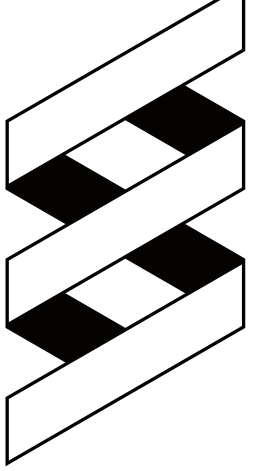


A promising single DNA-based assay to test for hemoglobinopathies, congenital adrenal hyperplasia, cystic fibrosis, spinal muscular atrophy and severe combined immunodeficiency for newborn screening



MRC
Holland

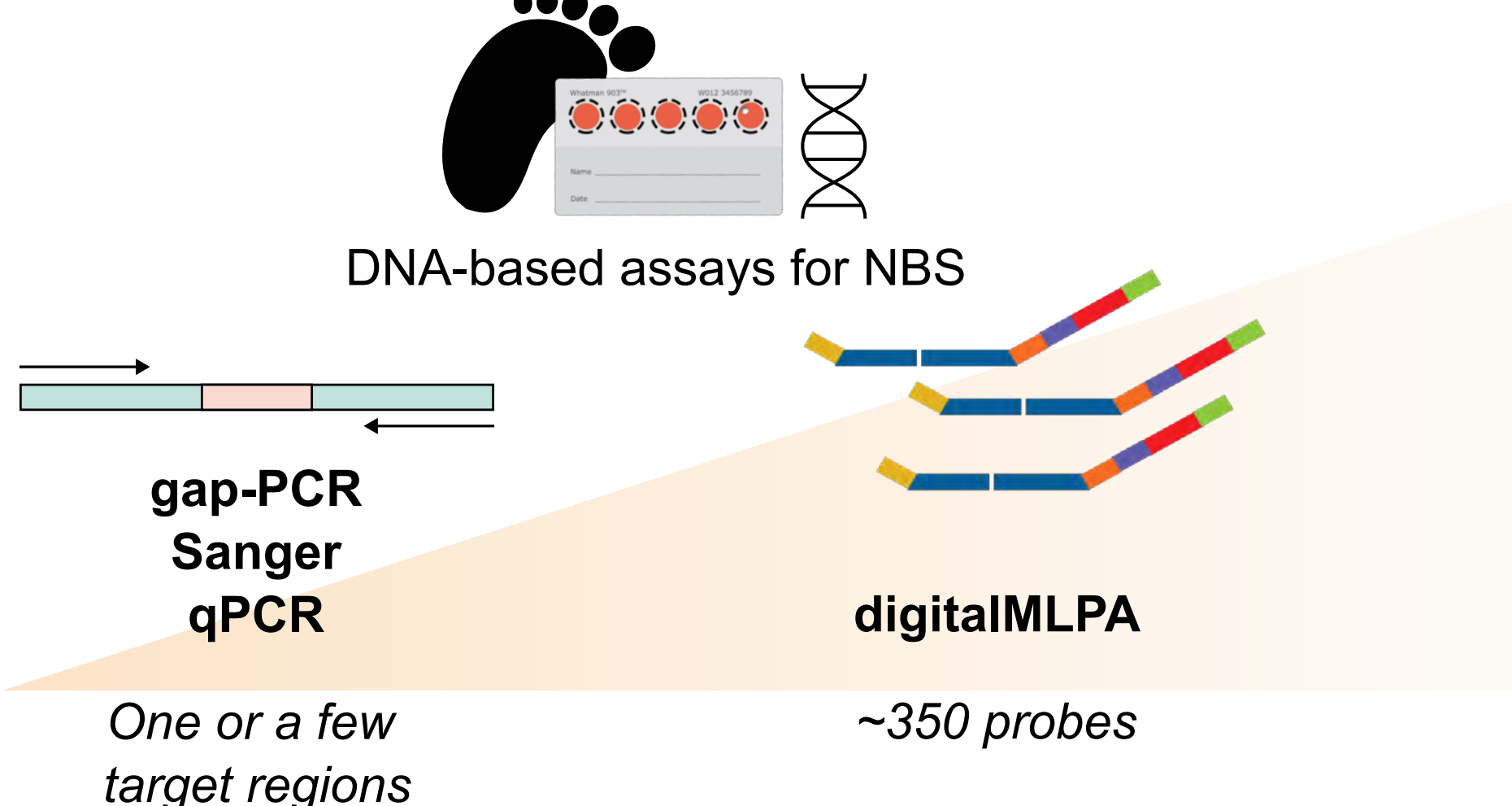
RESEARCH

P23.050.D

Joery den Hoed¹, Adinda Heuperman², Sen Kuilboer¹, Ingrid Pico-Knijnenburg², Terence Fabella^{1,3}, Mirjam van der Burg, Jan Schouten¹
1. MRC Holland, Amsterdam, the Netherlands; 2. Department of Pediatrics, Laboratory for Pediatric Immunology, Leiden University Medical Center, Leiden, The Netherlands
3. Human genetics department, Amsterdam UMC, Locatie Vrije Universiteit, Amsterdam, the Netherlands

digitalMLPA for the analysis of SNVs and CNVs associated with five newborn conditions

Newborn screening (NBS) programs rely primarily on biochemical tests for the detection of severe early-onset disorders. DNA-based techniques provide opportunities for confirmatory testing and expansion of newborn screening panels. However, currently used methods (e.g. Sanger sequencing, qPCR) often only target one or a handful of regions and therefore still require a condition-specific workflow. We are developing a **SALSA® digitalMLPA™** assay consisting of ~350 probes that detect single nucleotide variants (SNVs) and copy number variants (CNVs) associated with five conditions included in many NBS programs: severe combined immunodeficiency (SCID), spinal muscular atrophy (SMA), hemoglobinopathies (HbPs), cystic fibrosis (CF) and congenital adrenal hyperplasia (CAH; **Figure 1, Table 1**). In this study we highlight our results on SCID and HbPs.



digitalMLPA probemix (newborn test version)

SCID

TCRA/D
TCRB
TCRG
TREC

SMA

SMN1
SMN2

CF

CFTR

HbPs

HBA1/HBA2
HBB

CAH

CYP21A2

Figure 1. Left, schematic comparison of digitalMLPA to DNA-based assays currently used in NBS. Right, an overview of the targeted regions of the digitalMLPA probemix currently in development.

digitalMLPA: a two-day workflow using low amounts of DNA

digitalMLPA is a multiplex PCR-based method that uses Illumina sequencing platforms for amplicon detection. The workflow of digitalMLPA is illustrated in **Figure 2**.

