

**Genetic diversity of KELnull and KELel: a nationwide Austrian survey**

Günther E Körmöcz, Thomas Wagner, Christof Jungbauer, Maria Vadon, Norbert Ahrens, Willi Moll, Annelies Mühlbacher, Seyhan Özgül-Gülce, Thomas Kleinrath, Susanne Kilga-Nogler, Diether Schönitzer, and Christoph Gassner

Volume 47, April 2007 TRANSFUSION 703

**A novel KEL\*1,3 allele with weak Kell antigen exp confirming the cis-modifier effect of KEL3**

Günther E Körmöcz, Erwin A. Scharberg, and Christoph Gassner

Volume 49, April 2009 TRANSFUSION 733

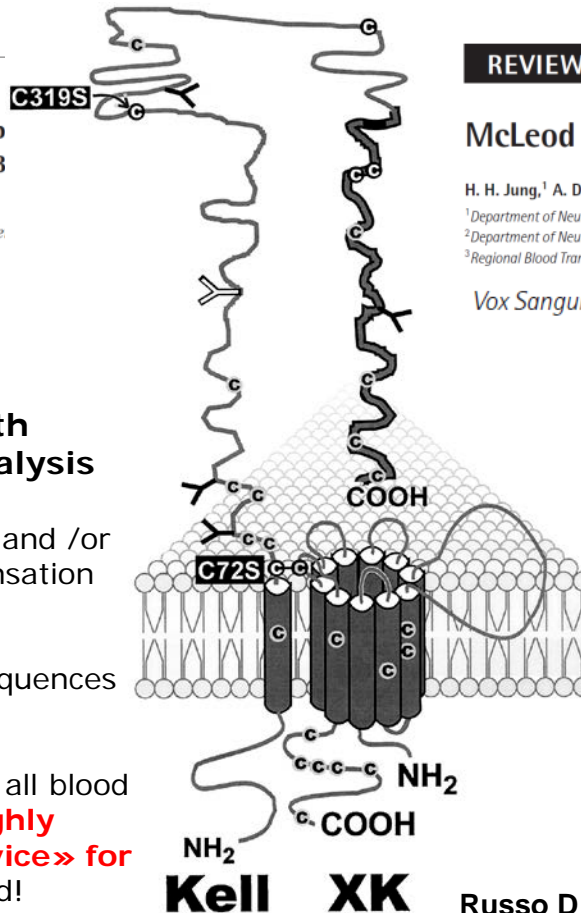
**ACADEMIC**

**10 to 20 results per year with need for further molecular analysis**

Usually laborious, involving sequencing and /or other methods. **UNPAYABLE**. Compensation partially via academic merit.

Findings **NEED TO BE PUBLISHED**. Sequences to be deposited in data-bases!

Consequence: No lab (?) is able to cover all blood groups. Prognosis: There will be **highly specialized labs with «academic service» for certain genes**, for «all» the world!



**Kell XK**

**McLeod phenotype associated with a XK missense mutation without hematologic, neuromuscular, or cerebral involvement**

Hans H. Jung, Martin Hergersberg, Marco Vogt, Jens Pahnke, Valerie Treyer, Benno Röthlisberger, Spyros S. Kollias, David Russo, and Beat M. Frey

928 TRANSFUSION Volume 43, July 2003

**REVIEW**

**McLeod syndrome: a neurohaematological disorder**

H. H. Jung,<sup>1</sup> A. Danek<sup>2</sup> & B. M. Frey<sup>3</sup>

<sup>1</sup>Department of Neurology, University Hospital Zürich, Zürich, Switzerland

<sup>2</sup>Department of Neurology, Hospital of the University of Munich Großhadern, Ludwig-Maximilians-Universität, Munich, Germany

<sup>3</sup>Regional Blood Transfusion Service, Swiss Red Cross, Zürich, Switzerland

*Vox Sanguinis* (2007) 93, 112–121

Russo D et al. *J. Biol. Chem.* 1998;273:13950-13956

# Number of D-A-CH donors and donations 2006-2009-(2011)

		first time donors (FTD)	number of all donors (D)	inhabitants (Mio)	donors per 1'000 inh.	repeat rate per year	sum EC	sum TC	n Dneg of all D (17,5%)	n Dneg of all FTD (17,5%)	
<b>D</b>	<b>Deutschland</b>	<b>2006</b>	0.18	2'846'415	82.3	35	1.71	4'867'408	249'035	483'891	86'990
	<b>Germany</b>	<b>2007</b>	0.18	2'978'888	82.2	36	1.63	4'868'063	278'630	506'411	93'263
		<b>2008</b>	0.19	2'946'183	82.0	36	1.68	4'942'220	287'853	500'851	96'898
		<b>2009</b>	0.20	3'143'222	81.9	38	1.58	4'966'271	288'559	534'348	109'536
<b>A</b>	<b>Österreich</b>	<b>2006</b>	0.17	354'973	8.3	43	1.38	491'605	19'808	60'345	10'164
	<b>Austria</b>	<b>2007</b>	0.16	330'797	8.3	40	1.50	495'913	28'562	56'235	9'169
		<b>2008</b>	0.16	338'958	8.3	41	1.47	499'609	29'082	57'623	8'983
		<b>2009</b>	0.14	364'788	8.4	44	1.32	480'129	30'330	62'014	8'550
<b>CH</b>	<b>Schweiz</b>	<b>2006</b>	0.09	240'690	7.5	32	1.44	347'684	20'032	42'121	3'621
	<b>Switzerland</b>	<b>2007</b>	0.11	241'063	7.6	32	1.46	353'063	21'265	42'186	4'433
		<b>2008</b>	0.12	253'953	7.7	33	1.41	358'903	25'626	44'442	5'220
		<b>2009</b>	0.12	260'377	7.8	33	1.39	363'213	26'823	45'566	5'175
	<b>BSD SRK AG Statistik</b>	<b>2010</b>	0.11	233'313	7.9	30	1.61	376'360	31'776	40'830	4'470
	<b>BSD SRK AG Statistik</b>	<b>2011</b>	0.13	227'945	8.0	29	1.63	371'016	33'032	39'890	5'010
<b>Alle "D-A-CH"</b>	<b>all "D-A-CH"</b>	<b>2006</b>	0.17	3'442'078	98.1	35	1.66	5'706'697	288'875	602'364	100'774
		<b>2007</b>	0.18	3'550'748	98.1	36	1.61	5'717'039	328'457	621'381	106'865
		<b>2008</b>	0.18	3'539'094	98.0	36	1.64	5'800'732	342'561	619'341	111'102
		<b>2009</b>	0.19	3'768'387	98.0	38	1.54	5'809'613	345'712	659'468	123'261

2006-2009, Prof. Dr. med. Barbara Blauhut, Linz, Austria  
 2010-2011, BSD SRK AG, yearly statistic

# Why high-throughput molecular immunohematology?

Screen donors with RARE blood groups!

Do the “dry-match” = “*in silico* cross-match”!



## Applying molecular immunohematology discoveries to standards of practice in blood banks: now is the time.

Denomme GA, Flegel WA.

Department of Pathology & Laboratory Medicine, Mount Sinai Hospital, New York, USA.

