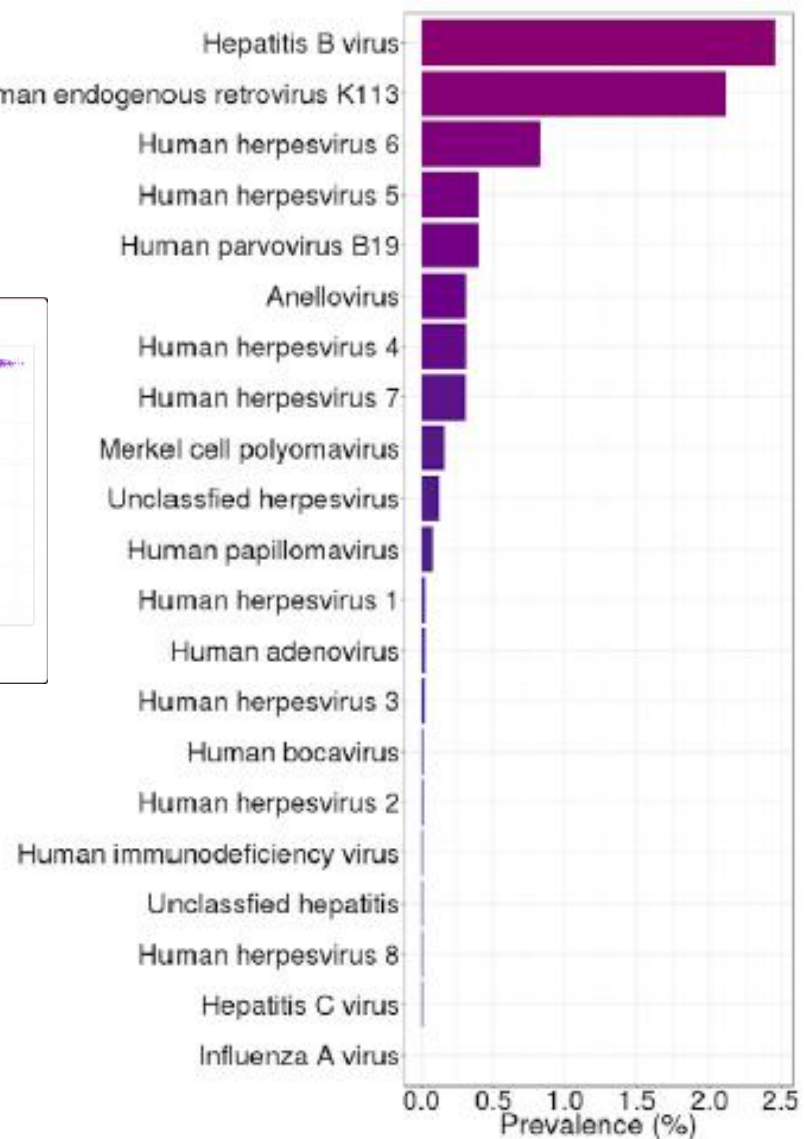


Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History

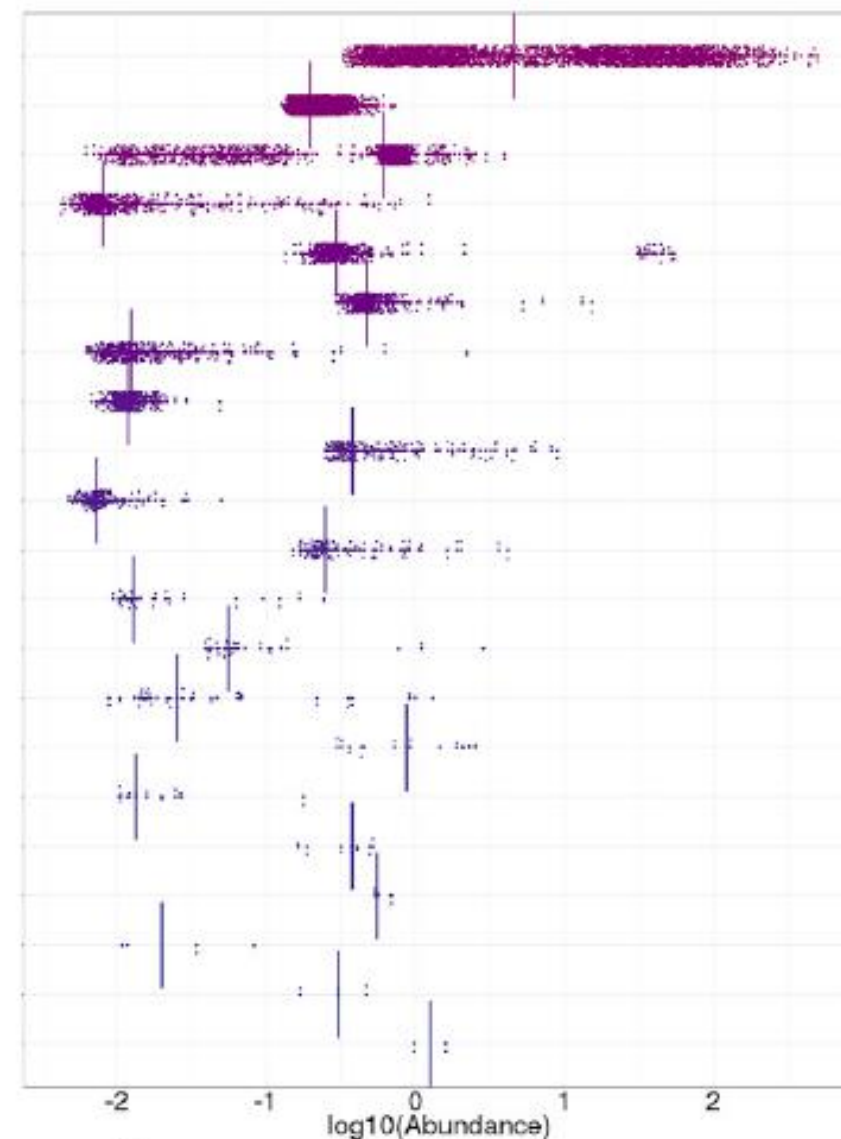
Cell 175, 347–359, October 4, 2018



A

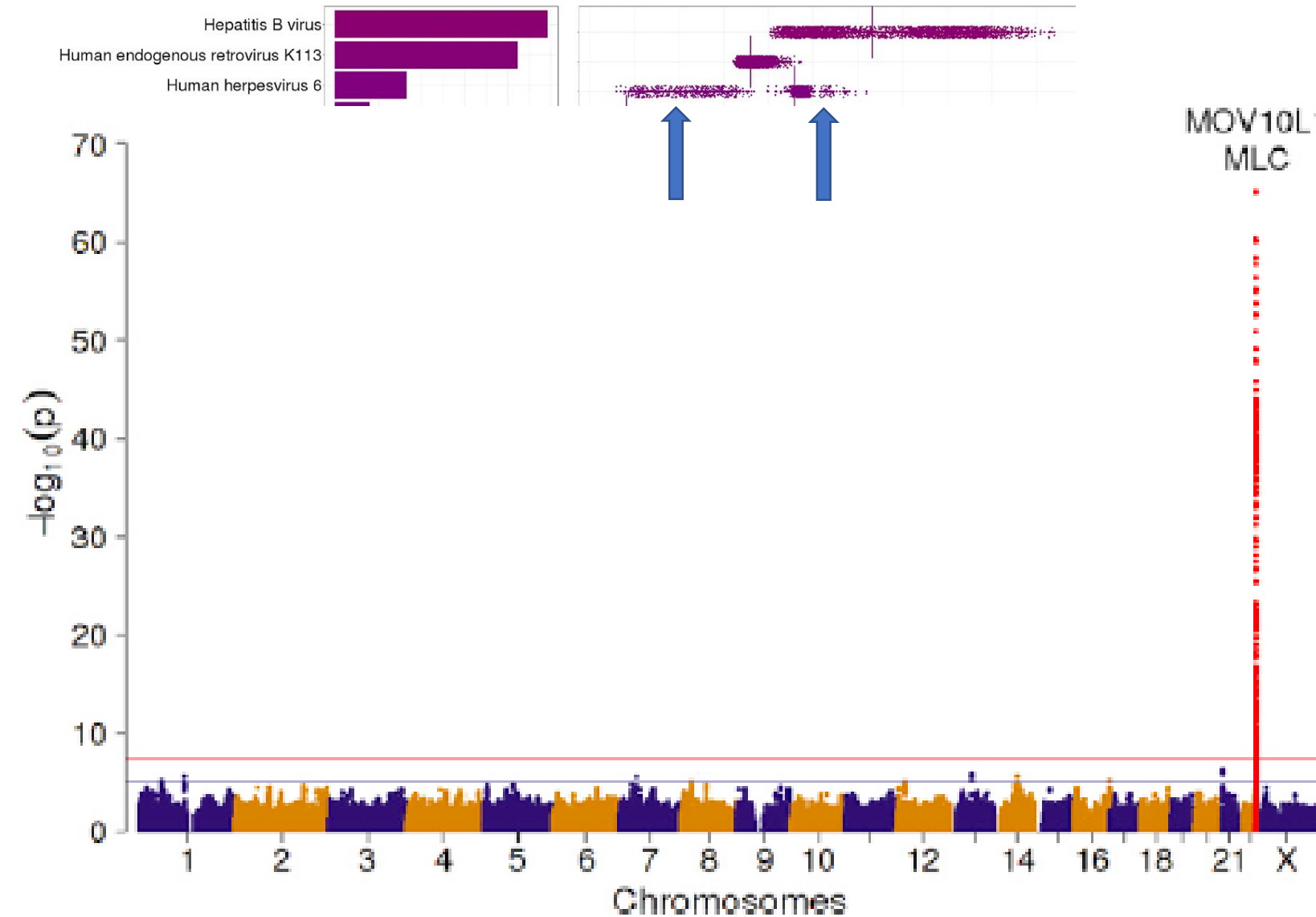


B

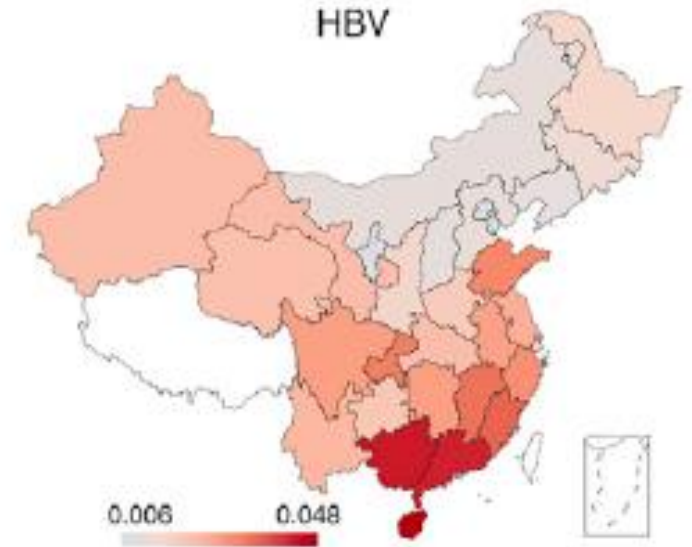


Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History

Cell 175, 347–359, October 4, 2018



E



IDENTIFICACION DEL MICROORGANISMO POR LA SEQUENCIACION DEL CELL-FREE DNA

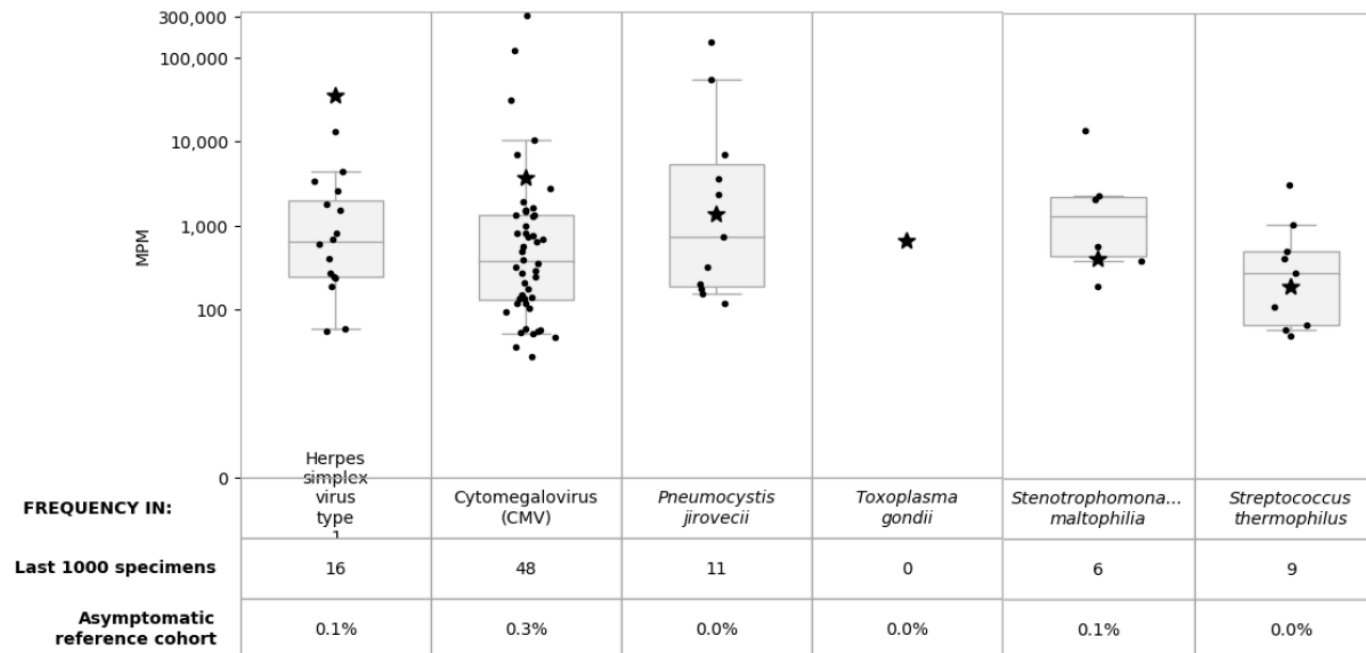


TEST RESULTS

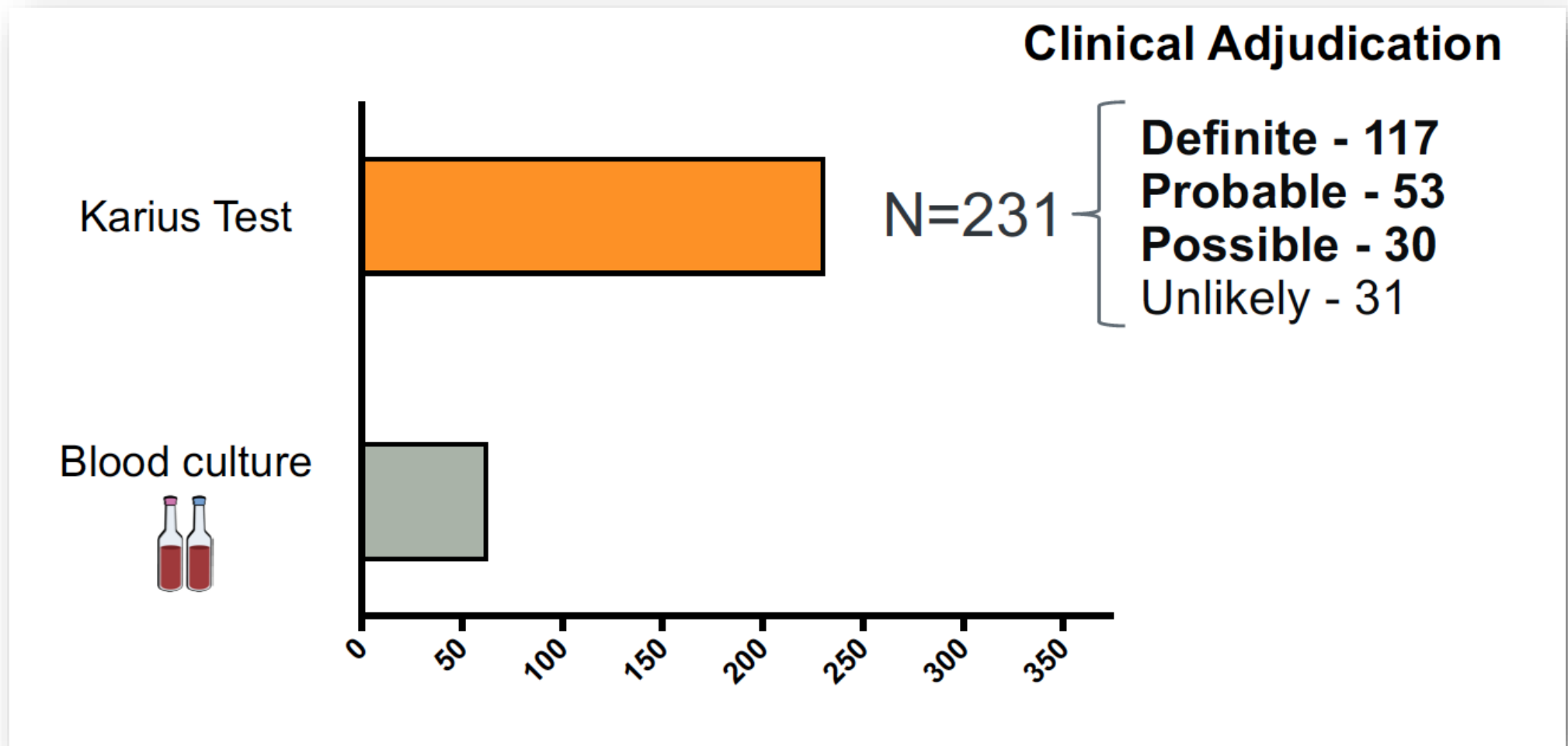
MICROORGANISM DETECTED	DNA MOLECULES PER MICROLITER (MPM)*	REFERENCE INTERVAL (MPM)**
Herpes simplex virus type 1 (HSV-1)	35,043	< 10
Cytomegalovirus (CMV)	3,672	< 10
<i>Pneumocystis jirovecii</i>	1,351	< 10
<i>Toxoplasma gondii</i>	663	< 10
<i>Stenotrophomonas maltophilia</i>	417	< 84