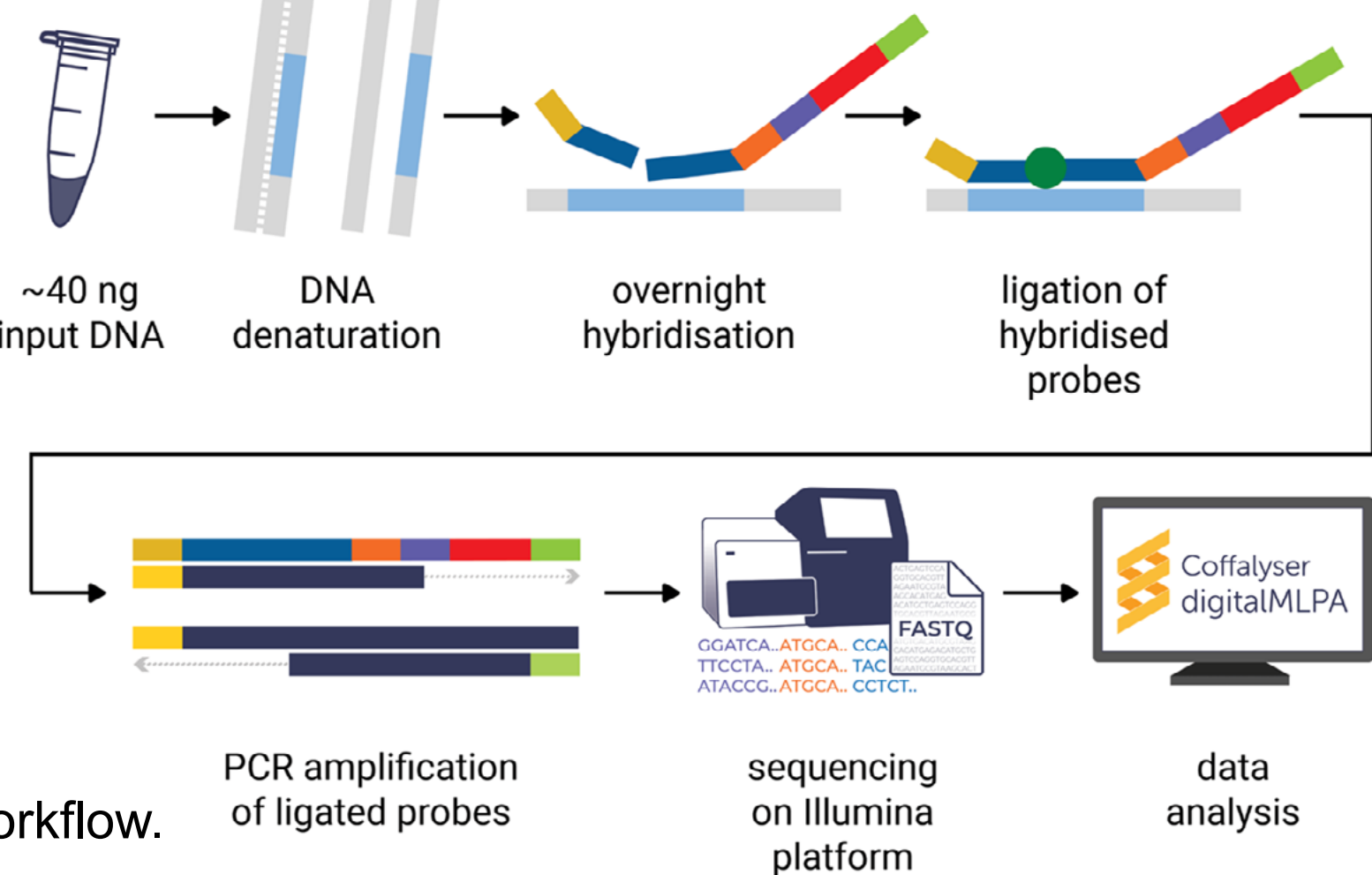


Figure 2. digitalMLPA workflow.

Table 1. Coverage of the probemix (in development)

Condition	Target	Coverage
SCID	T cell excision circles (TREC)	sjTREC and cjTREC
	TCRA, TCRB, TCRD, TCRG	Detection of rearrangements of the variable TCR regions
SMA	SMN1/SMN2	CNVs of SMN1 exon 7, SMN2 copy number determination
HbP	HBA1/HBA2	CNVs and 6 frequent pathogenic SNVs
	HBB	CNVs and 14 frequent pathogenic SNVs
CF	CFTR	CNVs and 33 frequent pathogenic SNVs
CAH	CYP21A2	CNVs and 11 frequent pathogenic SNVs

Detection of distinct HBA deletions as well as six frequent missense variants in HBA1 and HBA2