### Abstract

Lessons from more than 100 years of immunohematology exemplify that many critical discoveries were made serendipitously and their more rapid implementation could have benefited transfusion recipients and pregnancies. Constituents of blood that are not essential for the attempted therapeutic benefit of a transfusion are largely removed from today's blood products. We are now moving on to avoid unnecessary exposure to potentially harmful constituents of the therapeutically required cells, like blood group antigens that are foreign to the patient. Cost efficacy needs to be kept in mind but may eventually prove much better than anticipated, once hidden benefits are captured, as we show by examples from past immunohematologic developments. Here, we detail clinical applications for molecular immunohematology advances including "dry-matching" that will improve transfusion outcomes and argue for their widespread implementation by rapid timelines through standards of practice.

... almost all human blood group polymorphisms are known: Kp, Lu, Di, Wr, Yt, Co, Kn, Do, In, LW, Sc, Jr, Lan...

# Reasoning for molecular blood group typing

blood

2009 114: 248-256  
Prepublished online May 1, 2009;  
doi:10.1182/blood-2008-11-146860

## Red cell genotyping and the future of pretransfusion testing

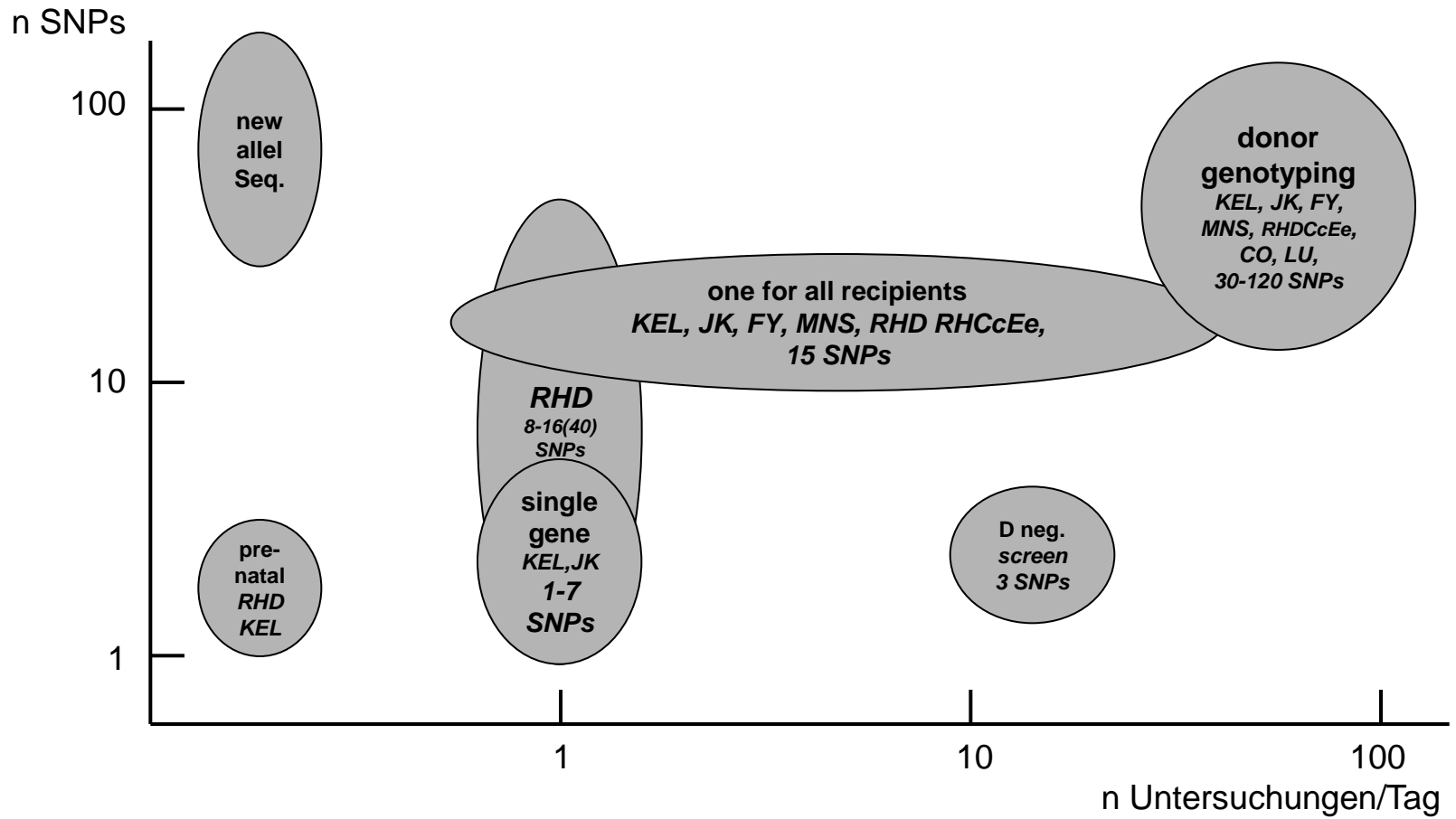
David J. Anstee

Table 1: Useful applications of red cell genotyping in transfusion medicine

- Fetal DNA typing
- Extensive blood group typing of donors for alloimmunized patients
- Determining the blood group of a recently transfused patient
- Screening blood donors to find rare blood group phenotypes
- Determining the frequency of blood group polymorphisms in a population
- Determining *RHD* zygosity for fathers of fetuses at risk for HDFN
- Blood group typing of patients with autoimmune hemolytic anemia

### Christoph Gassner:

1. Routine relevant determination of variant types of blood groups (e.g. *RHD*, *DARC*)
2. Screening RhD negatives for *RHD* (null) genes
3. "Academic" analysis of blood group phenotypes



