

XML schema files version 2.1



Applicable version of the XSD-schema

1. XSD main version like 2.1 and 2.2, will be updated annually, Q4 is preferred
Check the XSD update timeline based on known RFCs on <https://share.wmda.info/x/Glt0Ew>
2. Small changes that have no effect to the structure are possible to be arranged quarterly with version number like 2.2.1, 2.2.2
3. WMDA data upload system will always support 2 XSD versions
4. XSD transition period is one year for organisations.

File	Modified
File basicTypes.xsd version 2.1	Jul 06, 2017 by Former WMDA staff member
File Inventories.xsd version 2.1	Jul 06, 2017 by Former WMDA staff member
XML File ION-1234-D.xml	Jul 31, 2017 by Former WMDA staff member
Text File ChangeLog_v2.1.txt Changes from v2.0 to v2.1	Aug 03, 2017 by Riny Heijndael
XML File ION-1234-C.xml	Aug 10, 2017 by Former WMDA staff member
File Inventories-cbu-xml-gen.xsd For XSD version 2.1	Jul 11, 2019 by Zhihong He
File Inventories-donor-xml-gen.xsd For XSD version 2.1	Jul 29, 2019 by Zhihong He

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XML example files

[XML example file for cords](#)

[XML example file for donors](#)

Readable version :

The versions below of the xsd have been added for convenience only.

Inventory.xsd

```
<?xml version="1.0" encoding="UTF-8"?>
<xs:schema xmlns:xs="http://www.w3.org/2001/XMLSchema" elementFormDefault="qualified" attributeFormDefault="unqualified" version="2.1">
  <xs:include schemaLocation="basicTypes.xsd"/>
  <xs:complexType name="itemBaseType" abstract="true">
    <xs:annotation>
      <xs:documentation xml:lang="en">Abstract base type of donor and CBU items</xs:documentation>
    </xs:annotation>
    <xs:sequence>
      <xs:element name="ID">
        <xs:annotation>
          <xs:documentation xml:lang="en">Unique identifier of the donor/CBU: The value comprises the EMDIS hub code + donor identification allocated by the associated donor registry, where the sending organisation is an EMDIS member, otherwise the two digit ISO country code of the associated donor registry + donor identification allocated by the associated donor registry. For example: AU600196166, DE60E-35487, US087013165, SB45</xs:documentation>
        </xs:annotation>
        <xs:simpleType>
          <xs:restriction base="xs:string">
            <xs:maxLength value="17"/>
          </xs:restriction>
        </xs:simpleType>
      </xs:element>
      <xs:element name="GRID" minOccurs="0">
        <xs:annotation>
          <xs:documentation xml:lang="en">Global registration identifier of the donor/CBU.</xs:documentation>
        </xs:annotation>
      </xs:element>
    </xs:sequence>
  </xs:complexType>
</xs:schema>
```

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documentation>
    </xs:annotation>
    <xs:simpleType>
        <xs:restriction base="xs:string">
            <xs:length value="19"/>
        </xs:restriction>
    </xs:simpleType>
</xs:element>
<xs:element name="ATTR" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Describing attribute of the donor/CBU according to house
rules of the sending organization. </xs:documentation>
    </xs:annotation>
    <xs:simpleType>
        <xs:restriction base="xs:string">
            <xs:maxLength value="3"/>
        </xs:restriction>
    </xs:simpleType>
</xs:element>
<xs:element name="BIRTH_DATE" type="bareDateType">
    <xs:annotation>
        <xs:documentation xml:lang="en">Date of birth of the donor/CBU.</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="SEX" type="sexType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Biological gender of the donor/CBU. Mandatory for donors,
optional for CBUs.</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="ABO" type="aboType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Blood group (ABO) of the donor/CBU.</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="RHESUS" type="rhesusType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Rhesus (Rh) factor of the donor/CBU</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="ETHN" type="ethnType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Ethnic group of the donor/CBU</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="CCR5" type="ccr5Type" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">CCR5 status of the donor/CBU</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="HLA" type="hlaType">
    <xs:annotation>
        <xs:documentation xml:lang="en">HLA genotype of the donor/CBU</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="KIR" type="kirType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">KIR genotype of the donor/CBU</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="IDM" type="idmType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Infectious disease markers (IDM) and other relevant tests
of the donor/CBU</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="RSV_PAT" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Unique identifier of the patient the donor/CBU is reserved
for (STATUS=RS). The value comprises the EMDIS patient identification, where the patient search centre is an
EMDIS member, otherwise the value is empty. For example: AU9654021, DE275342, US2277450.</xs:documentation>
    </xs:annotation>

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        </xs:annotation>
        <xs:simpleType>
            <xs:restriction base="xs:string">
                <xs:maxLength value="17"/>
            </xs:restriction>
        </xs:simpleType>
    </xs:element>
    <xs:element name="STATUS" type="statusType">
        <xs:annotation>
            <xs:documentation xml:lang="en">Status of the donor/CBU</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="STAT_END_DATE" type="bareDateType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Date until which the current status will be applicable</xs:
documentation>
        </xs:annotation>
    </xs:element>
</xs:sequence>
</xs:complexType>
<xs:complexType name="donItemType">
    <xs:annotation>
        <xs:documentation xml:lang="en">A donor is an adult person who has consented to donate
haematopoietic progenitor cells to an unrelated patient.</xs:documentation>
    </xs:annotation>
    <xs:complexContent>
        <xs:extension base="itemBaseType">
            <xs:sequence>
                <xs:element name="STAT_REASON" type="statReasonDonType" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Additional information relevant to the donor status<
/xs:documentation>
                    </xs:annotation>
                </xs:element>
                <xs:element name="CONTACT_DATE" type="bareDateType" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Date of last confirmed contact</xs:documentation>
                    </xs:annotation>
                </xs:element>
                <xs:element name="CHECKUP_DATE" type="bareDateType" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Date of the last medical checkup</xs:documentation>
                    </xs:annotation>
                </xs:element>
                <xs:element name="WEIGHT" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Weight in kg</xs:documentation>
                    </xs:annotation>
                    <xs:simpleType>
                        <xs:restriction base="xs:short">
                            <xs:minInclusive value="1"/>
                            <xs:maxInclusive value="999"/>
                        </xs:restriction>
                    </xs:simpleType>
                </xs:element>
                <xs:element name="HEIGHT" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Height in cm</xs:documentation>
                    </xs:annotation>
                    <xs:simpleType>
                        <xs:restriction base="xs:short">
                            <xs:minInclusive value="1"/>
                            <xs:maxInclusive value="999"/>
                        </xs:restriction>
                    </xs:simpleType>
                </xs:element>
                <xs:element name="NMBR_TRANS" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Number of blood transfusions</xs:documentation>
                    </xs:annotation>
                    <xs:simpleType>