<i>Streptococcus thermophilus</i> (<i>Streptococcus salivarius</i> group)	193	< 10

* **Molecules Per Microliter** = number of DNA fragments present in one microliter of plasma

** **Reference Interval** = the 97.5th percentile MPM concentration detected in PPT plasma from a cohort of 684 asymptomatic donors



Analytical and clinical validation of a microbial cell-free DNA sequencing test for infectious disease



Metagenomics in pooled plasma, with identification of potential emerging infectious pathogens

TRANSFUSION 2018;58;633–637

Min Xu, Yashan Yang, Ya Zhou, Zhiyang Liu, Yu Liu, and Miao He

TABLE 2. Taxonomy of sequenced clones of pooled plasma from Chengdu

Category	Mean E value*	Pool 1 (DNA template)	Pool 2 (RNA template)	Total
<i>Homo sapiens</i>	$2 \times E^{-86}$	131	98	229
Bacteria				41
<i>Neisseria gonorrhoeae</i>	$4 \times E^{-10}$	3		
<i>Propionibacterium acnes</i>	$4 \times E^{-121}$		3	
<i>Bacillus pumilus</i>	$5 \times E^{-106}$	11		
<i>E. coli</i>	$2 \times E^{-91}$	2		
<i>Haemophilus influenzae</i>	$2 \times E^{-31}$	2		
<i>Ralstonia pickettii</i>	$3.3 \times E^{-89}$		19	
<i>O. tsutsugamushi</i>	$2 \times E^{-25}$	1		
Virus				18
Torque teno virus	$1 \times E^{-25}$	8		
Torque teno midi virus	$1 \times E^{-23}$	4		
Torque teno mini virus	$2 \times E^{-17}$	1		
Po-Circo-like virus 21	$4 \times E^{-9}$	1		
Adeno-associated virus 2	$8 \times E^{-8}$		3	
GB virus C	$1 \times E^{-134}$		1	
Parasite				2
<i>P. knowlesi</i>	$5 \times E^{-8}$	1		
<i>P. falciparum</i>	$5 \times E^{-5}$	1		
Unknown		160	231	391
Total		326	355	681

* $E < 10^{-5}$ is considered a significant similarity.