# Comercially available platforms for molecular blood group typing

platform	PCR-SSP, or ARMS	MALDI-TOF MS genotyping	Chip technology	Chip technology	Luminex technology (xMAP®)	Luminex technology (xMAP®)
<b>product example</b>	RBC Ready Gene	open	BLOODchip <sup>D</sup>	BioArray BeadChip™	BLOODchip ID LINE (xMAP®)	LIFECODES RBC-R assay
<b>company</b>	Inno-Train, Kronberg i.T., Germany	SEQUENOM®, San Diego, USA	Grifols, Barcelona, Spain	Immucor, Norcross, USA	Grifols, Barcelona, Spain	Gen-Probe, San Diego, USA
<b>commercial availability since</b>	1998	(2013)	2008	~ 2009	~ 2010	2010
<b>relevant early citation(s)</b>	Gassner et al 1996 ABO, Gassner et al 1997 RHD	Henk Garritsen, Transfus Med Hemother. 2009;36(3):181-187.	Avent, Flegel, Olsson, Transfus Med Hemother. 2009;36(3):162-167.	Hashmi G, Shariff T, Transfusion. 2005 May;45(5):680-8.	Drago F, Karpasitou K, Poli F., Transfus Med Hemother. 2009;36(3):157-160.	Drago F, Karpasitou K, Poli F., Transfus Med Hemother. 2009;36(3):157-160.
performance specs						
<b>tailoring of specificities ("unit")</b>	RBC Ready Gene ABO, 8 rctns., 4SNPs	module <i>RH</i> broad panel (3 MPX)	138 genetic polymorphisms	HAE BeadChip™	ID Core for 23 RBC antigens	RBC assay, 1 MPX, ~16 SNPs
	RBC Ready Gene CDE, 16 rctns., ~19 SNPs	module <i>RH</i> variant panel (2 MPX)	(including 12 SNPs for HPA)	RHCE BeadChip™	ID Core+ for 33 RBC antigens	RBC-R assay, 1 MPX, ~14 SNPs
	RBC Ready Gene KKD, 8 rctns., 5 SNPs	module <i>KEL, JK, FY</i> (1 MPX)	(including ABO genotyping)	RHD BeadChip™	ID HPA for 24 platelet antigens	.
	RBC Ready Gene MNS, 6 rctns., 4 SNPs	module <i>MNS</i> (2 MPX)	.	HPA BeadChip™	.	.
	RBC Ready Gene Rare ID, 16 rctns., 8 SNPs	module <i>RARE</i> blood group panel (2 MPX)	.	.	.	.
	and > 5 additional	module <i>HPNA</i> (1 MPX)	.	.	.	.
<b>highest level of certification</b>	CE self declared	in house validation in preparation	CE according to appendix II, list A (selected specificities)	CE according to appendix II, list A (some units)	n.a.	currently RUO, CE according to appendix II, list A in preparation
<b>single specificity (blood group) typing possible</b>	YES	(YES)	NO	(YES)	NO	NO
<b>single sample testing</b>	consists of 4 to 16 single PCR-SSPs per tailored specificity	consists of 1 to 5 MPX per module	consists of 1 MPX, analyzed on 1 individual chip	consists of 1 MPX, analyzed on 1 individual chip per tailored specificity	consists of 1 MPX, analyzed on 96-w MTP format	consists of 1 MPX, analyzed on 96-w MTP format
<b>single sample testing (cost efficiency)</b>	YES	NO (minimum of 96 MPX reactions in 96-w MTP format)	n.a.	n.a.	n.a.	1 sample, 1 unit (waste of sheath fluid, only)
<b>ideal number of samples processed per run (cost efficiency)</b>	e.g. 12 <i>KEL, JK, FY</i> genotypings, each consisting of 8 PCR-SSPs, processed in 96-w MTP format	384-w MTP format: 384 MPX reactions	24 samples	n.a.	96-w MTP format: 96 MPX reactions	96-w MTP format: 96 MPX reactions
<b>post DNA-prep</b>	2.5 h	10 h	10 h	6 h	5 h	4.5 h
Costs						
<b>hardware-1 description</b>	standard Agarose gel electrophoresis	384-w MTP format Sequenom Mass Spectrometer plus 2 X 96-w robots, plus 1 spotter	detailed instrument name n.a.	n.a.	detailed instrument name n.a.	Luminex® 100/200™
<b>hardware-1 costs (in Euro)</b>	negligible	~ 500.000,00	~ 105.000,00	~ 110.000,00	~ 40.000,00	~ 40.000,00
<b>consumables example 1</b>	RBC Ready Gene KKD, 8 rctns., 5 SNPs	module <i>KEL, JK, FY</i> (1 MPX)	BLOODchip <sup>D</sup>	HAE BeadChip™	ID Core for 23 RBC antigens	RBC assay, ~16 SNPs
<b>consumables example 2</b>	RBC Ready Gene MNS, 6 rctns., 4 SNPs	module <i>MNS</i> (2 MPX)	(including 12 SNPs for HPA)	.	ID Core+ for 33 RBC antigens	RBC-R assay, ~14 SNPs
<b>consumables example 3</b>	RBC Ready Gene Rare ID, 16 rctns., 8 SNPs	module <i>RARE</i> blood group panel (2 MPX)	(including ABO genotyping)	.	ID HPA for 12 HPA antigens	.
<b>consumables per sample and sum of examples 1-3 (in Euro)</b>	~ 75,00 to 90,00	~ 40,00 to 50,00	~ 185,00	~ 130,00	~ 85,00 to 98,00	~ 80,00 to 100,00

Matrix Assisted Laser Disorption Ionisation –  
**MALDI-**

Time Of Flight  
**TOF**

Mass Spectrometry  
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GenoTyping  
**GT**

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# MALDI-TOF principle on Js(a+b+), *KEL\*01* | *KEL\*02*

amplification primer  
GGCGCATCTCTGGTAAA 

CTTGAGGCTGGCGCATCTCTGGTAAATGGACTTCCTTAAACTTTAACCGAA **C** GCTGAGACTTCTGATGAGTCAGTATGGCCATTTCCCTTTCTTCAGAG

CTTGAGGCTGGCGCATCTCTGGTAAATGGACTTCCTTAAACTTTAACCGAA **C** GCTGAGACTTCTGATGAGTCAGTATGGCCATTTCCCTTTCTTCAGAG

*KEL\*07/07*, Js(a-b+)

 CGGTAAAGGGAAAGAAGT  
amplification primer

extension primer

TTAAACTTTAACCGAA **C** **5'882 Dalton**

**STEP 2: ddNTP extension**

CTTGAGGCTGGCGCATCTCTGGTAAATGGACTTCCTTAAACTTTAACCGAA **C** GCTGAGACTTCTGATGAGTCAGTATGGCCATTTCCCTTTCTTCAGAG

TTAAACTTTAACCGAA **T** **5'898 Dalton**

CTTGAGGCTGGCGCATCTCTGGTAAATGGACTTCCTTAAACTTTAACCGAA **T** GCTGAGACTTCTGATGAGTCAGTATGGCCATTTCCCTTTCTTCAGAG

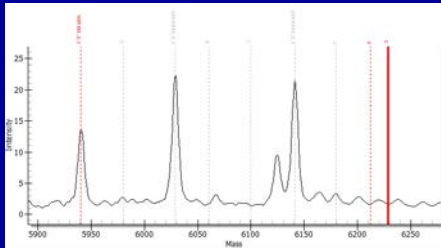
*KEL\*06/07*, Js(a+b+)

CTTGAGGCTGGCGCATCTCTGGTAAATGGACTTCCTTAAACTTTAACCGAA **T** GCTGAGACTTCTGATGAGTCAGTATGGCCATTTCCCTTTCTTCAGAG

CTTGAGGCTGGCGCATCTCTGGTAAATGGACTTCCTTAAACTTTAACCGAA **T** GCTGAGACTTCTGATGAGTCAGTATGGCCATTTCCCTTTCTTCAGAG

*KEL\*06/06*, Js(a+b-)

# spectrogram of three different Js<sup>a</sup>/Js<sup>b</sup> (KEL\*06 | KEL\*07) DNAs



**MALDI-TOF mass spectrometry**  
measures molecular weight (in Dalton)  
of extension primers (5'612)  
plus 1 extended base.

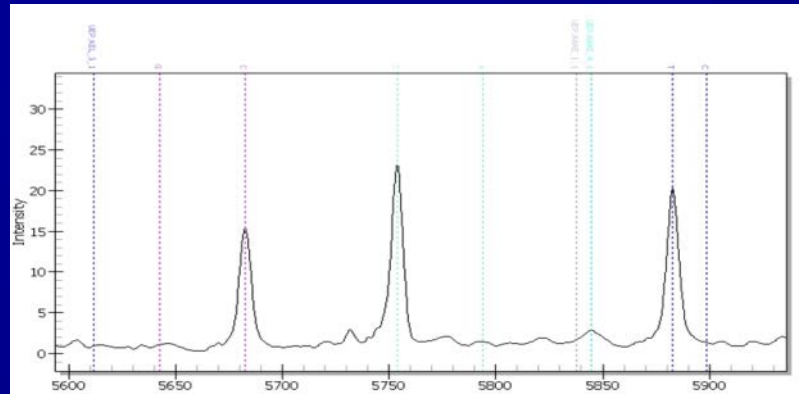
Heterozygous samples show 2 different  
molecular weights for those primers at  
about 5'882 and 5'898 Dalton (all  
indicated by arrow).