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        <xs:restriction base="xs:short">
            <xs:minInclusive value="0"/>
        </xs:restriction>
    </xs:simpleType>
</xs:element>
<xs:element name="NMBR_PREG" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Number of pregnancies</xs:documentation>
    </xs:annotation>
    <xs:simpleType>
        <xs:restriction base="xs:short">
            <xs:minInclusive value="0"/>
        </xs:restriction>
    </xs:simpleType>
</xs:element>
<xs:element name="NMBR_MARR" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Number of marrow donations</xs:documentation>
    </xs:annotation>
    <xs:simpleType>
        <xs:restriction base="xs:short">
            <xs:minInclusive value="0"/>
        </xs:restriction>
    </xs:simpleType>
</xs:element>
<xs:element name="NMBR_PBSC" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Number of PBSC donations</xs:documentation>
    </xs:annotation>
    <xs:simpleType>
        <xs:restriction base="xs:short">
            <xs:minInclusive value="0"/>
        </xs:restriction>
    </xs:simpleType>
</xs:element>
<xs:element name="COLL_TYPE" type="collTypeType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Collection type, i.e. the willingness of the donor
to donate in a specific manner</xs:documentation>
    </xs:annotation>
</xs:element>
</xs:sequence>
</xs:extension>
</xs:complexContent>
</xs:complexType>
<xs:complexType name="cbuItemType">
    <xs:annotation>
        <xs:documentation xml:lang="en">A cord blood unit (CBU) is a banked, frozen blood product extracted
from a newborn baby's umbilical cord.</xs:documentation>
    </xs:annotation>
    <xs:complexContent>
        <xs:extension base="itemBaseType">
            <xs:sequence>
                <xs:element name="STAT_REASON" type="statReasonCbuType" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Additional information relevant to the CBU status<
/xs:documentation>
                    </xs:annotation>
                </xs:element>
                <xs:element name="LOCAL_ID" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Identification of CBU locally at the associated CBB<
/xs:documentation>
                    </xs:annotation>
                    <xs:simpleType>
                        <xs:restriction base="xs:string">
                            <xs:maxLength value="17"/>
                        </xs:restriction>
                    </xs:simpleType>
                </xs:element>
            </xs:sequence>
        </xs:extension>
    </xs:complexContent>
</xs:complexType>
<xs:element name="BAG_ID" minOccurs="0">

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        <xs:annotation>
            <xs:documentation xml:lang="en">Identification as it appears on the bag. If more
than one bag is available then this data attribute is not populated</xs:documentation>
        </xs:annotation>
        <xs:simpleType>
            <xs:restriction base="xs:string">
                <xs:maxLength value="17"/>
            </xs:restriction>
        </xs:simpleType>
    </xs:element>
    <xs:element name="BANK_MANUF_ID" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Unique identifier of the CBB that manufactured the
CBBU: The value comprises the EMDIS hub code + id allocated by the associated EMDIS hub, where the cord registry
is an EMDIS member, otherwise the two digit ISO country code of the associated cord registry + id
identification allocated by the associated cord registry. For example: AUCBB1, SB890
        </xs:documentation>
        </xs:annotation>
        <xs:simpleType>
            <xs:restriction base="xs:string">
                <xs:maxLength value="10"/>
            </xs:restriction>
        </xs:simpleType>
    </xs:element>
    <xs:element name="BANK_DISTRIB_ID" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Unique identifier of the CBB distributing the CBBU:
: The value comprises the EMDIS hub code + id allocated by the associated EMDIS hub, where the cord registry is
an EMDIS member, otherwise the two digit ISO country code of the associated cord registry + id identification
allocated by the associated cord registry. For example: AUCBB1, SB890</xs:documentation>
        </xs:annotation>
        <xs:simpleType>
            <xs:restriction base="xs:string">
                <xs:maxLength value="10"/>
            </xs:restriction>
        </xs:simpleType>
    </xs:element>
    <xs:element name="COLL_DATE" type="bareDateType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Date that the CBBU was collected</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="PROC_DATE" type="bareDateType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Date that the processing started</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="PROC_METH" type="procMethType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Processing method used</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="PROC_METH_TYPE" type="procMethTypeType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Processing method type used</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="FREEZE_DATE" type="bareDateType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Date that the CBBU was frozen.</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="FREEZE_METH" type="freezeMethType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Freezing method used</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="PROD_MOD" type="prodModType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Product modifications made</xs:documentation>
        </xs:annotation>
    </xs:element>

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</xs:element>
<xs:element name="BAG_TYPE" type="bagTypeType" minOccurs="0">
  <xs:annotation>
    <xs:documentation xml:lang="en">Type of bag used (bag fractions / split unit)</xs:
documentation>
  </xs:annotation>
</xs:element>
<xs:element name="BAGS" minOccurs="0">
  <xs:annotation>
    <xs:documentation xml:lang="en">Number of bags for CBU sub units</xs:documentation>
  </xs:annotation>
  <xs:simpleType>
    <xs:restriction base="xs:short">
      <xs:minInclusive value="1"/>
      <xs:maxInclusive value="99"/>
    </xs:restriction>
  </xs:simpleType>
</xs:element>
<xs:element name="BACT_CULT" type="cultValueType" minOccurs="0">
  <xs:annotation>
    <xs:documentation xml:lang="en">Bacterial culture</xs:documentation>
  </xs:annotation>
</xs:element>
<xs:element name="FUNG_CULT" type="cultValueType" minOccurs="0">
  <xs:annotation>
    <xs:documentation xml:lang="en">Fungal culture</xs:documentation>
  </xs:annotation>
</xs:element>
<xs:element name="HEMO_STATUS" type="hemoStatusType" minOccurs="0">
  <xs:annotation>
    <xs:documentation xml:lang="en">Hemoglobinopathy screening status</xs:documentation>
  </xs:annotation>
</xs:element>
<xs:element name="VOL" minOccurs="0">
  <xs:annotation>
    <xs:documentation xml:lang="en">Collected volume before processing (without
additives) in ml</xs:documentation>
  </xs:annotation>
  <xs:simpleType>
    <xs:restriction base="xs:short">
      <xs:minInclusive value="1"/>
      <xs:maxInclusive value="9999"/>
    </xs:restriction>
  </xs:simpleType>
</xs:element>
<xs:element name="VOL_FRZN" minOccurs="0">
  <xs:annotation>
    <xs:documentation xml:lang="en">Total volume frozen (post processing, prior to
cryopreservation) in ml</xs:documentation>
  </xs:annotation>
  <xs:simpleType>
    <xs:restriction base="xs:short">
      <xs:minInclusive value="1"/>
      <xs:maxInclusive value="9999"/>
    </xs:restriction>
  </xs:simpleType>
</xs:element>
<xs:element name="TNC" type="xs:float" minOccurs="0">
  <xs:annotation>
    <xs:documentation xml:lang="en">Total number of nucleated cells (before processing)<
/xs:documentation>
  </xs:annotation>
</xs:element>
<xs:element name="TNC_FRZN" type="xs:float" minOccurs="0">
  <xs:annotation>
    <xs:documentation xml:lang="en">Total number of nucleated cells (post processing,
prior to cryopreservation)</xs:documentation>
  </xs:annotation>
</xs:element>
<xs:element name="RED_BC_FRZN" minOccurs="0">
  <xs:annotation>