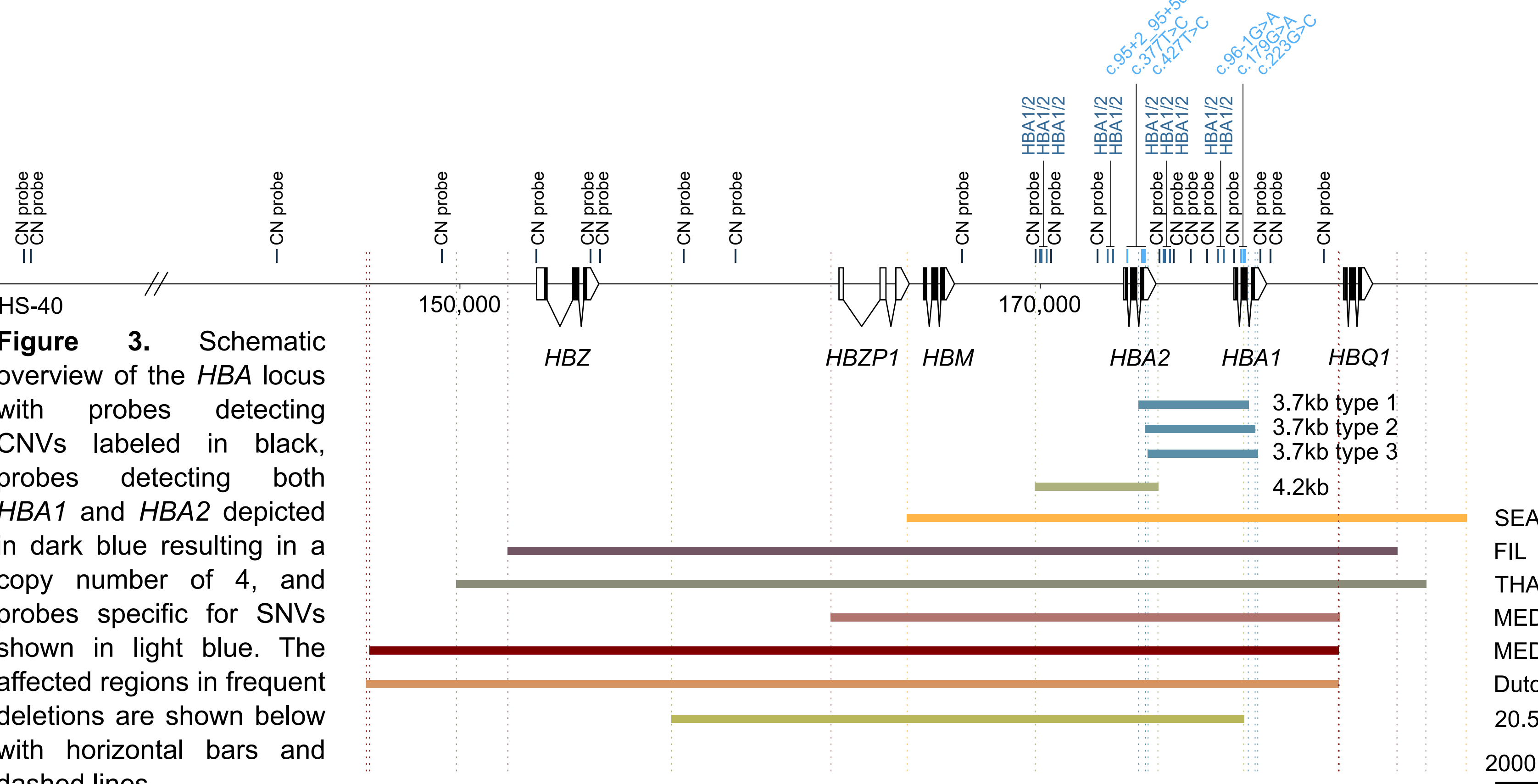


Figure 3. Schematic overview of the *HBA* locus with probes detecting CNVs labeled in black, probes detecting both *HBA1* and *HBA2* depicted in dark blue resulting in a copy number of 4, and probes specific for SNVs shown in light blue. The affected regions in frequent deletions are shown below with horizontal bars and dashed lines.

Alpha-thalassemia is caused by reduced production of the alpha-globin chain, encoded by *HBA1* and *HBA2*. The *HBA* locus is a complex region, with *HBA1* and *HBA2* being almost identical. About 85-90% of cases are caused by deletions of varying size in this region. Some of these deletions also affect *HBZ* (**Figure 3**), which causes embryonic lethality. The digitalMLPA probes are able to detect various of these frequent deletions (**Figure 3 and 4**).