Other specific peaks are results of other  
bloodgroup SNPs, detected in multiplex  
in the same PCR.

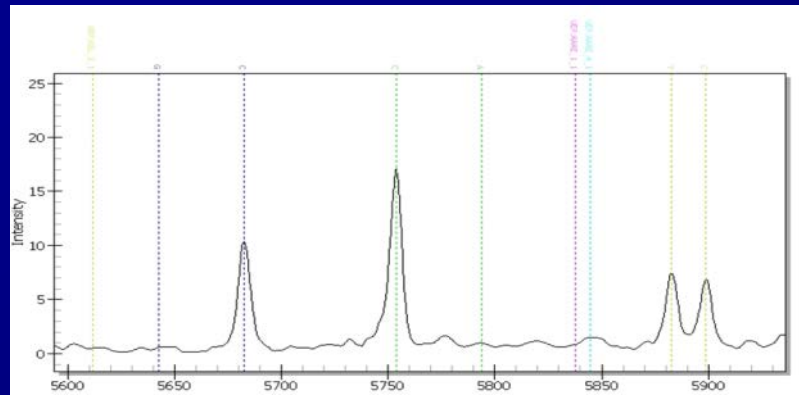
Primer unextended  
~5'612



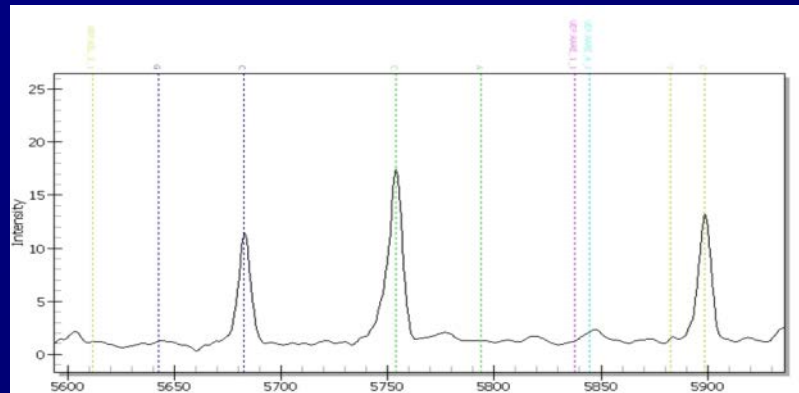
extended  
~5'882 | ~5'898



Js(a+b-)  
KEL6 | KEL6



Js(a+b+)  
KEL6 | KEL7

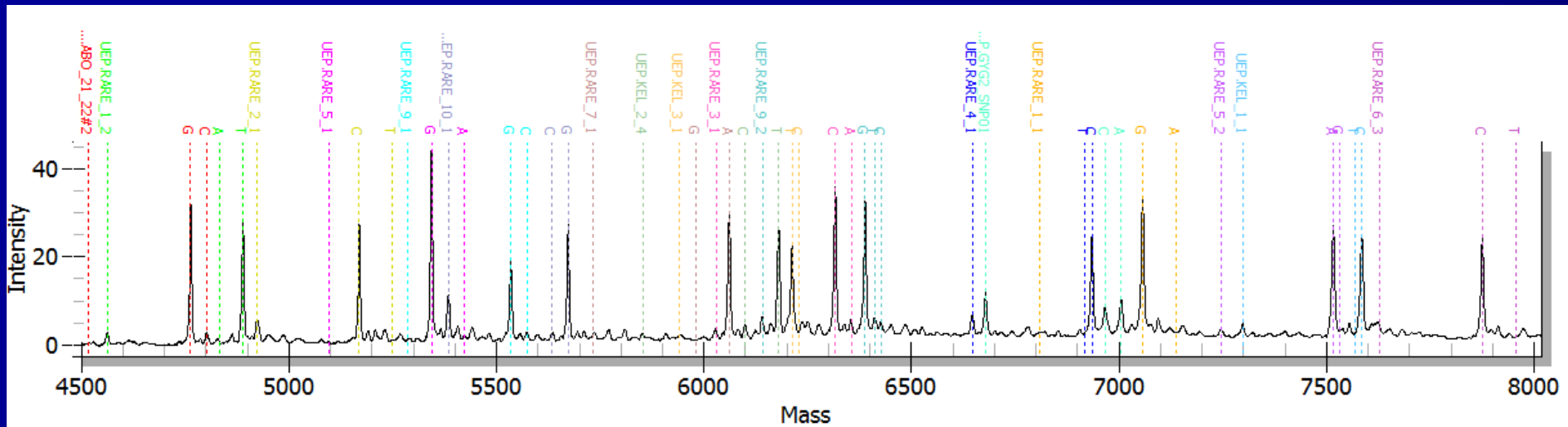


Js(a-b+)  
KEL7 | KEL7



Matrix Assisted Laser Desorption Ionisation – Time Of Flight

# MALDI-TOF spectrogram of a “RARE” multiplex including 22 assays (=22 SNPs)



Kk, Kp, Suter, KEL11/17,  
Lutheran, LU08/14, Auberger  
Diego, Wright,  
Cartwright,  
Colton,  
Knops, McCoy,  
Dombrock, Holley, Joseph  
Scianna,  
Landsteiner-Wiener,  
Cromer, Tc  
Indian

Primer ▲ ▲▲  
unextended ~7'298 extended ~7'569 | ~7'585

... 46 antigens

Matrix Assisted Laser Disruption Ionisation –  
**MALDI-**

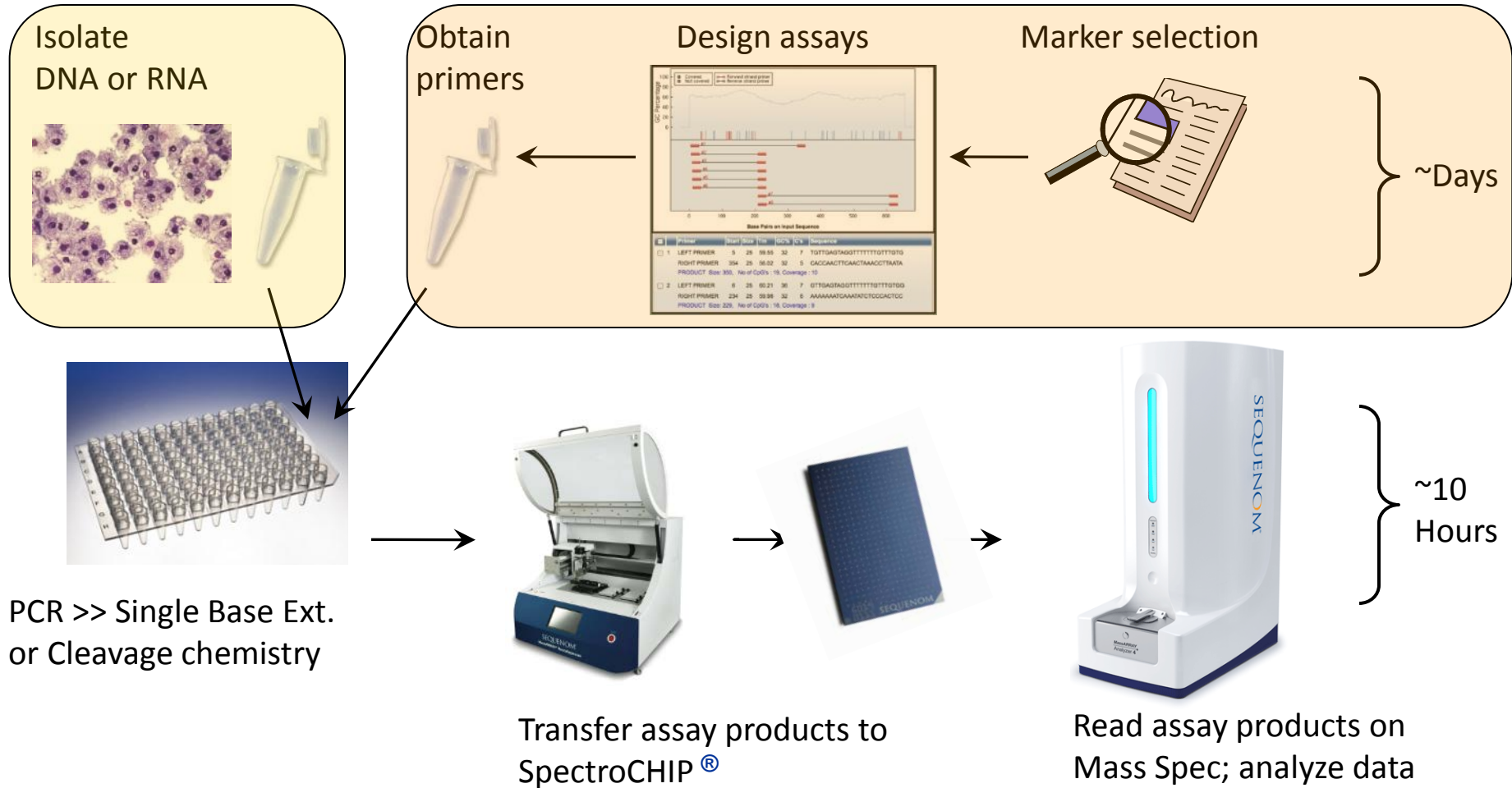
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# Typical MassARRAY<sup>®</sup> Assay Workflow