Metagenomics analysis of red blood cell and fresh-frozen plasma units

[Transfusion.](#) 2017 Jul;57(7):1787-1800

A

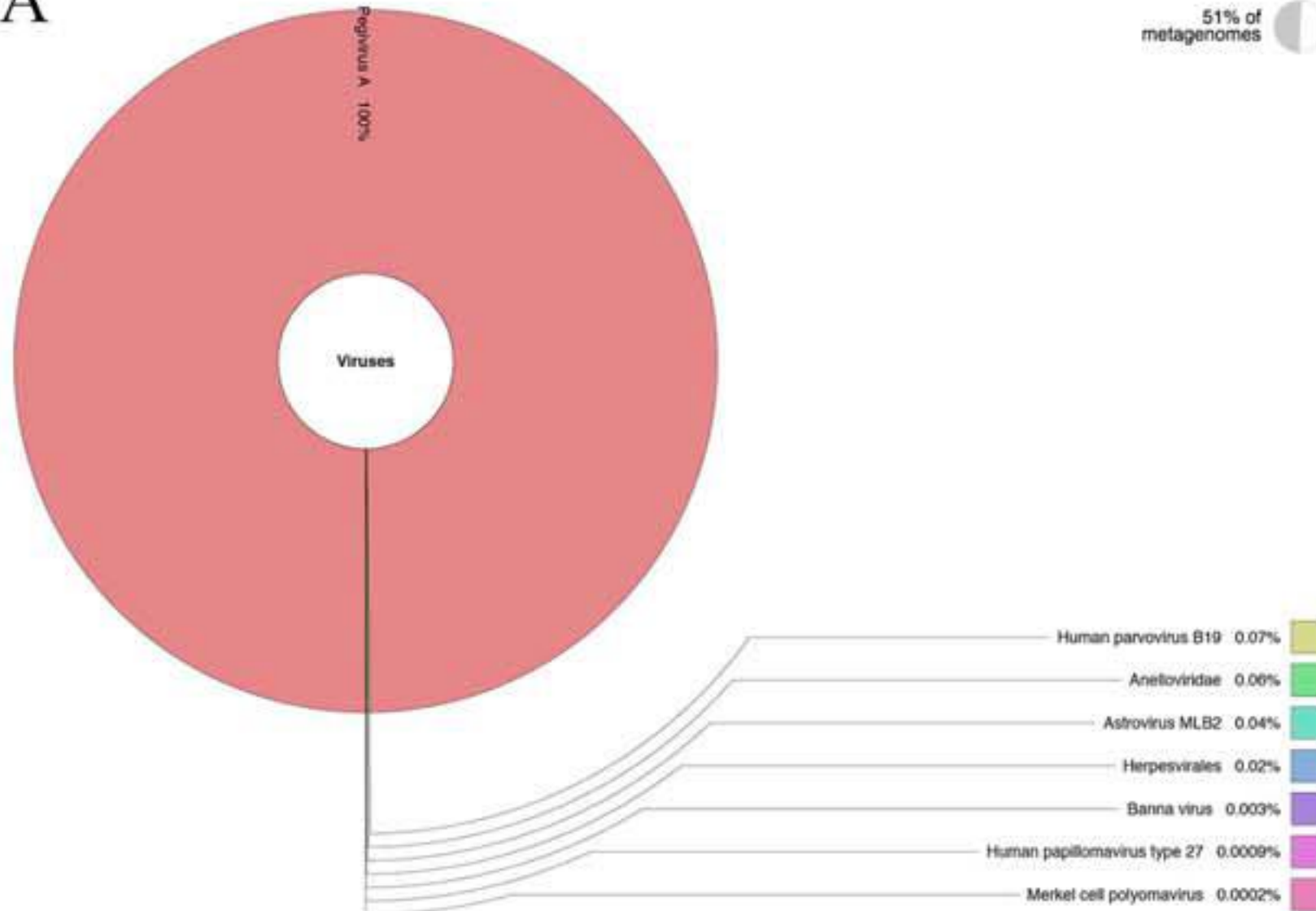


TABLE 2. Viral clusters detected in blood products by DNA-Seq

Pool	Type	Cluster	Virus representative	Reads	Max read depth	Genome coverage	ClusterID	Covered bases	Genome length
B2	RBCs	Small_anellovirus	Anelloviridae, small anellovirus	707	35	99.28	AY622909.1	2616	2,635
I2	FFP	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	462	17	89.6	FJ591158.1	4849	5,412
J2	FFP	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	347	19	84.79	FJ591158.1	4589	5,412
A2	RBCs	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	53	5	37.95	FJ591158.1	2054	5,412
F	RBCs	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	58	5	30.06	NC_000883.2	1682	5,596
J	FFP	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	36	4	26.23	NC_000883.2	1468	5,596
H	FFP	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	38	4	23.95	FJ591158.1	1296	5,412
B2	RBCs	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	25	4	19.99	FJ591158.1	1082	5,412
B2	RBCs	TT_virus	Anelloviridae, gammatorquevirus, torque teno midi virus 2	70	26	17.25	AB290919.1	561	3,253
K2	FFP	TT_virus	Anelloviridae, TTV	10	4	13.32	AM712003.1	501	3,760
N2	FFP	TT_virus	Anelloviridae, gammatorquevirus, torque teno midi virus 2	8	4	11.04	AB290919.1	359	3,253
D2	RBCs	Papillomavirus	Papillomaviridae, alphapapillomavirus, alphapapillomavirus 4	13	2	10.84	AB211993.1	849	7,831
J	FFP	TT_virus	Anelloviridae, TTV	10	4	10.76	AM711976.1	406	3,773
H2	FFP	TT_virus	Anelloviridae, gammatorquevirus, torque teno midi virus 2	10	4	9.04	AB290919.1	294	3,253
J	FFP	Small_anellovirus	Anelloviridae, small anellovirus 1	4	2	8.85	AY622908.1	199	2,249
I2	FFP	Small_anellovirus	Anelloviridae, small anellovirus	2	1	7.44	AY622909.1	196	2,635
L2	FFP	TT_virus	Anelloviridae, gammatorquevirus, torque teno midi virus 2	2	1	6.03	AB290919.1	196	3,253
I2	FFP	TTV-like_mini_virus	Anelloviridae, betatorquevirus, torque teno mini virus 9	2	1	5.97	AB038625.1	174	2,915
H2	FFP	Small_anellovirus	Anelloviridae, small anellovirus	4	3	5.96	AY622909.1	157	2,635
I	FFP	TT_virus	Anelloviridae, gammatorquevirus, torque teno midi virus 2	4	2	5.87	AB290919.1	191	3,253
J2	FFP	TT_virus	Anelloviridae, alphatorquevirus, TTV 19	2	1	5.25	AB025946.2	200	3,808
G2	RBCs	TT_virus	Anelloviridae, gammatorquevirus, torque teno midi virus 2	2	2	4.76	AB290919.1	155	3,253
I	FFP	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	2	1	3.7	FJ591158.1	200	5,412
E	RBCs	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	2	1	3.57	NC_000883.2	200	5,596
E2	RBCs	Merkel_cell_polyomavirus	Polyomaviridae, polyomavirus, MCPyV	3	2	2.9	EU375803.1	156	5,387
L2	FFP	Herpesvirus_6A	Herpesviridae, roseolovirus, human herpesvirus 6A	103	4	2.75	NC_001664.2	4383	159,322
F	RBCs	Herpesvirus_6A	Herpesviridae, roseolovirus, human herpesvirus 6A	69	8	1.9	KC465951.1	2988	156,885
E2	RBCs	Herpesvirus_6A	Herpesviridae, roseolovirus, human herpesvirus 6A	48	3	1.49	KC465951.1	2331	156,885
I2	FFP	Herpesvirus_7	Herpesviridae, roseolovirus, human herpesvirus 7	15	3	0.51	AF037218.1	787	153,080
E	RBCs	Herpesvirus_6B	Herpesviridae, roseolovirus, human herpesvirus 6B	35	7	0.4	AB021506.1	653	161,573
B2	RBCs	Herpesvirus_6A	Herpesviridae, roseolovirus, human herpesvirus 6A	11	4	0.36	KC465951.1	565	156,885
F	RBCs	Herpesvirus_6B	Herpesviridae, roseolovirus, human herpesvirus 6B	13	6	0.22	AF157706.1	364	162,114
M2	FFP	Saimiriine_herpesvirus_2	Herpesviridae, rhadinovirus, saimiriine herpesvirus 2	3	2	0.17	X64346.1	187	112,930
L2	FFP	Herpesvirus_6B	Herpesviridae, roseolovirus, human herpesvirus 6B	5	2	0.13	AF157706.1	215	162,114
M2	FFP	Herpesvirus_6B	Herpesviridae, roseolovirus, human herpesvirus 6B	4	2	0.11	AB021506.1	184	161,573
J	FFP	Herpesvirus_5	Herpesviridae, CMV, human herpesvirus 5	5	2	0.08	GQ466044.1	200	235,703