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        <xs:documentation xml:lang="en">Total number of nucleated red blood cells (post
processing, prior to cryopreservation)</xs:documentation>
    </xs:annotation>
    <xs:simpleType>
        <xs:restriction base="xs:float">
            <xs:minInclusive value="0.0E0"/>
            <xs:maxInclusive value="999.9E7"/>
        </xs:restriction>
    </xs:simpleType>
</xs:element>
<xs:element name="MNC_FRZN" type="xs:float" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Total Number of mononucleated cells (post
processing, prior to cryopreservation)</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="CD34PC" type="xs:float" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Total number of CD34+ cells (before processing)</xs:
documentation>
    </xs:annotation>
</xs:element>
<xs:element name="CD34PC_FRZN" type="xs:float" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Total number of CD34+ cells (post processing, prior
to cryopreservation)</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="CFU_FRZN" type="xs:float" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Total count of colony forming units (post
processing, prior to cryopreservation)</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="VIABILITY" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Viability as percentage value</xs:documentation>
    </xs:annotation>
    <xs:simpleType>
        <xs:restriction base="xs:short">
            <xs:minInclusive value="0"/>
            <xs:maxInclusive value="100"/>
        </xs:restriction>
    </xs:simpleType>
</xs:element>
<xs:element name="VIABILITY_DATE" type="bareDateType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Date that viability was tested</xs:documentation>
    </xs:annotation>
</xs:element>
<xs:element name="VIABILITY_CELLS" type="viabilityCellsType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Type of cells tested for viability</xs:
documentation>
    </xs:annotation>
</xs:element>
<xs:element name="VIABILITY_METHOD" type="viabilityMethodType" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Method used to calculate the viability</xs:
documentation>
    </xs:annotation>
</xs:element>
<xs:element name="ATT_SEG" minOccurs="0">
    <xs:annotation>
        <xs:documentation xml:lang="en">Number of attached segments available</xs:
documentation>
    </xs:annotation>
    <xs:simpleType>
        <xs:restriction base="xs:short">
            <xs:minInclusive value="0"/>
            <xs:maxInclusive value="99"/>

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        </xs:restriction>
      </xs:simpleType>
    </xs:element>
    <xs:element name="DNA_SMPL" type="xs:boolean" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">DNA samples available?</xs:documentation>
      </xs:annotation>
    </xs:element>
    <xs:element name="OTH_SMPL" type="xs:boolean" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Samples other than DNA available?</xs:documentation>
      </xs:annotation>
    </xs:element>
    <xs:element name="CT_COMPLETE_DATE" type="bareDateType" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Date of completion of confirmatory typing (CT)</xs:
documentation>
      </xs:annotation>
    </xs:element>
    <xs:element name="CT_SMPL_TYPE" type="ctSmplTypeType" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Confirmatory typing (CT) sample type</xs:
documentation>
      </xs:annotation>
    </xs:element>
    <xs:element name="AL_RED_BC" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Number of red cell fraction aliquots</xs:
documentation>
      </xs:annotation>
      <xs:simpleType>
        <xs:restriction base="xs:short">
          <xs:minInclusive value="0"/>
          <xs:maxInclusive value="99"/>
        </xs:restriction>
      </xs:simpleType>
    </xs:element>
    <xs:element name="AL_SER" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Number of serum aliquots available</xs:
documentation>
      </xs:annotation>
      <xs:simpleType>
        <xs:restriction base="xs:short">
          <xs:minInclusive value="0"/>
          <xs:maxInclusive value="99"/>
        </xs:restriction>
      </xs:simpleType>
    </xs:element>
    <xs:element name="SER_QUANT" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Total quantity of serum available in ml</xs:
documentation>
      </xs:annotation>
      <xs:simpleType>
        <xs:restriction base="xs:decimal">
          <xs:minInclusive value="0.0"/>
          <xs:maxInclusive value="99.9"/>
          <xs:fractionDigits value="1"/>
        </xs:restriction>
      </xs:simpleType>
    </xs:element>
    <xs:element name="AL_PLA" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Number of plasma aliquots available</xs:
documentation>
      </xs:annotation>
      <xs:simpleType>
        <xs:restriction base="xs:short">
          <xs:minInclusive value="0"/>
          <xs:maxInclusive value="99"/>

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        </xs:restriction>
      </xs:simpleType>
    </xs:element>
    <xs:element name="PLA_QUANT" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Total quantity of plasma available in ml</xs:
documentation>
      </xs:annotation>
      <xs:simpleType>
        <xs:restriction base="xs:decimal">
          <xs:minInclusive value="0.0"/>
          <xs:maxInclusive value="99.9"/>
          <xs:fractionDigits value="1"/>
        </xs:restriction>
      </xs:simpleType>
    </xs:element>
    <xs:element name="MAT" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Data of the mother of the infant associated with
the CBU</xs:documentation>
      </xs:annotation>
      <xs:complexType>
        <xs:sequence>
          <xs:element name="ID" minOccurs="0">
            <xs:annotation>
              <xs:documentation xml:lang="en">Identification used to identify the
maternal donor as assigned by the registry</xs:documentation>
            </xs:annotation>
            <xs:simpleType>
              <xs:restriction base="xs:string">
                <xs:maxLength value="15"/>
              </xs:restriction>
            </xs:simpleType>
          </xs:element>
          <xs:element name="ID_BANK" minOccurs="0">
            <xs:annotation>
              <xs:documentation xml:lang="en">Identification used by associated CBU
manufacturer to identify maternal details</xs:documentation>
            </xs:annotation>
            <xs:simpleType>
              <xs:restriction base="xs:string">
                <xs:maxLength value="15"/>
              </xs:restriction>
            </xs:simpleType>
          </xs:element>
          <xs:element name="HLA" minOccurs="0">
            <xs:annotation>
              <xs:documentation xml:lang="en">HLA genotype</xs:documentation>
            </xs:annotation>
            <xs:complexType>
              <xs:complexContent>
                <xs:extension base="hlaType"/>
              </xs:complexContent>
            </xs:complexType>
          </xs:element>
          <xs:element name="IDM" minOccurs="0">
            <xs:annotation>
              <xs:documentation xml:lang="en">Infectious disease markers (IDM) and
other relevant tests</xs:documentation>
            </xs:annotation>
            <xs:complexType>
              <xs:complexContent>
                <xs:extension base="idmType"/>
              </xs:complexContent>
            </xs:complexType>
          </xs:element>
          <xs:element name="AL_SER" minOccurs="0">
            <xs:annotation>
              <xs:documentation xml:lang="en">Number of serum aliquots available</xs:
documentation>
            </xs:annotation>

```