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# projects to come ... participants are **exemplary** and not confirmed yet

Financial support granted by the Humanitarian Foundation of the Swiss Red Cross, Blutspende Zürich, Blutspende SRK Schweiz and Sequenom GmbH.

**RHD** *broad* / *RHCE*

3<sub>(30)</sub>

**RHD** *high*

2<sub>(20)</sub>

**KELL**-*JK*-*FY*

1<sub>(15)</sub>

**MNS**

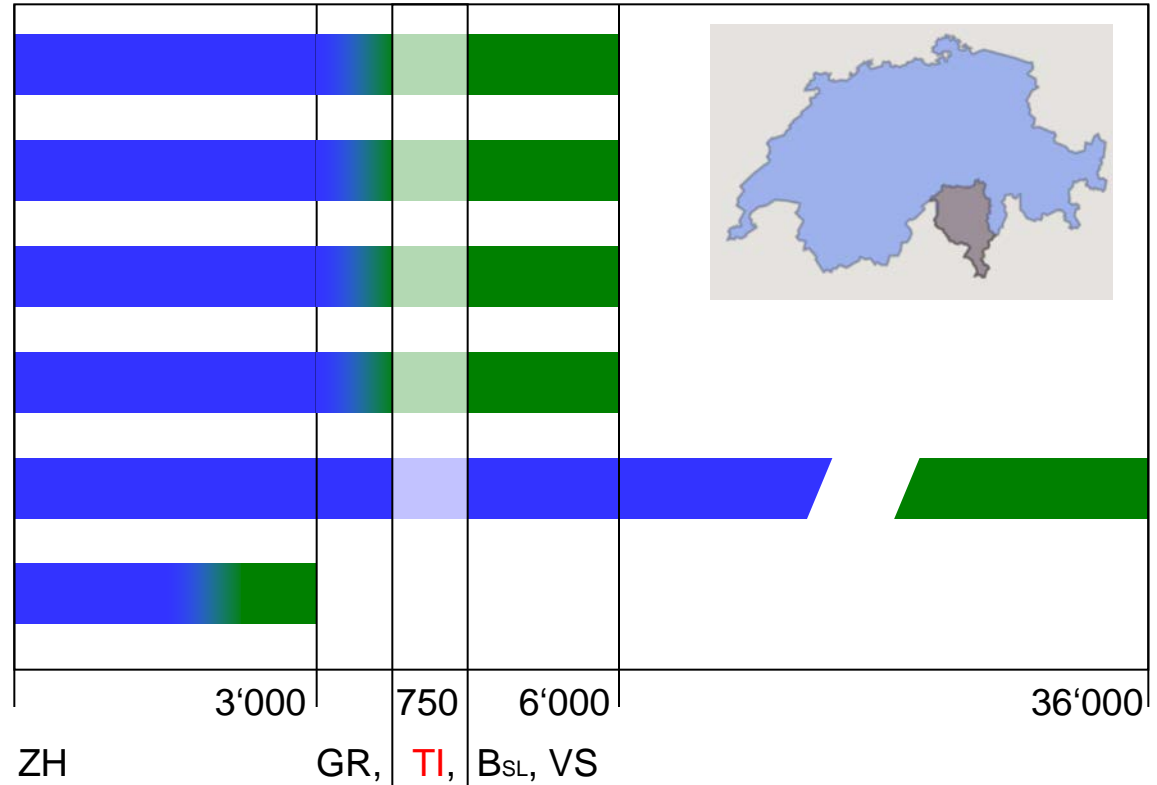
2<sub>(10)</sub>

**Public** *vs RARE*

2<sub>(25)</sub>

**HPA / HNA**

1<sub>(14)</sub>



From 2011 for 3 years:

3'000 DNAs for **HPA/HNA**

36'000 DNAs for **Public vs Rare**

6'000 DNAs for **RHDCE, KEL, JK, FY, MNS**

50% (minimum) of all DNAs will be from the **canton of Zurich**.  
other 50% (maximum) from **other Swiss areas**.

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# MALDI-TOF MS GT modules KEL-JK-FY, MNSs, “rare”

module name	genes	positions on genes, (trivial) (allele) names, additional information	n MPX	n SNPs	n alleles	n antigens
<b>KEL-JK-FY</b>			<b>1</b>	<b>15</b>	<b>21</b>	<b>19</b>
	KEL	K/k, Kp, Js, e.g. KEL(ISVS3+1g>a)null & 5 others, KEL(1719C>T)mod		9	11	10
	SLC14A1	Jk, JK(IVS5-1g>a)null & 2 others, JK(582C>G)		3	6	4
	DARC	Fy, -67T>C, FYX		3	4	5
	GYG2, AMXY	cross-ID-control		2	2	0
<b>MNSs§</b>	GYPA, GYPB, GYPE	<b>currently under development</b>	<b>2</b>	<b>11</b>	<b>15</b>	<b>16</b>
<b>"rare antigens"</b>			<b>2</b>	<b>22</b>	<b>34</b>	<b>46</b>
	KEL	K/k, Kp, Js, KEL11/17		4	5	8
	LU	Lu, LU8/14, Au		3	4	6
	Band 3	Di, Wr		2	3	4
	ACHE	Yt		1	2	2
	AQP1	Co		1	2	2
	CR-1	Kn, McC, Sl		3	4	6
	ART4	Do, Hy, Jo		3	4	6
	ICAM4	LW		1	2	2
	ERMAP	SC		1	2	2
	DAF	Cr, Tc		2	4	6
	CD44	In		1	2	2
	GYG2, AMXY, ABO	cross-ID-control, ABO positions: 261, 802, 803		5	6	0