TABLE 3. Viral clusters detected in blood products by RNA-Seq

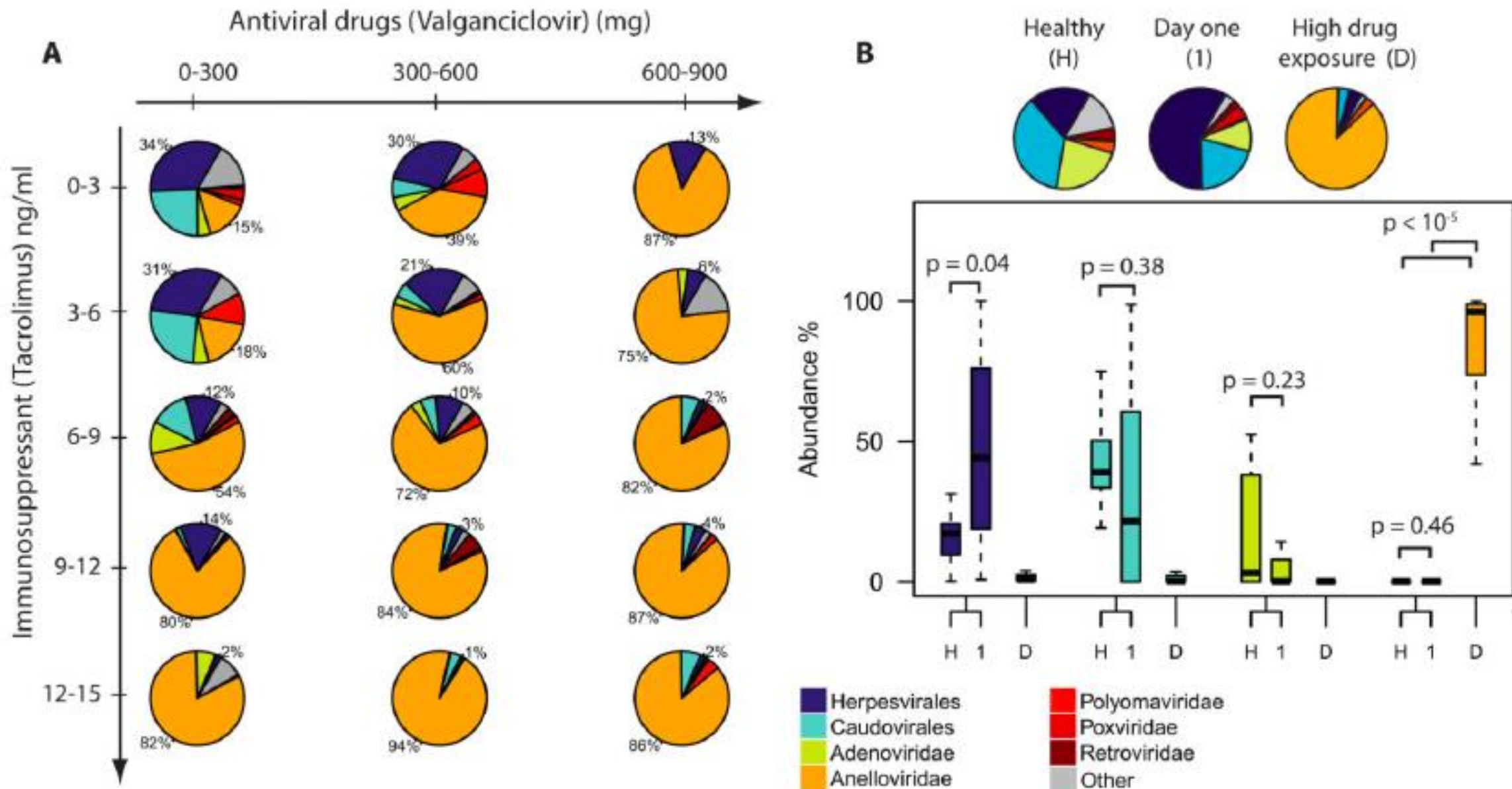
Pool	Type	Cluster	Virus representative	Reads	Max read depth	Genome coverage	ClusterID	Covered bases	Genome length
L2	FFP	Pegivirus	Flaviviridae, pegivirus,HPgV	1,391,071	67612	99.81	D90600.1	9377	9,395
B2	RBC	Pegivirus	Flaviviridae, pegivirus,HPgV	3,570	190	83.09	NC_001710.1	7804	9,392
A2	RBC	Pegivirus	Flaviviridae, pegivirus,HPgV	694	50	67.55	NC_001710.1	6344	9,392
K2	FFP	Pegivirus	Flaviviridae, pegivirus,HPgV	206	17	45.84	D90600.1	4307	9,395
B2	RBC	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	40	7	29.72	NC_000883.2	1663	5,596
P	FFP	Astrovirus	Astroviridae, astrovirus MLB2	517	72	29.11	JF742759.1	1781	6,119
J2	FFP	Pegivirus	Flaviviridae, pegivirus,HPgV	158	34	11.91	NC_001710.1	1119	9,392
G2	RBC	Pegivirus	Flaviviridae, pegivirus,HPgV	18	2	10.57	NC_001710.1	993	9,392
K	RBC	Pegivirus	Flaviviridae, pegivirus,HPgV	17	2	10.45	NC_001710.1	981	9,392
C2	RBC	Pegivirus	Flaviviridae, pegivirus,HPgV	18	3	9.73	NC_001710.1	914	9,392
E2	RBC	Xenotropic_MuLV-related_virus	Retroviridae, gammaretrovirus, murine leukemia-related retroviruses	21	4	8.85	FN692043.2	724	8,185
D2	RBC	Xenotropic_MuLV-related_virus	Retroviridae, gammaretrovirus, murine leukemia-related retroviruses	19	5	7.72	FN692043.2	632	8,185
C2	RBC	Xenotropic_MuLV-related_virus	Retroviridae, gammaretrovirus, murine leukemia-related retroviruses	17	4	7.64	FN692043.2	625	8,185
M2	FFP	Pegivirus	Flaviviridae, pegivirus,HPgV	209	59	6.77	NC_001710.1	636	9,392
L2	FFP	GB_virus_C	Flaviviridae, pegivirus, GB virus C variant troglodytes	597	646	6.1	AF070476.1	564	9,250
K	RBC	Xenotropic_MuLV-related_virus	Retroviridae, gammaretrovirus, murine leukemia-related retroviruses	11	3	5.77	FN692043.2	472	8,185
G2	RBC	Xenotropic_MuLV-related_virus	Retroviridae, gammaretrovirus, murine leukemia-related retroviruses	12	4	4.8	FN692043.2	393	8,185
P	FFP	Merkel_cell_polyomavirus	Polyomaviridae, polyomavirus, MCPyV	5	2	3.71	EU375803.1	200	5,387
A2	RBC	Parvovirus	Parvoviridae, erythroparvovirus, primate erythroparvovirus 1	9	5	3.25	FJ591158.1	176	5,412
E2	RBC	Pegivirus	Flaviviridae, pegivirus, HPgV	4	1	3.19	NC_001710.1	300	9,392
M	RBC	Xenotropic_MuLV-related_virus	Retroviridae, gammaretrovirus, murine leukemia-related retroviruses	7	3	2.75	FN692043.2	225	8,185
