REFERENCES
1) Clinical and Laboratory Standards Institute (CLSI). *Establishing Molecular Testing in Clinical Laboratory Environments; Approved Guideline.* CLSI document MM19-A. Clinical and Laboratory Standards Institute, Wayne, PA; 2011.
2) Department of Health and Human Services, Centers for Medicare and Medicaid Services. Clinical laboratory improvement amendments of 1988; final rule. *Fed Register*. 2003(Jan 24): [42CFR1256(d)(3)(i) and (ii)].

HSC.36795 Internal Controls - Nucleic Acid Amplification — Phase II

In nucleic acid amplification procedures, internal controls are run to detect a false negative reaction secondary to extraction failure or the presence of an inhibitor, when appropriate.

NOTE: The laboratory should be able to distinguish a true negative result from a false negative due to failure of extraction or amplification. Demonstration that another sequence can be successfully amplified in the same specimen should be sufficient to resolve this issue. For quantitative amplification assays, the effect of partial inhibition must also be addressed.

The internal control should not be smaller than the target amplicon.

Evidence of Compliance:
- ✓ Records of assay validation and monitoring statistics for test result trends

REFERENCES
1) Department of Health and Human Services, Centers for Medicare and Medicaid Services. Clinical laboratory improvement amendments of 1988; final rule. *Fed Register.* 2003(Jan 24): [42CFR493.1256(d)(3)(iv)(v)].

HSC.36975 DNA Contamination — Phase II

There is a process to detect and control for DNA contamination.

NOTE: Contamination must be monitored in different areas by wipe tests using the regular detection for testing. There are records of the results of monitoring and corrective action taken when contamination is detected.

HSC.37162 Molecular Weight Markers — Phase II

Known molecular weight markers that span the range of expected bands are used for each electrophoretic run.

Evidence of Compliance:
- ✓ Records of appropriate markers with each run

HSC.37349 Amplification Quality — Phase II

For hybridization techniques, there are records that the different components and steps are monitored and acceptable, including the amount and integrity of amplified product and the signal intensity produced by each probe.

REFERENCES
1) Clark JR, Scott SD, Jack AL, et al. Monitoring of chimerism following allogeneic haematopoietic stem cell transplantation (HSCT): Technical recommendations for the use of short tandem repeat (STR) based techniques, on behalf of the United Kingdom National External Quality Assessment Service for Leucocyte Immunophenotyping Chimerism Working Group. *Br J Haematol.* 2015;168(1):26-37.

HSC.37536 Pre-Analytic Testing Requirements — Phase II

The conditions (temperature, salt concentration, probe concentration, etc.) for pre-hybridization, hybridization, and solid-phase support systems are optimized to consistently produce accurate results.

HSC.37723 Probe Labeling Validation — Phase II

The method of probe labeling is validated to detect the target sequence without a false positive signal for non-target sequences.

Evidence of Compliance:
- ✓ Records of in-house validation study data

HSC.37910 Re-Probing **Phase II**

If re-probing a solid-phase nucleic acid sample is performed, there are records of complete stripping of the previous probe before re-probing.

MOLECULAR HLA TYPING

HSC.38060 HLA Typing Level of Resolution **Phase II**

The level of resolution of HLA typing is adequate for the clinical programs, including donor registries, and the type of cell, tissue, or organ to be transplanted and meets the requirements of relevant accrediting agencies.

NOTE: Laboratories performing testing for NMDP donors must follow NMDP policies for resolution of typing ambiguities. Alternative allele combinations must be resolved when they contain one or more alleles in the common or intermediate categories of the CIWD 3.0.0 catalog.

For hematopoietic progenitor cell transplant, the laboratory must perform HLA typing at the level of resolution and including the loci required by the agreements with the transplant center and/or donor registry. For example, high resolution typing of HLA-A, B, C, DRB1 and DPB1 is mandatory for patient and unrelated donor matching per NMDP.

When performing HLA typing of deceased donors for the purpose of solid organ allocation in the United States, report the following loci as required by OPTN policies: A, B, Bw4, Bw6, C, DRB1, DRB3/4/5, DQA1, DQB1, and DPB1.

REFERENCES

1) Organ Procurement and Transplantation Network (OPTN) Policies. Policy 4: Histocompatibility. US Department of Health and Human Services. Effective Date: December 5, 2022.
2) Foundation for the Accreditation of Cellular Therapy (FACT) and Joint Accreditation Committee ISCT and EBMT (JACIE). FACT-JACIE International Standards for Hematopoietic Cellular Therapy Product Collection, Processing, and Administration. 8th Edition, December 14, 2021.
3) National Marrow Donor Program (NMDP)/Be The Match. US Transplant Center Participation Criteria. Document #A00228. Effective January 30, 2023.
4) National Marrow Donor Program. NMDP Policy for HLA Confirmatory Typing Requirements for Unrelated Adult Donors and HLA Typing Requirement for Patients. Document Number: P00079. Effective date: February 27, 2021.
5) Hurley CK, et al. Common, intermediate and well-documented HLA alleles in world populations: CIWD version 3.0.0. *HLA.* 2020;95(6):516-531.

HSC.38097 Sequence-Based Typing **Phase II**

For sequence-based typing, there are records of the following:

- **Templates with sufficient specificity for a locus or allele**
- **Appropriate monitoring of all steps**
- **Adequate electrophoretogram quality to support the sequence results**
- **Definition of a sequence following a procedure for accurate assignment of HLA alleles**

NOTE: Records must include the HLA locus and allele specificity of the template, the source of the sequence data base used (annually updated), and procedures to resolve ambiguous combinations. Assignment of alleles for HLA loci must be done by comparing the sequence data with the sequences of all alleles that are recognized by the World Health Organization (WHO) Nomenclature Committee for Factors of the HLA System.