# MALDI-TOF MS GT modules RH, HPA-HNA

module name	genes	positions on genes, (trivial) (allele) names, additional information	n MPX	n SNPs	n alleles	n antigens
<b>RH</b>	<b>RHCE, RHD</b>		<b>5</b>	<b>49</b>	<b>~79</b>	<b>28</b>
	RHC, RHc , RHCw	122, 201, 307, i2		4	3	4
	RHE, Rhe	676 generic and on RHCE only		2	2	2
	RHD exons	-132, i1+18, 455, 514, 787, 916, 968, i7-327, 1048, 1170, 1193, 1359		12	~45	2
	RHD categories & partials	VII, DFL, DOL, DVL-2, V(697A), weak type 4.0-3, 11, 15, DNB, DAU		11	11	18
	RHD weaks	1, 1.1, 2, 3, 5, 17		6	6	0
	RHD DELs	delA147, IVS3+1g>a, IVS3+2T>A, K409K, X418L		5	5	2
	RHD nulls	W16X, Dces type 1 & 2, RHD-CE(2-9)-D 2 subtypes, RHDpsi, Y401X		9	7	0
	GYG2, AMXY, ABO	cross-ID-control, ABO positions: 261, 803		5	5	0
<b>HPNA</b>	e.g. ITGB3, FCGR3b, SLC44A2		<b>1</b>	<b>13</b>	<b>25</b>	<b>23</b>
	HPA	HPA-1 to 6, 15		7	14	14
	HNA	HNA-1, 3 to 5		6	9	9
	AMXY	cross-ID-control		1	2	0
		redundancy of "rare" to "KEL-JK-FY"		-3	-4	-6
		<b>total different blood (platelet, granulocyte) groups</b>	<b>11</b>	<b>107</b>	<b>170</b>	<b>132</b>
		<b>total different cross-ID-controls</b>		<b>5</b>	<b>6</b>	n.a.

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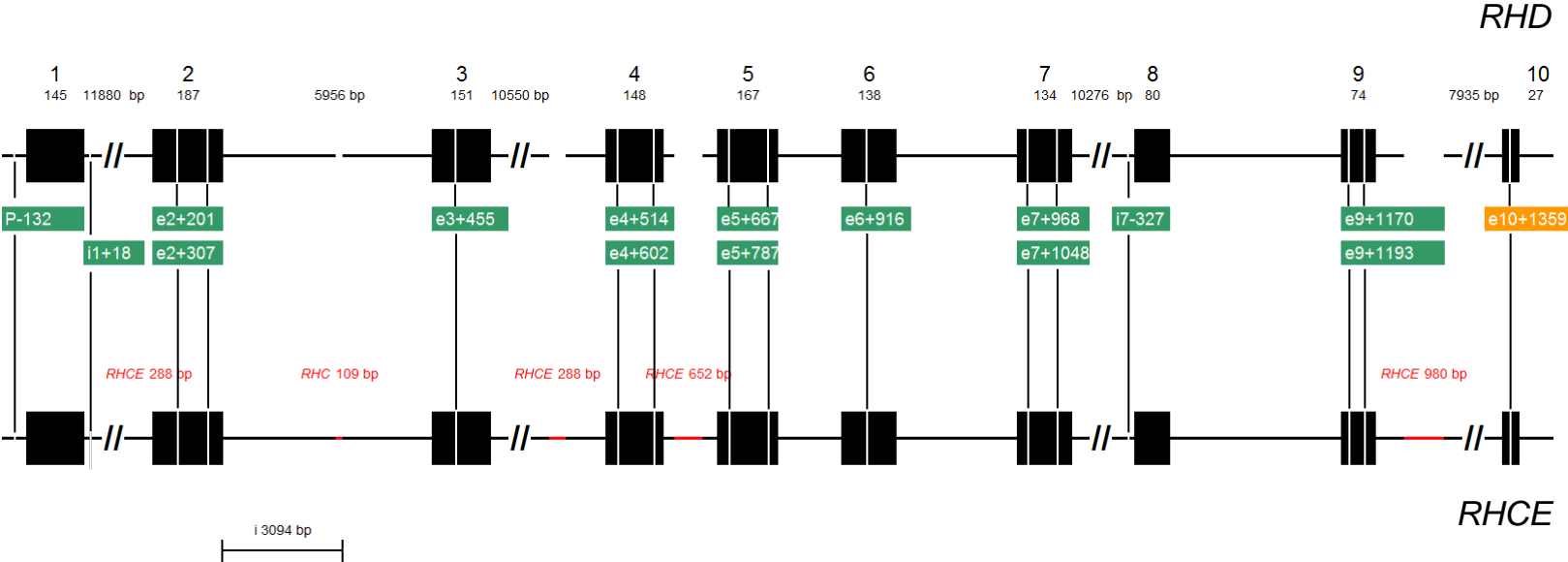
# MALDI-TOF MS GT results on “rare typing“ 3.040 individuals

antigen	ISBT allele	observed "rare" allele frequency (%), MALDI-TOF MS	n observed "rare" homozygous carriers (in 3.040)	n expected "rare" homozygous carriers (in 3.040)	n expected "rare" homozygous carriers (in 36.000)	n expected "rare" homozygous carriers in Switzerland (8 Mio)
K	<i>KEL*01</i>	0.0395	4	4.7	56	
Kp <sup>a</sup>	<i>KEL*02.03</i>	0.0107	1	0.3	4	
Js <sup>a</sup>	<i>KEL*02.06</i>	0.0008	0	0.0	0	5.5
KEL17	<i>KEL*02.17</i>	0.0013	0	0.0	0	14.2
Lu <sup>a</sup>	<i>LU*01</i>	0.0370	5	4.1	49	
LU14	<i>LU*02.14</i>	0.0093	2	0.3	3	
LU19	<i>LU*02.19</i>	0.3182	313	303.9	3646	
Di <sup>a</sup>	<i>DI*01</i>	0.0002	0	0.0	0	0.2
Wr <sup>a</sup>	<i>DI*02.03</i>	0.0003	0	0.0	0	0.9
Yt <sup>b</sup>	<i>YT*02</i>	0.0648	14	12.6	151	
Co <sup>b</sup>	<i>CO*02</i>	0.0333	2	3.3	40	
Kn <sup>b</sup>	<i>KN*02</i>	0.0283	5	2.4	29	
McC <sup>b</sup>	<i>KN*01.06</i>	0.0003	0	0.0	0	0.9
Vil	<i>KN*01.07</i>	0.0018	0	0.0	0	26.7
Do <sup>a</sup>	<i>DO*01</i>	0.4061	487	495.8	5936	
Hy neg	<i>DO*02.-04</i>	0.0007	0	0.0	0	3.5
Jo <sup>a</sup> neg	<i>DO*01.-05</i>	0.0000	0	0.0	0	0.0
LW <sup>b</sup>	<i>LW*07</i>	0.0040	0	0.0	1	
SC:2	<i>SC*02</i>	0.0000	0	0.0	0	0.0
Cr <sup>a</sup> neg	<i>CROM*-01</i>	0.0002	0	0.0	0	0.2
Tc <sup>b</sup>	<i>CROM*01.03</i>	0.0002	0	0.0	0	0.2
Tc <sup>c</sup>	<i>CROM*01.04</i>	0.0008	0	0.0	0	5.6
In <sup>a</sup>	<i>IN*01</i>	0.0000	0	0.0	0	0.0