B2	RBC	GB_virus_C	Flaviviridae, pegivirus, GB virus C variant troglodytes	15	11	2.57	AF070476.1	238	9,250
M	RBC	Pegivirus	Flaviviridae, pegivirus, HPgV	4	2	2.18	NC_001710.1	205	9,392
A2	RBC	GB_virus_C	Flaviviridae, pegivirus, GB virus C variant troglodytes	5	4	1.78	AF070476.1	165	9,250
G2	RBC	Saimirine_herpesvirus_2	Herpesviridae, rhadinovirus, saimiriine herpesvirus 2	3	1	0.16	X64346.1	177	112,930
N	FFP	Herpesvirus_5	Herpesviridae, CMV, human herpesvirus 5	34	21	0.07	X17403.1	168	229,354

TABLE 4. Detection of bacterial sequences in blood products

Pool	Type	Bacterium name	TaxonID	Genome length	Reads	Genome coverage
G	RBCs	<i>P. acnes</i>	1747	3,361,368	10,128	35.67
E	RBCs	<i>P. acnes</i>	1747	3,361,368	4,617	35.04
D2-DNA	RBCs	<i>P. acnes</i>	1747	3,361,368	3,508	19.56
I	FFP	<i>P. acnes</i>	1747	3,361,368	1,681	15.72
P	FFP	<i>P. acnes</i>	1747	3,361,368	28,288	6.08
N	FFP	<i>P. acnes</i>	1747	3,361,368	46,286	5.68
F2-RNA	RBCs	<i>P. acnes</i>	1747	3,361,368	83,428	3.64
O	FFP	<i>P. acnes</i>	1747	3,361,368	34,261	3
L2-RNA	FFP	<i>P. acnes</i>	1747	3,361,368	86,069	2.26
J2-RNA	FFP	<i>P. acnes</i>	1747	3,361,368	82,316	2.25
I2-RNA	FFP	<i>P. acnes</i>	1747	3,361,368	178,762	2.17
H2-RNA	FFP	<i>P. acnes</i>	1747	3,361,368	153,175	2.02
M2-RNA	FFP	<i>P. acnes</i>	1747	3,361,368	188,189	1.77
K2-RNA	FFP	<i>P. acnes</i>	1747	3,361,368	54,336	1.49
F2-RNA	RBCs	<i>M. luteus</i>	1270	2,501,097	57,864	1.33
N2-RNA	FFP	<i>P. acnes</i>	1747	3,361,368	80,183	1.15
J2-RNA	FFP	<i>S. epidermidis</i>	1282	2,586,069	9,552	0.8
D2-RNA	RBCs	<i>P. acnes</i>	1747	3,361,368	2,007	0.68
K2-RNA	FFP	<i>M. luteus</i>	1270	2,501,097	102,210	0.65
A2-RNA	RBCs	<i>M. luteus</i>	1270	2,501,097	1,580	0.61
G2-RNA	RBCs	<i>P. acnes</i>	1747	3,361,368	850	0.58
A2-RNA	RBCs	<i>P. acnes</i>	1747	3,361,368	1,500	0.55
L	RBCs	<i>P. acnes</i>	1747	3,361,368	447	0.53
E2-RNA	RBCs	<i>P. acnes</i>	1747	3,361,368	1,211	0.51
F2-RNA	RBCs	<i>C. aurimucosum</i>	169292	2,819,226	52,071	0.42
N2-RNA	FFP	<i>M. luteus</i>	1270	2,501,097	26,043	0.38
J2-RNA	FFP	<i>M. luteus</i>	1270	2,501,097	26,623	0.36
C2-RNA	RBCs	<i>P. acnes</i>	1747	3,361,368	830	0.35
C2-RNA	RBCs	<i>C. metallidurans</i>	119219	6,913,352	387	0.22
C2-RNA	RBCs	<i>M. luteus</i>	1270	2,501,097	215	0.22

