



Unleash the Power of Transplant Matching with Hybrid Capture

Margot D.,
Stem cell transplant recipient

High-throughput, high-resolution,
automation-friendly HLA typing

No long-range PCR =
No amplification inefficiencies

Can process up to 192 samples per
run with data upload at 1 min/sample*

Available as CE/IVD and research use only products. For local regulatory status, please contact CareDx.

AlloSeq Tx Offers a Single Tube Workflow and No Long Range PCR Inefficiencies

High-volume typing with easy, simple workflow

Eliminating the need for upfront PCR means no risk of PCR artifacts such as allele drop out or amplification imbalance. Combined with early pooling and single tube workflow, you can have confidence in robust and reliable genotype calling.

STEP

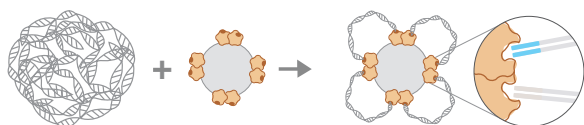
1

Whole Genome Library Generation

🕒 3.5 hrs / 2 hrs hands-on

LESS INPUT DNA
REQUIRED: >50NG
OF INPUT DNA

More permissive to
**LOWER QUALITY
DNA LIKE BUCCAL
SWAB SAMPLES**



Tagmentation

Genomic DNA is bound, fragmented and tagged by bead-linked transposomes - one sample per well



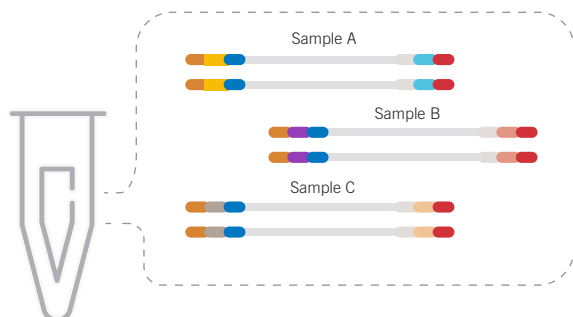
Wash beads

To remove any unbound DNA

Index PCR amplification

Clean up & size selection

Early indexing
leads to
**REDUCED RISK
OF SAMPLE
SWITCHING**



Pool all the sample libraries into a single tube

No manual quantification of DNA is required prior to pooling

SINGLE TUBE WORKFLOW

Additional genes can be added without impacting workflow

STEP

2

Hybrid Capture

🕒 5.5 hrs / 2 hrs hands-on

NO LONG RANGE
PCR MEANS:

CONSISTENT
ALLELE BALANCE

REDUCED ALLELE
DROP OUT RATES

NO PCR ARTIFACTS

READS GENERATED
ARE PROPORTIONAL
TO GENE COPY
NUMBER

Hybridize probes

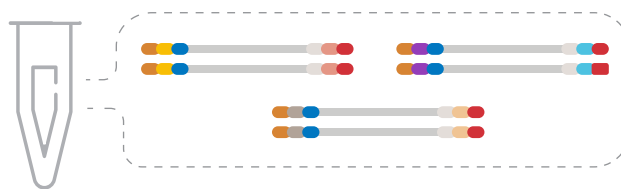
🕒 90 min or overnight
at 62°C

Capture target
fragments

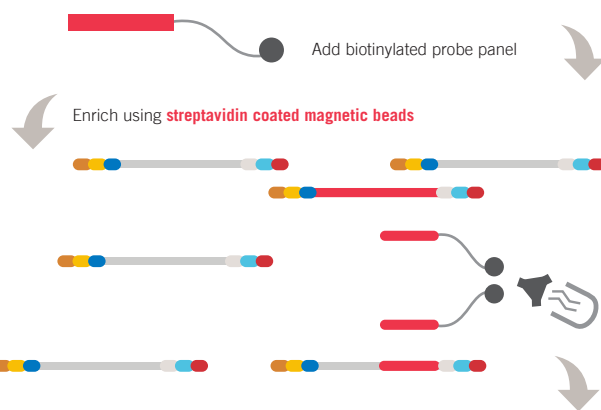
Amplify

Clean up

POOLED SAMPLE LIBRARIES



GENES OF INTEREST CAPTURE



ENRICHED LIBRARY



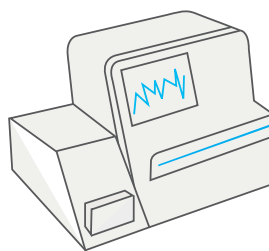
ENRICHED AND INDEXED LIBRARY READY FOR SEQUENCING

STEP

3

Sequencing

🕒 17-24 hrs / 15 min hands-on



Sequencing on the
Illumina platforms

MiSeq, MiniSeq, iSeq

STEP

4

Software Analysis

🕒 30 min / 24 sample import

 AlloSeq Assign

1 MIN/SAMPLE IMPORT

*as per internal testing - will depend on multiple factors

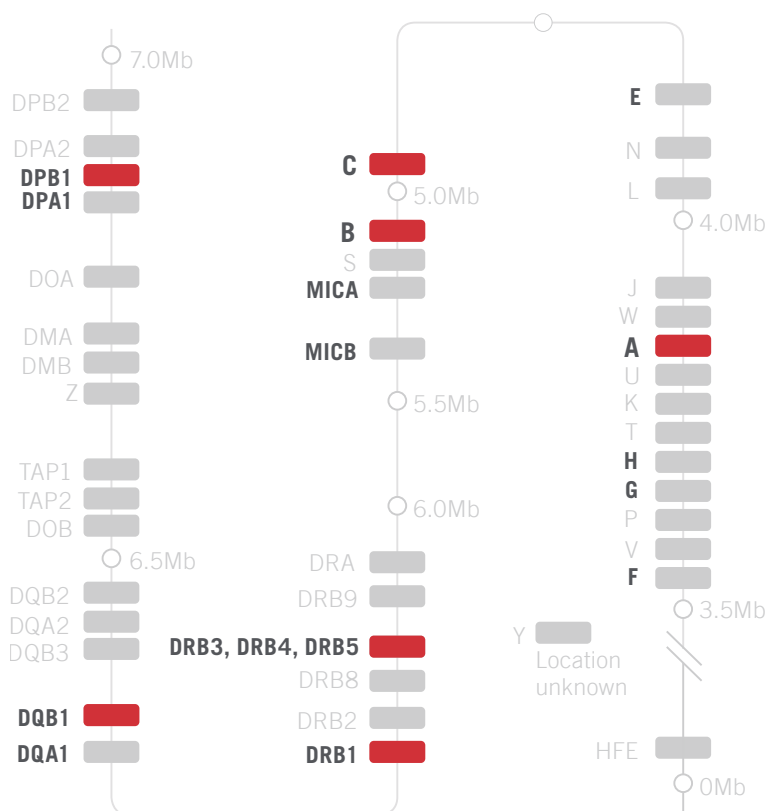
FAST DATA IMPORT SPEED
LEADS TO FAST ANALYSIS

AUTOMATIC COMMENCEMENT OF
ANALYSIS FOLLOWING COMPLETION
OF SEQUENCING RUN.

Customizable results exportable into LIMS.

AlloSeq Tx9 Enables High Throughput and High Quality Data for Faster Identification of Better Matched Donors

With the ability to match the 9 classic HLA loci at the highest resolution, AlloSeq Tx9** accommodates volunteer donor registries with local and international requirements.



CLASSICAL HLA GENES

GENE	RESOLUTION	COVERAGE
HLA-A	4th field	Full Gene
HLA-B	4th field	Full Gene
HLA-C	4th field	Full Gene
HLA-DRB1	3rd field	Full Exon
HLA-DRB3/4/5	3rd field	Full Exon
HLA-DQB1	3rd field	Full Exon
HLA-DPB1	3rd field	Full Exon

PRODUCT

AlloSeq Tx9 (RUO)

AlloSeq Tx9 (CE-IVD)

NO. RXNS

96

96

TARGETED GENES

HLA-A, -B, -C, -DRB1, -DRB3/DRB4/DRB5, -DQB1, -DPB1

HLA-A, -B, -C, -DRB1, -DRB3/DRB4/DRB5, -DQB1, -DPB1

PRODUCT CODE

ASTX9.1(96)-A-RUO
ASTX9.1(96)-B-RUO

ASTX9.1(96)-A-IVD
ASTX9.1(96)-B-IVD

AlloSeq Tx9, 96 reaction kits, are available as CE/IVD and research use only products.
For local regulatory status, please contact CareDx.

For inquiries, contact your CareDx representative or reach out to us:

Americas – orders-US@caredx.com

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