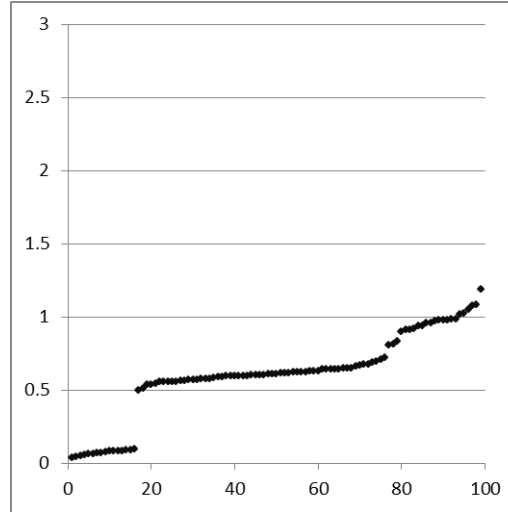
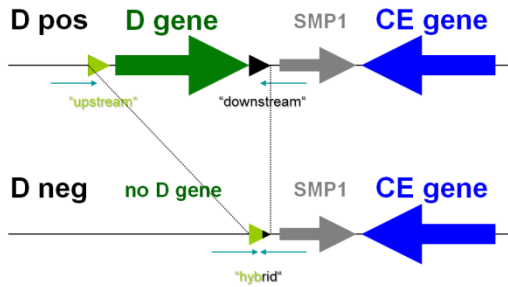
# MALDI-TOF MS results on HPA/HNA typing 1.520 individuals

group system	allele	allele-frequency MALDI-TOF MS	allele-frequency Switzerland	allele-frequency Austria	allele-frequency Germany
HPA	1b	0.147	0.191	0.148	0.161
	2b	0.090	0.109	0.082	0.090
	3b	0.334	0.407	0.388	0.414
	4b	0.000	0.000	0.000	0.000
	5b	0.106	0.066	0.108	0.083
	15b	0.490	n.a.	0.500	n.a.
HNA	1b	0.621	n.a.	n.a.	0.601
	1c	0.033	n.a.	n.a.	0.008
	3b	0.207	n.a.	n.a.	0.256
	4b	0.117	n.a.	n.a.	0.092
	5b	0.276	n.a.	n.a.	0.269

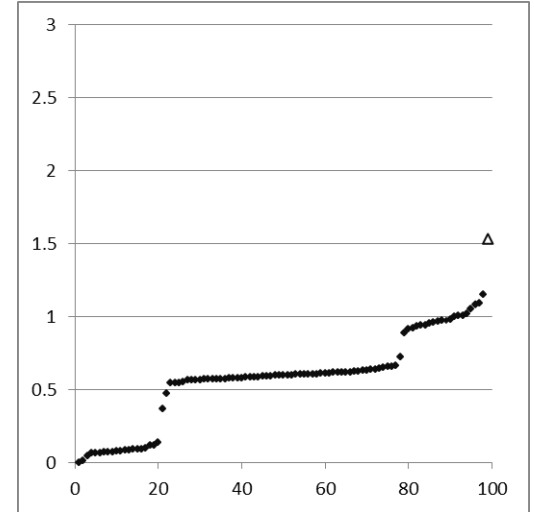
# Specificities: *RHD*: zygosity is detectable...



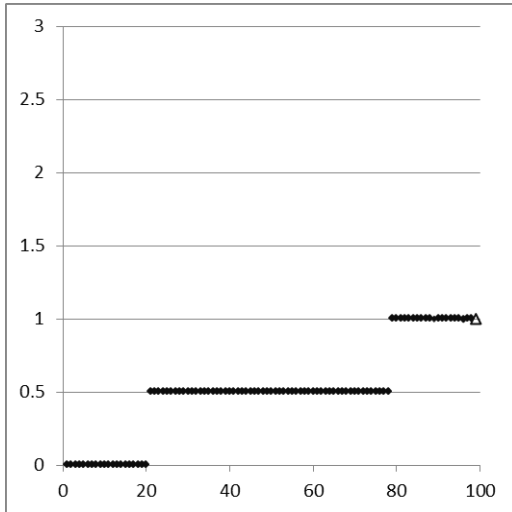
# MALDI-TOF MS GT results on *RHD* zygosity