Temporal Response of the Human Virome to Immunosuppression and Antiviral Therapy

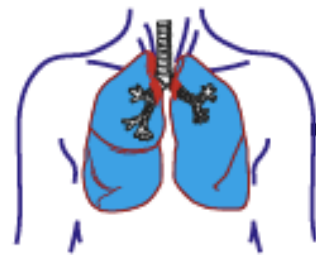
Cell. 2013 November 21; 155(5): 1178–1187.



Noninvasive monitoring of infection and rejection after lung transplantation

www.pnas.org/cgi/doi/10.1073/pnas.1517494112

Collect plasma samples post lung transplant (51 patients, 398 samples)

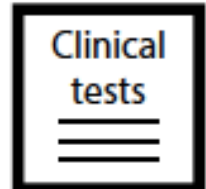


Quantify cell-free DNA (cfDNA) level

Correlate cfDNA level with clinical tests

Donor-derived cfDNA

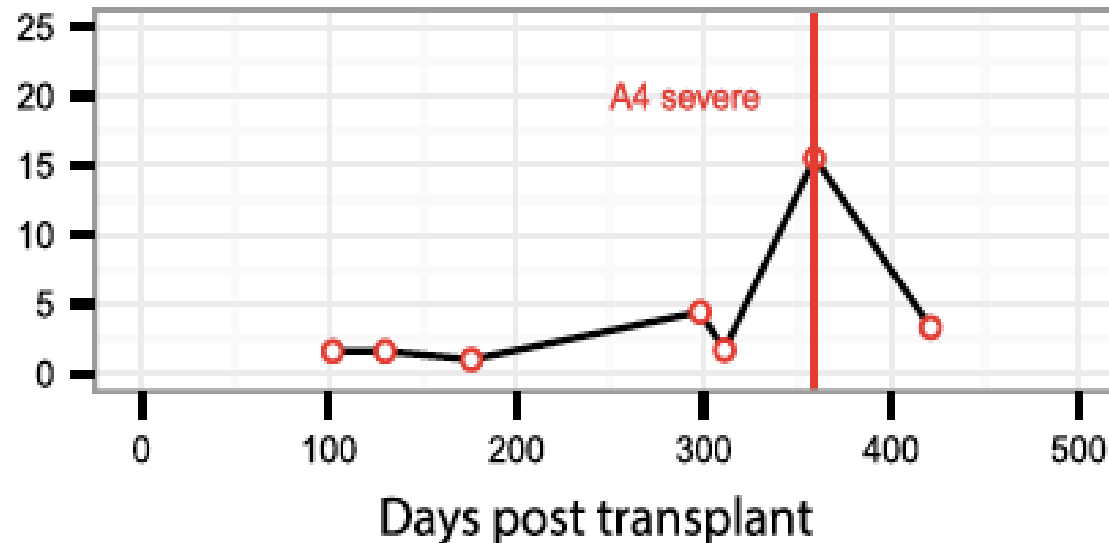
Rejection (Biopsy)



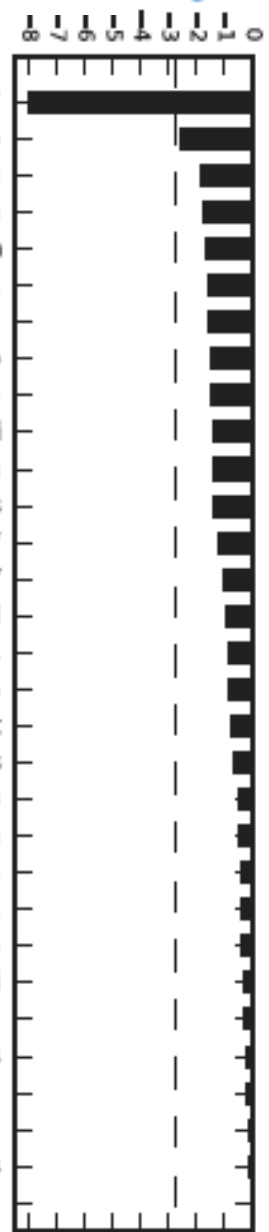
Infection-derived cfDNA

Infection (Culture, qPCR)




Donor DNA (%)

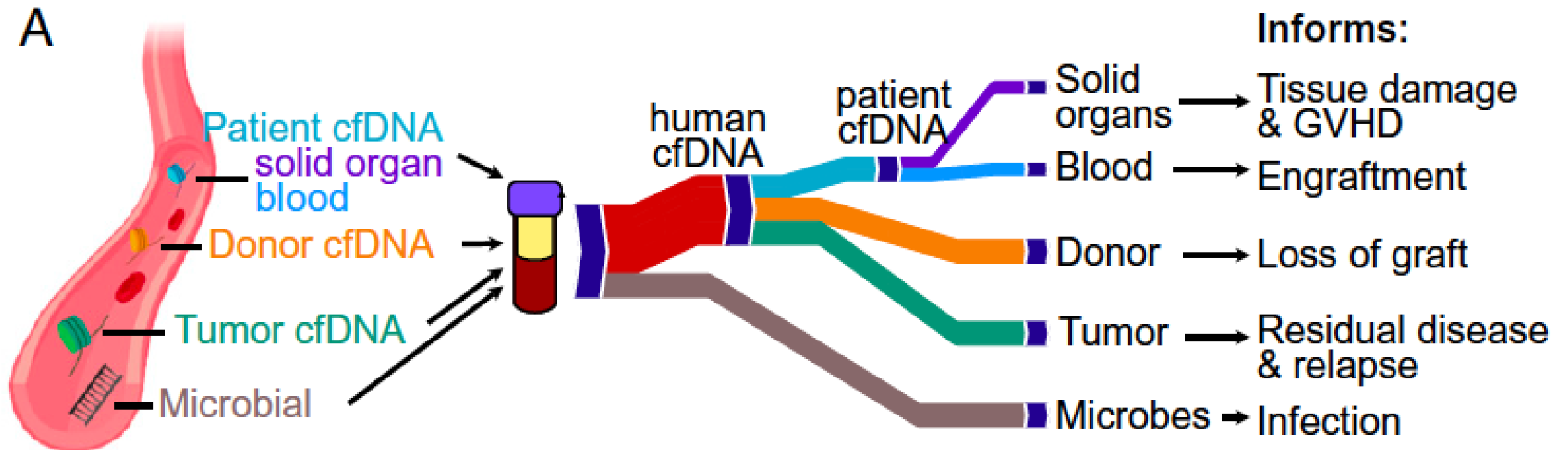


CMV
Pseudomonas aeruginosa
Scedosporium boydii
Gram Negative Rods
Penicillium
Staph aureus
Candida parapsilosis
M.pseudo
Klebsiella pneumonia
E.coli
Mixed flora
Micrococcus
RSV
EBV
Gram Positive Cocci
MRSA
Pseudomonas maltophilia
Yeast
Enterococcus
Parainfluenza 3
Serratia rubidaea
Aspergillus fumigatus
Candida glabrata
Aspergillus
Citrobacter freundii
Aspergillus niger
Gram Positive Rods
Corynebacterium avium complex
Emmericella nidulans
Metapneumovirus
Mycobacterium indicus pranii



Cell-free DNA profiling informs all major complications of hematopoietic cell transplantation

Alexandre Pellan Cheng^a, Matthew Pellan Cheng^{b,c}, Conor James Loy^d , Joan Sasing Lenz^a, Kaiwen Chen^{b,c}, Sami Smalling^a, Philip Burnham^e, Kaitlyn Marie Timblin^{b,c}, José Luis Orejas^{b,c}, Emily Silverman^{b,c}, Paz Polak^{f,g}, Francisco M. Marty^{c,h} , Jerome Ritz^{b,h} , and Iwijn De Vlaminc^{a,1}



Virome Analysis of Transfusion Recipients Reveals a Novel Human Virus That Shares Genomic Features with Hepaciviruses and Pegiviruses

Amit Kapoor,^a Arvind Kumar,^a Peter Simmonds,^b Nishit Bhuva,^a Lokendra Singh Chauhan,^a Bohyun Lee,^a Amadou Alpha Sall,^c Zhezhen Jin,^a Stephen S. Morse,^a Beth Shaz,^f Peter D. Burbelo,^g W. Ian Lipkin^a

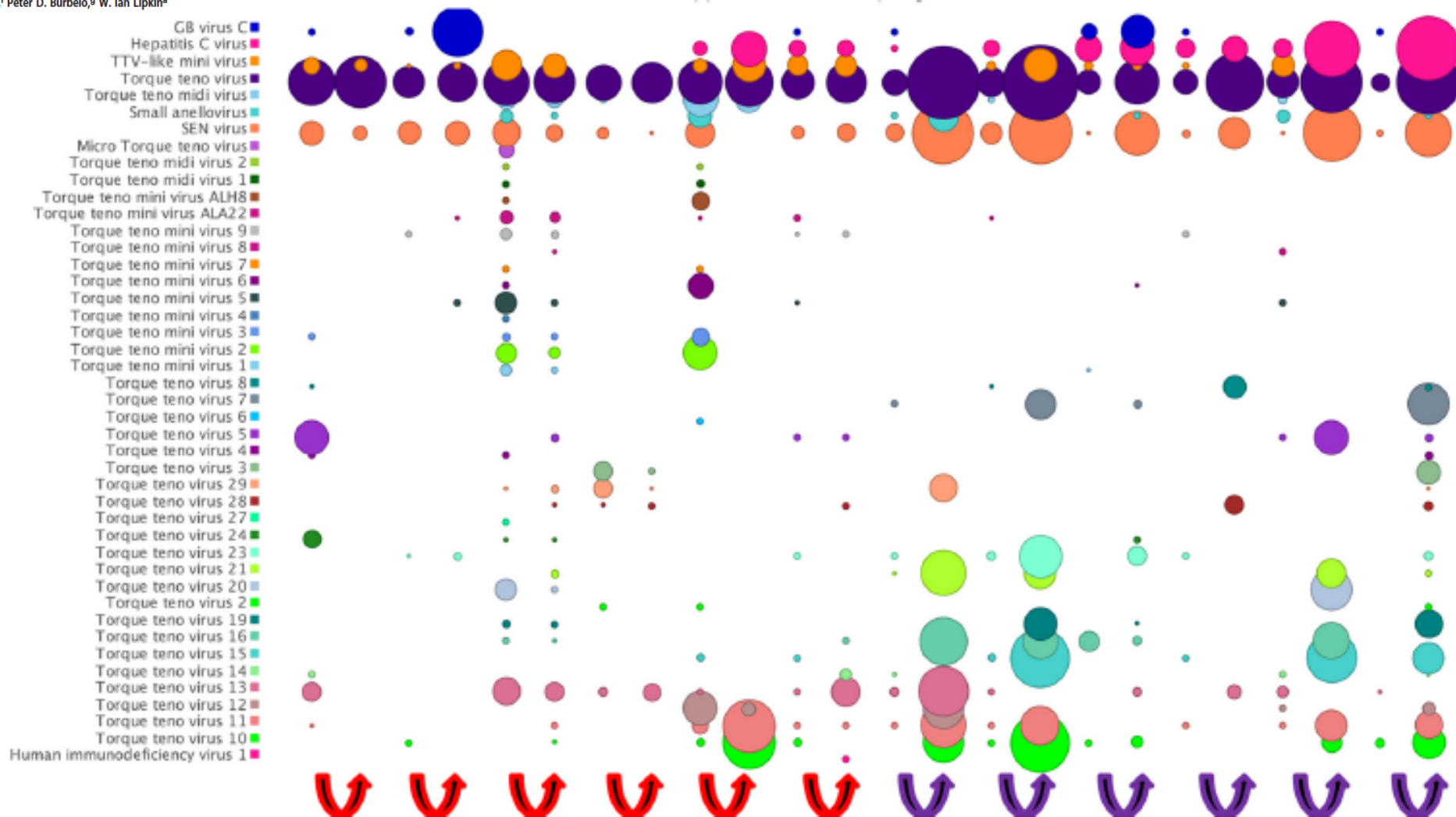


FIG 1 Virome analysis of TTVS pre- and posttransfusion samples. (Top) Statistical analysis of total virus sequences (left), anellovirus sequences (middle), and virus-like unclassified sequences (right) in pre- and posttransfusion samples. (Bottom) Metagenomic binning of all viruses sequences in pre- and posttransfusion samples from twelve TTVS subjects. Red arrows represent pre- and posttransfusion sample pairs that were similar in amount of total virus sequences, and purple arrows represent pre- and posttransfusion sample pairs where posttransfusion samples had significantly larger amounts of total virus sequences.

12

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