```

        <xs:simpleType>
          <xs:restriction base="xs:short">
            <xs:minInclusive value="0"/>
            <xs:maxInclusive value="99"/>
          </xs:restriction>
        </xs:simpleType>
      </xs:element>
    <xs:element name="SER_QUANT" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Total quantity of serum available in ml<
/xs:documentation>
      </xs:annotation>
      <xs:simpleType>
        <xs:restriction base="xs:decimal">
          <xs:minInclusive value="0.0"/>
          <xs:maxInclusive value="99.9"/>
          <xs:fractionDigits value="1"/>
        </xs:restriction>
      </xs:simpleType>
    </xs:element>
    <xs:element name="AL_PLA" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Number of plasma aliquots available</xs:
documentation>
      </xs:annotation>
      <xs:simpleType>
        <xs:restriction base="xs:short">
          <xs:minInclusive value="0"/>
          <xs:maxInclusive value="99"/>
        </xs:restriction>
      </xs:simpleType>
    </xs:element>
    <xs:element name="PLA_QUANT" minOccurs="0">
      <xs:annotation>
        <xs:documentation xml:lang="en">Total quantity of plasma available in
ml</xs:documentation>
      </xs:annotation>
      <xs:simpleType>
        <xs:restriction base="xs:decimal">
          <xs:minInclusive value="0.0"/>
          <xs:maxInclusive value="99.9"/>
          <xs:fractionDigits value="1"/>
        </xs:restriction>
      </xs:simpleType>
    </xs:element>
  </xs:sequence>
</xs:complexType>
</xs:element>
</xs:sequence>
</xs:extension>
</xs:complexContent>
</xs:complexType>
<xs:complexType name="inventoryType">
  <xs:annotation>
    <xs:documentation xml:lang="en">Type representing an inventory of donors and/or cord blood units
(CBUs)</xs:documentation>
  </xs:annotation>
  <xs:sequence>
    <xs:element name="DONOR" type="donItemType" minOccurs="0" maxOccurs="unbounded">
      <xs:annotation>
        <xs:documentation xml:lang="en">A donor is an adult person who has consented to donate
haematopoietic progenitor cells, that is, HPC(M) or HPC(A) and similar products to an unrelated patient.</xs:
documentation>
      </xs:annotation>
    </xs:element>
    <xs:element name="CBU" type="cbuItemType" minOccurs="0" maxOccurs="unbounded">
      <xs:annotation>
        <xs:documentation xml:lang="en">A cord blood unit (CBU) is a banked, frozen blood product
extracted from a newborn baby's umbilical cord.</xs:documentation>
      </xs:annotation>
    </xs:element>
  </xs:sequence>

```

```

        </xs:sequence>
        <xs:attribute name="LISTING_ORGANIZATION" type="ionType" use="required">
          <xs:annotation>
            <xs:documentation xml:lang="en">Organisation that lists the donor/cbu provided as ION</xs:
documentation>
          </xs:annotation>
        </xs:attribute>
        <xs:attribute name="POOL" type="ionType" use="required">
          <xs:annotation>
            <xs:documentation>Physical location of the donors/CBUs of the inventory provided as ION</xs:
documentation>
          </xs:annotation>
        </xs:attribute>
        <xs:attribute name="CONTENT_TYPE" type="contentTypeType" use="required">
          <xs:annotation>
            <xs:documentation xml:lang="en">Type of the inventory items, i.e. donor or CBU</xs:
documentation>
          </xs:annotation>
        </xs:attribute>
        <xs:attribute name="UPDATE_MODE" type="updateModeType" use="required">
          <xs:annotation>
            <xs:documentation xml:lang="en">Update mode of the inventory, i.e. FULL or DIFF</xs:
documentation>
          </xs:annotation>
        </xs:attribute>
        <xs:attribute name="SNAPSHOT_TIME" type="xs:dateTime" use="optional">
          <xs:annotation>
            <xs:documentation xml:lang="en">Timestamp of the 'data snapshot' (in UTC)</xs:documentation>
          </xs:annotation>
        </xs:attribute>
      </xs:complexType>
      <xs:element name="INVENTORIES">
        <xs:annotation>
          <xs:documentation xml:lang="en">Root element representing a set of inventories</xs:documentation>
        </xs:annotation>
        <xs:complexType>
          <xs:sequence>
            <xs:element name="INVENTORY" type="inventoryType" maxOccurs="unbounded"/>
          </xs:sequence>
          <xs:attribute name="CREATION_TIME" type="xs:dateTime" use="required">
            <xs:annotation>
              <xs:documentation xml:lang="en">Creation timestamp of the inventories (in UTC)</xs:
documentation>
            </xs:annotation>
          </xs:attribute>
        </xs:complexType>
      </xs:element>
    </xs:schema>

```

basicTypes.xsd

```

<?xml version="1.0" encoding="UTF-8"?>
<xs:schema xmlns:xs="http://www.w3.org/2001/XMLSchema" elementFormDefault="qualified" attributeFormDefault="
unqualified" version="2.1">
  <xs:simpleType name="updateModeType">
    <xs:annotation>
      <xs:documentation xml:lang="en">Inventory update mode</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:string">
      <xs:enumeration value="FULL"/>
      <xs:enumeration value="DIFF"/>
    </xs:restriction>
  </xs:simpleType>
  <xs:simpleType name="contentTypeType">
    <xs:annotation>
      <xs:documentation xml:lang="en">Inventory content type</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:string">

```

```

        <xs:enumeration value="C">
            <xs:annotation>
                <xs:documentation xml:lang="en">CBU</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="D">
            <xs:annotation>
                <xs:documentation xml:lang="en">Donor</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="B">
            <xs:annotation>
                <xs:documentation xml:lang="en">Both</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
    </xs:restriction>
</xs:simpleType>
<xs:simpleType name="ionType">
    <xs:annotation>
        <xs:documentation xml:lang="en">Issuing Organisation Number (ION) allocated by ICBBA (e.
g. 7748 ~ ABMDR)</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:short">
        <xs:minInclusive value="1000"/>
        <xs:maxInclusive value="9999"/>
    </xs:restriction>
</xs:simpleType>
<xs:simpleType name="sexType">
    <xs:annotation>
        <xs:documentation xml:lang="en">Sex</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:string">
        <xs:enumeration value="M">
            <xs:annotation>
                <xs:documentation xml:lang="en">Male</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="F">
            <xs:annotation>
                <xs:documentation xml:lang="en">Female</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
    </xs:restriction>
</xs:simpleType>
<xs:simpleType name="aboType">
    <xs:annotation>
        <xs:documentation xml:lang="en">Blood group</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:string">
        <xs:enumeration value="A">
            <xs:annotation>
                <xs:documentation xml:lang="en">Blood group A</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="B">
            <xs:annotation>
                <xs:documentation xml:lang="en">Blood group B</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="O">
            <xs:annotation>
                <xs:documentation xml:lang="en">Blood group O (letter O!)</xs:
documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="AB">
            <xs:annotation>
                <xs:documentation xml:lang="en">Blood group AB</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
    </xs:restriction>

```

```

</xs:simpleType>
<xs:simpleType name="rhesusType">
  <xs:annotation>
    <xs:documentation xml:lang="en">Rhesus</xs:documentation>
  </xs:annotation>
  <xs:restriction base="xs:string">
    <xs:enumeration value="P">
      <xs:annotation>
        <xs:documentation xml:lang="en">Positive</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="N">
      <xs:annotation>
        <xs:documentation xml:lang="en">Negative</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
  </xs:restriction>
</xs:simpleType>
<xs:simpleType name="ethnType">
  <xs:annotation>
    <xs:documentation xml:lang="en">Ethnic group</xs:documentation>
  </xs:annotation>
  <xs:restriction base="xs:string">
    <xs:enumeration value="AFNA">
      <xs:annotation>
        <xs:documentation xml:lang="en">African: North Africa</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="AFSS">
      <xs:annotation>
        <xs:documentation xml:lang="en">African: Sub-Saharan Africa</xs:
documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="ASSW">
      <xs:annotation>
        <xs:documentation xml:lang="en">Asian: Southwest Asia (Middle East,
Turkey)</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="ASSO">
      <xs:annotation>
        <xs:documentation xml:lang="en">Asian: Southern Asia (India, Pakistan,
Bangladesh, Sri Lanka, Bhutan, Nepal)</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="ASCE">
      <xs:annotation>
        <xs:documentation xml:lang="en">Asian: Central Asia (Eastern Russia,
Kazakhstan, Uzbekistan, Kyrgyzstan, Tajikistan)</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="ASSE">
      <xs:annotation>
        <xs:documentation xml:lang="en">Asian: Southeast Asia (China, Mongolia,
Burma, Laos, Cambodia, Thailand, Vietnam, Taiwan)</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="ASNE">
      <xs:annotation>
        <xs:documentation xml:lang="en">Asian: North and Northeast Asia (Japan,
North Korea, South Korea)</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="ASOC">
      <xs:annotation>
        <xs:documentation xml:lang="en">Asian: Oceania (Pacific Islands
excluding Japan, Australia, Taiwan, Sakhalin, Aleutian Islands)</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="CAEU">

```

```

        <xs:annotation>
            <xs:documentation xml:lang="en">Caucasian: Mainland Europe, Greenland,
Iceland, Western Russia)</xs:documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="CAER">
        <xs:annotation>
            <xs:documentation xml:lang="en">Caucasian: Eastern Russia</xs:
documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="CANA">
        <xs:annotation>
            <xs:documentation xml:lang="en">Caucasian: North America (USA, Canada,
Mexico)</xs:documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="CAAU">
        <xs:annotation>
            <xs:documentation xml:lang="en">Caucasian: Australia (Australia, New
Zealand)</xs:documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="HICA">
        <xs:annotation>
            <xs:documentation xml:lang="en">Hispanic: Central America, Caribbean<
/xs:documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="HISA">
        <xs:annotation>
            <xs:documentation xml:lang="en">Hispanic: South America</xs:
documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="AF">
        <xs:annotation>
            <xs:documentation xml:lang="en">African: unspecific</xs:documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="AS">
        <xs:annotation>
            <xs:documentation xml:lang="en">Asian: unspecific</xs:documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="CA">
        <xs:annotation>
            <xs:documentation xml:lang="en">Caucasian: unspecific</xs:documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="HI">
        <xs:annotation>
            <xs:documentation xml:lang="en">Hispanic: unspecific</xs:documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="MX">
        <xs:annotation>
            <xs:documentation xml:lang="en">Mixed / multiple</xs:documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="OT">
        <xs:annotation>
            <xs:documentation xml:lang="en">Other (e.g. Australian Aborigine)</xs:
documentation>
        </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="UK">
        <xs:annotation>
            <xs:documentation xml:lang="en">Unknown</xs:documentation>
        </xs:annotation>
    </xs:enumeration>

```

```

        </xs:restriction>
    </xs:simpleType>
    <xs:simpleType name="ccr5Type">
        <xs:annotation>
            <xs:documentation xml:lang="en">CCR5 status</xs:documentation>
        </xs:annotation>
        <xs:restriction base="xs:string">
            <xs:enumeration value="DD">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Deletion (delta 32) - homozygous</xs:
documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="WW">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Wildtype - homozygous</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="DW">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Deletion (delta 32) / wildtype -
heterozygous</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
        </xs:restriction>
    </xs:simpleType>
    <xs:simpleType name="collTypeType">
        <xs:annotation>
            <xs:documentation xml:lang="en">Collection type</xs:documentation>
        </xs:annotation>
        <xs:restriction base="xs:string">
            <xs:enumeration value="M">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Marrow</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="P">
                <xs:annotation>
                    <xs:documentation xml:lang="en">PBSC</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="B">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Both</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
        </xs:restriction>
    </xs:simpleType>
    <xs:simpleType name="procMethType">
        <xs:annotation>
            <xs:documentation xml:lang="en">Processing method</xs:documentation>
        </xs:annotation>
        <xs:restriction base="xs:string">
            <xs:enumeration value="HES">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Hydroxy-Ethyl-Starch</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="DGS">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Density Gradient Separation</xs:
documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="CEN">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Centrifuge</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="FIL">
                <xs:annotation>

```

```

        <xs:documentation xml:lang="en">Filtration</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="FIC">
      <xs:annotation>
        <xs:documentation xml:lang="en">FICOL</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="PER">
      <xs:annotation>
        <xs:documentation xml:lang="en">PERCOL</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="OTH">
      <xs:annotation>
        <xs:documentation xml:lang="en">Other</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
  </xs:restriction>
</xs:simpleType>
<xs:simpleType name="procMethTypeType">
  <xs:annotation>
    <xs:documentation xml:lang="en">Processing method type</xs:documentation>
  </xs:annotation>
  <xs:restriction base="xs:string">
    <xs:enumeration value="MAN">
      <xs:annotation>
        <xs:documentation xml:lang="en">Manual</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="SPX">
      <xs:annotation>
        <xs:documentation xml:lang="en">Sepax</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="OTP">
      <xs:annotation>
        <xs:documentation xml:lang="en">Optipress II</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="AXP">
      <xs:annotation>
        <xs:documentation xml:lang="en">AXP</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="OTH">
      <xs:annotation>
        <xs:documentation xml:lang="en">Other</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
  </xs:restriction>
</xs:simpleType>
<xs:simpleType name="freezeMethType">
  <xs:annotation>
    <xs:documentation xml:lang="en">Freezing method</xs:documentation>
  </xs:annotation>
  <xs:restriction base="xs:string">
    <xs:enumeration value="C">
      <xs:annotation>
        <xs:documentation xml:lang="en">Controlled rate</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="M">
      <xs:annotation>
        <xs:documentation xml:lang="en">Manual</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
  </xs:restriction>
</xs:simpleType>
<xs:simpleType name="prodModType">
  <xs:annotation>

```



```

        <xs:documentation xml:lang="en">Product modification</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:string">
        <xs:enumeration value="BCE">
            <xs:annotation>
                <xs:documentation xml:lang="en">Buffy Coat Enriched</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="DNE">
            <xs:annotation>
                <xs:documentation xml:lang="en">Density Enriched</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="PLR">
            <xs:annotation>
                <xs:documentation xml:lang="en">Plasma Reduced (Volume reduction only)</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="PRR">
            <xs:annotation>
                <xs:documentation xml:lang="en">Plasma and RBC Reduced</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="RBR">
            <xs:annotation>
                <xs:documentation xml:lang="en">RBC Reduced (depletion)</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="NOT">
            <xs:annotation>
                <xs:documentation xml:lang="en">Not reduced</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="OTH">
            <xs:annotation>
                <xs:documentation xml:lang="en">Other</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
    </xs:restriction>
</xs:simpleType>
<xs:simpleType name="bagTypeType">
    <xs:annotation>
        <xs:documentation xml:lang="en">Type of bag used (bag fractions / split unit)</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:string">
        <xs:enumeration value="80/20"/>
        <xs:enumeration value="50/50"/>
        <xs:enumeration value="40/60"/>
        <xs:enumeration value="NS">
            <xs:annotation>
                <xs:documentation xml:lang="en">No split</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
    </xs:restriction>
</xs:simpleType>
<xs:simpleType name="cultValueType">
    <xs:annotation>
        <xs:documentation xml:lang="en">Culture value</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:string">
        <xs:enumeration value="P">
            <xs:annotation>
                <xs:documentation xml:lang="en">Positive</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="N">
            <xs:annotation>

```

```

        <xs:documentation xml:lang="en">Negative</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="D">
      <xs:annotation>
        <xs:documentation xml:lang="en">Not done</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
  </xs:restriction>
</xs:simpleType>
<xs:simpleType name="hemoStatusType">
  <xs:annotation>
    <xs:documentation xml:lang="en">Hemoglobinopathy screening status</xs:documentation>
  </xs:annotation>
  <xs:restriction base="xs:string">
    <xs:enumeration value="DN">
      <xs:annotation>
        <xs:documentation xml:lang="en">Screening done, normal results</xs:
documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="DU">
      <xs:annotation>
        <xs:documentation xml:lang="en">Screening done, unusual findings</xs:
documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="NS">
      <xs:annotation>
        <xs:documentation xml:lang="en">No screening done</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="CD">
      <xs:annotation>
        <xs:documentation xml:lang="en">Can be done at time of release</xs:
documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="NC">
      <xs:annotation>
        <xs:documentation xml:lang="en">Cannot be done</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="DT">
      <xs:annotation>
        <xs:documentation xml:lang="en">Thalassemia</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="DD">
      <xs:annotation>
        <xs:documentation xml:lang="en">Drepanocytosis</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
  </xs:restriction>
</xs:simpleType>
<xs:simpleType name="statusType">
  <xs:annotation>
    <xs:documentation xml:lang="en">Status</xs:documentation>
  </xs:annotation>
  <xs:restriction base="xs:string">
    <xs:enumeration value="AV">
      <xs:annotation>
        <xs:documentation xml:lang="en">Available</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="TU">
      <xs:annotation>
        <xs:documentation xml:lang="en">Temporarily unavailable, reason
specified in STAT_REASON</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
  </xs:restriction>

```

```

        <xs:enumeration value="RS">
            <xs:annotation>
                <xs:documentation xml:lang="en">Reserved for the patient specified in
the RSV_PAT</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="DE">
            <xs:annotation>
                <xs:documentation xml:lang="en">Deleted; only applicable for update
mode DIFF</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
    </xs:restriction>
</xs:simpleType>
<xs:simpleType name="statReasonDonType">
    <xs:annotation>
        <xs:documentation xml:lang="en">Status reason (donor)</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:string">
        <xs:enumeration value="DO">
            <xs:annotation>
                <xs:documentation xml:lang="en">Donor is too old</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="DD">
            <xs:annotation>
                <xs:documentation xml:lang="en">Donor died</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="MR">
            <xs:annotation>
                <xs:documentation xml:lang="en">Medical reasons</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="PR">
            <xs:annotation>
                <xs:documentation xml:lang="en">Personal reasons</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="TX">
            <xs:annotation>
                <xs:documentation xml:lang="en">After transplantation</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="MO">
            <xs:annotation>
                <xs:documentation xml:lang="en">Donor moved</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="UC">
            <xs:annotation>
                <xs:documentation xml:lang="en">Unable to contact donor</xs:
documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="TQ">
            <xs:annotation>
                <xs:documentation xml:lang="en">Typing questionable</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="OT">
            <xs:annotation>
                <xs:documentation xml:lang="en">Other reasons</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="UK">
            <xs:annotation>
                <xs:documentation xml:lang="en">Unknown</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
    </xs:restriction>

```

```

</xs:simpleType>
<xs:simpleType name="statReasonCbuType">
  <xs:annotation>
    <xs:documentation xml:lang="en">Status reason (CBU)</xs:documentation>
  </xs:annotation>
  <xs:restriction base="xs:string">
    <xs:enumeration value="QR">
      <xs:annotation>
        <xs:documentation xml:lang="en">Quarantined</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="AD">
      <xs:annotation>
        <xs:documentation xml:lang="en">Administrative</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="CD">
      <xs:annotation>
        <xs:documentation xml:lang="en">CBU destroyed or damaged</xs:
documentation>
        </xs:annotation>
      </xs:enumeration>
    <xs:enumeration value="DS">
      <xs:annotation>
        <xs:documentation xml:lang="en">Distributed for infusion</xs:
documentation>
        </xs:annotation>
      </xs:enumeration>
    <xs:enumeration value="XP">
      <xs:annotation>
        <xs:documentation xml:lang="en">Expired</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="MR">
      <xs:annotation>
        <xs:documentation xml:lang="en">Medical reasons</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="OT">
      <xs:annotation>
        <xs:documentation xml:lang="en">Other reasons</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="UK">
      <xs:annotation>
        <xs:documentation xml:lang="en">Unknown</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
  </xs:restriction>
</xs:simpleType>
<xs:simpleType name="idmValueType">
  <xs:annotation>
    <xs:documentation xml:lang="en">IDM result value set: P, N</xs:documentation>
  </xs:annotation>
  <xs:restriction base="xs:string">
    <xs:enumeration value="P">
      <xs:annotation>
        <xs:documentation xml:lang="en">Positive</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
    <xs:enumeration value="N">
      <xs:annotation>
        <xs:documentation xml:lang="en">Negative</xs:documentation>
      </xs:annotation>
    </xs:enumeration>
  </xs:restriction>
</xs:simpleType>
<xs:simpleType name="idmValueExtType">
  <xs:annotation>
    <xs:documentation xml:lang="en">Extended IDM result value set: P,G,M,B,H,O,N</xs:
documentation>
  </xs:annotation>

```

```

        </xs:annotation>
        <xs:restriction base="xs:string">
            <xs:enumeration value="P">
                <xs:annotation>
                    <xs:documentation xml:lang="en">IgG or IgM positive, test did not
differentiate</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="G">
                <xs:annotation>
                    <xs:documentation xml:lang="en">IgG positive, IgM negative</xs:
documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="M">
                <xs:annotation>
                    <xs:documentation xml:lang="en">IgG negative, IgM positive</xs:
documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="B">
                <xs:annotation>
                    <xs:documentation xml:lang="en">IgG positive, IgM positive</xs:
documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="H">
                <xs:annotation>
                    <xs:documentation xml:lang="en">IgG positive, IgM not tested</xs:
documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="N">
                <xs:annotation>
                    <xs:documentation xml:lang="en">IgG negative, IgM negative</xs:
documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="O">
                <xs:annotation>
                    <xs:documentation xml:lang="en">IgG negative, IgM not tested</xs:
documentation>
                </xs:annotation>
            </xs:enumeration>
        </xs:restriction>
    </xs:simpleType>
    <xs:simpleType name="viabilityCellsType">
        <xs:annotation>
            <xs:documentation xml:lang="en">Type of cells tested for viability</xs:documentation>
        </xs:annotation>
        <xs:restriction base="xs:string">
            <xs:enumeration value="TNC"/>
            <xs:enumeration value="CD34PC"/>
            <xs:enumeration value="CD45PC"/>
        </xs:restriction>
    </xs:simpleType>
    <xs:simpleType name="viabilityMethodType">
        <xs:annotation>
            <xs:documentation xml:lang="en">Method used for viability test</xs:documentation>
        </xs:annotation>
        <xs:restriction base="xs:string">
            <xs:enumeration value="7A">
                <xs:annotation>
                    <xs:documentation xml:lang="en">7AAD</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
            <xs:enumeration value="PI">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Proprium Iodide</xs:documentation>
                </xs:annotation>
            </xs:enumeration>
        </xs:restriction>
    </xs:simpleType>

```

```

        <xs:enumeration value="TB">
            <xs:annotation>
                <xs:documentation xml:lang="en">Trypan Blue</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
        <xs:enumeration value="OT">
            <xs:annotation>
                <xs:documentation xml:lang="en">Other</xs:documentation>
            </xs:annotation>
        </xs:enumeration>
    </xs:restriction>
</xs:simpleType>
<xs:simpleType name="ctSmplTypeType">
    <xs:annotation>
        <xs:documentation xml:lang="en">Confirmatory typing sample type</xs:documentation>
    </xs:annotation>
    <xs:restriction base="xs:string">
        <xs:enumeration value="AS">
            <xs:annotation>
                <xs:documentation xml:lang="en">CBU contiguous attached segment</xs:
documentation>
                    </xs:annotation>
                </xs:enumeration>
                <xs:enumeration value="WB">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Whole blood sample</xs:documentation>
                    </xs:annotation>
                </xs:enumeration>
                <xs:enumeration value="RC">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Red cell fraction (pellet)</xs:
documentation>
                            </xs:annotation>
                        </xs:enumeration>
                        <xs:enumeration value="FP">
                            <xs:annotation>
                                <xs:documentation xml:lang="en">Blood spotted filter paper</xs:
documentation>
                                    </xs:annotation>
                                </xs:enumeration>
                                <xs:enumeration value="ED">
                                    <xs:annotation>
                                        <xs:documentation xml:lang="en">Extracted DNA</xs:documentation>
                                    </xs:annotation>
                                </xs:enumeration>
                            </xs:restriction>
                        </xs:simpleType>
                    <xs:simpleType name="kirLocusType">
                        <xs:annotation>
                            <xs:documentation xml:lang="en">KIR locus type</xs:documentation>
                        </xs:annotation>
                        <xs:restriction base="xs:string">
                            <xs:enumeration value="POS">
                                <xs:annotation>
                                    <xs:documentation xml:lang="en">Presence of KIR gene</xs:documentation>
                                </xs:annotation>
                            </xs:enumeration>
                            <xs:enumeration value="NEG">
                                <xs:annotation>
                                    <xs:documentation xml:lang="en">Absence of KIR gene</xs:documentation>
                                </xs:annotation>
                            </xs:enumeration>
                        </xs:restriction>
                    </xs:simpleType>
                <xs:simpleType name="schemaVersionType">
                    <xs:annotation>
                        <xs:documentation xml:lang="en">Version of the XML Schema Definition (XSD)</xs:
documentation>
                            </xs:annotation>
                        <xs:restriction base="xs:string">
                            <xs:pattern value="[1-9]\d?\.\d{1,2}"/>

```

```

        </xs:restriction>
    </xs:simpleType>
    <xs:simpleType name="bareDateType">
        <xs:annotation>
            <xs:documentation xml:lang="en">Date without timezone information</xs:documentation>
        </xs:annotation>
        <xs:restriction base="xs:date">
            <xs:pattern value="^[^:Z]*"/>
        </xs:restriction>
    </xs:simpleType>
    <xs:complexType name="idmType">
        <xs:annotation>
            <xs:documentation xml:lang="en">Infectious disease markers (IDM) and other relevant
tests</xs:documentation>
        </xs:annotation>
        <xs:sequence>
            <xs:element name="CMV" type="idmValueExtType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">CMV status</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="CMV_NAT" type="idmValueType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">CMV NAT status</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="CMV_DATE" type="bareDateType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Date of CMV test</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="HBS_AG" type="idmValueType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Hepatitis B status (hepatitis B surface
antigen)</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="ANTI_HBC" type="idmValueType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Hepatitis B status (antibody to
hepatitis B core antigen)</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="ANTI_HBS" type="idmValueType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Hepatitis B status (antibody to
hepatitis B surface antigen)</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="ANTI_HCV" type="idmValueType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Hepatitis C status (antibody to
hepatitis C virus)</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="ANTI_HIV_12" type="idmValueType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">Anti-HIV 1/2 status</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="HIV_1_NAT" type="idmValueType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">HIV-1 NAT status</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="HIV_P24" type="idmValueType" minOccurs="0">
                <xs:annotation>
                    <xs:documentation xml:lang="en">HIV p24 status</xs:documentation>
                </xs:annotation>
            </xs:element>
            <xs:element name="HCV_NAT" type="idmValueType" minOccurs="0">

```

```

        <xs:annotation>
            <xs:documentation xml:lang="en">HCV NAT status</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="ANTI_HTLV" type="idmValueType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Antibody to HTLV I/II</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="SYPHILIS" type="idmValueType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Syphilis status</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="WNV" type="idmValueType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">WNV status</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="CHAGAS" type="idmValueType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Chagas status</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="EBV" type="idmValueExtType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">EBV status</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="TOXO" type="idmValueExtType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Toxoplasmosis status</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="HBV_NAT" type="idmValueType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">HBV NAT status</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="PB19_NAT" type="idmValueType" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">ParvoB19 NAT status</xs:documentation>
        </xs:annotation>
    </xs:element>
    <xs:element name="ALT" minOccurs="0">
        <xs:annotation>
            <xs:documentation xml:lang="en">Alanine aminotransferase status in
units per litre</xs:documentation>
        </xs:annotation>
        <xs:simpleType>
            <xs:restriction base="xs:short">
                <xs:minInclusive value="1"/>
            </xs:restriction>
        </xs:simpleType>
    </xs:element>
</xs:sequence>
</xs:complexType>
<xs:complexType name="kirType">
    <xs:annotation>
        <xs:documentation xml:lang="en">KIR genotype</xs:documentation>
    </xs:annotation>
    <xs:sequence>
        <xs:element name="KIR2DL1" type="kirLocusType" minOccurs="0">
            <xs:annotation>
                <xs:documentation xml:lang="en">KIR gene 2DL1</xs:documentation>
            </xs:annotation>
        </xs:element>
        <xs:element name="KIR2DL2" type="kirLocusType" minOccurs="0">
            <xs:annotation>
                <xs:documentation xml:lang="en">KIR gene 2DL2</xs:documentation>
            </xs:annotation>
        </xs:element>
    </xs:sequence>
</xs:complexType>

```


[illegible]

```

        <xs:element name="KIR3DP1" type="kirLocusType" minOccurs="0">
            <xs:annotation>
                <xs:documentation xml:lang="en">KIR gene 3DP1</xs:documentation>
            </xs:annotation>
        </xs:element>
        <xs:element name="KIR_GL" minOccurs="0">
            <xs:annotation>
                <xs:documentation xml:lang="en">URI that refers to a GL-string
registered with a GL-service or direct GL-string for absence / presence. Field is not used at the moment and
should therefore always be empty.</xs:documentation>
            </xs:annotation>
            <xs:simpleType>
                <xs:restriction base="xs:string">
                    <xs:maxLength value="255"/>
                </xs:restriction>
            </xs:simpleType>
        </xs:element>
    </xs:sequence>
</xs:complexType>
<xs:complexType name="hlaSerFieldsType">
    <xs:annotation>
        <xs:documentation xml:lang="en">HLA values obtained by serological typing methods</xs:
documentation>
    </xs:annotation>
    <xs:sequence>
        <xs:element name="FIELD1">
            <xs:simpleType>
                <xs:restriction base="xs:string">
                    <xs:maxLength value="5"/>
                </xs:restriction>
            </xs:simpleType>
        </xs:element>
        <xs:element name="FIELD2">
            <xs:simpleType>
                <xs:restriction base="xs:string">
                    <xs:maxLength value="5"/>
                </xs:restriction>
            </xs:simpleType>
        </xs:element>
    </xs:sequence>
</xs:complexType>
<xs:complexType name="hlaDnaFieldsType">
    <xs:annotation>
        <xs:documentation xml:lang="en">HLA values obtained by DNA based typing methods</xs:
documentation>
    </xs:annotation>
    <xs:sequence>
        <xs:element name="FIELD1">
            <xs:simpleType>
                <xs:restriction base="xs:string">
                    <xs:maxLength value="20"/>
                </xs:restriction>
            </xs:simpleType>
        </xs:element>
        <xs:element name="FIELD2">
            <xs:simpleType>
                <xs:restriction base="xs:string">
                    <xs:maxLength value="20"/>
                </xs:restriction>
            </xs:simpleType>
        </xs:element>
    </xs:sequence>
</xs:complexType>
<xs:complexType name="hlaLocusType">
    <xs:annotation>
        <xs:documentation xml:lang="en">HLA locus type comprising SER and DNA fields</xs:
documentation>
    </xs:annotation>
    <xs:sequence>
        <xs:element name="SER" type="hlaSerFieldsType" minOccurs="0" maxOccurs="1"/>
        <xs:element name="DNA" type="hlaDnaFieldsType" minOccurs="0" maxOccurs="1"/>
    </xs:sequence>
</xs:complexType>

```

```

        </xs:sequence>
    </xs:complexType>
    <xs:complexType name="hlaLocusDnaOnlyType">
        <xs:annotation>
            <xs:documentation xml:lang="en">HLA locus type comprising DNA fields only</xs:
documentation>
            </xs:annotation>
            <xs:complexContent>
                <xs:restriction base="hlaLocusType">
                    <xs:sequence>
                        <xs:element name="SER" type="hlaSerFieldsType" minOccurs="0" maxOccurs="
0"/>
                        <xs:element name="DNA" type="hlaDnaFieldsType" minOccurs="0" maxOccurs="
1"/>
                    </xs:sequence>
                </xs:restriction>
            </xs:complexContent>
        </xs:complexType>
    <xs:complexType name="hlaType">
        <xs:annotation>
            <xs:documentation xml:lang="en">HLA genotype</xs:documentation>
        </xs:annotation>
        <xs:sequence>
            <xs:element name="A" type="hlaLocusType" minOccurs="0"/>
            <xs:element name="B" type="hlaLocusType" minOccurs="0"/>
            <xs:element name="C" type="hlaLocusType" minOccurs="0"/>
            <xs:element name="DRB1" type="hlaLocusType" minOccurs="0"/>
            <xs:element name="DRB3" type="hlaLocusDnaOnlyType" minOccurs="0"/>
            <xs:element name="DRB4" type="hlaLocusDnaOnlyType" minOccurs="0"/>
            <xs:element name="DRB5" type="hlaLocusDnaOnlyType" minOccurs="0"/>
            <xs:element name="DQA1" type="hlaLocusDnaOnlyType" minOccurs="0"/>
            <xs:element name="DQB1" type="hlaLocusType" minOccurs="0"/>
            <xs:element name="DPA1" type="hlaLocusDnaOnlyType" minOccurs="0"/>
            <xs:element name="DPB1" type="hlaLocusDnaOnlyType" minOccurs="0"/>
        </xs:sequence>
    </xs:complexType>
</xs:schema>

```