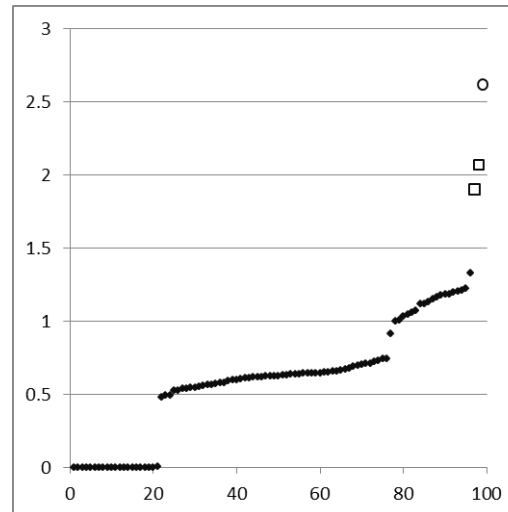
*RH* Intron 1, +18



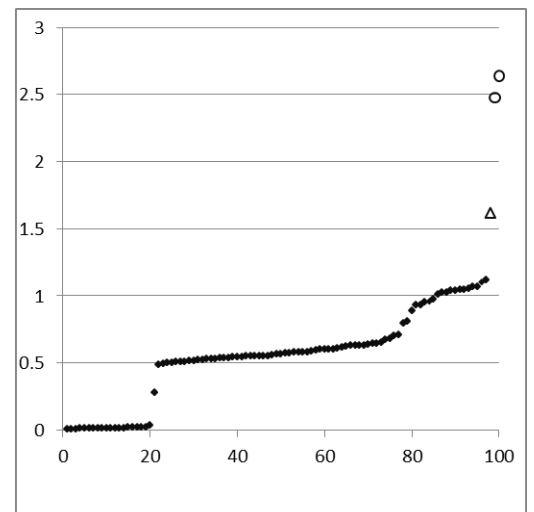
*RH* exon 3, 455



theoretically

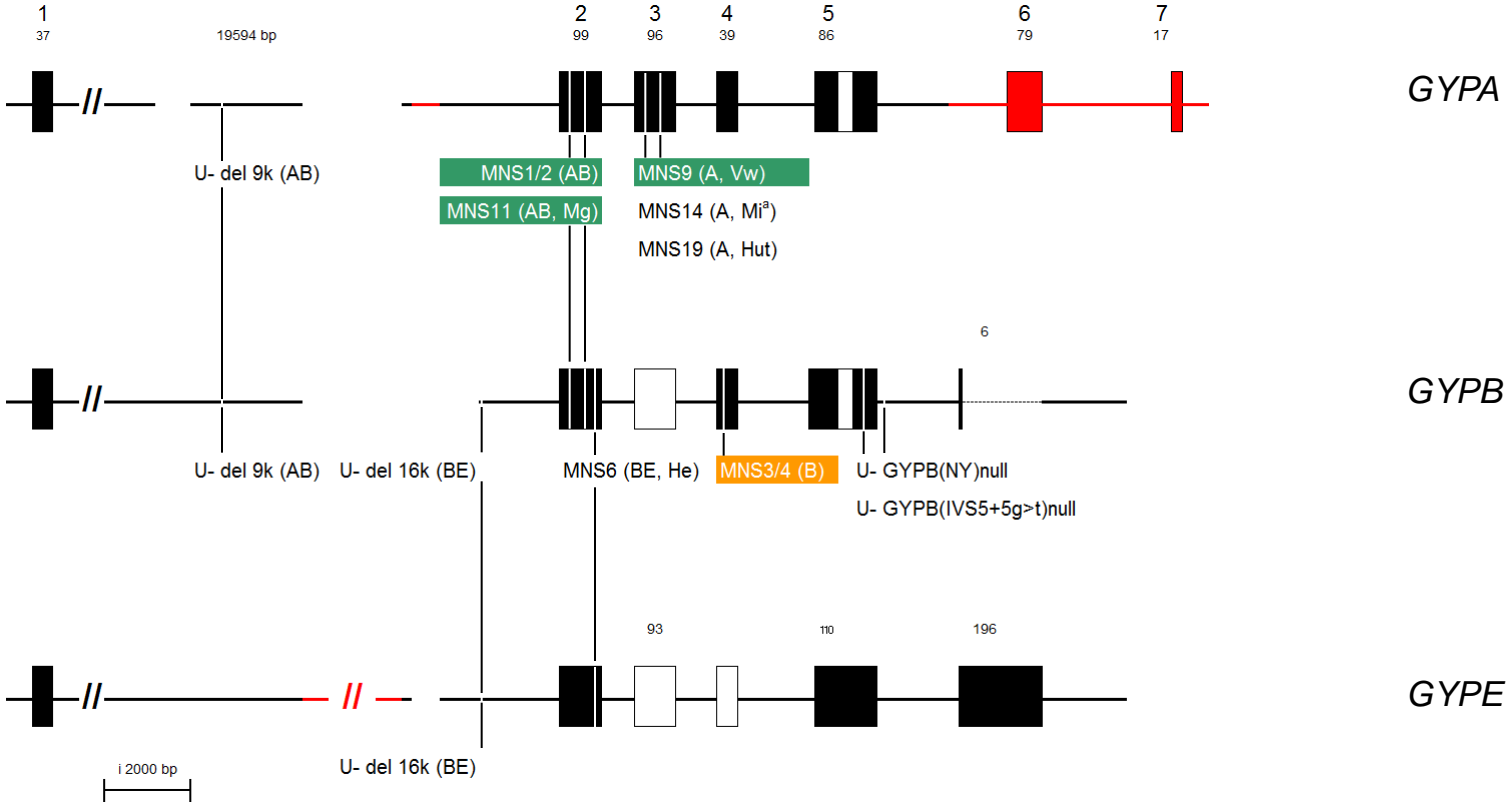


*RH* exon 6, 916



*RH* exon 9, 1170

# Specificities: *MNS*, prototype 2





Matrix Assisted Laser Disruption Ionisation –  
**MALDI-**

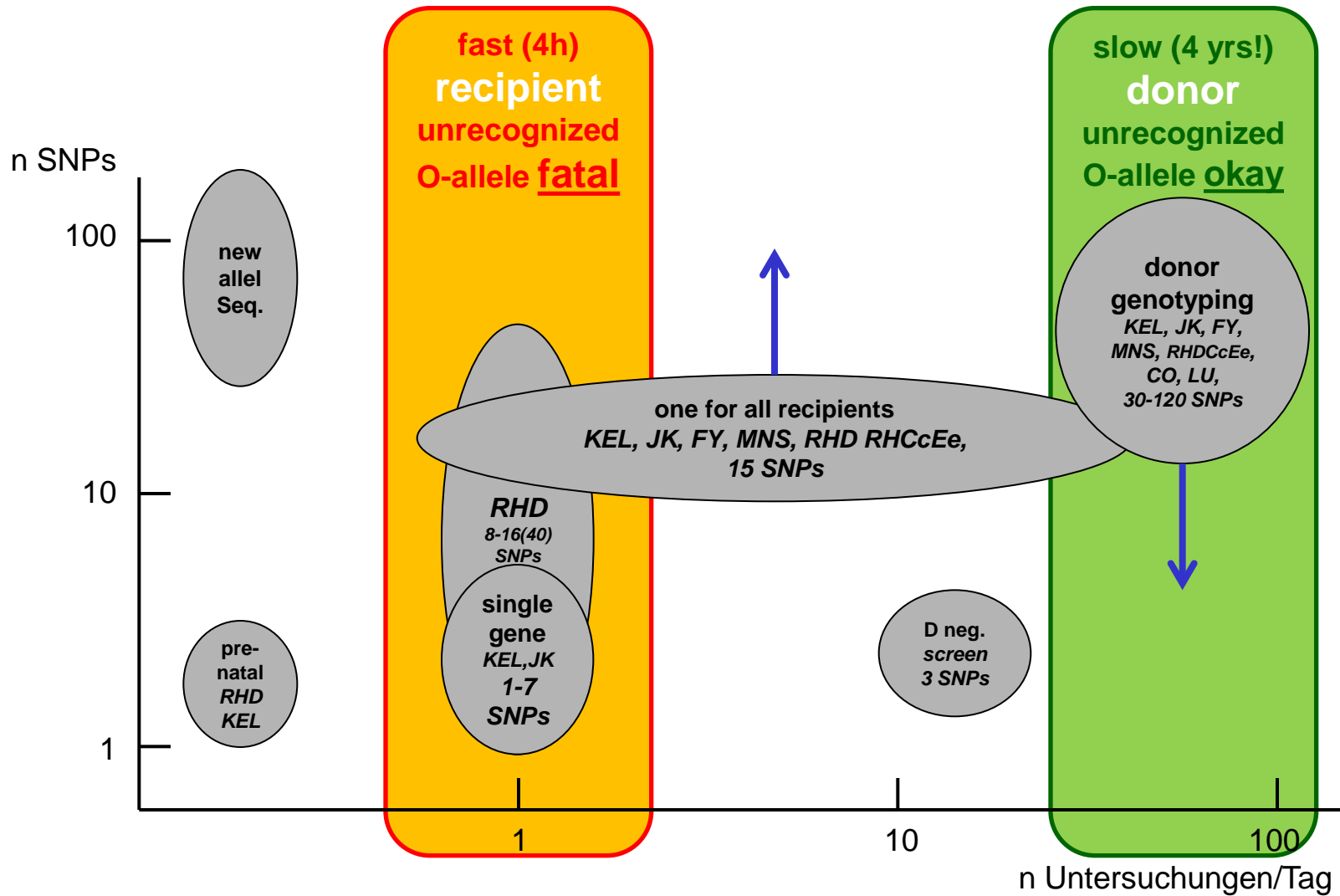
Time Of Flight  
**TOF**

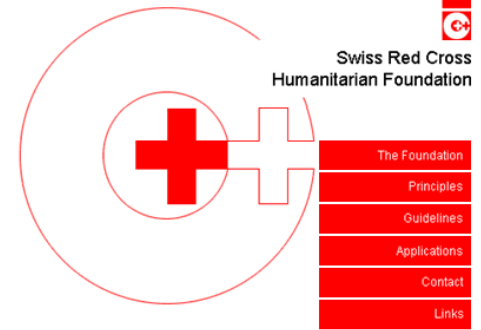
Mass Spectrometry  
**MS**

GenoTyping  
**GT**

- technological principle
- hardware
- a Swiss project
- the modules
- current results
- **conclusion**

# Methods & Indication | Resolution & Throughput





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PERSONELL, ADMIN, QM, IT, SCREENING, CENTERS & DRIVE-OUTS Blutspende Zürich, Schlieren, Switzerland**