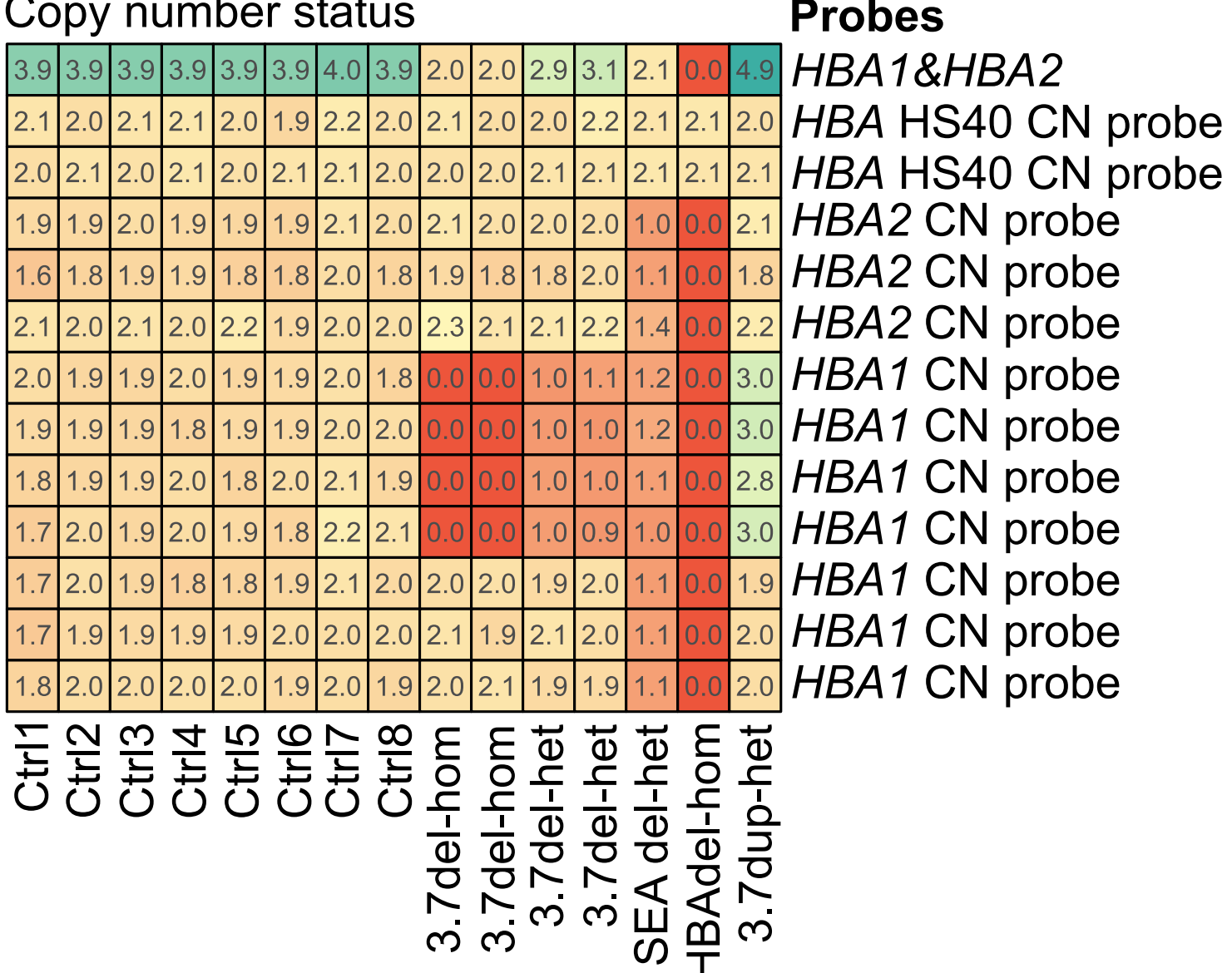


Figure 4. Heatmap indicating the copy number status of 15 samples (columns) obtained using a selection of *HBA1*/*HBA2* probes (rows). The top row shows the median signal for the probes that recognize both *HBA1* and *HBA2*. Values represent the copy number status.

Combined detection of TCR recombination and TREC circles as measure for T cells in blood-derived DNA

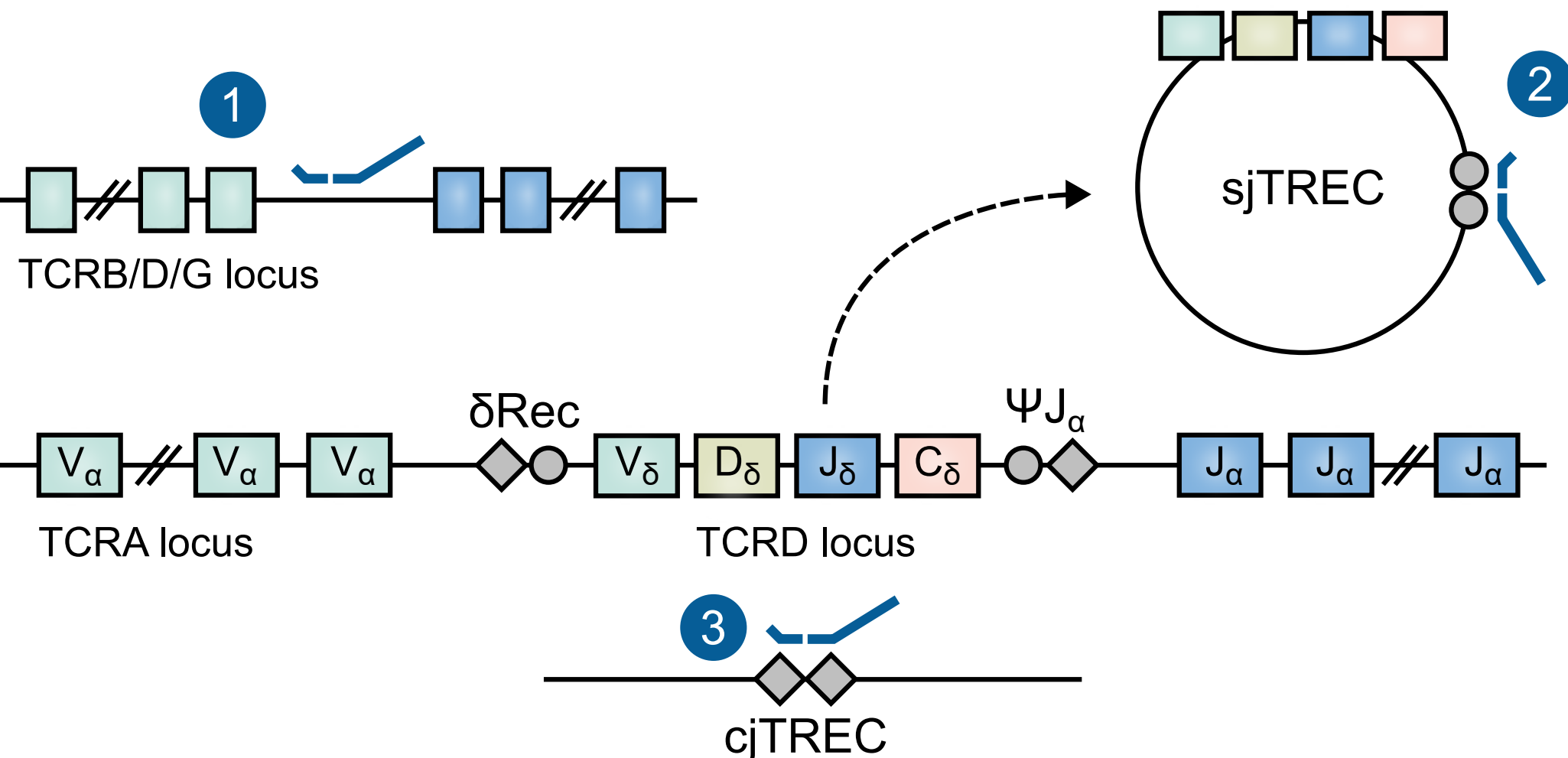


Figure 5. Overview of the detection of T cell DNA using three probe types 1) Probes located between variable rearrangement regions of the TCRs are no longer present in T cells, resulting in a decreased probe ratio in blood-derived DNA. 2) Probes recognizing the signal joint of TREC circles are specific for naive T cells. 3) Probes recognizing the coding joint in the TCR delta locus are specific for T cells.

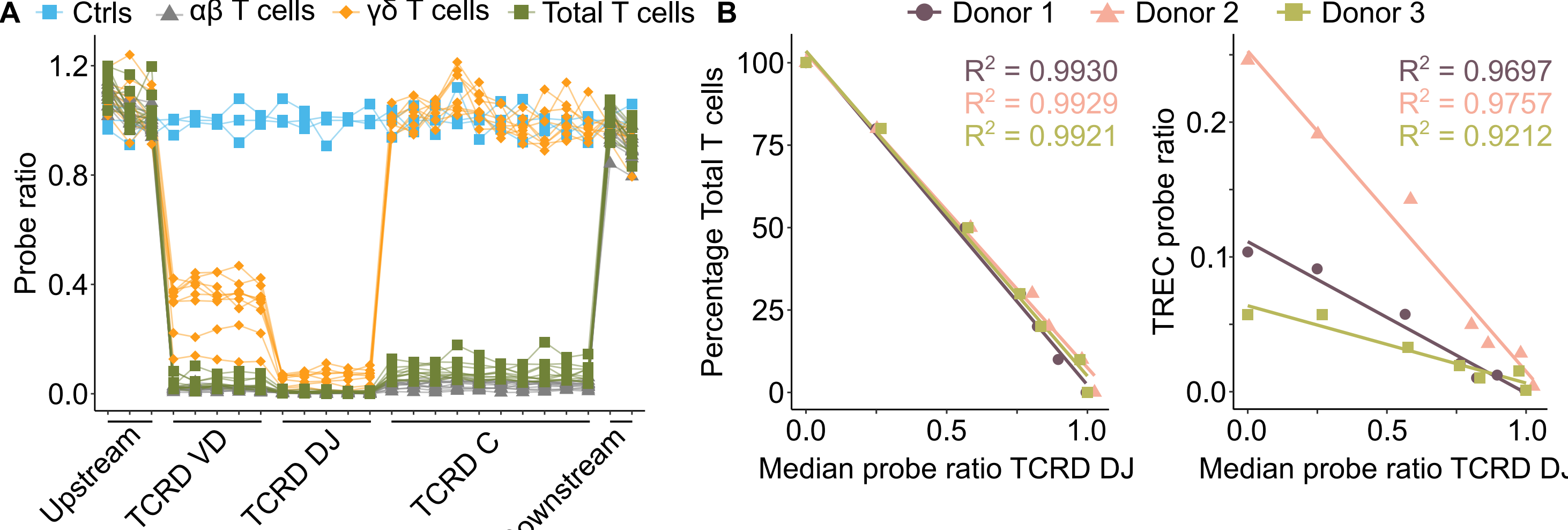



Figure 6. A) Probe ratios of the TCRD locus in samples of different T cell types **B)** Left, correlation between the median probe ratio for the TCRD DJ region and increasing amounts of T cell DNA in a fibroblast-derived DNA background. Right, correlation between the median probe ratio for the TCRD DJ region and the ratio of probes targeting TRECs.

For further information, please contact:
Joery den Hoed at j.denhoed@mrcholland.com or
Jan Schouten at j.schouten@mrcholland.com


digitalMLPA is for research use only. Not for use in diagnostic procedures.

The product described concerns a trial version that is not available for general purchase.

Conclusions




This digitalMLPA assay (newborn test version) can reliably detect distinct frequent deletions in the complex *HBA* locus associated with alpha-thalassemias.



A probe set with a two-fold approach to detect the presence of T cell DNA in a blood-derived sample holds promise as a novel approach to screen for SCID.

Taken together, this SALSA® digitalMLPA™ probemix (newborn test version) is a promising DNA-based assay for testing of multiple early-onset conditions.

Interested in our product?
Scan the QR code to be involved and receive the latest news



Download the poster here:

