

2402: Disease Classification

The Disease Classification Form is required for all transplants, including subsequent transplants on the comprehensive report form track and cellular therapy infusions when the indication is malignant hematologic disorder, non-malignant disorder or solid tumor.

All transplant centers participating in the CIBMTR must submit a Disease Classification Form (Form 2402) for each allogeneic (related or unrelated) hematopoietic cell transplant (HCT). The Disease Classification Form is a requirement of the SCTOD for all United States transplant centers when either the stem cell donation or the transplant occurs within the United States. For more information regarding the SCTOD, see General Instructions, Stem Cell Therapeutics Outcomes Database.

Although data regarding recipients receiving autologous HCT are not required to be submitted as part of the C.W. Bill Young Transplant Program, the CIBMTR is highly committed to collecting data on these recipients for research studies. Centers choosing to report autologous data to the CIBMTR must report on all autologous transplants performed at their center. For more information regarding data reporting for autologous HCT, see General Instructions, Autologous Hematopoietic Stem Cell Transplant.

The Disease Classification Form may be submitted to the CIBMTR up to two weeks prior to the start of the recipient's preparative regimen. The Disease Classification Form is due the day of infusion (day 0), and is past due if not received by that date.

The Disease Classification Form is designed to capture important details regarding the recipient's primary disease for which the reported HCT is being given. Key reporting areas differ depending on the disease reported (question 1), but may include disease type, subtype, transformations, cytogenetic and molecular markers, disease-specific laboratory results, staging, and disease status.

For recipients receiving a subsequent HCT:

Transplant centers must submit a Disease Classification Form for all subsequent HCTs; this includes recipients assigned to the TED Forms **and** the Comprehensive Report Forms by the form selection algorithm.

For the majority of subsequent HCTs, the recipient will remain on the original follow-up form track (TED or CRF) assigned by the form selection algorithm. For more information regarding center type and the form selection algorithm, see General Instructions, Center Type and Data Collection Forms. A recipient may need to change tracks if enrolled on a study that requires comprehensive forms.

For recipients of multiple transplants, transplant centers are not granted access to a subsequent Disease Classification Form in FormsNet3SM until the Post-TED (Form 2450) or Post-Infusion Data Form (Form 2100) from the previous transplant has been completed.

[Links to Sections of the Form:](#)

[Q1-2: Primary Disease for HCT](#)

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[Q164-167: Acute Leukemias of Ambiguous Lineage and Other Myeloid Neoplasms](#)

[Q168-178: Chronic Myelogenous Leukemia](#)

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Manual Updates:

Sections of the Forms Instruction Manual are frequently updated. The most recent updates to the manual can be found below. For additional information, select the manual section and review the updated text.

If you need to reference the historical Manual Change History for this form, please [click here](#) or reference the retired manual section on the [Retired Forms Manuals](#) webpage.

Date	Manual Section	Add/Remove/Modify	Description
8/19/2020	2402: Disease Classification	Add	Blue information box added above question 412 to indicate questions 412 – 441 refer to the labs and assessments performed at the diagnosis of the primary disease for transplant.
8/19/2020	2402: Disease Classification	Modify	Updated the Common Disease Transformation table for CLL to NHL, found in question 1-2. When a recipient transforms from CLL to NHL, multiple sections of the Disease Classification (2402) Form are not required to be completed.
8/18/2020	2402: Disease Classification	Add	Blue information box added above Q279 to provide instructions on how to report CALR testing: If CALR testing was performed but the lab report does not specify the type, select “not done” for questions 284 and 285 and specify the results as either “positive” or “negative” for question 286.
7/7/2020	2402: Disease Classification	Removed	Updated question 92 by removing the strike through sentence: This question is optional for international centers. This question is required to be answered for both domestic and international centers.

6/11/2020	2402: Disease Classification	Add	Clarification added on how to report the diagnosis date for recipients with congenital immunodeficiency in question 1: If the recipient was diagnosed prenatally (in utero) or was diagnosed with a congenital immunodeficiency , report the date of birth as the date of diagnosis.
6/11/2020	2402: Disease Classification	Modify	Updated the “Complete multiple disease sections of the Disease Classification Form?” column of Common Disease Transformations table above question 1 for the following transformations: MDS or MPN to AML: Yes – AML and MDS / or MPN ; JMML to AML: Yes – AML and MDS / MPN (select questions only); CLL to NHL (i.e., Richter’s Syndrome): No Yes – NHL and CLL
6/11/2020	2402: Disease Classification	Add	Added red warning box at the top of question 1 to provide clarification (red text) on what assessments to report for the “at diagnosis” time point if a previous infusion has been reported to the CIBMTR and relapse or progression occurred: For many diseases, the CIBMTR data collection forms capture disease assessments at multiple timepoints pre- and post-infusion. If the indication for this recipient’s HCT / Cellular Therapy is relapsed / progressive disease and they have had a previous transplant that was reported to the CIBMTR, only disease assessments performed after the disease relapse / progression occurred need to be reported. In this case, the disease assessments “at diagnosis” would be the disease assessments performed at the time relapse / progression occurred (prior to the initiation of therapy). Some pre-infusion forms on the Case Report Form (CRF) track have different reporting rules, depending on if a pre-infusion CRF had been previously completed for the recipient. Carefully review the Disease-Specific CRF manuals for additional information.
6/9/2020	2402: Disease Classification	Add	Provided clarification to question 371 that the molecular response should only be reported based on the detected driver mutations.
6/3/2020	2402: Disease Classification	Add	Added clarification on how to report the pre-HCT disease status for recipient with amyloidosis who do not receive therapy. If therapy was not given to treat amyloidosis, report “Unknown”
5/29/2020	2402: Disease Classification	Add	Added clarification that chromosomal microarrays / chromosomal genomic arrays should be reported within the FISH assessments data fields.
5/19/2020	2402: Disease Classification	Modify	Updated disease indication mentioned in guidance for answering question 101 from AML to ALL.
5/13/2020	2402: Disease Classification	Modify	Updated the following disease status criteria for hairy cell leukemia for question 378: Complete Remission, Stable Disease, and Progressive Disease.
5/13/2020	2402: Disease Classification	Modify	Updated questions 23 and 115 so that, wherever indicated, “microarray” is now “chromosomal microarray”.
5/13/2020	2402: Disease Classification	Modify	Updated question 389 to include criteria the the PET or combination PET / CT scan must meet to answer “yes” for this question.
5/9/2020	2402: Disease Classification	Modify	Version 5 of the 2402: Pre-TED Disease Classification section of the Forms Instructions Manual released. Version 5 corresponds to revision 5 of the Form 2402.

Q1-2: Primary Disease for HCT / Cellular Therapy

* Disease Classification Questions

The newest versions of the TED Forms use the World Health Organization (WHO) disease classifications. The Disease Classification questions contain all of the established WHO disease types and subtypes. The “other, specify” category should be used only if the recipient’s disease is not one of the listed options. For more information regarding disease classification, consult a transplant physician, contact the CIBMTR Customer Service Center, or visit the WHO website at: <http://www.who.int/classifications/icd/en/>.

Several of the Disease Classification questions ask for “*Status at Transplantation*.” Although there are many interpretations of disease response criteria, **when reporting data to the CIBMTR, use the guidelines in this manual to determine disease status**. A majority of the disease response criteria are established by an international working group. Citations of resources used to define disease responses are included where applicable.

If the recipient’s status is unclear, consult with the transplant physician for further information or contact the CIBMTR Customer Service Center.

! Subsequent HCT / Cellular Therapy for Disease Relapse:

For many diseases, the CIBMTR data collection forms capture disease assessments at multiple time points pre- and post-infusion. If the indication for this recipient’s HCT / Cellular Therapy is relapsed / progressive disease and they have had a previous infusion that was reported to the CIBMTR, only disease assessments performed after the disease relapse / progression need to be reported. In this case, the disease assessments “at diagnosis” would be the disease assessments performed at the time of relapse / progression occurred (prior to the initiation of therapy). Some pre-infusion forms on the Case Report Form (CRF) track have different reporting rules, depending on if a pre-infusion CRF had been previously complete for the recipient. Carefully review the Disease-Specific CRF manuals for additional information.

* Malignant vs. Non-Malignant

Malignant diseases involve cells dividing without control that can spread to other parts of the body through blood and lymph systems. These diseases are usually characterized by unlimited, aggressive growth, invasion of surrounding tissues, and metastasis.

Non-malignant diseases involve cell overgrowth, but lack the malignant properties of cancer.

The CIBMTR database disease codes are represented in parentheses after the disease subtype on the Disease Classification questions and can be helpful in mapping diagnosis [e.g., Myeloid Sarcoma (295)], and determining if the disease is malignant or non-malignant. Disease codes (10-299) indicate a malignant disease, with the exception of Paroxysmal Nocturnal Hemoglobinuria (PNH) (56). A disease code of (300) or above indicates a non-malignant disease, with the exception of disease code (900), which could indicate either a malignant or non-malignant disease.

If the indication for HCT is due to a combination of diseases or a transformation of one disease to another, it may be necessary to report multiple disease classifications. The tables below list how common examples of disease combinations and transformations should be reported using the Disease Classification questions.

Common Disease Combinations

Disease Combinations	Report Primary Disease as:	Report disease diagnosis date of:	Complete multiple disease sections of the Disease Classification Form?
FAN or SAA <u>and</u> AML	AML	AML	No
FAN or SAA <u>and</u> MDS	MDS	MDS	No
MYE <u>and</u> AMY	MYE	MYE	No

Common Disease Transformations

Disease Transformation	Report primary disease as:	Report disease diagnosis date of:	Complete multiple disease sections of the Disease Classification Form?
MDS or MPN <u>to</u> AML	AML	AML	Yes – AML <u>and</u> MDS or MPN
JMML <u>to</u> AML	AML	AML	Yes – AML <u>and</u> MDS (select questions only)
NHL <u>to</u> another NHL	Second NHL diagnosis	Second NHL diagnosis	No
HL <u>to</u> NHL*	NHL	NHL	No
CLL <u>to</u> NHL (i.e., Richter's Syndrome)	NHL	NHL	No

AML=Acute Myelogenous Leukemia; AMY=Amyloidosis; CLL=Chronic Lymphocytic Leukemia; FAN=Fanconi Anemia; MDS=Myelodysplastic Syndrome; MPS=Myeloproliferative Disease; MYE=Multiple Myeloma; NHL=Non-Hodgkin Lymphoma; SAA=Severe Aplastic Anemia.

*Ensure that the disease process is a transformation from Hodgkin lymphoma to Non-Hodgkin lymphoma (typically diffuse large B-cell lymphoma), rather than the distinct entity "B-cell lymphoma, unclassifiable, with features indeterminate between DLBCL and classical Hodgkin Lymphoma."

Question 1: Date of diagnosis for primary disease for HCT:

The date of diagnosis is important because the interval between diagnosis and HCT is often a significant indicator for the recipient's prognosis post-HCT.

Report the date of the first pathological diagnosis (e.g., bone marrow or tissue biopsy) of the disease. Enter the date the sample was collected for examination. If the diagnosis was determined at an outside center, and no documentation of a pathological or laboratory assessment is available, the dictated date of diagnosis

within a physician note may be reported. Do not report the date symptoms first appeared.

If the recipient was diagnosed prenatally (*in utero*) or was diagnosed with a **congenital** immunodeficiency, report the date of birth as the date of diagnosis.

If the exact pathological diagnosis date is not known, use the process described in [General Instructions, Guidelines for Completing Forms](#).

If this is a subsequent HCT for a new malignancy (or other new indication), report the date of diagnosis of the new malignancy.

! Erythropoietic protoporphyria (EPP): Historically, if the primary disease for transplant was erythropoietic protoporphyria, the primary disease for transplant was reported as “Other Disease.” However, the primary disease for transplant should be reported as “Inherited Abnormalities of Erythrocyte Differentiation or Function” in question 2 and specify the classification as “Other hemoglobinopathy” in question 359.

Question 2: What was the primary disease for which the HCT was performed?

Select the primary disease for which the recipient is receiving the HCT and continue with the appropriate disease classification questions.

Last modified: Aug 19, 2020

Q3-95: Acute Myelogenous Leukemia

Acute Myelogenous Leukemia (AML) is a cancer of the white blood cells. It is characterized by the rapid proliferation of abnormal, immature myelocytes, known as myeloblasts, in the bone marrow. This accumulation of blasts in the marrow prevents the formation of healthy red blood cells, white blood cells, and/or platelets. Normal myeloblasts develop into neutrophils, basophils, and eosinophils, which are all white blood cells that fight infection. In AML, the leukemic myeloblasts do not fully develop and are unable to fight infection. The symptoms of AML result from a drop in red blood cell, platelet, and normal white blood cell counts caused by the replacement of normal bone marrow with leukemic cells.

Certain prognostic indicators are associated with poorer outcomes. These include advanced age (50+ years of age), AML arising from MDS or secondary / therapy-related AML, and certain genetic mutations that are described in greater detail later in this manual.

Question 3: Specify the AML classification

Indicate the disease classification at diagnosis

Report the most specific entity that applies to the recipient. For example, if the recipient was classified using both cytogenetic data and the M5 FAB classification, the more specific cytogenetic data should be reported for classification purposes.

Question 4: Did AML transform from MDS or MPN?

AML often evolves from MDS or MPN. This transformation is typically distinguished by the percentage of blasts in the bone marrow

AML that transforms from MDS or MPN has a lower survival prognosis because of the association with unfavorable cytogenetic abnormalities.

AML can also evolve from Juvenile Myelomonocytic Leukemia (JMML). JMML is a rare form of chronic leukemia that affects young children, usually before the age of five. JMML results from DNA mutations in cells called monocytes. Normal monocytes attack invading microorganisms and assist lymphocytes in carrying out immune functions. Abnormal monocytes in JMML accumulate in the bone marrow and interfere with the production of normal white blood cells, red blood cells, and platelets.

If AML transformed from MDS or MPN (including JMML), check “Yes” and complete both the **AML and MDS / MPN** disease classification sections of this form. If AML did not transform from MDS or MPS, check “No.”

If MDS / MPN is suspected, but not confirmed by documented laboratory or pathologic findings, or if there is documentation of MDS / MPN **concurrent** with AML, check “No.”

Question 5: Is the disease (AML) therapy related?

Agents such as radiation or systemic therapy used to treat other diseases (e.g., Hodgkin lymphoma, non-Hodgkin lymphoma, or breast cancer) can damage the marrow and lead to a secondary malignancy such as AML. If the diagnosis of AML is therapy-related, check “Yes.”

If the diagnosis of AML is not therapy-related, check “No.”

- If AML was preceded by therapy-related MDS, check “No.”
- If the recipient developed AML after an environmental exposure (e.g., exposure to benzene), check “No.”

If it is unknown whether or not the diagnosis of AML was therapy-related, check “Unknown.”

Question 6: Did the recipient have a predisposing condition?

A predisposing condition is a condition that contributes to the susceptibility of developing leukemia. Therefore, diagnosis of the condition increases the likelihood that the recipient will develop leukemia. If the recipient has a documented history of a predisposing condition, check “Yes” and continue with question 7. If there is no history of a predisposing condition or if predisposition is unknown, indicate “No” or “Unknown” and continue with question 9.

Question 7-8: Specify condition:

Bloom syndrome is an autosomal recessive genetic disorder characterized by excessive chromosome breakage and corresponding rearrangements, proportional dwarfism, and sun sensitivity. The chromosomal instability seen in Bloom syndrome is generally assumed to be responsible for these individuals' predisposition to malignancy.

Down syndrome is also a chromosomal disorder (trisomy 21). It is characterized by an additional chromosome 21. Down syndrome patients exhibit a particular set of facial characteristics, growth deficiency, and cognitive impairment. Although Down syndrome patients have a reduced risk of developing many common malignancies, they have an increased risk of developing leukemia.

Fanconi anemia is a rare genetic blood disorder that prevents the body from producing a sufficient number of new blood cells to function properly. Abnormal blood cells may also be produced. These patients are short in stature, exhibit skeletal anomalies, and have an increased risk of developing solid tumors and leukemias.

Dyskeratosis congenita (DKC), also known as Zinsser-Engman-Cole syndrome, involves progressive bone marrow failure. Patients with DKC experience skin hyperpigmentation, nail dystrophy, and oral leukoplakia (a white patch / plaque that cannot be rubbed off).

Indicate the recipient's predisposing condition prior to the diagnosis of leukemia. If the recipient has a

documented history of a predisposing condition but it is not listed as an option in question 7, select “Other condition” and specify the condition in question 8.

* At Diagnosis, Last Evaluation, and In Between

Questions 9-83 ask about testing performed at different time points prior to HCT. For reporting purposes, use the definitions below to determine where to report testing on the Disease Classification Form.

At Diagnosis: Any testing performed between the date of diagnosis (question 1) and the start of any treatment for AML.

In Between: Any pre-infusion testing which cannot be reported as part of “At Diagnosis” or “Last Evaluation.”

Last Evaluation: Testing performed during the recipient’s work-up for HCT or cellular therapy (generally within 30 days of the start of the preparative regimen or infusion).

Question 9: Were cytogenetics tested (karyotyping or FISH)? (at diagnosis)

Cytogenetic analysis is the study of chromosomes. Cytogenetic assessment involves testing blood or bone marrow for the presence of a known chromosomal abnormality which reflects the recipient’s disease.

Testing methods you may see include conventional chromosome analysis (karyotyping) or fluorescence in situ hybridization (FISH). For more information about cytogenetic testing and terminology, see [Appendix C. Cytogenetic Assessments](#).

Karyotyping is performed by culturing cells (growing cells under controlled conditions) until they reach the dividing phase. Techniques are then performed to visualize the chromosomes during cell division so that various bands and reconfigurations can be seen. Banding pattern differentiation and chromosomal reconfiguration demonstrate evidence of disease.

FISH is a sensitive technique that assesses a large number of cells. This technique uses special probes that recognize and bind to fragments of DNA. These probes are mixed with cells from the recipient’s blood or bone marrow. A fluorescent “tag” is then used to visualize the binding of the probe to the diseased cells.

Table 3. Examples of AML Cytogenetic Findings Categorized by Prognosis

Favorable	Intermediate	Poor
t(15;17) t(8;21) inv(16) or t(16;16)	Normal +8 t(9;11) <i>All other abnormalities</i>	≥ 3 abnormalities 5- or 5q- 7- or 7q- t(9;22)

Indicate whether cytogenetic studies were performed at diagnosis. Do not report any testing performed after treatment for AML has started. If cytogenetic studies were obtained at diagnosis, check “Yes” and go to question 10. If cytogenetic studies were not obtained at this time point or it is not known whether chromosome studies were performed, indicate “No” or “Unknown” respectively and go to question 23.

Question 10-11: Were cytogenetics tested via FISH?

If FISH studies were performed at diagnosis (see [note box](#) above question 9), report “Yes” for question 10 and indicate whether clonal abnormalities were detected in question 11. Do not report any testing performed after treatment for AML has started. If FISH studies were not performed at this time point, report “No” for question 10 and go to question 16. Examples of this include: no FISH study performed or FISH sample was inadequate.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.



Question 12 is disabled and cannot be answered at this time.

Question 12-15: Specify cytogenetic abnormalities (FISH)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 12, then continue with question 13.

Specify the number of abnormalities detected by FISH at diagnosis (see note box above question 9) in question 13. After indicating the number of abnormalities in question 13, select all abnormalities detected in questions 14-15.

If a clonal abnormality is detected, but not listed as an option in question 15, select “Other abnormality” and specify the abnormality in question 15. If multiple “Other abnormalities” were detected, report “see attachment” in question 15 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 16-17: Were cytogenetics tested via karyotyping?

If karyotyping was performed at diagnosis (see note box above question 9), report “Yes” for question 16 and indicate whether clonal abnormalities were detected in question 17. Do not report any testing performed after treatment for AML has started. If karyotyping was not performed at this time point, indicate “No” and go to question 22. Examples of this include: karyotyping was not performed or karyotyping sample was inadequate.



Question 18 is disabled and cannot be answered at this time.

Question 18-21: Specify cytogenetic abnormalities (karyotyping)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 18, then continue with question 19.


Report the number of abnormalities detected by karyotyping at diagnosis (see note box above question 9) in

question 19. After indicating the number of abnormalities in question 19, select all abnormalities detected in questions 20-21.

If a clonal abnormality is detected, but not listed as an option in question 20, select “Other abnormality” and specify the abnormality in question 21. If multiple “Other abnormalities” were detected, report “see attachment” in question 21 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 22: Was documentation submitted to the CIBMTR?

Indicate if a karyotyping or FISH testing report is attached to support the cytogenetic findings reported in questions 9-21. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

 Questions capturing molecular marker results are intended to capture **molecular abnormalities** identified by **molecular methods**. Additional testing methods, such as FISH and chromosomal microarray, may identify molecular marker results but should **not** be reported in the molecular section(s) of the Pre-TED Disease Classification (2402) Form. Abnormalities identified by karyotyping, FISH, or chromosomal microarray should only be reported in the cytogenetic section of the Pre-TED Disease Classification (2402) Form.

Question 23: Were tests for molecular markers performed (e.g., PCR, NGS)? (at diagnosis)

Molecular markers for disease refer to specific genetic sequences which are believed to be associated with the recipient’s primary disease. Testing for these sequences is often performed using PCR based methods; however, lower sensitivity testing, including FISH, may also be used to detect molecular markers. Once a marker has been identified, these methods can be repeated to detect minimal residual disease (MRD) in the recipient’s blood, marrow, or tissue. Molecular assessments include polymerase chain reaction (PCR) amplification to detect single specific disease markers; however, molecular methods are evolving and now include Sanger sequencing, and next generation sequencing (e.g., Illumina, Roche 454, Proton / PGM, SOLiD).

If testing for molecular markers was performed at diagnosis (see note box above question 9), report “Yes” and go to question 24.

If molecular marker testing was not performed at diagnosis or it is not known if testing was done, report “No” or “Unknown” respectively and go to question 36.

Question 24-35: Specify results

For each molecular marker in questions 24-33, report whether testing was “Positive,” “Negative,” or “Not done” at diagnosis (see note box above question 9). If tests identified a molecular marker other than those listed in questions 24-33, report the result in question 34 and specify the marker in question 35.

If multiple “Other molecular marker[s]” were tested, report one instance (i.e., copy) of question 34-35 for each “Other molecular marker” tested. If greater than 3 “Other molecular marker[s]” were tested, do the following::

- report one instance of question 34-35; and
- report “Positive” if any of the “Other molecular marker[s]” were positive, otherwise, report “Negative;” and
- report “see attachment” in question 35; and
- attach any / all reports documenting the results of testing for “Other molecular marker[s].”

If CEBPA is reported as “Positive” (question 24) question 25 must be completed. If the lab report does not specify whether the detected marker was biallelic / homozygous or monoallelic / heterozygous, confirm with the laboratory whether this information can be determined prior to reporting “Unknown.”

If FLT3-ITD is reported as “Positive” (question 27) questions 28 and 29 must be completed. If the allelic ratio is known, report “Known” for question 28 and report the value in question 29. If the lab report does not specify the allelic ratio, confirm with the laboratory whether this information can be determined prior to reporting “Unknown.”

Table 4. Common Molecular Markers Associated with AML

Molecular Abnormality	Characteristics
CEBPA	CEBPA, <i>aka</i> CCAAT/enhancer binding protein α , is a transcription factor required for the differentiation of granulocytes. Numerous CEBPA mutations have been identified in relation to AML, with the majority of patients displaying biallelic mutations ultimately resulting in the down regulation of gene activity. Decreased gene activity results in decreased differentiation potential for immature granulocytes. An estimated 7-15% of AML patients have CEBPA mutations and CEBPA mutations are generally found in M1 and M2 subtypes in conjunction with intermediate-risk cytogenetics. Studies show an association with more favorable outcomes. ¹
FLT3-D835 point mutation	FLT3 encodes a receptor tyrosine kinase. The FLT3-D835 point mutation, <i>aka</i> FLT3-TKD, is an activating mutation impacting tyrosine-kinase domains. FLT3 mutations are found in up to 1/3 of all AML patients. The clinical significance of TKD activation remains unclear. FLT3-D385 mutations are often found in conjunction with other mutations. Overall, FLT3-D385 is not considered a favorable or poor prognostic indicator. However, in certain combinations with other mutations, there are associations with both improved and diminished survival. ²³
FLT3-ITD mutation	FLT3 encodes a receptor tyrosine kinase. The FLT3-ITD (internal tandem duplication) interferes with certain down regulation functions within receptor tyrosine kinases, leading to activation of TK activity. FLT3 mutations are found in up to 1/3 of all AML patients. FLT3-ITD is considered a poor prognostic factor. Sorafenib (Nexavar) has been shown to initially improve disease response in FLT3-ITD-positive AML. ⁴
IDH1	Isocitrate Dehydrogenase (IDH) is an oxidative enzyme involved in the citric acid cycle. IDH1 mutations result in incorrect catalytic activity, leading to increased levels of an oncometabolite, 2-hydroxyglutarate. The pathologic activity of IDH1 mutations is still being studied, but it has been suggested that IDH mutations may be a distinct mechanism in AML pathogenesis;

	research models show they may cause an accumulation of hematopoietic progenitor cells. Early research suggests IDH1 mutation may be a less favorable prognostic indicator. ⁵
IDH2	Isocitrate Dehydrogenase (IDH) is an oxidative enzyme involved in the citric acid cycle. IDH2 is a mitochondrial homolog to IDH1. Much like IDH1 mutations, IDH2 mutations result in incorrect catalytic activity, leading to increased levels of (D)-2-hydroxyglutarate. The pathologic activity of IDH2 mutations are still being studied, but it has been suggested that IDH mutations may be a distinct mechanism in AML pathogenesis; research models show they may cause an accumulation of hematopoietic progenitor cells. Early research suggests IDH2 mutation may be a more favorable prognostic indicator, unlike IDH1 mutation, though there may be differences based on where the IDH2 mutation occurs in gene. ⁶
KIT	KIT encodes a receptor tyrosine kinase. The KIT mutations at exons 8 and 17 are associated with activation of encoded proteins, resulting in activation impacting tyrosine-kinase domains. Patients with t(8;21) and inv(16) cytogenetics are frequently screened for KIT mutations, which adversely affect prognosis in these patients. ⁷
NPM1	NPM1 encodes a protein responsible for multiple cellular functions, including the regulation of the ARF-p53 tumor suppressor pathway. Mutations in NPM1 result in gene over-expression and subsequent inactivation of ARF-p53 tumor suppression pathway. NPM1 mutations are one of the most common molecular markers seen in AML and are associated with improved survival. ⁸
Other molecular marker	Assessments for other molecular markers known or believed to be associated with AML may be performed. If these studies are performed, indicate “positive” or “negative” and specify the marker in question 56.

¹ Lin L, Chen C, Lin D, Tsay W, Tang J, Yeh Y, Shen H, Su F, Yao M, Huang S, Tien H. (2005). Characterization of CEBPA Mutations in Acute Myeloid Leukemia: Most patients with CEBPA mutations have biallelic mutations and show a distinct immunophenotype of the leukemic cells. *Clin Cancer Res*, 11, 1372-9.

² Mead AJ, Linch DC, Hills RK, Wheatley K, Burnett AK, Gale RE. (2007). FLT3 tyrosine kinase domain mutations are biologically distinct from and have a significantly more favorable prognosis than FLT3 international tandem duplications in patient with acute myeloid leukemia. *Blood*, 110, 1262-70.

³ Whitman SP, Ruppert AS, Radmacher, MD, et al. (2008). FLT3 D835/I836 mutations are associated with poor disease-free survival and a distinct gene-expression signature among younger adults with de novo cytogenetically normal acute myeloid leukemia lacking FLT3 internal tandem duplications. *Blood*, 111, 1552-59.

⁴ Man CH, Fung TK, Ho C, et al. (2011). Sorafenib treatment of FLT-ITD+ acute myeloid leukemia: favorable initial outcome and mechanisms of subsequent non-responsiveness associated with the emergence of a D835 mutation. *Blood*, 119 (22), 5133-43.

⁵ Marucci G, Maharry K, Wu YZ, et al. (2010). IDH1 and IDH2 Gene Mutations Identify Novel Molecular Subsets Within De Novo Cytogenetically Normal Acute Myeloid Leukemia: A Cancer and Leukemia Group B Study. *J Clin Oncol*, 28(14), 2348-55.

⁶ Green CL, Evans CM, Zhao L, et al. (2011). The prognostic significance of IDH2 mutations in AML depends on the location of the mutation. *Blood*, 118(2), 409-12.

⁷ Döhner K, Döhner H. (2008).Molecular characterization of acute myeloid leukemia. *Haematologica*, 93(7), 976-82.

⁸ Varhaak RGW, Goudswaard CS, van Putten W, et al. (2005).Mutations in nucleophosmin (NPM1) in acute myeloid leukemia (AML): association with other gene abnormalities and previously established gene expression signatures and their favorable prognostic significance. *Blood*, 106(12), 3747-54.


Question 36: Were cytogenetics tested (karyotyping or FISH)? (between diagnosis and last evaluation)

See question 9 for a description of cytogenetic tests. Indicate whether cytogenetic studies were performed between diagnosis and the last evaluation prior to infusion (see note above question 9). If cytogenetic studies were obtained during this time, check “Yes” and go to question 37. If cytogenetic studies were not obtained at this time point or it is not known whether chromosome studies were performed, indicate “No” or “Unknown” respectively and go to question 50.

Question 37-38: Were cytogenetics tested via FISH?

If FISH studies were performed between diagnosis and the last evaluation prior to infusion (see note box above question 9), report “Yes” for question 37 and indicate whether clonal abnormalities were detected in question 38. If multiple FISH assessments were performed, report “Abnormalities Identified” if any testing showed clonal abnormalities during this period. If FISH studies were not performed during this period, report “No” for question 37 and go to question 43. Examples of this include: no FISH study performed or all FISH samples were inadequate.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.

 Question 39 is disabled and cannot be answered at this time.

Question 39-42: Specify cytogenetic abnormalities (FISH)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 39, then continue with question 40.

Report the number of abnormalities detected by FISH between diagnosis and the last evaluation prior to infusion (see note box above question 9) in question 40. If FISH studies showed different clonal abnormalities during this time, report the total number of clonal abnormalities detected. After indicating the number of clonal abnormalities in question 40, select all clonal abnormalities detected during this period in questions 41-42. This includes all clonal abnormalities detected any FISH assessment performed during this period.

If a clonal abnormality is detected, but not listed as an option in question 41, select “Other abnormality” and specify the abnormality in question 42. If multiple “Other abnormalities” were detected, report “see attachment” in question 42 and attach the final report(s) for any other abnormalities detected. For further

instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 43-44: Were cytogenetics tested via karyotyping?

If karyotyping was performed between diagnosis and the last evaluation prior to infusion (see note box above question 9), report “Yes” for question 43 and indicate whether clonal abnormalities were detected in question 44. If multiple karyotypes were performed, report “Abnormalities Identified” if any testing showed clonal abnormalities during this period. If karyotyping was not performed during this period, report “No” for question 43 and go to question 49. Examples of this include: no karyotyping performed or all karyotype samples were inadequate.



Question 45 is disabled and cannot be answered at this time.

Question 45-48: Specify cytogenetic abnormalities (karyotyping)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 45, then continue with question 46.

Report the number of abnormalities detected by karyotyping between diagnosis and the last evaluation prior to infusion (see note box above question 9) in question 46. If karyotype studies showed different clonal abnormalities during this time, report the total number of clonal abnormalities detected. After indicating the number of clonal abnormalities in question 46, select all clonal abnormalities detected during this period in questions 47-48. This includes all clonal abnormalities detected any karyotype performed during this period.

If a clonal abnormality is detected, but not listed as an option in question 47, select “Other abnormality” and specify the abnormality in question 48. If multiple “Other abnormalities” were detected, report “see attachment” in question 48 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 49: Was documentation submitted to the CIBMTR?

Indicate if a karyotyping or FISH testing report is attached to support the cytogenetic findings reported in questions 36-48. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).



Questions capturing molecular marker results are intended to capture **molecular abnormalities** identified by **molecular methods**. Additional testing methods, such as FISH, may identify molecular marker results but should **not** be reported in the molecular section(s) of the Pre-TED Disease Classification (2402) Form. Abnormalities identified by karyotyping, FISH, or microarray should only be reported in the cytogenetic section of the Pre-TED Disease Classification (2402) Form.

Question 50: Were tests for molecular markers performed (e.g., PCR, NGS)? (between diagnosis and last evaluation)

See question 21 for a description of testing for molecular markers. Indicate whether testing for molecular markers was performed between diagnosis and the last evaluation prior to infusion (see note above question 9). If testing for molecular markers was performed during this time, check “Yes” and go to question 51. If cytogenetic studies were not obtained during this period or it is not known whether testing for molecular markers was performed, indicate “No” or “Unknown” and go to question 63.

Question 51-62: Specify results

For each molecular marker in questions 51-60, report whether testing was “Positive,” “Negative,” or “Not done” between diagnosis and the last evaluation prior to infusion (see note box above question 9). If tests identified a molecular marker other than those listed in questions 51-60, report the result in question 61 and specify the marker in question 62.

If multiple “Other molecular marker[s]” were tested, report one instance (i.e., copy) of question 61-62 for each “Other molecular marker” tested. If greater than 3 “Other molecular marker[s]” were tested, do the following:

- report one instance of question 61-62; and
- report “Positive” if any of the “Other molecular marker[s]” were positive, otherwise, report “Negative;” and
- report “see attachment” in question 62; and
- attach any / all reports documenting the results of testing for “Other molecular marker[s].”

If CEBPA is reported as “Positive” (question 51) question 52 must be completed. If the lab report does not specify whether the detected marker was biallelic / homozygous or monoallelic / heterozygous, confirm with the laboratory whether this information can be determined prior to reporting “Unknown.”

If FLT3-ITD is reported as “Positive” (question 54) questions 55 and 56 must be completed. If the allelic ratio is known, report “Known” for question 55 and report the value in question 56. If the lab report does not specify the allelic ratio, confirm with the laboratory whether this information can be determined prior to reporting “Unknown.”

Question 63: Were cytogenetics tested (karyotyping or FISH)? (at last evaluation)

See question 9 for a description of cytogenetic testing. Indicate whether cytogenetic studies were performed at the last evaluation prior to infusion (see note box above question 9). If cytogenetic studies were obtained at this time point, check “Yes” and go to question 64. If cytogenetic studies were not obtained at this time point or it is not known whether chromosome studies were performed, indicate “No” or “Unknown” respectively and go to question 77.

Questions 64-65: Were cytogenetics tested via FISH?

If FISH studies were performed at the last evaluation prior to infusion (see note box above question 9), report “Yes” for question 64 and indicate whether clonal abnormalities were detected in question 65. If FISH studies were not performed at this time point, report “No” for question 64 and go to question 70. Examples of this include: no FISH study performed or FISH sample was inadequate.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.

! Question 66 is disabled and cannot be answered at this time.

Question 66-69: Specify cytogenetic abnormalities (FISH)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 66, then continue with question 67.

Report the number of abnormalities detected by FISH at the last evaluation prior to infusion (see note box above question 9) in question 67. After indicating the number of abnormalities in question 67, select all abnormalities detected in questions 68-69.

If a clonal abnormality is detected, but not listed as an option in question 68, select “Other abnormality” and specify the abnormality in question 69. If multiple “Other abnormalities” were detected, report “see attachment” in question 69 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 70-71: Were cytogenetics tested via karyotyping?

If karyotyping was performed at the last evaluation prior to infusion (see note box above question 9), report “Yes” for question 70 and indicate whether clonal abnormalities were detected in question 71. If karyotyping was not performed at this time point, indicate “No” and go to question 76. Examples of this include: karyotyping was not performed or karyotyping sample was inadequate.

! Question 72 is disabled and cannot be answered at this time.

Question 72-75: Specify cytogenetic abnormalities (karyotyping)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 72, then continue with question 73.

Report the number of abnormalities detected by karyotyping at the last evaluation prior to infusion (see note box above question 9) in question 73. After indicating the number of abnormalities in question 73, select all abnormalities detected in questions 74-75.

If a clonal abnormality is detected, but not listed as an option in question 74, select “Other abnormality” and specify the abnormality in question 75. If multiple “Other abnormalities” were detected, report “see attachment” in question 75 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 76: Was documentation submitted to the CIBMTR?

Indicate if a karyotyping or FISH testing report is attached to support the cytogenetic findings reported in questions 63-75. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

✿ Questions capturing molecular marker results are intended to capture **molecular abnormalities** identified by **molecular methods**. Additional testing methods, such as FISH, may identify molecular marker results but should **not** be reported in the molecular section(s) of the Pre-TED Disease Classification (2402) Form. Abnormalities identified by karyotyping, FISH, or microarray should only be reported in the cytogenetic section of the Pre-TED Disease Classification (2402) Form.

Question 77: Were tests for molecular markers performed (e.g., PCR, NGS)? (at last evaluation)

See question 21 for a description of testing for molecular markers. If testing for molecular markers was performed at the last evaluation prior to infusion (see note box above question 9), report “Yes” and go to question 78. If molecular marker testing was not performed at this time point or it is not known if testing was done, report “No” or “Unknown” respectively and go to question 90.

Question 78-89: Specify results

For each molecular marker in questions 78-87, report whether testing was “Positive,” “Negative,” or “Not done” at the last evaluation prior to infusion (see note box above question 9). If tests identified a molecular marker other than those listed in questions 78-87, report the result in question 88 and specify the marker in question 89.

If multiple “Other molecular marker[s]” were tested, report one instance (i.e., copy) of question 88-89 for each “Other molecular marker” tested. If greater than 3 “Other molecular marker[s]” were tested, do the following:

- report one instance of question 88-89; and
- report “Positive” if any of the “Other molecular marker[s]” were positive, otherwise, report “Negative;” and
- report “see attachment” in question 89; and
- attach any / all reports documenting the results of testing for “Other molecular marker[s].”

If CEBPA is reported as “Positive” (question 78) question 79 must be completed. If the lab report does not specify whether the detected marker was biallelic / homozygous or monoallelic / heterozygous, confirm with the laboratory whether this information can be determined prior to reporting “Unknown.”

If FLT3-ITD is reported as “Positive” (question 81) questions 82 and 83 must be completed. If the allelic ratio is known, report “Known” for question 82 and report the percent in question 83. If the lab report does not specify the allelic ratio, confirm with the laboratory whether this information can be determined prior to reporting “Unknown.”

Question 90: Did the recipient have central nervous system leukemia at any time prior to the start of the preparative regimen / infusion?

Central nervous system (CNS) involvement by leukemia may be detected via pathologic examination of cerebrospinal fluid or tumor tissue as well as by radiological examinations (e.g., MRI, PET/CT, MIBG, etc.). If the recipient had documented involvement of AML in the CNS, report “Yes” for question 90. If all CNS testing was negative since the time of diagnosis, report “No.” If testing for CNS involvement was not performed from the time of diagnosis to the time of HCT / cellular therapy, report “Unknown.”

Question 91: What was the disease status (based on hematologic test results)?

Indicate the disease status of AML at the last assessment prior to the start of the preparative regimen. Refer to the AML Response Criteria section of the Forms Instructions Manual for definitions of each response. For reporting purposes, consider complete remission with incomplete hematologic recovery (CRi) a complete remission (CR1, CR2, or CR3+).

If the recipient did not receive any treatment for AML from the time of diagnosis to the start of the preparative regimen / infusion, report “No treatment” and go to question 95.

If the recipient’s disease status is primary induction failure at the time of HCT / cellular therapy, go to question 95.

If the recipient’s disease status is CR / CRi at the time of HCT / cellular therapy, go to question 92.

If the recipient’s disease status is relapse at the time of HCT / cellular therapy, go to question 94.

Question 92: How many cycles of induction therapy were required to achieve 1st complete remission (CR)? (includes CRi)

Chemotherapy is initially given as induction therapy intended to bring the disease into remission. Recipients usually have one to two cycles of induction therapy; disease prognosis is considered less favorable if the patient fails to achieve remission with the first induction therapy and even poorer if patients fail two or more induction therapies.¹ An example of a common induction therapy for all AML subtypes (except M3) is a combination of an anthracycline and cytarabine, commonly known as “7+3.” In this regimen, cytarabine is typically administered for seven days at a dose of 100 mg/m²/day. The anthracycline (usually daunorubicin

at 45 to 60 mg/m²/day or idarubicin at 12 mg/m²/day) is generally given on the first three days the cytarabine is given.

The second phase of chemotherapy is known as consolidation therapy. The goal of consolidation therapy is to destroy any remaining leukemia cells and sustain remission. An example of a common consolidation therapy for all AML subtypes (except M3) is high-dose cytarabine, commonly referred to as “HiDAC.” In this regimen, cytarabine is typically administered at a dose exceeding 10 g/m² per cycle.

Maintenance chemotherapy may follow consolidation therapy. Maintenance chemotherapy is given in lower doses and is intended to prolong a remission. Maintenance therapy is used less commonly for the treatment of AML than other malignancies. Treatment may also be administered for relapsed disease. Much like induction therapy, treatment for relapse is intended to bring the disease back into remission. Systemic therapeutic agents used to induce remission following relapse often differ from those used in the initial induction, since the disease is often resistant to many of the agents used earlier in the disease course and is considered high-risk with a poor prognosis. Allogeneic HCT is often considered the only potential “cure” for relapsed disease.

Indicate the number of cycles of induction therapy that were required to achieve the first CR.

¹ Ravandi F, Cortes J, Faderl S, et al. (2010). Characteristics and outcome of patients with acute myeloid leukemia refractory to one cycle of high-dose cytarabine-based induction therapy. *Blood*, 116(26):5818-23.

Question 93: Was the recipient in remission by flow cytometry?

Question 93 will only be answered if CR has been reported for question 91. Flow cytometry assessment is a method of analyzing peripheral blood, bone marrow, or tissue preparations for multiple unique cell characteristics. Its primary clinical purpose in the setting of leukemias is to quantify blasts in the peripheral blood or bone marrow, or to identify unique cell populations through immunophenotyping. Flow cytometry assessment may also be referred to as “MRD,” or minimal residual disease, testing.

Flow cytometric remission is a treatment response in which no blasts can be detected.

If flow cytometric abnormalities associated with the recipient’s disease were identified previously, but the criteria above were met at the last evaluation prior to the start of the preparative regimen, indicate “yes.”

If flow cytometric abnormalities associated with the recipient’s disease were identified at the last evaluation prior to the start of the preparative regimen, indicate “no.”

Indicate “unknown” if flow cytometric abnormalities associated with the recipient’s disease were identified previously and no flow cytometry assessment was performed prior to the start of the preparative regimen.

Indicate “not applicable” if one of the following applies:

- No flow cytometry assessments were performed at any time prior to the start of the preparative regimen.
- Flow cytometric abnormalities were not identified on previous testing and no flow cytometric abnormalities were identified at the last evaluation prior to the start of the preparative regimen.

This question is optional for international centers.

Question 94: Date of most recent relapse:

Enter the date of the most recent relapse prior to the start of the preparative regimen / infusion. If reporting a pathological evaluation (e.g., bone marrow) or blood/serum assessment (e.g., CBC, peripheral blood smear), enter the date the sample was collected. If extramedullary disease was detected by radiographic examination (e.g., X-ray, CT scan, MRI scan, PET scan), enter the date the imaging took place. If the physician determines cytogenetic or molecular relapse, enter the date the sample was collected for cytogenetic or molecular evaluation. If the physician determines evidence of relapse following a clinical assessment during an office visit, report the date of assessment.

If the exact date is not known, use the process for reporting partial or unknown dates as described in [General Instructions, General Guidelines for Completing Forms](#).

Question 95: Date assessed

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen. The date reported should be that of the most disease-specific assessment within the pre-transplant work-up period (approximately 30 days). Clinical and hematologic assessments include pathological evaluation (e.g., bone marrow biopsy), radiographic examination (e.g., X-ray, CT scan, MRI scan, PET scan), and laboratory assessment (e.g., CBC, peripheral blood smear), in addition to clinician evaluation and physical examination. Enter the date the sample was collected for pathological and laboratory evaluations; enter the date the imaging took place for radiographic assessments.

If the exact date is not known, use the process for reporting partial or unknown dates as described in [General Instructions, Guidelines for Completing Forms](#).

Last modified: Jul 07, 2020

Q96-163: Acute Lymphoblastic Leukemia



Acute Lymphoblastic Lymphoma

Due to the aggressive nature of precursor T- and precursor B-cell lymphoblastic lymphoma (or lymphoma / leukemia), the primary disease reported for recipients with these malignancies should be acute lymphoblastic leukemia (T-cell lymphoblastic leukemia / lymphoma or B-cell ALL, NOS {L1 / L2}).

Acute Lymphoblastic Leukemia (ALL) is a cancer of the white blood cells. It is characterized by the rapid proliferation of abnormal, immature lymphocytes, known as lymphoblasts, in the bone marrow. This accumulation of blasts in the marrow prevents the formation of healthy red blood cells, white blood cells and/or platelets. Normal lymphoblasts develop into B and T lymphocytes that fight infection. In ALL, the leukemic lymphoblasts do not fully develop and therefore cannot fight infection. The symptoms of ALL are caused by the replacement of normal bone marrow with leukemic cells, resulting in a drop in red blood cells, platelets, and normal white blood cells. It is estimated that 80-85% of ALL cases occur in children, with peak incidence of pediatric ALL at age 5. Biologically, adult and pediatric ALL are very different. Pediatric cases are more often characterized by favorable prognostic indicators including a precursor B-cell population, TEL / AML1 fusion gene, and/or hyperdiploidy; adult cases are more often characterized by poor prognostic indicators including a precursor T-cell population and / or BCR / ABL fusion gene.¹

¹ Sallan S. Myths and Lessons from the Adult/Pediatric Interface in Acute Lymphoblastic Leukemia. ASH Education Book, 1st edition. 2006:128-32.

Question 96: Specify ALL classification

Indicate the disease classification at diagnosis.

Due to the aggressive nature of precursor T- and precursor B-cell lymphoblastic lymphoma (or lymphoma / leukemia), the primary disease reported for recipients with these malignancies should be acute lymphoblastic leukemia.

If the cytogenetic or molecular abnormalities present at diagnosis are listed on the Pre-TED form, check the sub-type rather than “B-cell ALL, NOS” option.

Question 97: Did the recipient have a predisposing condition?

A predisposing condition is a condition that contributes to the susceptibility of developing leukemia. Therefore, diagnosis of the condition increases the likelihood that the recipient will develop leukemia. If the recipient has a documented history of a predisposing condition, check “Yes” and continue with question 98. If there is no history of a predisposing condition or if predisposition is unknown, indicate “No” or “Unknown” and continue with question 100.

Question 98-99: Specify condition:

Aplastic anemia is an acquired or inherited disorder of the bone marrow characterized by pancytopenia, where the body does not produce a sufficient number of new blood cells. Inherited aplastic anemias include Fanconi anemia (specified separately on this form), Shwachman-Diamond anemia, Diamond-Blackfan anemia, and dyskeratosis congenita. Acquired aplastic anemia may develop after exposures to toxins, radiation, and/or chemotherapy, or may result from an autoimmune condition such as systemic lupus erythematosus (SLE) or rheumatoid arthritis (RA). The majority of presenting signs and symptoms in aplastic anemia patients are directly related to their low blood counts and include fatigue, dizziness, shortness of breath, abnormal bleeding or bruising, and frequent infections.

Bloom syndrome is an autosomal recessive genetic disorder characterized by excessive chromosome breakage and corresponding rearrangements, proportional dwarfism, and sun sensitivity. The chromosomal instability seen in Bloom syndrome is generally assumed to be responsible for these individuals' predisposition to malignancy.

Down syndrome is also a chromosomal disorder (trisomy 21). It is characterized by an additional chromosome 21. Down syndrome patients exhibit a particular set of facial characteristics, growth deficiency, and cognitive impairment. Although Down syndrome patients have a reduced risk of developing many common malignancies, they have an increased risk of developing leukemia.

Fanconi anemia is a rare genetic blood disorder that prevents the body from producing a sufficient number of new blood cells to function properly. Abnormal blood cells may also be produced. These patients are short in stature, exhibit skeletal anomalies, and have an increased risk of developing solid tumors and leukemias.

Indicate the recipient's predisposing condition prior to the diagnosis of leukemia. If the recipient has a documented history of a predisposing condition but it is not listed as an option in question 98, select "Other condition" and specify the condition in question 99.

Question 100: Were tyrosine kinase inhibitors (i.e., imatinib mesylate) given for pre-HCT therapy at any time prior to the start of the preparative regimen?

Report whether the recipient received any tyrosine kinase inhibitor from the diagnosis of ALL to the start of the preparative regimen / infusion. Examples include: Imatinib mesylate is also known as Gleevec, Glivec, STI-571, or CGP57148B.

This question is optional for international centers.

 **At Diagnosis, Last Evaluation, and In Between**

Questions 101-163 ask about testing performed at different time points prior to HCT. For reporting purposes, use the definitions below to determine where to report testing on the Disease Classification Form.

At Diagnosis: Any testing performed between the date of diagnosis (question 1) and the start of any treatment for ALL.

In Between: Any testing which cannot be reported as part of either of the two above time points.

Last Evaluation: Testing performed during the recipient's work-up for HCT or cellular therapy (generally within 30 days of the start of the preparative regimen or infusion).

Question 101: Were cytogenetics tested (conventional or FISH)? (at diagnosis)

Cytogenetic analysis is the study of chromosomes. Cytogenetic assessment involves testing blood or bone marrow for the presence of a known chromosomal abnormality which reflects the recipient's disease. Testing methods you may see include conventional chromosome analysis (karyotyping) or fluorescence in situ hybridization (FISH). For more information about cytogenetic testing and terminology, see [Appendix C. Cytogenetic Assessments](#).

Karyotyping is performed by culturing cells (growing cells under controlled conditions) until they reach the dividing phase. Techniques are then performed to visualize the chromosomes during cell division so that various bands and reconfigurations can be seen. Banding pattern differentiation and chromosomal reconfiguration demonstrate evidence of disease.

FISH is a sensitive technique that assesses a large number of cells. This technique uses special probes that recognize and bind to fragments of DNA. These probes are mixed with cells from the recipient's blood or bone marrow. A fluorescent "tag" is then used to visualize the binding of the probe to the diseased cells.

Table 5. Examples of ALL Cytogenetic Findings Categorized by Prognosis (Adult Precursor B-cell ALL)

Favorable	Intermediate	Poor	Very Poor
High hyperdiploidy (51-65 chromosomes)	Normal 11q abnormalities del(6q) del(17p) del(9p) del(12p) -13/del(13q) t(14q32) t(10;14) Low hyperdiploidy (47-50 chromosomes) Tetraploidy (> 80 chromosomes)	-7/del(7p) +8 11q23 abnormalities/ MLL t(1;19) t(17;19) t(5;14) t(9;22)	≥ 5 abnormalities t(4;11) t(8;14)


² Pullarkat V, Slovak ML, Kopecky KJ, Forman SJ, Appelbaum FR. Impact of cytogenetics on the outcome of adult acute lymphoblastic leukemia: results of Southwest Oncology Group 9400 study. *Blood*. 2008;111(5):2563-72.

Indicate whether cytogenetic studies were performed at diagnosis. Do not report any testing performed after treatment for ALL has started. If cytogenetic studies were obtained at diagnosis, check “Yes” and go to question 102. If cytogenetic studies were not obtained at this time point or it is not known whether chromosome studies were performed, indicate “No” or “Unknown” respectively and go to question 115.

Question 102-103: Were cytogenetics tested via FISH?

If FISH studies were performed at diagnosis (see [note box](#) above question 95), report “Yes” for question 102 and indicate whether clonal abnormalities were detected in question 103. Do not report any testing performed after treatment for ALL has started. If FISH studies were not performed at this time point, report “No” for question 102 and go to question 108. Examples of this include: no FISH study performed, or FISH sample was inadequate.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.

 Question 104 is disabled and cannot be answered at this time.

Question 104-107: Specify cytogenetic abnormalities (FISH)


Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 104, then continue with question 105.

Report the number of abnormalities detected by FISH at diagnosis (see note box above question 101) in question 105. After indicating the number of abnormalities in question 105, select all abnormalities detected in questions 106-107.

If a clonal abnormality is detected, but not listed as an option in question 106, select “Other abnormality” and specify the abnormality in question 107. If multiple “Other abnormalities” were detected, report “see attachment” in question 107 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 108-109: Were cytogenetics tested via karyotyping?

If karyotyping was performed at diagnosis (see [note box](#) above question 101), report “Yes” for question 108 and indicate whether clonal abnormalities were detected in question 109. Do not report any testing performed after treatment for ALL has started. If karyotyping was not performed at this time point, indicate “No” and go to question 115. Examples of this include: karyotyping was not performed or karyotyping sample was inadequate.

 Question 110 is disabled and cannot be answered at this time.

Question 110-113: Specify cytogenetic abnormalities (karyotyping)


Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 110, then continue with question 111.

Report the number of abnormalities detected by karyotyping at diagnosis (see note box above question 101) in question 111. After indicating the number of abnormalities in question 111, select all abnormalities detected in questions 112-113.

If a clonal abnormality is detected, but not listed as an option in question 112, select “Other abnormality” and specify the abnormality in question 113. If multiple “Other abnormalities” were detected, report “see attachment” in question 112 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 114: Was documentation submitted to the CIBMTR?

Indicate if a karyotyping or FISH testing report is attached to support the cytogenetic findings reported in questions 101-113. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

 Questions capturing molecular marker results are intended to capture **molecular abnormalities** identified by **molecular methods**. Additional testing methods, such as FISH or chromosomal microarray, may identify molecular marker results but should **not** be reported in the molecular section(s) of the Pre-TED Disease Classification (2402) Form. Abnormalities identified by karyotyping, FISH, or chromosomal microarray should only be reported in the cytogenetic section of the Pre-TED Disease Classification (2402) Form.

Question 115: Were tests for molecular markers performed (e.g., PCR)? (at diagnosis)

Molecular markers for disease refer to specific genetic sequences which are believed to be associated with the recipient’s primary disease. Testing for these sequences is often performed using PCR based methods; however, lower sensitivity testing, including FISH, may also be used to detect molecular markers. Once a marker has been identified, these methods can be repeated to detect minimal residual disease (MRD) in the recipient’s blood, marrow, or tissue. Molecular assessments include polymerase chain reaction (PCR) amplification to detect single specific disease markers; however, molecular methods are evolving and now include Sanger sequencing, and next generation sequencing (e.g., Illumina, Roche 454, Proton / PGM, SOLiD).

If testing for molecular markers was performed at diagnosis (see [note box](#) above question 101), report “Yes” and go to question 116.

If molecular marker testing was not performed at diagnosis or it is not known if testing was done, report “No” or “Unknown” respectively and go to question 120.

Table 6. Common Molecular Markers Associated with ALL

Molecular Abnormality	Characteristics
BCR-ABL	BCR-ABL, <i>aka</i> Philadelphia chromosome, refers to the tyrosine kinase gene fusion resulting from the translocation of material from chromosome 9 (ABL) onto chromosome 22 (BCR). Molecular weight varies depending on exact location of the translocation; isoform p190 is typically seen in ALL. Tyrosine kinase inhibitor therapies such as imatinib mesylate (Gleevec) target and block ABL from fusing with BCR. Presence of BCR-ABL gene fusion is associated with poorer outcomes. ³
TEL-AML/AML1	TEL-AML1, <i>aka</i> ETV6-RUNX1, is a fusion gene resulting from the translocation of chromosomes 12 and 21. It is the most common fusion gene seen in childhood precursor B-cell ALL. Research in murine models shows that cell lines expressing TEL-AML1 proliferate more slowly than the non-expressing cell lines, but evade inhibition of proliferation typically regulated by tissue growth factor β (TGF- β), ultimately leading to the growth of the leukemic cell population. TEL-AML1 is considered a favorable prognostic indicator. ⁴⁵
Other molecular marker	Assessments for other molecular markers known or believed to be associated with ALL may be performed. If these studies were performed, indicate “positive” or “negative” and specify the marker in question 99.

³ Wassmann B, Pfeifer H, Scheuring UJ, et al. (2004). Early prediction of response in patients with relapsed or refractory Philadelphia chromosome-positive acute lymphoblastic leukemia (Ph+ALL) treated with imatinib. *Blood*, 103(4):1495-8.

⁴ Ford AM, Palmi C, Bueno C, et al. (2009). The TEL-AML1 leukemia fusion gene dysregulates the TGF- β pathway in early B lineage progenitor cells. *J Clin Invest*, 119(4):826-36.

⁵ Jamil A, Kahwash S, Ruyman FB, Klopfenstein KJ. (2000). TEL/AML-1 fusion gene: its frequency and prognostic significance in childhood acute lymphoblastic leukemia. *Cancer Genet Cytogenet*, 122(2):73-8.

Question 116-119: Specify results

For each molecular marker in questions 116-117, report whether testing was “Positive,” “Negative,” or “Not done” at diagnosis (see note box above question 101). If tests identified a molecular marker other than those listed in questions 116-117, report the result in question 118 and specify the marker in question 119.

If multiple “Other molecular marker[s]” were tested, report one instance (i.e., copy) of question 118-119 for each “Other molecular marker” tested. If greater than 3 “Other molecular marker[s]” were tested, do the following:

- report one instance of question 118-119; and
- report “Positive” if any of the “Other molecular marker[s]” were positive, otherwise, report “Negative;” and
- report “see attachment” in question 119; and
- attach any / all reports documenting the results of testing for “Other molecular marker[s].”

Question 120: Were cytogenetics tested (karyotyping or FISH)? (between diagnosis and last evaluation)

See [question 101](#) for a description of cytogenetic tests. Indicate whether cytogenetic studies were performed between diagnosis and the last evaluation prior to HCT / cellular therapy (see note above question 101). If cytogenetic studies were obtained during this time, check “Yes” and go to question 121. If cytogenetic studies were not obtained at this time point or it is not known whether chromosome studies were performed, indicate “No” or “Unknown” respectively and go to question 134.

Question 121-122: Were cytogenetics tested via FISH?

If FISH studies were performed between diagnosis and the last evaluation prior to Infusion (see note box above question 101), report “Yes” for question 121 and indicate whether clonal abnormalities were detected in question 122. If multiple FISH assessments were performed, report “Abnormalities Identified” if any testing showed clonal abnormalities during this period. If FISH studies were not performed during this period, report “No” for question 121 and go to question 127. Examples of this include: no FISH study performed, or all FISH samples were inadequate.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.



Question 123 is disabled and cannot be answered at this time.

Question 123-126: Specify cytogenetic abnormalities (FISH)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 123, then continue with question 124.

Report the number of abnormalities detected by FISH between diagnosis and the last evaluation prior to Infusion (see note box above question 101) in question 124. If FISH studies showed different clonal abnormalities during this time, report the total number of clonal abnormalities detected. After indicating the number of clonal abnormalities in question 124, select all clonal abnormalities detected during this period in questions 125-126. This includes all clonal abnormalities detected any FISH assessment performed during this period.

If a clonal abnormality is detected, but not listed as an option in question 125, select “Other abnormality” and specify the abnormality in question 126. If multiple “Other abnormalities” were detected, report “see attachment” in question 126 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 127-128: Were cytogenetics tested via karyotyping?

If karyotyping was performed between diagnosis and the last evaluation prior to Infusion (see note box above question 101), report “Yes” for question 127 and indicate whether clonal abnormalities were detected in question 128. If multiple karyotypes were performed, report “Abnormalities Identified” if any testing

showed clonal abnormalities during this period. If karyotyping was not performed during this period, report “No” for question 127 and go to question 133. Examples of this include: no karyotyping performed or all karyotype samples were inadequate.



Question 129 is disabled and cannot be answered at this time.

Question 129-132: Specify cytogenetic abnormalities (karyotyping)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 129, then continue with question 130.

Report the number of abnormalities detected by karyotyping between diagnosis and the last evaluation prior to Infusion(see note box above question 101) in question 130. If karyotype studies showed different clonal abnormalities during this time, report the total number of clonal abnormalities detected. After indicating the number of clonal abnormalities in question 130 select all clonal abnormalities detected during this period in questions 131-132. This includes all clonal abnormalities detected any karyotype performed during this period.

If a clonal abnormality is detected, but not listed as an option in question 131, select “Other abnormality” and specify the abnormality in question 132. If multiple “Other abnormalities” were detected, report “see attachment” in question 132 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 133: Was documentation submitted to the CIBMTR?

Indicate if a karyotyping or FISH testing report is attached to support the cytogenetic findings reported in questions 120-132. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).



Questions related to capturing molecular marker results are intended to capture **molecular abnormalities** identified by **molecular methods**. Additional testing methods, such as FISH, may identify molecular marker results but should **not** be reported in the molecular section(s) of the Pre-TED Disease Classification (2402) Form. Abnormalities identified by karyotyping, FISH, or microarray should only be reported in the cytogenetic section of the Pre-TED Disease Classification (2402) Form.

Question 134: Were tests for molecular markers performed (e.g., PCR)? (between diagnosis and last evaluation)

See question 115 for a description of testing for molecular markers. Indicate whether testing for molecular markers was performed between diagnosis and the last evaluation prior to Infusion(see note above question 101). If testing for molecular markers was performed during this time, check “Yes” and go to question 135. If

molecular markers were not obtained during this period or it is not known whether testing for molecular markers was performed, indicate “No” or “Unknown” respectively and go to question 139.

Question 135-138: Specify results

For each molecular marker in questions 135-136, report whether testing was “Positive,” “Negative,” or “Not done” between diagnosis and the last evaluation prior to Infusion (see note box above question 101). If tests identified a molecular marker other than those listed in questions 135-136, report the result in question 137 and specify the marker in question 138.

If multiple “Other molecular marker[s]” were tested, report one instance (i.e., copy) of question 137-138 for each “Other molecular marker” tested. If greater than 3 “Other molecular marker[s]” were tested, do the following:

- report one instance of question 137-138; and
- report “Positive” if any of the “Other molecular marker[s]” were positive, otherwise, report “Negative;” and
- report “see attachment” in question 138; and
- attach any / all reports documenting the results of testing for “Other molecular marker[s].”

Question 139: Were cytogenetics tested (karyotyping or FISH)? (at last evaluation)

See question 101 for a description of cytogenetic testing. Indicate whether cytogenetic studies were performed at the last evaluation prior to infusion (see note box above question 101). Do not report any testing performed after treatment for ALL has started. If cytogenetic studies were obtained at this time point, check “Yes” and go to question 139. If cytogenetic studies were not obtained at this time point or it is not known whether chromosome studies were performed, indicate “No” or “Unknown” respectively and go to question 153.

Question 140-141: Were cytogenetics tested via FISH?

If FISH studies were performed at the last evaluation prior to HCT / cellular therapy (see note box above question 101), report “Yes” for question 140 and indicate whether clonal abnormalities were detected in question 141. If FISH studies were not performed at this time point, report “No” for question 140 and go to question 146. Examples of this include: no FISH study performed or FISH sample was inadequate.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.



Question 142 is disabled and cannot be answered at this time.

Question 142-145: Specify cytogenetic abnormalities (FISH)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable

in question 142, then continue with question 143.

Report the number of abnormalities detected by FISH at the last evaluation prior to infusion (see note box above question 101) in question 143. After indicating the number of abnormalities in question 132, select all abnormalities detected in questions 144-145.

If a clonal abnormality is detected, but not listed as an option in question 144, select “Other abnormality” and specify the abnormality in question 145. If multiple “Other abnormalities” were detected, report “see attachment” in question 145 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 146-147: Were cytogenetics tested via karyotyping?

If karyotyping was performed at the last evaluation prior to infusion (see note box above question 101), report “Yes” for question 146 and indicate whether clonal abnormalities were detected in question 147. If karyotyping was not performed at this time point, indicate “No” and go to question 146. Examples of this include: karyotyping was not performed or karyotyping sample was inadequate.



Question 148 is disabled and cannot be answered at this time.

Question 148-151: Specify cytogenetic abnormalities (karyotyping)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string if applicable in question 148, then continue with question 149.

Report the number of abnormalities detected by karyotyping at the last evaluation prior to infusion (see note box above question 101) in question 149. Only consider clonal abnormalities associated with the recipient's ALL when completing questions 149-151. After indicating the number of abnormalities in question 149, select all abnormalities detected in questions 150-151.

If a clonal abnormality is detected, but not listed as an option in question 150, select “Other abnormality” and specify the abnormality in question 151. If multiple “Other abnormalities” were detected, report “see attachment” in question 151 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 152: Was documentation submitted to the CIBMTR?

Indicate if a karyotyping or FISH testing report is attached to support the cytogenetic findings reported in questions 139-151. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

* Questions capturing molecular marker results are intended to capture **molecular abnormalities** identified by **molecular methods**. Additional testing methods, such as FISH, may identify molecular marker results but should **not** be reported in the molecular section(s) of the Pre-TED Disease Classification (2402) Form. Abnormalities identified by karyotyping, FISH, or microarray should only be reported in the cytogenetic section of the Pre-TED Disease Classification (2402) Form.

Question 153: Were tests for molecular markers performed (e.g., PCR)? (at last evaluation)

See question 115 for a description of testing for molecular markers. If testing for molecular markers was performed at the last evaluation prior to infusion (see note box above question 101), report “Yes” and go to question 154. If molecular marker testing was not performed at this time point or it is not known if testing was done, report “No” or “Unknown” respectively and go to question 158.

Question 154-157: Specify results

For each molecular marker in questions 154-155, report whether testing was “Positive,” “Negative,” or “Not done” at the last evaluation prior to infusion (see note box above question 101). If tests identified a molecular marker other than those listed in questions 154-155, report the result in question 156 and specify the marker in question 157.

If multiple “Other molecular marker[s]” were tested, report one instance (i.e., copy) of question 156-157 for each “Other molecular marker” tested. If greater than 3 “Other molecular marker[s]” were tested, do the following:

- report one instance of question 154-157; and
- report “Positive” if any of the “Other molecular marker[s]” were positive, otherwise, report “Negative;” and
- report “see attachment” in question 157; and
- attach any / all reports documenting the results of testing for “Other molecular marker[s].”

Question 158: Did the recipient have central nervous system leukemia at any time prior to the start of the preparative regimen / infusion?

Central nervous system (CNS) involvement by leukemia may be detected via pathologic examination of cerebrospinal fluid or tumor tissue as well as by radiological examinations (e.g., MRI, PET/CT, MIBG, etc.). If the recipient had documented involvement of ALL in the CNS, report “Yes” for question 158. If all CNS testing was negative since the time of diagnosis, report “No.” If testing for CNS involvement was not performed from the time of diagnosis to the time of HCT / cellular therapy, report “Unknown.”

Question 159: What was the disease status (based on hematological test results)?

Indicate the disease status of ALL at the last evaluation prior to the start of the preparative regimen. Refer

to the ALL Response Criteria section of the Forms Instructions Manual for definitions of each response. For reporting purposes, consider complete remission with incomplete hematologic recovery (CRi) a complete remission (CR1, CR2, or CR3+).

If the recipient did not receive any treatment for ALL from the time of diagnosis to the start of the preparative regimen / infusion, report “No treatment” and go to question 163.

If the recipient’s disease status is primary induction failure at the time of HCT / cellular therapy, go to question 163.

If the recipient’s disease status is CR / CRi at the time of HCT / cellular therapy, go to question 160.

If the recipient’s disease status is relapse at the time of HCT / cellular therapy, go to question 162.

Question 160: How many cycles of induction therapy were required to achieve CR?

Chemotherapy is initially given as induction therapy intended to bring the disease into remission. Recipients usually have one to two cycles of induction therapy. An example of a common induction therapy for precursor B-cell ALL in children with higher-risk prognostic indicators is a combination of vincristine, prednisone, an anthracycline, and L-asparaginase given over 4-6 weeks. Patients with a rapid response, defined as < 5% blasts within 7 to 14 days of starting induction, have improved outcomes.¹

¹ Gaynon PS, Desai AA, Bostrom BC, et al. Early response to therapy and outcome in childhood acute lymphoblastic leukemia: a review. *Cancer*. 1997;80(9):1717-26.

The second phase of chemotherapy is known as consolidation therapy. The goal of consolidation therapy is to destroy any remaining leukemia cells and sustain remission. An example of a consolidation therapy for precursor B-cell ALL in children is daunorubicin and cytarabine; several studies support the use of consolidation therapy in ALL.

Maintenance therapy typically involves daily doses of mercaptopurine and weekly doses of methotrexate. Treatment continues for 2-3 years for most children with ALL. Treatment may also be administered for relapsed disease. Much like induction therapy, treatment for relapse is intended to bring the disease back into remission. Systemic therapeutic agents used to induce remission following relapse often differ from those used during initial induction, since the disease is considered high-risk with a poor prognosis and is often resistant to many of the agents used earlier in the disease course. Allogeneic HCT is often considered the only potential “cure” for relapsed disease, if the patient has not already been transplanted.

Indicate the number of cycles of induction therapy that were required to achieve the first CR.

Question 161: Was the recipient in remission by flow cytometry?

Question 161 will only be answered if CR has been reported for question 159. Flow cytometry assessment is a method of analyzing peripheral blood, bone marrow, or tissue preparations for multiple unique cell

characteristics. Its primary clinical purpose in the setting of leukemias is to quantify blasts in the peripheral blood or bone marrow, or to identify unique cell populations through immunophenotyping. Flow cytometry assessment may also be referred to as “MRD,” or minimal residual disease, testing.

Flow cytometric remission is a treatment response in which no blasts can be detected.

If flow cytometric abnormalities associated with the recipient’s disease were identified previously, but the criteria above were met at the last evaluation prior to the start of the preparative regimen, indicate “yes.”

If flow cytometric abnormalities associated with the recipient’s disease were identified at the last evaluation prior to the start of the preparative regimen, indicate “no.”

Indicate “unknown” if flow cytometric abnormalities associated with the recipient’s disease were identified previously and no flow cytometry assessment was performed prior to the start of the preparative regimen.

Indicate “not applicable” if one of the following applies:

- No flow cytometry assessments were performed at any time prior to the start of the preparative regimen.
- Flow cytometric abnormalities were not identified on previous testing and no flow cytometric abnormalities were identified at the last evaluation prior to the start of the preparative regimen.

Question 162: Date of most recent relapse:

Enter the date of the most recent relapse prior to the start of the preparative regimen. If reporting a pathological evaluation (e.g., bone marrow) or blood/serum assessment (e.g., CBC, peripheral blood smear), enter the date the sample was collected. If extramedullary disease was detected by radiographic examination (e.g., X-ray, CT scan, MRI scan, PET scan), enter the date the imaging took place. If the physician determines cytogenetic or molecular relapse, enter the date the sample was collected for cytogenetic or molecular evaluation. If the physician determines evidence of relapse following a clinical assessment during an office visit, report the date of assessment.

If the exact date is not known, use the process for reporting partial or unknown dates as described in [General Instructions, Guidelines for Completing Forms](#).

Question 163: Date assessed

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen. The date reported should be that of the most disease-specific assessment within the pre-transplant work-up period (approximately 30 days). Clinical and hematologic assessments include pathological evaluation (e.g., bone marrow biopsy), radiographic examination (e.g., X-ray, CT scan, MRI scan, PET scan), and laboratory assessment (e.g., CBC, peripheral blood smear), in addition to clinician evaluation and physical examination. Enter the date the sample was collected for pathological and laboratory evaluations; enter the

date the imaging took place for radiographic assessments.

If the exact date is not known, use the process for reporting partial or unknown dates as described in [General Instructions, Guidelines for Completing Forms](#).

Last modified: May 29, 2020

Q164-167: Acute Leukemias of Ambiguous Lineage and Other Myeloid Neoplasms

Questions 164-165: Specify other acute leukemia classification

Indicate the other acute leukemia disease classification at diagnosis. If the subtype is not listed, report as “other leukemia” and specify the reported disease.

- Acute undifferentiated leukemia is a type of AML characterized by immature predominating cells that cannot be classified.
- Biphenotypic, bilineage, or hybrid leukemias have characteristics representative of both myeloid and lymphoid lineages.
- Mast cell leukemia is characterized by an increased number of tissue mast cells in the peripheral blood.

Question 166: What was the disease status (based on hematological test results)?

Indicate the disease status of acute leukemia at the last evaluation prior to the start of the preparative regimen.

Table 7. Disease Status of Acute Leukemia

Disease Status	Definition
Primary Induction Failure (PIF)	The patient received treatment for acute leukemia but never achieved complete remission at any time . PIF is not limited by the number of unsuccessful treatments; this disease status only applies to recipients who have <i>never been in complete remission</i> .
Complete Remission (CR)	<p>Hematologic complete remission is defined as meeting all of the following response criteria for at least four weeks.</p> <ul style="list-style-type: none"> • < 5% blasts in the bone marrow • Normal maturation of all cellular components in the bone marrow • No extramedullary disease (e.g., CNS, soft tissue disease) • Neutrophils $\geq 1,000/\mu\text{L}$ • Platelets $\geq 100,000/\mu\text{L}$ • Transfusion independent <p>In some cases, there may not be a four-week interval between completion of therapy and the pre-transplant disease assessment; in this case, CR should still be reported as the status at transplant, since it represents the “best assessment” prior to HCT. This is an exception to the criteria that CR be durable beyond four weeks; the pre-transplant disease status should not be changed based on early relapse or disease assessment post-transplant.</p>

	<p>Include recipients with persistent cytogenetic or molecular abnormalities who meet the above CR criteria for hematologic CR.</p> <p>Include recipients meeting the above CR criteria regardless of how many courses of therapy were required to achieve CR.</p> <p>The number of this complete remission can be determined by using the following guidelines:</p> <ul style="list-style-type: none"> • 1st CR: no prior relapse • 2nd CR: one prior relapse • 3rd or higher: two or more prior relapses
Relapse (REL)	<p>Relapse is defined as the recurrence of disease after CR, meeting the following criteria:</p> <ul style="list-style-type: none"> • $\geq 5\%$ blasts in the marrow or peripheral blood • Extramedullary disease • Reappearance of cytogenetic and/or molecular abnormalities associated with diagnosis that, <u>in the judgment of a physician</u>, are at a level representing relapse • Disease presence determined by a physician upon clinical assessment <p>The number of this relapse can be determined by using the following guidelines:</p> <ul style="list-style-type: none"> • 1st relapse: one prior CR • 2nd relapse: two prior CRs • 3rd or higher: three or more CRs <p>Do not include a partial response (PR) when determining number of relapse. Recipients who achieve a PR to treatment should be classified as either PIF or relapse; PR in acute leukemia is generally of short duration and is unlikely to predict clinical benefit.</p>
No Treatment	<p>The recipient was diagnosed with acute leukemia and never received therapeutic agents; include patients who have received only supportive therapy, including growth factors and/or blood transfusions.</p>

Question 167: Date assessed

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen. The date reported should be that of the most disease-specific assessment within the pre-transplant work-up period (approximately 30 days). Clinical and hematologic assessments include pathological evaluation (e.g., bone marrow biopsy), radiographic examination (e.g., X-ray, CT scan, MRI scan, PET scan), and laboratory assessment (e.g., CBC, peripheral blood smear), in addition to clinician evaluation and physical examination. Enter the date the sample was collected for pathological and laboratory evaluations; enter the date the imaging took place for radiographic assessments.

If the exact date is not known, use the process for reporting partial or unknown dates as described in [General Instructions, Guidelines for Completing Forms](#).

Last modified: Jan 27, 2020

Q168-178: Chronic Myelogenous Leukemia

Chronic myelogenous leukemia (CML) is a slow-progressing cancer of the myeloid white blood cells. It is characterized by increased proliferation of immature white blood cells (granulocytes) with damaged DNA, or blasts, which accumulate in the blood and bone marrow. Normal blasts develop into white blood cells that fight infection. The symptoms of CML are caused by the replacement of normal bone marrow with leukemic cells, resulting in fewer red blood cells, platelets, and normal white blood cells.

Question 168: Was therapy given prior to this HCT?

If the recipient received therapy to treat CML prior to this HCT, check “yes” and go to question 169. Do not report a prior HCT or cellular therapy as these are captured separately on the Pre-TED Form (Form 2400). If the recipient did **not** receive therapy to treat CML, check “no” and go to question 175.

Question 169-174: CML treatment

Indicate the therapy the recipient received to treat CML prior to this HCT. If the recipient’s treatment consisted of a combination of chemotherapeutic agents, check the “combination chemotherapy” box **and** each drug included in the combination from the list provided. The “other, specify” category should only be used if the drug is not one of the listed options. For example, if the recipient received a combination of interferon and cytarabine, check all of the following: “combination chemotherapy,” “interferon,” and “other, specify: cytarabine.”

Question 175: What was the disease status?

Indicate the disease status of CML at the last evaluation prior to the start of the preparative regimen (or infusion if no preparative regimen was given). Refer to the CML Response Criteria section for a description of each disease response.

If the recipient is in complete hematologic response or chronic phase at the start of the preparative regimen, go to question 176. Otherwise, go to question 177.

Question 176: Specify level of response

If the recipient’s best response to therapy (question 175) is “complete hematologic remission” or “chronic phase,” specify the cytogenetic / molecular response. Refer to Table 8 for definitions of cytogenetic and molecular responses.

Table 8. Definitions of Cytogenetic and Molecular Responses to Therapy

Response	Definition
Complete molecular remission (<i>most favorable</i>)	0% BCR / ABL transcripts detected in peripheral blood or bone marrow

Major molecular remission	> 0 – 0.1% BCR / ABL transcripts detected in peripheral blood or bone marrow
Complete cytogenetic response	0% Ph+ cells detected in bone marrow
Partial cytogenetic response	> 0 – 35% Ph+ cells in bone marrow
Minor cytogenetic response	> 35 – 65% Ph+ cells in bone marrow
Minimal cytogenetic response	> 65 – 95% Ph+ cells in bone marrow
No cytogenetic response (<i>least favorable</i>)	> 95% Ph+ cells in bone marrow.

Definitions taken from Hughes, T. P., Ross, D. M. & Melo, J. V. Handbook of chronic myeloid leukemia. (Adis, 2014).

The above responses are listed from most favorable (complete molecular remission) to least favorable (no cytogenetic response). Centers should report the most favorable response achieved. For example, if a recipient has achieved a major molecular remission by PCR testing as well as a complete cytogenetic response by karyotyping / FISH, the center should report “major molecular remission” for question 176.

Question 177: Number

Indicate the number of times the recipient has been in the disease phase reported in question 175.

Question 178: Date assessed

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen. The date reported should be that of the most disease-specific assessment within the pre-transplant work-up period (approximately 30 days). Clinical and hematologic assessments include pathological evaluation (e.g., bone marrow biopsy), radiographic examination (e.g., X-ray, CT scan, MRI scan, PET scan), and laboratory assessment (e.g., CBC, peripheral blood smear), in addition to clinician evaluation and physical examination. Enter the date the sample was collected for pathological and laboratory evaluations; enter the date the imaging took place for radiographic assessments.

If the exact date is not known, use the process for reporting partial or unknown dates as described in [General Instructions, Guidelines for Completing Forms](#).

Last modified: Jan 27, 2020

Q179-259: Myelodysplastic Diseases

✿ Transformation to AML

If the recipient is being transplanted for AML that has transformed from MDS, the primary disease for HCT must be reported as AML. Disease Classification questions must be completed for both AML and MDS.

The **myelodysplastic syndromes (MDS)** are a group of clonal hematopoietic stem cell diseases characterized by cytopenia(s), dysplasia (abnormal growth or development leading to an alteration in size, shape, and organization of the cell) in one or more of the major myeloid cell lines (WBC, RBC, and/or platelets), ineffective hematopoiesis, and an increased risk of developing acute myelogenous leukemia (AML). MDS occurs primarily in older adults, with a median age of 70 years. The majority of recipients present with symptoms related to cytopenias. Most recipients present with anemia requiring RBC transfusions.

Primary or *de novo* MDS occurs without a known history of chemotherapy or radiation exposure. Some inherited hematologic disorders, such as Fanconi anemia, dyskeratosis congenita, Shwachman-Diamond syndrome, and Diamond-Blackfan syndrome are associated with an increased risk of MDS.

Question 179: What was the MDS subtype at diagnosis?

Please indicate the MDS subtype at diagnosis. For a list of MDS subtypes and their diagnostic criteria, see Appendix H.



Questions 180-181 refer to MDS, unclassifiable; if the diagnosis was other than an MDS unclassifiable continue with question 182.

Question 180: Specify Myelodysplastic syndrome, unclassifiable (MDS-U)

Specify the Myelodysplastic syndrome, unclassifiable (MDS-U) and continue with question 181.

Question 181: Was documentation submitted to the CIBMTR (e.g. pathology report used for diagnosis)?

Indicate whether documentation was submitted to the CIBMTR (e.g., pathology report). For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 182: Was the disease (MDS) therapy-related?

Agents such as radiation or systemic therapy used to treat other diseases (e.g., Hodgkin lymphoma, non-Hodgkin lymphoma, or breast cancer) can damage the marrow and lead to a secondary malignancy, such as MDS.

If the diagnosis of MDS is therapy-related, select “yes.” If the diagnosis of MDS is not therapy-related, select “no.” If it is unknown if the MDS is therapy-related, select “unknown.”

Do not report “yes” if the recipient developed MDS after an environmental exposure (e.g., exposure to benzene).

Question 183: Did the recipient have a predisposing condition?

A predisposing condition contributes to the susceptibility of developing MDS. Therefore, diagnosis of the condition increases the likelihood that the recipient will develop MDS. If the recipient has a documented history of a predisposing condition, select “yes” and continue with question 184. If there is no history of a predisposing condition or if predisposition is unknown, indicate “no” or “unknown” and continue with question 186.

Questions 184-185: Specify condition:

Specify the recipient’s predisposing condition.

Aplastic anemia may progress to MDS and/or AML. Aplastic anemia is a broad classification referring to bone marrow failure characterized by pancytopenia and marrow hypoplasia. If aplastic anemia is selected and the recipient is on the CRF track, the Aplastic Anemia Pre-HCT (2028) Form will come due.

DDX41-associated familial MDS is a rare germline heterozygous mutation. DDX41 represents a class of tumor suppressor genes in myeloid neoplasms.

Diamond-Blackfan anemia is a rare genetic disorder that affects the ability of the marrow from producing red blood cells. These recipients may present with anemia, recipients may also exhibit physical abnormalities such as: small head size, cleft lip, webbed neck, defects of the hands and a short stature. Fanconi anemia is a rare genetic blood disorder that prevents the body from producing a sufficient number of new blood cells to function properly. Abnormal blood cells may also be produced. These recipients are short in stature, exhibit skeletal abnormalities, and have an increased risk of developing solid tumors, MDS, and leukemias. If Fanconi anemia is selected and the recipient is on the CRF track, the Fanconi Anemia Pre-HCT (2029) Form will come due.

GATA2 deficiency is a rare genetic disorder which can cause a variety of issues including viral and bacterial infections, cytopenias, myelodysplasia, myeloid leukemias, pulmonary alveolar proteinosis and lymphedema

Li-Fraumeni syndrome is a rare genetic disorder which increases the risk of developing several types of cancers, notably: breast cancer, osteosarcoma, sarcoma, brain tumors and leukemias. Li-Fraumeni syndromes are associated with mutations in the TP53 gene.

Paroxysmal nocturnal hemoglobinuria (PNH) is a rare genetic disorder of the blood cells. The disease is characterized by destruction of red blood cells. blood clots and impaired bone marrow function. PNH is very closely related and often derives from aplastic anemia. If PNH is selected and the recipient is on the CRF

track, the Aplastic Anemia Pre-HCT (2028) Form will come due

RUNX1 deficiency was previously known as “familial platelet disorder with propensity to myeloid malignancies”. Recipients with RUNX1 deficiencies typically present with mild to moderate thrombocytopenia with normal-sized platelets, functional platelets defects leading to prolonged bleeding and an increased risk to develop myelodysplastic syndromes (MDS), acute myeloid leukemia (AML), or T-cell acute lymphoblastic leukemia (T-ALL).

SAMD9- or SAMD9L-associated familial MDS are germline mutations which can result in a spectrum of multisystem disorders that carry a markedly increased risk of developing myeloid malignancies.

Shwachman-Diamond syndrome (SDS) is a rare autosomal recessive disorder in which is characterized by exocrine pancreatic insufficiency, bone marrow dysfunction, and skeletal abnormalities.

Telomere biology disorder (including dyskeratosis congenita) are a complex set of inherited conditions defined by the presence of very short telomeres. Telomere biology disorder can be characterized by bone marrow failure and lung disease.

If the recipient had a predisposing condition not listed above, select “other condition” and specify the condition in question 185.

A list of entities that would fall into the “other condition” category include: ETV6-related familial thrombocytopenia, ANKRD26-related familial thrombocytopenia, SRP72-related familial aplastic anemia/ MDS, MBD4-related familial leukemia, Bloom Syndrome, Noonan Syndrome, Neurofibromatosis, Downs Syndrome, ATG2B/GSKIP duplication (chromosome 14q32.2), MECOM-associated syndrome.

Report laboratory results from prior to the start of first treatment of the primary disease for which the HCT is being performed. If the recipient’s MDS transformed, report the studies from the original diagnosis.

Question 186: Date CBC drawn

These questions are intended to capture the laboratory studies performed at the diagnosis of MDS. Testing may be performed multiple times around the time of diagnosis; report the most recent laboratory results performed prior to the start of first treatment of the primary disease for HCT. If the recipient’s MDS transformed, report the studies from the original diagnosis.

Report the date the sample was drawn and continue with question 187.

Question 187-188: WBC

Indicate whether the white blood cell (WBC) count was “known” or “unknown” at diagnosis. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 188. If “unknown,” continue with question 189.

Question 189-190: Neutrophils

Indicate whether the neutrophil percentage in the blood was “known” or “unknown” at diagnosis. If “known,” report the value documented on the laboratory report in question 190. If “unknown,” continue with question 191.

Question 191-192: Blasts in the blood

Indicate whether the percent blasts in the peripheral blood is “known” or “unknown” at diagnosis. If “known,” report the laboratory value in question 192. If the percent blasts in blood at diagnosis is not known, report “unknown” and go to question 193. **Note**, blasts are not typically seen in the peripheral blood. If blasts are NOT reported on the differential you can still report “known” in question 191 and “0%” in question 192.

Question 193-194: Hemoglobin

Indicate whether the hemoglobin was “known” or “unknown” at diagnosis. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 194. If “unknown,” continue with question 196.

Question 195: Were RBCs transfused \leq 30 days before the date the CBC was drawn?

Transfusions temporarily increase the red blood cell count. It is important to distinguish between a recipient whose body is creating these cells and a recipient who requires transfusions to support the counts.

Indicate if red blood cells were transfused less than or equal to 30 days prior to the date the CBC was drawn as reported in question 186.

Question 196-197: Platelets

Indicate whether the platelet count was “known” or “unknown” at diagnosis. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 197. If “unknown,” continue with question 199.

Question 198: Were platelets transfused \leq 7 days before date the CBC was drawn?

Transfusions temporarily increase the platelet count. It is important to distinguish between a recipient whose body is creating the platelets and a recipient who requires transfusions to support the counts.

Indicate if platelets were transfused less than or equal to 7 days prior to the date the CBC was drawn as reported in question 186.

Question 199-200: Blasts in bone marrow

If the bone marrow pathology report states a range for blasts, enter the average of the range rounded to the nearest whole number (e.g., if 0-5%, enter 3%).

If the report indicates “sheets of blasts” or “packed marrow,” report 100%.
If the report states > n% blasts, enter (n +1)% on the form. For example, if the laboratory report indicates > 90% blasts, report 91%.
If the report states < n% blasts, enter (n -1)% on the form. For example, if the laboratory report indicates < 5% blasts, report 4%.

Indicate whether the percentage of blasts in the bone marrow was “known” or “unknown” at diagnosis. If “known,” report the percentage documented on the laboratory report in question 200. If “unknown,” continue with question 201.

If multiple methods were used to detect the percentage of blasts in the bone marrow, the aspirate differential is the most preferred method followed by flow cytometry and IHC.

Question 201: Were cytogenetics tested (karyotyping or FISH)?

Cytogenetics is the study of chromosomes. Cytogenetic assessment involves testing blood or bone marrow for the presence of known chromosomal abnormalities that reflect the recipient’s disease. Testing methods include conventional chromosome analysis (karyotyping) or fluorescence in situ hybridization (FISH). For more information about cytogenetic testing and terminology, see Appendix C, Cytogenetic Assessments.

Indicate if cytogenetic studies were obtained at diagnosis. If cytogenetic studies were obtained, select “yes” and continue with question 202.

If no cytogenetic studies were obtained or it is unknown if chromosome studies were performed, select “no” or “unknown” and continue with question 218.

Question 202: Were cytogenetics tested via FISH?

If FISH studies were performed at diagnosis, report “yes” and continue with question 203.

If FISH studies were not performed at diagnosis, report “no” and go to question 210. Examples include: no FISH study performed or FISH sample was inadequate. See Appendix C, Cytogenetic Assessments, for assistance interpreting FISH results.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.

Question 203: Sample source:

Indicate if the sample was from “bone marrow” or from “peripheral blood” and continue with question 204. If multiple sources were used to test FISH, the most preferred sample is the bone marrow.

Question 204: Results of tests:

If FISH assessments identified abnormalities, indicate “abnormalities identified” and continue with question

205.

If FISH assessments were unremarkable, indicate “no abnormalities” identified, continue with question 209.

! Question 205 is disabled and cannot be answered at this time.

Questions 205-208: Specify cytogenetic abnormalities (FISH)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string, if applicable, in question 205, then continue with question 206.

Report the number of abnormalities detected by FISH at diagnosis in question 206. After indicating the number of abnormalities in question 206, select all abnormalities detected in question 207. If a clonal abnormality is detected, but not listed as an option in question 207, select “other abnormality” and specify the abnormality in question 208.

If multiple “other abnormalities” were detected, report “see attachment” in question 208 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 209: Was documentation submitted to the CIBMTR?

Indicate whether documentation was submitted to the CIBMTR (e.g., pathology report, FISH report). For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 210: Were cytogenetics tested via karyotyping?

If karyotyping was performed at diagnosis report “yes” and continue with question 211.

If karyotyping was not performed at this time point, indicate “no” and continue with question 218. Examples of this include: karyotyping was not performed, or karyotyping sample was inadequate.

Question 211: Sample source:

Indicate if the sample was from “bone marrow” or from “peripheral blood” and continue with question 212. If multiple sources were used for karyotyping assessments, the most preferred sample is the bone marrow.

Question 212: Results of tests:

If karyotyping assessments identified abnormalities, indicate “abnormalities identified” and continue with question 213.

If karyotyping assessments yielded no evaluable metaphases or there were no abnormalities identified, indicate as such and continue with question 217.



Question 213 is disabled and cannot be answered at this time.

Question 213-216: Specify cytogenetic abnormalities (karyotyping)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string, if applicable, in question 213, then continue with question 214.

Report the number of abnormalities detected by karyotyping at diagnosis in question 214. After indicating the number of abnormalities in question 214, select all abnormalities detected in question 215. If a clonal abnormality is detected, but not listed as an option in question 215, select “other abnormality” and specify the abnormality in question 216.

If multiple “other abnormalities” were detected, report “see attachment” in question 216 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 217: Was documentation submitted to the CIBMTR?

Indicate whether documentation was submitted to the CIBMTR (e.g., FISH report, karyotype report). For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 218: Did the recipient progress or transform to a different MDS subtype or AML between diagnosis and the start of the preparative regimen / infusion?

Indicate if the recipient’s disease progressed to AML or transformed into a different MDS subtype between initial diagnosis and the start of the preparative regimen / infusion. Approximately one third of MDS cases transform into AML, signifying a poorer prognosis. Progression to AML is defined by an increase in blood or bone marrow blasts equal to or greater than 20%.

MDS subtypes may also transform / progress from one into another. A progression from one subtype of MDS to another indicates that the number of cytopenias, number of blasts, and/or morphology of marrow sufficiently qualified them for a higher grade (i.e., more severe) MDS. For example, an MDS classified as MDS-SLD at diagnosis whose blast count rises to 8% as documented on bone marrow aspirate would have progressed to MDS-EB-1.

Conversely, do not report a progression / transformation if the recipient’s assessments after diagnosis show that they qualify for a lower grade (i.e., less severe MDS). For example, a recipient who is diagnosed with MDS-EB-2, but whose assessments show that they meet the criteria for MDS-EB-1 as a response to treatment, would not qualify as a progression or transformation. In this example, the disease is lower grade (i.e., less severe), rather than a higher grade (i.e., more severe) so it should not be reported as a progression/transformation. See the table below for guidance in determining the severity of MDS progressions and transformations.

Grade of MDS Progression/Transformations

Lower Grade	>>>>>	>>>>>	>>>>>	Higher Grade
MDS-SLD / MDS-RS-SLD / MDS-RS-MLD / Childhood MDS	MDS-MLD	MDS-EB-1	MDS-EB-2	AML
JMML/CMML	—	—	—	AML

Indicate if the recipient's disease progressed to AML or transformed from one MDS subtype to another. If the recipient's disease transformed or progressed, select "yes" and continue with question 219. If there was no documented transformation or progression, select "no" and continue with question 223.

Question 219: Specify the MDS subtype after transformation:

Indicate the recipient's current MDS subtype after transformation. If the recipient experienced more than one transformation after diagnosis, report the most recent subtype. For a list of MDS subtypes and their diagnostic criteria, see Appendix H.

If the recipient progressed or transformed to MDS unclassifiable, continue with question 220. If the disease transformed to AML, continue with question 222. If MDS progresses to AML and the recipient is on the CRF track, the Acute Myelogenous Leukemia (AML) Pre-HCT (2010) Form will also come due.

For all other progressions or transformations continue with question 221.

Question 220: Specify Myelodysplastic syndrome, unclassifiable (MDS-U)

The classification of myelodysplastic syndrome, unclassifiable (MDS-U) would be based off the bone marrow biopsy pathology report and can be reported as one of the following:

- MDS-U with 1% blood blasts
- MDS-U with single lineage dysplasia and pancytopenia
- MDS-U based on defining cytogenetic abnormality

Specify the Myelodysplastic syndrome, unclassifiable (MDS-U) using the definitions listed in on the form and continue with question 221.

Question 221: Specify the date of the most recent transformation:

Report the date of assessment that determined the most recent disease transformation (i.e., if there were multiple transformations, report the most recent). Report the date of the pathological evaluation (e.g., bone marrow) or blood/serum assessment (e.g., CBC, peripheral blood smear). Enter the date the sample was collected for pathological and laboratory evaluations.

If the exact date is not known, use the process for reporting partial or unknown dates as described in General Instructions, Guidelines for Completing Forms.

Question 222: Date of MDS Diagnosis

If the recipient's MDS transformed to AML prior to HCT, report the date of diagnosis of MDS. If the exact date is not known, use the process for reporting partial or unknown dates as described in General Instructions, Guidelines for Completing Forms.

Ensure the date of diagnosis for AML has been reported in question 1, AML is reported as the primary disease for HCT in question 2, and the AML section of the Disease Classification Form has been complete appropriately. Go to the signature line.

Question 223: Date CBC drawn:

Report the date the CBC was drawn at the last evaluation prior to the start of the preparative regimen / infusion and continue with question 224. If multiple assessments were performed, report the most recent one prior to the start of the preparative regimen / infusion.

Question 224-225: WBC

Indicate whether the white blood cell (WBC) count was "known" or "unknown" at the last evaluation prior to the start of the preparative regimen / infusion. If "known," report the laboratory count and unit of measure documented on the laboratory report in question 225. If "unknown," continue with question 226.

Questions 226-227: Neutrophils

Indicate whether the neutrophil percentage in the blood was "known" or "unknown" at the last evaluation prior to the start of the preparative regimen / infusion. If "known," report the value documented on the laboratory report in question 227. If "unknown," continue with question 228.

Question 228-229: Blasts in the blood

Indicate whether the percent blasts in the peripheral blood is "known" or "unknown" at the last evaluation prior to the start of the preparative regimen / infusion. If "known," report the laboratory value in question 229. If the percent blasts in blood at diagnosis is not known, report "unknown" and go to question 230. **Note**, blasts are not typically seen in the peripheral blood. If blasts are NOT reported on the differential you can still report "known" in question 228 and "0%" in question 229.

Question 230-231: Hemoglobin

Indicate whether the hemoglobin was "known" or "unknown" at the last evaluation prior to the start of the preparative regimen / infusion. If "known," report the laboratory count and unit of measure documented on the laboratory report in question 231. If "unknown," continue with question 233.

Question 232: Were RBCs transfused \leq 30 days before the date the CBC was drawn?

Transfusions temporarily increase the red blood cell count. It is important to distinguish between a recipient whose body is creating these cells and a recipient who requires transfusions to support the counts.

Indicate if red blood cells were transfused less than or equal to 30 days prior to the date the CBC was drawn as reported in question 223.

Question 233-234: Platelets

Indicate whether the platelet count was “known” or “unknown” at the last evaluation prior to the start of the preparative regimen / infusion. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 234. If “unknown,” continue with question 236.

Question 235: Were platelets transfused \leq 7 days before the date the CBC was drawn?

Transfusions temporarily increase the platelet count. It is important to distinguish between a recipient whose body is creating the platelets and a recipient who requires transfusions to support the counts.

Indicate if platelets were transfused less than or equal to 7 days prior to the date the CBC was drawn as reported in question 223.

Questions 236-237: Blasts in bone marrow:

- * If the bone marrow pathology report states a range for blasts, enter the average of the range rounded to the nearest whole number (e.g., if 0-5%, enter 3%).
- If the report indicates “sheets of blasts” or “packed marrow,” report 100%.
- If the report states $> n\%$ blasts, enter $(n+1)\%$ on the form. For example, if the laboratory report indicates $> 90\%$ blasts, report 91%.
- If the report states $< n\%$ blasts, enter $(n-1)\%$ on the form. For example, if the laboratory report indicates $< 5\%$ blasts, report 4%.

Indicate whether the percentage of blasts in the bone marrow was “known” or “unknown” at the last evaluation prior to the start of the preparative regimen / infusion. If “known,” report the percentage documented on the pathology report in question 237. If “unknown,” continue with question 238

If multiple assessments were performed at the last evaluation, report the most recent assessment prior to the start of the preparative regimen / infusion.

Question 238: Were cytogenetics tested (karyotyping or FISH)?

Cytogenetics is the study of chromosomes. Cytogenetic assessment involves testing blood or bone marrow for the presence of known chromosomal abnormalities that reflect the recipient’s disease. Testing methods include conventional chromosome analysis (karyotyping) or fluorescence in situ hybridization (FISH). For more information about cytogenetic testing and terminology, see Appendix C, Cytogenetic Assessments.

Indicate if cytogenetic studies were obtained at the last evaluation prior to the preparative regimen / infusion. If cytogenetic studies were obtained, select “yes” and continue with question 239.

If no cytogenetic studies were obtained or it is unknown if chromosome studies were performed, select “no” or “unknown” and continue with question 255.

Question 239: Were cytogenetics tested via FISH?

Indicate if FISH studies were performed at the last evaluation prior to the start of the preparative regimen / infusion. If “yes,” continue with question 240.

If FISH studies were not performed at the last evaluation prior to the start of the preparative regimen / infusion, report “no” and continue with question 247. Examples include: no FISH study performed, or FISH sample was inadequate. See Appendix C, Cytogenetic Assessments, for assistance interpreting FISH results.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.

Question 240: Sample source:

Indicate if the sample was from “bone marrow” or from “peripheral blood” and continue with question 241. If multiple sources were used to test FISH, the most preferred sample is the bone marrow.

If FISH studies were performed on multiple samples at the last evaluation prior to the start of the preparative regimen / infusion, the bone marrow results are the preferred sample source to report.

Question 241: Results of tests:

If FISH assessments identified abnormalities, indicate “abnormalities identified” and continue with question 242.

If FISH assessments were unremarkable, indicate “no abnormalities” identified, continue with question 246.



Question 242 is disabled and cannot be answered at this time.

Questions 242-245: Specify cytogenetic abnormalities (FISH)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string, if applicable, in question 242, then continue with question 243.

Report the number of abnormalities detected by FISH at the last evaluation prior to the preparative regimen / infusion in question 243. After indicating the number of abnormalities in question 243, select all abnormalities detected in question 244.

If a clonal abnormality is detected, but not listed as an option in question 244, select “other abnormality” and specify the abnormality in question 245. If multiple “other abnormalities” were detected, report “see attachment” in question 245 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 246: Was documentation submitted to the CIBMTR?

Indicate whether documentation was submitted to the CIBMTR (e.g., FISH report). For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 247: Were cytogenetics tested via karyotyping?

Indicate if karyotyping was performed at the last evaluation prior to the preparative regimen / infusion. If “yes,” continue with question 248.

If karyotyping was not performed at the last evaluation prior to the start of the preparative regimen / infusion, indicate “no” and continue with 255. Examples of this include: karyotyping was not performed, or karyotyping sample was inadequate.

Question 248: Sample source:

Indicate if the sample was from “bone marrow” or from “peripheral blood” and continue with question 249. If karyotyping studies were performed on multiple samples at the last evaluation prior to the start of the preparative regimen / infusion, the bone marrow results are the preferred sample source to report

Question 249: Results of tests:

If karyotyping assessments identified abnormalities, indicate “abnormalities identified” and continue with question 250.

If karyotyping assessments yielded no evaluable metaphases or there were no abnormalities identified, indicate such and continue with question 254.



Question 250 is disabled and cannot be answered at this time.

Question 251-253: Specify cytogenetic abnormalities (karyotyping)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string, if applicable, in question 250, then continue with question 251.

Report the number of abnormalities detected by karyotyping prior to the start of the preparative regimen / infusion in question 251. After indicating the number of abnormalities in question 251, select all abnormalities detected in question 252.

If a clonal abnormality is detected, but not listed as an option in question 252, select “other abnormality” and specify the abnormality in question 253. If multiple “other abnormalities” were detected, report “see attachment” in question 253 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 254: Was documentation submitted to the CIBMTR?

Indicate whether documentation was submitted to the CIBMTR (e.g., karyotype report). For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 255: What was the disease status?

Indicate the disease status of MDS at the last evaluation prior to the start of the preparative regimen / infusion. **Refer to the MDS Response Criteria section of the Forms Instructions Manual for definitions of each disease response.**



“Never Treated” is not an option choice on the current revision of the Pre-TED: Disease Classification Form. When completing this form, centers should report “No Response (NR) / Stable Disease (SD)” for recipients who have only received supportive care prior to transplant.

Question 256: Specify the cell line examined to determine HI status:

Indicate the cell line examined to determine hematologic improvement. To determine the cell line, review the Hematologic Improvement criteria listed in the MDS Response Criteria section of the Forms Instructions Manual.

If the cell lines examined to determine hematologic improvement included “Hematologic Improvement – Erythroid (HI-E),” continue with question 257.

If the cell lines examined to determine hematologic improvement only included “Hematologic Improvement – Platelets (HI-P)” and/or “Hematologic Improvement – Neutrophils (HI-N),” continue with question 259.

Question 257: Specify transfusion dependence:

If the recipient’s pre-transplant disease status included hematologic improvement – erythroid, indicate the transfusion dependence at the time of determining disease status at last evaluation prior to start of the preparative regimen / infusion.

Select “Non-transfused (NTD)” if the recipient was without RBC transfusions as supportive care for the disease within a period of 16 weeks prior to the start of the preparative regimen / infusion and continue with question 259.

Select “Low-transfusion burden (LTB)” if the recipient had 3-7 RBC transfusions within a period of 16 weeks in at least 2 transfusion episodes with a maximum of 3 RBC transfusions in 8 weeks prior to the start of the preparative regimen / infusion and continue with question 259.

Select “High-transfusion burden (HTB)”- if the recipient had ≥ 8 RBCs transfusions within a period of 16 weeks or ≥ 4 within 8 weeks prior to the start of the preparative regimen / infusion and continue with question 258.



Question 258 is disabled and should not be answered.

Question 258: Specify the response achieved:

Question 258 was inadvertently included in this revision of the form. It should be disabled and should not be answered.

Question 259: Date assessed:

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen / infusion. The date reported should be that of the most disease-specific assessment within the pre-transplant work-up period (approximately 30 days). Clinical and hematologic assessments include pathological evaluation (e.g., bone marrow biopsy), radiographic examination (e.g., X-ray, CT scan, MRI scan, PET scan), and laboratory assessment (e.g., CBC, peripheral blood smear), in addition to clinician evaluation and physical examination. Enter the date the sample was collected for pathological and laboratory evaluations; enter the date the imaging took place for radiographic assessments.

If the exact date is not known, use the process for reporting partial or unknown dates as described in General Instructions, Guidelines for Completing Forms.

Last modified: May 29, 2020

Q260-372: Myeloproliferative Diseases

* Transformation to AML:

If the recipient is being transplanted for AML that has transformed from MPN, the primary disease for HCT must be reported as AML. Disease Classification questions must be completed for both AML and MPN.

* Transformation to Myelofibrosis:

Recipients transplanted for post-essential thrombocythemia myelofibrosis (post-ET MF) or post-polycythemia myelofibrosis (post-PV MF) will be reported as ET or PV at diagnosis (Q260). Question: 'Did the recipient progress or transform to a different MPN subtype or AML between diagnosis and the start of the preparative regimen / infusion?' must be answered "Yes".

Myeloproliferative Neoplasms (MPN) are characterized by the overproduction of blood cells (red blood cells, white blood cells, and/or platelets) or collagen in the bone marrow. Often the MPN will be identified because of a blood test for another condition, as some recipients are asymptomatic. Common symptoms found in the array of myeloproliferative disorders include fatigue and the enlargement of the spleen (splenomegaly).

Question 260: What was the MPN subtype at diagnosis?

Indicate the MPN subtype at diagnosis and continue with question 263.

If the MPN subtype is "Myeloproliferative neoplasm (MPN), unclassifiable" continue with question 262. If the MPN subtype is "Systemic mastocytosis" continue with question 261.

Question 261: Specify systemic mastocytosis

Specify the systemic mastocytosis sub-type / variant and continue with question 263.

The diagnosis of systemic mastocytosis can be made when the major criterion and at least 1 minor criterion are present, or when ≥ 3 minor criteria are present.

- Major criterion: Multifocal dense infiltrates of mast cells (≥ 15 mast cells in aggregates) detected in sections of bone marrow and/or other extracutaneous organs(s).
- Minor criteria:
 1. In biopsy sections of bone marrow or other extracutaneous organs, $>25\%$ of the mast cells in the infiltrate are spindle-shaped or have atypical morphology; or $>25\%$ of all mast cells in bone marrow aspirate smears are immature or atypical.
 2. Detection of an activating point mutation at codon 816 of KIT in the bone marrow, blood or another extracutaneous organ.

3. Mast cells in bone marrow, blood or another extracutaneous organ express CD25, with or without CD2, in addition to normal mast cell markers.
4. Serum total tryptase is persistently >20 ng/ml, unless there is an associated myeloid neoplasm, in which case this parameter is not valid.

The diagnostic criteria for the systemic mastocytosis sub-types/variants are as follows. Each sub-type/variant meets the general criteria for systemic mastocytosis with additional criteria for each.

1. **Indolent systemic mastocytosis:** Low mast cell burden; no evidence of an associated hematologic neoplasm; skin lesions are almost invariably present; no “C” findings
2. **Smoldering systemic mastocytosis:** ≥ 2 “B” findings and no “C” findings; high mast cell burden; no evidence of an associated hematologic neoplasm; does not meet criteria for mast cell leukemia
3. **Systemic mastocytosis with an associated hematologic neoplasm:** Meets the criteria for an associated hematologic neoplasm (i.e., MDS, MPN,AML, lymphoma or another hematological neoplasm classified as a distinct entity in the WHO classification).
4. **Aggressive systemic mastocytosis:** ≥ 1 “C” findings; does not meet the criteria for mast cell leukemia; skin lesions are usually absent.
5. **Mast Cell leukemia:** Bone marrow biopsy shows diffuse infiltrate of atypical, immature mast cells; bone marrow aspirate smears show $\geq 20\%$ mast cells. In classic cases, mast cells account for $\geq 10\%$ of the peripheral blood WBC, but the aleukemic variant (in which mast cells account for $< 10\%$) is more common. Skin lesions are usually absent

“B” (burden of disease) and “C” (cytoreduction-requiring) findings in systemic mastocytosis.

“B” findings

1. BM biopsy showing $>30\%$ infiltration by MC (focal, dense aggregates) and/or serum total tryptase level >200 ng/mL
2. Signs of dysplasia or myeloproliferation, in non-MC lineage(s), but insufficient criteria for definitive diagnosis of a hematopoietic neoplasm (AHNMD), with normal or slightly abnormal blood counts.
3. Hepatomegaly without impairment of liver function, and/or palpable splenomegaly without hypersplenism, and/or lymphadenopathy on palpation or imaging.

“C” findings

1. Bone marrow dysfunction manifested by one or more cytopenia(s) (ANC $< 1.0 \times 10^9/L$, Hgb < 10 g/dL, or platelets $< 100 \times 10^9/L$), but no obvious non-mast cell hematopoietic malignancy.
2. Palpable hepatomegaly with impairment of liver function, ascites and/or portal hypertension.
3. Skeletal involvement with large osteolytic lesions and/or pathological fractures.
4. Palpable splenomegaly with hypersplenism.

5. Malabsorption with weight loss due to gastrointestinal mast cell infiltrates.

Question 262: Was documentation submitted to the CIBMTR (e.g. pathology report used for diagnosis)?

Indicate whether documentation for “myeloproliferative neoplasm, unclassifiable” was submitted to the CIBMTR (e.g., pathology report). For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Questions 263: Did the recipient have constitutional symptoms (> 10% weight loss in six months, night sweats, unexplained fever higher than 37.5°C) in six months before diagnosis?

Indicate if constitutional symptoms were present at diagnosis. Constitutional symptoms are often called “B” symptoms and include unexplained fever greater than 38°C (100.4°F), night sweats, or unexplained weight loss in the six months prior to diagnosis. Indicate “yes” if any constitutional symptoms were present at or six months prior to diagnosis.

Indicate “no” if constitutional symptoms were not present at or prior to diagnosis. Indicate “unknown” if it is not possible to determine the presence or absence of constitutional symptoms at or six months prior to diagnosis.

Question 264: Date CBC drawn

These questions are intended to capture the laboratory studies performed at that diagnosis of MPN. Testing may be performed multiple times at diagnosis; report the most recent laboratory results performed prior to the start of first treatment of the primary disease for HCT. If the recipient’s MPN transformed, report the studies from the original diagnosis.

Report the date the sample was collected for testing and continue with question 265.

Questions 265-266: WBC

Indicate whether the white blood cell (WBC) count was “known” or “unknown” at diagnosis. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 266. If “unknown,” continue with question 267.

Questions 267-268: Neutrophils

Indicate whether the neutrophil percentage in the blood was “known” or “unknown” at diagnosis. If “known,” report the value documented on the laboratory report in question 268. If “unknown,” continue with question 269.

Questions 269-270: Blasts in blood

Indicate whether the percent blasts in the peripheral blood is “known” or “unknown” at the time of diagnosis.

If “known,” report the laboratory value in question 270. **Note**, blasts are not typically found in the peripheral blood. If blasts are not noted on the differential, you can still indicate “known” and report “0%” in question 270.

If the percent blasts in blood at diagnosis is not known, report “unknown” and go to question 271.

Questions 271-272: Hemoglobin

Indicate whether the hemoglobin was “known” or “unknown” at diagnosis. If “known,” report the laboratory value and unit of measure documented on the laboratory report in question 272. If “unknown,” continue with question 274.

Question 273: Was RBC transfused \leq 30 days before the CBC sample date?

Transfusions temporarily increase the red blood cell count. It is important to distinguish between a recipient whose body is creating these cells and a recipient who requires transfusions to support the counts.

Indicate if red blood cells were transfused less than or equal to 30 days prior to the date reported in question 264.

Questions 274-275: Platelets

Indicate whether the platelet count was “known” or “unknown” at diagnosis. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 275. If “unknown,” continue with question 277.

Question 276: Were platelets transfused \leq 7 days before the CBC sample date?

Transfusions temporarily increase the platelet count. It is important to distinguish between a recipient whose body is creating the platelets and a recipient who requires transfusions to support the counts.

Indicate if platelets were transfused less than or equal to 7 days prior to the date reported in question 264

Questions 277-278: Blasts in bone marrow

- ✿ If the bone marrow pathology report states a range for blasts, enter the average of the range rounded to the nearest whole number (e.g., if 0-5%, enter 3%).
- If the report indicates “sheets of blasts” or “packed marrow,” report 100%.
- If the report states $> n\%$ blasts, enter $(n+1)\%$ on the form. For example, if the laboratory report indicates $> 90\%$ blasts, report 91%.
- If the report states $< n\%$ blasts, enter $(n-1)\%$ on the form. For example, if the laboratory report indicates $< 5\%$ blasts, report 4%.

Indicate whether the percentage of blasts in the bone marrow was “known” or “unknown” at the diagnosis. If “known,” report the percentage documented on the laboratory report in question 278. If “unknown,” continue

with question 279.



Questions 283-286 CALR Testing: If CALR testing was performed but the lab report does not specify the type, select “not done” for questions 284 and 285 and specify the results as either “positive” or “negative” for question 286.

Question 279-288: Were tests for driver mutations performed?

Testing for driver mutations may be performed by different methods including next generation sequencing (NGS), polymerase chain reaction (PCR), microarray, and fluorescence in situ hybridization (FISH). If testing was performed by any / all of these methods at diagnosis, report “yes” and report the results for the most recent test(s) in questions 280-288.

If testing for driver mutations were not performed or is unknown, report “no” or “unknown” and continued with question 290.

Question 289: Was documentation submitted to the CIBMTR (e.g. pathology report used for diagnosis)?

Indicate whether documentation was submitted to the CIBMTR (e.g., pathology report). For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 290: Were cytogenetics tested (karyotyping or FISH)?

Cytogenetics is the study of chromosomes. Cytogenetic assessment involves testing blood or bone marrow for the presence of known chromosomal abnormalities that reflect the recipient’s disease. Testing methods include conventional chromosome analysis (karyotyping) or fluorescence in situ hybridization (FISH). For more information about cytogenetic testing and terminology, see Appendix C, Cytogenetic Assessments.

Indicate if cytogenetic studies were obtained at diagnosis. If cytogenetic studies were obtained, select “yes” and continue with question 291.

If no cytogenetic studies were obtained or it is unknown if chromosome studies were performed, select “no” or “unknown” and continue with question 307.

Question 291: Were cytogenetics tested via FISH?

Indicate if FISH studies were performed at diagnosis. If FISH studies were performed, report “yes” and continue with question 292.

If FISH studies were not performed at diagnosis, report “no” and continue question 299. Examples include: no FISH study performed, or FISH sample was inadequate. See Appendix C, Cytogenetic Assessments, for assistance interpreting FISH results.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.

Question 292: Sample source:

Indicate if the sample was from “bone marrow” or from “peripheral blood” and continue with question 293. If multiple sources were used to test FISH, the most preferred sample is the bone marrow.

Question 293: Results of tests:

If FISH assessments identified abnormalities, indicate “abnormalities identified” and continue with question 294.

If FISH assessments were unremarkable, indicate “no abnormalities” identified, continue with question 298.



Question 294 is disabled and cannot be answered at this time.

Question 294-297: Specify cytogenetic abnormalities (FISH)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string, if applicable, in question 294, then continue with question 295.

Report the number of abnormalities detected by FISH at diagnosis in question 295, then select all abnormalities detected in question 296.

If a clonal abnormality is detected, but not listed as an option in question 296, select “other abnormality” and specify the abnormality in question 297. If multiple “other abnormalities” were detected, report “see attachment” in question 297 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 298: Was documentation submitted to the CIBMTR?

Indicate whether documentation was submitted to the CIBMTR (e.g., pathology report, FISH report). For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 299: Were cytogenetics tested via karyotyping?

Indicate if karyotyping was performed at diagnosis. If karyotyping was performed, report “yes” and continue with question 300.

If karyotyping was not performed at diagnosis, report “no” and continue with question 307. Examples of this include: karyotyping was not performed, or karyotyping sample was inadequate.

Question 300: Sample source:

Indicate if the sample was from “bone marrow” or from “peripheral blood” and continue with question 301. If multiple sources were used for karyotyping analyses, the most preferred sample is the bone marrow.

Question 301: Results of tests:

If karyotyping assessments identified abnormalities, indicate “abnormalities identified” and continue with question 302.

If karyotyping assessments yielded no evaluable metaphases or there were no abnormalities identified, indicate such and continue with question 306.



Question 302 is disabled and cannot be answered at this time.

Question 302-305: Specify cytogenetic abnormalities (karyotyping)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string, if applicable, in question 302, then continue with question 303.

Report the number of abnormalities detected by karyotyping at diagnosis in question 303. After indicating the number of abnormalities in question 303, select all abnormalities detected in question 304.

If a clonal abnormality is detected, but not listed as an option in question 304, select “other abnormality” and specify the abnormality in question 305. If multiple “other abnormalities” were detected, report “see attachment” in question 305 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 306: Was documentation submitted to the CIBMTR?

Indicate whether documentation was submitted to the CIBMTR (e.g., karyotype report). For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 307: Did the recipient progress or transform to a different MPN subtype or AML between diagnosis and the start of the preparative regimen / infusion?**Transformation to AML**

If the recipient is being transplanted for AML that has transformed from MPN, the primary disease for HCT must be reported as AML. Disease Classification questions must be completed for both AML and MPN.

MPN subtypes may also transform/progress from one into another. Indicate if the recipient’s disease progressed to AML or transformed into a different MPN subtype between initial diagnosis and the start of the preparative regimen / infusion. Progression to AML is defined by an increase in blood or bone marrow blasts equal to or greater than 20%.

If the recipient’s disease did transform or progress, select “yes” and continue with question 308. If there was

no documented transformation or progression, select “no” and continue with question 311.

Question 308: Specify the MDS subtype after transformation:

Indicate the recipient’s current MPN subtype after transformation. If the recipient experienced more than one transformation after diagnosis, report the most recent subtype. For a list of MPN subtypes and their diagnostic criteria, see Appendix H.

If the disease transformed to AML, continue with question 310.

For all other progressions or transformations, continue with question 309.

Question 309: Specify the date of the most recent transformation:

Report the date of assessment that determined the most recent disease transformation (i.e., if there were multiple transformations, report the most recent). Report the date of the pathological evaluation (e.g., bone marrow) or blood/serum assessment (e.g., CBC, peripheral blood smear). Enter the date the sample was collected for pathological and laboratory evaluations.

If the exact date is not known, use the process for reporting partial or unknown dates as described in General Instructions, Guidelines for Completing Forms.

Question 310: Date of MDS Diagnosis

If the recipient’s MPN transformed to AML prior to HCT, report the date of diagnosis of MPN. If the exact date is not known, use the process for reporting partial or unknown dates as described in General Instructions, Guidelines for Completing Forms.

Ensure the date of diagnosis for AML has been reported in question 1, AML is reported as the primary disease for HCT in question 2, and the AML section of the Disease Classification Form has been completed. Go to the signature line.

Question 311: Specify transfusion dependence at the last evaluation prior to the start of the preparative regimen / infusion:

Indicate the transfusion dependence for the recipient at the last evaluation prior to the start of the preparative regimen / infusion.

Select “Non-transfused (NTD)” if the recipient was without RBC transfusions as supportive care for the disease within a period of 16 weeks prior to the start of the preparative regimen / infusion.

Select “Low-transfusion burden (LTB)” if the recipient had 3-7 RBC transfusions within a period of 16 weeks in at least 2 transfusion episodes with a maximum of 3 RBC transfusions in 8 weeks prior to the start of the preparative regimen / infusion.

Select “High-transfusion burden (HTB)”- if the recipient had ≥ 8 RBCs transfusions within a period of 16 weeks or ≥ 4 within 8 weeks prior to the start of the preparative regimen / infusion.

Questions 312: Did the recipient have constitutional symptoms (> 10% weight loss in six months, night sweats, unexplained fever higher than 37.5°C) in six months before the last evaluation prior to the start of the preparative regimen / infusion?

Report “yes” if constitutional symptoms were present within six months before the last evaluation prior to the preparative regimen / infusion. Constitutional symptoms are often called “B” symptoms and include unexplained fever greater than 38°C (100.4°F), night sweats, or unexplained weight loss in the six months before the last evaluation prior to the start of the preparative regimen / infusion.

Report “no” if constitutional symptoms were not present at this timepoint.

Report “unknown” if it is not possible to determine the presence or absence of constitutional symptoms at this timepoint.

Question 313: Did the recipient have splenomegaly at last evaluation prior to the start of the preparative regimen / infusion?

Indicate if the recipient had splenomegaly at the last evaluation. Splenomegaly is often documented during the physician’s physical assessment of the recipient and represents an abnormal finding. Splenomegaly can also be detected by imaging techniques such as ultrasonography, CT or MRI.

Indicate “yes” if splenomegaly was present at the last evaluation prior to the start of the preparative regimen / infusion and continue with question 314.

Indicate “no” if splenomegaly was not present at the last evaluation and continue with question 317.

Indicate “unknown” if it is not possible to determine the presence or absence of splenomegaly at this timepoint and continue with question 317.

Indicate “not applicable” if the question does not apply to the recipient (e.g. prior splenectomy) and continue with question 317.

Question 314: Specify the method used to measure spleen size

Indicate the method used to measure the spleen size.

If the method selected is “physical assessment,” continue with question 315.

If the method selected is “ultrasound” or “CT / MRI” continue with question 316.

If spleen size is measured using multiple methods, report the most accurate assessment. Ultrasound is the most specific and preferred assessment.

Question 315: Specify the spleen size below the left coastal margin

Indicate the size of the spleen in centimeters, measured below the left coastal margin as assessed by physical exam then continue with question 317.

Question 316: Specify the spleen size in centimeters

Indicate the size of the spleen in centimeters, as assessed by imaging (ultrasound, CT / MRI) then continue with question 317.

Question 317: Did the recipient have hepatomegaly

Indicate if the recipient had hepatomegaly at the last evaluation prior to the start of the preparative regimen / infusion. Hepatomegaly is often documented during the physician's physical assessment of the recipient and represents an abnormal finding.

Indicate "yes" if hepatomegaly was present at the last evaluation and continue with question 318.

Indicate "no" if hepatomegaly was not present at this timepoint and continue with question 321.

Indicate "unknown" if it is not possible to determine the presence or absence of hepatomegaly at this timepoint and continue with question 321.

Question 318: Specify the method used to measure liver size

Indicate the method used to measure the liver size.

If the method selected is "physical assessment" continue with question 319.

If the method selected is "ultrasound" or "CT / MRI" continue with question 320. If liver size is measured using multiple methods, report the most accurate assessment. Ultrasound is the most specific and preferred assessment.

Question 319: Specify the liver size below the right coastal margin

Indicate the size of the liver in centimeters, measured below the right coastal margin as assessed by physical exam then continue with question 321.

Question 320: Specify the liver size in centimeters

Indicate the size of the liver in centimeters, as assessed by imaging (ultrasound, CT / MRI) then continue with question 321.

Question 321: Date CBC drawn

Report the date of the CBC was drawn at the last evaluation prior to the start of the preparative regimen /

infusion and continue with question 322. If multiple CBCs were drawn, report the most recent one prior to the start of the preparative regimen / infusion.

Question 322-323: WBC

Indicate whether the white blood cell (WBC) count was “known” or “unknown” at the last evaluation prior to the start of the preparative regimen / infusion. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 323. If “unknown,” continue with question 324.

Questions 324-325: Neutrophils

Indicate whether the neutrophil percentage in the blood was “known” or “unknown” at the last evaluation prior to the start of the preparative regimen / infusion. If “known,” report the value documented on the laboratory report in question 325. If “unknown,” continue with question 326.

Question 326-327: Blasts in the blood

Indicate whether the percent blasts in the peripheral blood is “known” or “unknown” at the last evaluation prior to the start of the preparative regimen / infusion.

If “known,” report the laboratory value in question 327. **Note**, blasts are not typically found in the peripheral blood. If blasts are not noted on the differential, you can still indicate “known” and report “0%” in question 327.

If the percent blasts in blood at the last evaluation prior to the start of the preparative regimen / infusion is not known, report “unknown” and go to question 328.

Question 328-329: Hemoglobin

Indicate whether the hemoglobin was “known” or “unknown” at the last evaluation prior to the start of the preparative regimen / infusion. If “known,” report the laboratory value and unit of measure documented on the laboratory report in question 329. If “unknown,” continue with question 331.

Question 330: Was RBCs transfused ≤ 30 days before the CBC sample date?

Transfusions temporarily increase the red blood cell count. It is important to distinguish between a recipient whose body is creating these cells and a recipient who requires transfusions to support the counts.

Indicate if red blood cells were transfused less than or equal to 30 days prior to the CBC sample date reported in question 321.

Question 331-332: Platelets

Indicate whether the platelet count was “known” or “unknown” at the last evaluation prior to the start of the preparative regimen / infusion. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 332. If “unknown,” continue with question 334.

Question 333: Were platelets transfused \leq 7 days before date of test?

Transfusions temporarily increase the platelet count. It is important to distinguish between a recipient whose body is creating the platelets and a recipient who requires transfusions to support the counts.

Indicate if platelets were transfused less than or equal to 7 days prior to the CBC sample date reported in question 321.

Questions 334-335: Blasts in bone marrow:

- ✿ If the bone marrow pathology report states a range for blasts, enter the average of the range rounded to the nearest whole number (e.g., if 0-5%, enter 3%).
- If the report indicates “sheets of blasts” or “packed marrow,” report 100%.
- If the report states $> n\%$ blasts, enter $(n+1)\%$ on the form. For example, if the laboratory report indicates $> 90\%$ blasts, report 91%.
- If the report states $< n\%$ blasts, enter $(n-1)\%$ on the form. For example, if the laboratory report indicates $< 5\%$ blasts, report 4%.

Indicate whether the percentage of blasts in the bone marrow was “known” or “unknown” at the last evaluation prior to the start of the preparative regimen / infusion. If “known,” report the percentage documented on the pathology report in question 335. If “unknown,” continue with question 336.

Question 336-345: Were tests for driver mutations performed?

Testing for driver mutations may be performed by different methods including next generation sequencing (NGS), polymerase chain reaction (PCR), microarray, and fluorescence in situ hybridization (FISH). If testing was performed by any / all of these methods at the last evaluation prior to the start of the preparative regimen / infusion, report “yes” and report the results for the most recent test(s) in questions 337-345.

If testing for driver mutations were not performed or is unknown, report “no” or “unknown” and continued with question 347.

Question 346: Was documentation submitted to the CIBMTR (e.g. pathology report used for diagnosis)?

Indicate whether documentation was submitted to the CIBMTR (e.g., pathology report). For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 347: Were cytogenetics tested (karyotyping or FISH)?

Cytogenetics is the study of chromosomes. Cytogenetic assessment involves testing blood or bone marrow for the presence of known chromosomal abnormalities that reflect the recipient’s disease. Testing methods include conventional chromosome analysis (karyotyping) or fluorescence in situ hybridization (FISH). For more information about cytogenetic testing and terminology, see Appendix C, Cytogenetic Assessments.

Indicate if cytogenetic studies were obtained at the last evaluation prior to the preparative regimen / infusion. If cytogenetic studies were obtained, select “yes” and continue with question 348.

If no cytogenetic studies were obtained or it is unknown if chromosome studies were performed, select “no” or “unknown” and continue with question 364.

Question 348: Were cytogenetics tested via FISH?

If FISH studies were performed at the last evaluation prior to the start of the preparative regimen / infusion, report “yes” for question 348 and continue with question 349. If FISH studies were not performed at this time point, report “no” for question 348 and go to question 356. Examples include: no FISH study performed, or FISH sample was inadequate. See Appendix C, Cytogenetic Assessments, for assistance interpreting FISH results.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.

Question 349: Sample source:

Indicate if the sample was from “bone marrow” or from “peripheral blood” and continue with question 349. If multiple sources were used to test FISH, the most preferred sample is the bone marrow.

Question 350: Results of tests:

If FISH assessments identified abnormalities, indicate “abnormalities identified” and continue with question 351.

If FISH assessments were unremarkable, indicate “no abnormalities” identified, continue with question 355.



Question 351 is disabled and cannot be answered at this time.

Questions 351-354: Specify cytogenetic abnormalities (FISH)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string, if applicable, in question 351, then continue with question 352.

Report the number of abnormalities detected by FISH at the last evaluation prior to the preparative regimen / infusion in question 352. After indicating the number of abnormalities in question 352, select all abnormalities detected in question 353.

If a clonal abnormality is detected, but not listed as an option in question 353, select “other abnormality” and specify the abnormality in question 354. If multiple “other abnormalities” were detected, report “see attachment” in question 354 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 355: Was documentation submitted to the CIBMTR?

Indicate whether documentation was submitted to the CIBMTR (e.g., pathology report, FISH report). For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 356: Were cytogenetics tested via karyotyping?

If karyotyping was performed at the last evaluation prior to the preparative regimen / infusion, report “yes” and continue with question 357. If karyotyping was not performed at this time point, indicate “no” and continue with 364. Examples of this include: karyotyping was not performed, or karyotyping sample was inadequate.

Question 357: Sample source:

Indicate if the sample was from “bone marrow” or from “peripheral blood” and continue with question 358. If multiple sources were used to for karyotyping analyses, the most preferred sample is the bone marrow.

Question 358: Results of tests:

If karyotyping assessments identified abnormalities, indicate “abnormalities identified” and continue with question 359.

If karyotyping assessments yielded no evaluable metaphases or there were no abnormalities identified, indicate such and continue with question 363.



Question 359 is disabled and cannot be answered at this time.

Question 359-362: Specify cytogenetic abnormalities (karyotyping)

Report the International System for Human Cytogenetic Nomenclature (ISCN) compatible string, if applicable, in question 359, then continue with question 360.

Report the number of abnormalities detected by karyotyping at the last evaluation prior to the start of the preparative regimen / infusion. After indicating the number of abnormalities in question 360, select all abnormalities detected in question 361.

If a clonal abnormality is detected, but not listed as an option in question 361, select “other abnormality” and specify the abnormality in question 362. If multiple “other abnormalities” were detected, report “see attachment” in question 362 and attach the final report(s) for any other abnormalities detected.

For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#).

Question 363: Was documentation submitted to the CIBMTR?

Indicate whether documentation was submitted to the CIBMTR (e.g., karyotype report). For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 364: What was the disease status?

Indicate the disease status of MPN at the last assessment prior to the start of the preparative regimen / infusion. **Refer to the MPN Response Criteria section of the Forms Instructions Manual for definitions of each disease response.**


If the disease status is “Clinical Improvement (CI)” continue with question 365. If the disease status is “Not Assessed” continue with question 369. For all other disease statuses go to question 368.

Question 365: Was an anemia response achieved?

Specify if an anemia response has been achieved at the last evaluation prior to the preparative regimen / infusion and continue with question 366.

An anemia response is characterized by a ≥ 20 g/L (or > 2.0 g/dL) increase in hemoglobin level (for transfusion-independent recipients) or by becoming transfusion-independent (transfusion-dependent recipients).

Question 366: Was a spleen response achieved?

 If a spleen response does not apply to the recipient (e.g. prior splenectomy) as documented in question 313, this question will be disabled and should not be answered.

Specify if a spleen response has been achieved at the last evaluation prior to the preparative regimen / infusion and continue with question 367.

A spleen response is achieved when a baseline splenomegaly that is palpable at 5-10 cm below the left costal margin (LCM) becomes not palpable or baseline splenomegaly that is palpable at > 10 cm below the LCM, decreases by $\geq 50\%$.

A baseline splenomegaly that is palpable at < 5 cm, below the LCM, is not eligible for spleen response.

A spleen response can be documented by a physician or confirmed by MRI / computed tomography showing $\geq 35\%$ spleen volume reduction.

Question 367: Was a symptom response achieved?

The Myeloproliferative Neoplasm Symptom Assessment Form Total Symptom Score (MPN-SAF TSS) is used to evaluate the recipient’s symptom response. The MPN-SAF TSS is used to provide an accurate

assessment of MPN symptom burden. The evaluation tool allows recipients with MPN to report their symptom severity at the worst level. They rate their symptom severity on a scale from zero to ten, zero being absent to ten being the worst imaginable. Adding the scores for all symptoms together will result in the recipient's MPN-SAF TSS. See Table 1 below for an example of this assessment:

Table 1. Myeloproliferative Neoplasm Symptom Assessment Form Total Symptom Score (MPN-SAF TSS)

Symptom	1 to 10 (0 if absent) ranking – 1 is most favorable and 10 least favorable
Please rate your fatigue (weariness, tiredness) by circling the one number that best describes your WORST level of fatigue during the past 24 hours	(No fatigue) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Circle the one number that describes how, during the past week how much difficulty you have had with each of the following symptoms.	—
Filling up quickly when you eat (early satiety)	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Abdominal discomfort	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Inactivity	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Problems with concentration – Compared to prior to my MPD	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Numbness / tingling (in my hands and feet)	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Night sweats	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Itching (pruritus)	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Bone pain (diffuse not joint pain or arthritis)	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Fever (>100 F)	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)
Unintentional weight loss last 6 months	(Absent) 0 1 2 3 4 5 6 7 8 9 10 (Worst imaginable)

A symptom response is achieved when there is a $\geq 50\%$ reduction in the Myeloproliferative Neoplasm Symptom Assessment Form Total Symptom Score (MPN-SAF TSS).

Specify if a symptom response has been achieved at the last evaluation prior to preparative regimen / infusion and continue with question 368.

Question 368: Date assessed:

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen / infusion. The date reported should be that of the most disease-specific assessment within the pre-transplant work-up period (approximately 30 days). Clinical and hematologic assessments include pathological evaluation (e.g., bone marrow biopsy), radiographic examination (e.g., X-ray, CT scan, MRI scan, PET scan), and laboratory assessment (e.g., CBC, peripheral blood smear), in addition to clinician evaluation and physical examination. Enter the date the sample was collected for pathological and laboratory evaluations; enter the date the imaging took place for radiographic assessments.

If the exact date is not known, use the process for reporting partial or unknown dates as described in General Instructions, Guidelines for Completing Forms.

Question 369: Specify the cytogenetic response:

Specify the recipient's cytogenetic response at the last evaluation prior to the start of the preparative regimen / infusion.

If there is eradication of the previous reported abnormality select "Complete response (CR)" and continue with question 370.

If there is a $\geq 50\%$ reduction in abnormal metaphases, select "Partial Remission (PR)" and continue with question 370.

Select "Re-emergence of pre-existing cytogenetic abnormality" if the cytogenetic abnormality was eradicated and reemerged at the last evaluation and continue with question 370.

If cytogenetic response was not tested at the last evaluation select "Not assessed" and continue with question 371.

Select "not applicable" if cytogenetic abnormalities were never identified and continue with question 371.

If the recipient does not meet the criteria for CR or PR, select "None of the above" and continue with question 371 (e.g. if a new cytogenetic abnormality is identified but there is also eradication of a previous abnormality).

Example: A recipient had 10 abnormal metaphases (out of 20) at diagnosis. At the last evaluation prior to the start of the preparative regimen, they had 2 abnormal metaphases (out of 20). As this is a $\geq 50\%$ reduction in abnormal metaphases, "Partial Remission (PR)" should be reported.

Question 370: Date assessed:

Report the date the cytogenetic response was established. Enter the date the sample was collected for pathologic evaluation (e.g., bone marrow biopsy) or blood/serum assessment (e.g., CBC, peripheral blood smear).

Question 371: Specify the molecular response:

Specify the recipient's molecular response at the last evaluation prior to the start of the preparative regimen / infusion, based on the four driver mutations (JAK2, CALR, MPL, and CSF3R) listed in questions 280 – 288.

If there is eradication of the previously reported driver mutation (JAK2, CALR, MPL, and/or CSF3R), select "Complete response (CR)" and continue with question 372.

If there is a 50% decrease in allele burden of the driver mutation (JAK2, CALR, MPL, and/or CSF3R), select "Partial Remission (PR)" and continue with question 372.

Example: A recipient was found to have a molecular mutation identified (JAK2, CALR, MPL, and/or CSF3R) in 80% of cells examined at diagnosis. At their last evaluation prior to transplant, the molecular mutation was only identified in 40% of cells examined. The number of cells with the molecular mutation identified decreased from 80% to 40%, which is a 50% reduction. In this case, "Partial Remission" should be reported as their molecular response.

Select "Re-emergence of pre-existing molecular abnormality" if the molecular abnormality (JAK2, CALR, MPL, and/or CSF3R) was eradicated and reemerged at the last evaluation and continue with question 372.

Select "not applicable" if JAK2, CALR, MPL, and CSF3R were never identified and go to first name.

If molecular response was not tested at the last evaluation select "Not assessed" and go to first name. If the recipient does not meet the criteria for CR or PR select "None of the above" and go to first name.

Question 372: Date assessed:

Report the date the molecular response was established. Enter the date the sample was collected for pathologic evaluation (e.g., bone marrow biopsy) or blood/serum assessment (e.g., CBC, peripheral blood smear).

Last modified: Aug 18, 2020

Q373-379: Other Leukemia

CLL, or chronic lymphocytic leukemia, is characterized by $\geq 5 \times 10^9/L$ monoclonal lymphocytes with a CLL phenotype (usually co-expressed CD5 and CD23). The term SLL, or small lymphocytic lymphoma is used for non-leukemic cases with the tissue morphology and immunophenotype of CLL.

Hairy cell leukemia is characterized by the presence of abnormal B-lymphocytes in the bone marrow, peripheral blood, and spleen.

PLL, or prolymphocytic leukemia, is a type of CLL and is characterized by increased presence of immature prolymphocytes in the bone marrow and peripheral blood.

Question 373-374: Specify the other leukemia classification

Indicate the other leukemia disease classification at diagnosis. If the subtype is not listed, report as “other leukemia” and specify the reported disease in question 373.

Question 375: Was any 17p abnormality detected?

Cytogenetics is the study of chromosomes. Cytogenetic assessment involves testing blood or bone marrow for the presence of a known chromosomal abnormality that reflects the recipient’s disease. Testing methods you may see include conventional chromosome analysis (karyotyping) or fluorescence *in situ* hybridization (FISH). For more information about cytogenetic testing and terminology, see [Appendix C](#).

Indicate if cytogenetic studies detected any 17p abnormality at any time prior to the start of the preparative regimen.

If “yes” and the disease classification is CLL, continue with question 376. If “yes” and the disease classification is PLL, continue with question 378.

If cytogenetic studies did not detect any 17p abnormality at any time prior to the start of the preparative regimen, select “no” and continue with question 379.

Question 376: Did a histologic transformation to diffuse large B-cell lymphoma (Richter syndrome) occur at any time after CLL diagnosis?

Histologic transformation may occur after CLL diagnosis. Indicate if CLL transformed into diffuse large B-cell lymphoma (known as Richter’s transformation or Richter’s syndrome). If CLL transformed, select “yes” and continue with question 380. If CLL did not transform, select “no” and continue with question 378.

Question 377: What was the disease status? (Atypical CML)

Indicate the disease status for atypical CML at the last evaluation prior the start of the preparative regimen (or infusion of no preparative regimen was given). If no treatment was given prior to HCT, submit the form.

Otherwise, continue with question 378.

Disease Status of Atypical CML

Primary Induction Failure (PIF)

The patient received treatment for atypical CML **but never achieved complete remission at any time**. PIF is not limited by the number of unsuccessful treatments; this disease status only applies to recipients who have *never been in complete remission*.

Complete Remission (CR)

All of the following criteria are met and maintained for four or more weeks:

- Marrow with normal maturation of all cellular components
 - ≤ 5% blasts in the marrow
 - No signs or symptoms of the disease
- If the timeframe between achieving CR and the start date of the HCT (i.e., day 0) is less than four weeks, and the recipient is believed to be in CR, report the status at transplantation as CR.

*Important: if within four weeks following transplant the recipient's status is determined to **not be CR**, an Error Correction Form must be submitted to change the pre-HCT status.*

Include recipients with persistent cytogenetic abnormalities who otherwise meet all the criteria of CR.

Report that the recipient is in CR at the time of transplant no matter how many courses of therapy it may have taken to achieve that CR.

The number of this complete remission can be determined by using the following guidelines:

- 1st CR: no prior relapse
- 2nd CR: one prior relapse
- 3rd or higher: two or more prior relapses

Relapse (REL)

Recurrence of disease after CR. Relapse is defined as:

- > 5% blasts in the marrow
- Extramedullary disease
- Reappearance of cytogenetic abnormalities and/or molecular markers associated with the diagnosis at levels that, as determined by a physician, represent relapse.

The number of this relapse can be determined by using the following guidelines:

- 1st relapse: one prior CR
- 2nd relapse: two prior CRs
- 3rd or higher: three or more CRs

No treatment

The recipient was diagnosed with atypical CML and never treated.

Question 378: What was the disease status? (CLL, PLL, Hairy cell leukemia, Other leukemia)

Indicate the disease status for CLL / SLL, PLL, hairy cell leukemia, or other leukemia at the last evaluation prior the start of the preparative regimen (or infusion if no preparative regimen was given) and continue with question 235.

If reporting **CLL / SLL** or **PLL**, refer to the [CLL Response Criteria](#) section of the Forms Instructions Manual for definitions of each response.

Disease Status of Hairy Cell Leukemia¹

Untreated

The recipient was diagnosed with hairy cell leukemia and never treated.

Complete Remission (CR)

Disappearance of all evidence of disease.

Requires **all** of the following:

- Neutrophils $\geq 1.5 \times 10^9$
- Hemoglobin ≥ 11.0 g/dL (without transfusion)
- Platelets $\geq 100 \times 10^9/L$
- Absence of hairy cells on peripheral blood smear and on bone marrow examination
- No palpable lymphadenopathy or hepatosplenomegaly

Partial Remission (PR)

Requires **all** of the following:

- $\geq 50\%$ reduction in the absolute hairy cell count in the peripheral blood and the bone marrow
- $\geq 50\%$ improvement of all cytopenias
- $\geq 50\%$ reduction in abnormal lymphadenopathy or hepatosplenomegaly

Stable Disease (SD)

Not meeting the criteria for any of the other disease response criteria.

Progressive Disease

Requires one or more of the following:

- $\geq 25\%$ increase in the absolute hairy cell count in the peripheral blood and/or bone marrow
- $\geq 25\%$ decrease in any of the hematologic parameters (i.e., neutrophils, hemoglobin or platelets)
- $\geq 25\%$ increase in abnormal lymphadenopathy or hepatosplenomegaly

Not assessed

No assessment of organomegaly, peripheral blood counts, absolute hairy cell count in the bone marrow or the peripheral blood smear was done at any time after treatment.

Relapse (untreated)

Relapse after CR:

- Reappearance of hairy cells in the peripheral blood smear and/or bone marrow (regardless of the degree of infiltration)
- Development of peripheral blood cytopenias
- Splenomegaly

Relapse after PR:

- $\geq 50\%$ increase of residual hairy cells in the marrow
- Development of cytopenias
- Splenomegaly insufficient to qualify as PR

OR

- Reappearance of hairy cells in the bone marrow of those patients who had been classified as partial responders based on residual splenomegaly only

¹ Saven, A., Burian, C., Koziol, J. A., & Piro, L. D. (1998). Long-term follow-up of patients with hairy cell leukemia after cladribine treatment. *Blood*, 92(6), 1918-1926.

Other leukemia:

To determine the disease status, use the criteria for the leukemia that most closely resembles the disease for which this form is being completed. For questions, contact the CIBMTR Customer Service Center.

Question 379: Date assessed:

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen. The date reported should be that of the most disease-specific assessment within the pre-transplant work-up

period (approximately 30 days). Clinical and hematologic assessments include pathological evaluation (e.g., bone marrow biopsy), radiographic examination (e.g., X-ray, CT scan, MRI scan, PET scan), and laboratory assessment (e.g., CBC, peripheral blood smear), in addition to clinician evaluation and physical examination. Enter the date the sample was collected for pathological and laboratory evaluations; enter the date the imaging took place for radiographic assessments.

If the exact date is not known, use the process for reporting partial or unknown dates as described in [General Instructions, Guidelines for Completing Forms](#).

Last modified: Aug 21, 2020

Q380-397: Hodgkin and Non-Hodgkin Lymphoma

Hodgkin lymphoma (HL or Hodgkin disease) is a cancer of the immune system that is marked by the presence of a type of cell called the Reed-Sternberg cell. The two major types of Hodgkin lymphoma are classical Hodgkin lymphoma (90-95% of cases) and nodular lymphocyte-predominant Hodgkin lymphoma (5-10% of cases).

Classical Hodgkin lymphoma can be further subdivided into four histologic subtypes: nodular sclerosis (NS), mixed cellularity (MC), lymphocyte deplete (LD), and lymphocyte rich (LR). Symptoms include the painless enlargement of lymph nodes, spleen, or other immune tissue. Generalized pruritus is also common and may precede the diagnosis by months. The most common sites of involvement include cervical, supraclavicular, and mediastinal lymph nodes. Central nervous system involvement may occur in rare cases. Other symptoms include fever, weight loss, fatigue, and/or night sweats.

Non-Hodgkin lymphoma (NHL) is a large group of cancers derived from lymphocytes (white blood cells). Non-Hodgkin lymphomas can occur at any age and are often marked by enlarged lymph nodes, fever, night sweats and weight loss. There are many different types of non-Hodgkin lymphoma. These types can be divided into aggressive (fast-growing), intermediate, or indolent (slow-growing) and can develop from either B-cells or T-cells. See Table 10.

Lymphomas that occur after bone marrow or stem cell transplantation are usually B-cell non-Hodgkin lymphomas and are collectively known as **post-transplant lymphoproliferative disorders (PTLD)**.



Acute Lymphoblastic Leukemia / Lymphoma

Due to the aggressive nature of precursor B- and precursor T-cell lymphoblastic lymphoma (or lymphoma / leukemia), the primary disease to report for recipients with these malignancies should be acute lymphoblastic leukemia (B-cell lymphoblastic leukemia / lymphoma or early T-cell precursor lymphoblastic leukemia).

Hodgkin Lymphoma (HL) and non-Hodgkin Lymphoma (NHL) are WHO disease classification subtypes of lymphoma. HL and NHL can transform into other disease subtypes. NHL can transform into other NHL subtypes, or into HL subtypes, but HL will rarely transform into NHL. Additionally, HL and NHL can occur at the same time and most likely classified as “B-cell lymphoma, unclassifiable, with features intermediate between DLBCL and classical Hodgkin lymphoma”.

In order to complete the correct Disease Classification questions for a recipient who has a history of both HL and NHL, **it is important to determine which disease is active prior to the start of the preparative regimen. A physician must make this determination.**


The following two scenarios are examples of the data reporting practice for recipients with a combination of

HL and NHL.

Scenario 1: A recipient is being transplanted for active NHL, but has a history of HL that is in remission at the start of the preparative regimen. Report the active NHL on the Disease Classification questions, and report HL as a prior malignancy on the Pre-TED Form (Form 2400).

Scenario 2: A recipient is being transplanted for both active NHL and active HL. Report this as NHL using “Other B-cell Lymphoma” and specify in question 269. Complete the Disease Classification questions for NHL. This only applies when the NHL and HL have been diagnosed at different times (i.e., two primaries).

Question 380-381: Specify the lymphoma histology (at infusion)

 **Double-hit or triple-hit lymphomas** – Rearrangements of MYC and BCL2 and/or BCL6 constitute a single category in the updated WHO classification and should be reported as “High-grade B-cell lymphoma, with MYC and BCL2 and/or BCL6 rearrangements” on CIBMTR forms.

Indicate the histology for which the recipient is receiving a transplant or cellular therapy. If the histology is “Other B-cell lymphoma” or “Other T-cell / NK-cell lymphoma,” specify the histology in question 381.

Go to question 382 if either of the following histologies were reported in question 381:

- Diffuse, large B-cell lymphoma – Activated B-cell type (non-GCB)
- Diffuse, large B-cell lymphoma – Germinal center B-cell type

Otherwise, go to question 383.

Question 382: Assignment of DLBCL subtype:

DLBCL subtypes may be identified using different techniques including immunohistochemistry (IHC) and gene expression profiling. IHC involves staining a tissue sample and determining the presence of cell surface markers via microscopy. Gene expression profiling utilized molecular techniques.

Report the method used to determine the DLBCL subtype. Indicate “Unknown” if the method cannot be determined from the available source documentation.

Question 383: Is the lymphoma histology reported at transplant a transformation from CLL?

In some cases, CLL may evolve to a more aggressive diffuse large B-cell lymphoma (DLBCL). This is commonly referred to as Richter’s syndrome or Richter’s transformation. In a sub-set of CLL cases, the transformation may be to Hodgkin lymphoma (HL).

If the histology reported at infusion (question 380) is a transformation from CLL, indicate “Yes,” and go to question 384.

If the histology reported at infusion is not a transformation from CLL, indicate “No” and go to question 385.

Question 384: Was any 17p abnormality detected?

Report “Yes” if an abnormality was ever detected (by any method) on the short arm of chromosome 17 since the date of diagnosis of CLL. This includes any 17p abnormality detected after transformation to lymphoma and go to question 386. Report “No” if a 17p abnormality was not detected and go to question 389.

Question 385: Is the lymphoma histology reported at transplant a transformation from a different lymphoma histology (not CLL)?

Transformation may occur when a slow-growing lymphoma with an indolent clinical history changes to a more aggressive lymphoma histologically and clinically. An example of a common transformation would include follicular lymphoma evolving to a diffuse large B-cell lymphoma (DLBCL).

If a histologic transformation occurred after or concurrently with diagnosis, indicate “Yes” and go to question 386. If a histologic transformation did not occur, indicate “No” and go to question 389.

Question 386-387: Specify the original lymphoma histology (prior to transformation)

Report the histology of the recipient’s primary disease at diagnosis. If the histology is “Other B-cell lymphoma” or “Other T-cell / NK-cell lymphoma,” specify the histology in question 387.

Question 388: Date of original lymphoma diagnosis

Report the date of diagnosis for the histology specified in questions 386-387. If the exact pathological diagnosis date is not known, use the process described in General Instructions, [General Guidelines for Completing Forms](#).

Question 389: Was a PET (or combination PET / CT) scan performed? (at last evaluation prior to the start of the preparative regimen / infusion)

Report “Yes” and go to question 390 if a PET scan was performed within three months prior to the start of the preparative regimen / infusion and meets the following criteria:

- Was performed within three months prior to the start of the preparative regimen / infusion and
- Was performed after the last pre-infusion line of therapy started

Combination PET / CT may also be reported, but a CT scan alone should not be captured here. Centers may report a PET scan performed during the most recent line of therapy so long as it is the most recent scan and was done within noted period. Report “No” and go to question 395 if a PET scan was not performed within this period.

Question 390: Was the PET (or PET / CT) scan positive for lymphoma involvement at any disease site?

Report “Yes” if the most recent PET scan prior to the start of the preparative regimen / infusion detected the recipient’s primary disease. Otherwise, report “No.”

Question 391-392: Date of PET scan

Questions 391-392 refer to the PET scan used to answer question 389. If the date of this PET scan is known, report “Known” and specify the date in question 392. If the date is only partially known (e.g., the month and year are known, but not the day) report “Known”, and use the process described in General Instructions, [General Guidelines for Completing Forms](#) to complete question 392. If the date cannot be determined / estimated, report “Unknown” and go to question 393.

Question 393-394: Deauville (five-point) score of the PET (or PET/CT) scan

Questions 393-394 refer to the PET scan used to answer question 389. Report whether the five-point PET score is known. This information is typically documented in the PET report. Consult the appropriate transplant physician if the results are unclear. If “Known,” report the score in question 394. Otherwise, report “Unknown” for question 393 and go to question 395. If the PET scan result is only documented as an ‘X’, report this as “Unknown” for question 393.

If multiple scores are documented, report the highest.

Question 395: What was the disease status?

The recipient’s pre-HCT disease status may be evaluated by a PET scan, CT scan, or both. If possible, complete question 395 using the metabolic (PET) criteria provided in the [Lymphoma Response Criteria](#) section of the manual. If it is not possible to use metabolic criteria to report the recipient’s disease (e.g., insufficient PET scan(s), non-PET-avid disease), use the radiographic criteria instead.

Indicate the disease status at the last evaluation prior to the start of the preparative regimen. When determining the disease status, compare the restaging assessments immediately prior to the preparative regimen to the assessments at baseline. “Baseline” is defined as the disease at diagnosis or at relapse/ progression. When a transformation has occurred (e.g., follicular lymphoma (FL) transformed to DLBCL), count the response number (CR1, REL2, etc.) beginning with the transformed lymphoma (in this case the DLBCL). Do not include the responses to the lymphoma sub-type prior to the transformation.

Question 396: Total number of lines of therapy received (between diagnosis and HCT / infusion)

A single line of therapy refers to any agents administered during the same time period with the same intent (induction, consolidation, etc.). If a recipient’s disease status changes resulting in a change to treatment, this should be considered a new line of therapy. Additionally, if therapy is changed because a favorable disease response was not achieved, this should be considered a new line of therapy.

Indicate how many lines of therapy the recipient received prior to the start of the preparative regimen /

infusion.

Question 397: Date assessed:

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen. Report the date imaging took place for the radiographic assessment (CT, MRI, PET, or PET/CT). Report the date the sample was collected for pathological evaluation (e.g., bone marrow biopsy). If no radiographic or pathologic assessment was performed within one month prior to transplant, report the most recent office visit in which the physician evaluated the recipient's disease status.

If the exact date is not known, use the process for reporting partial or unknown dates as described in General Instructions, [General Guidelines for Completing Forms](#).

Last modified: May 13, 2020

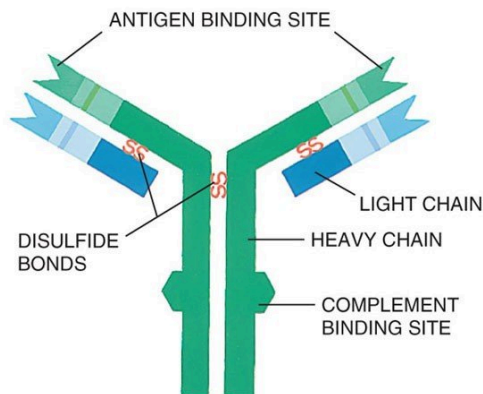
Q398-445: Multiple Myeloma / Plasma Cell Disorder

One kind of white blood cell, the plasma cell (also called plasma B cells, plasmocytes, or effector B cells), produces proteins called antibodies or immunoglobulins (Igs) that are part of our defense system against foreign substances (called antigens). Antibodies are produced in response to such things as viruses, bacteria, and other infectious agents.

Multiple myeloma is a cancer that leads to the proliferation of malignant plasma cells (myeloma cells). Myeloma cells usually proliferate in the bone marrow. When myeloma cells grow into isolated masses in other sites, these masses are called plasmacytomas. Health problems caused by multiple myeloma can affect the bones, immune system, kidneys, and red blood cell count.

The immunoglobulins (antibodies) produced by healthy plasma cells are composed of pairs of heavy chains and light chains (see graphic below). Healthy plasma cells create many different kinds of immunoglobulins that are classified by their heavy chain type into five categories (IgG, IgA, IgM, IgD, or IgE). The light chain types are designated kappa (κ) or lambda (λ). The whole Ig molecule is then labeled IgG kappa, IgG lambda, IgA kappa, IgA lambda, etc. These protein levels can be measured in blood serum and/or urine.

Structure of an Immunoglobulin (Antibody)



Secretory Multiple Myeloma:

Healthy plasma cells make immunoglobulins (antibodies) of all types. With the proliferation of malignant plasma cells, the level of one immunoglobulin type increases in the blood and/or urine. This abnormal immunoglobulin type is called the monoclonal immunoglobulin, monoclonal protein (M-protein/M-spike/M-component), or paraprotein. In most cases, the normal immunoglobulins are reciprocally depressed. Patients with this condition are said to have *secretory myeloma*.

Some myeloma patients make only an excess of the light chain portion of the immunoglobulin molecule (i.e., only monoclonal kappa or lambda light chains). The light chain is also called Bence Jones protein. In most

patients whose myeloma cells only make light chains, this paraprotein may not be detectable in the blood, but only in the urine. These patients are said to have *light-chain-only disease*. Ninety-seven percent of patients diagnosed with multiple myeloma have a detectable paraprotein in the blood serum and/or urine.

Distribution of Monoclonal Proteins in Secretory Multiple Myeloma¹²

Monoclonal Proteins at Diagnosis	Percent
<i>Source of monoclonal proteins</i>	
Serum monoclonal proteins	80%
Urine monoclonal proteins	75%
<i>Type of monoclonal proteins</i>	
IgG	50-54%
IgA	20%
Monoclonal light chain (light-chain-only disease)	20%
IgD	2%

¹ Kyle RA, et al. Review of 1027 patients with newly diagnosed multiple myeloma. *Mayo Clin Proc.* 2003;78(1):21-33.

² International Myeloma Working Group. Criteria for the classification of monoclonal gammopathies, multiple myeloma and related disorders: a report of the International Myeloma Working Group. *Br J Haem.* 2003;121(5):749-57.

Nonsecretory Multiple Myeloma:

In some myeloma patients, the malignant plasma cells do not produce an excess of the heavy chain or light chain portion of the immunoglobulin molecule; therefore, a paraprotein is not detectable in the serum or urine. These patients are said to have nonsecretory myeloma (i.e., the absence of a paraprotein on immunofixation). Immunofixation detects the specific immunoglobulins after separating the proteins into bands on an electrophoresis gel. Nonsecretory myeloma accounts for 3% of myeloma cases.

Amyloidosis:

Amyloidosis is a disease in which abnormally folded proteins build up in different tissues of the body. In the most common amyloidosis, AL amyloidosis, the abnormally folded protein is the light chain component of an immunoglobulin. These light chains may build up in a variety of tissues, but the most common sites of build-up are the heart, kidneys, liver and nerves. According to the Amyloidosis Foundation, AL Amyloidosis is a relatively rare disorder, with 1200-3200 new cases reported each year in the United States. The disease mostly impacts men and people over 40.³

³ Amyloidosis Foundation. Amyloidosis – Primary AL. 15 Apr. 2013. Accessed at: <http://www.amyloidosis.org/TreatmentInformation/primaryAL.html>
Accessibility verified on October 21, 2013.

Question 398-399: Specify the multiple myeloma / plasma cell disorder (PCD) classification:

Indicate the multiple myeloma / plasma cell disorder (PCD) disease classification at diagnosis. If the subtype is not listed, report as “other plasma cell disorder” and specify the reported disease.

Plasma Cell Disorders and Characteristics**Multiple Myeloma (symptomatic)⁴**

Diagnostic criteria for symptomatic multiple myeloma requires clonal bone marrow plasma cells in $\geq 10\%$ or biopsy proven bony or extramedullary plasmacytoma and any one or more of the following myeloma-defining events:

1. Evidence of end organ damage (i.e., CRAB features) that can be attributed to the underlying plasma cell proliferative disorder, specifically:

- Hypercalcemia: serum calcium >1 mg/dL (> 0.25 mmol/L) higher than the ULN or > 11 mg/dL (> 2.75 mmol/L)
- Renal insufficiency: creatinine clearance < 40 ml/min or serum creat >2 mg/dL (> 177 μ mol/L)
- Anemia: hemoglobin > 2 g/dL (> 20 g/L) below the LLN or a hemoglobin <10 g/dL (< 100 g/dL)
- Bone lesions: one or more osteolytic lesions on skeletal x-ray, CT or PET-CT

2. Any one or more of the following biomarkers of malignancy:

- Clonal bone marrow plasma percentage $\geq 60\%$
- Involved : uninvolved serum free light chain ratio ≥ 100
- > 1 focal lesion on MRI studies (each lesion must be ≥ 5 mm in size)

⁴ (2015, October 29). International Myeloma Working Group (IMWG) Criteria for the Diagnosis of Multiple Myeloma. Retrieved February 15, 2017, from <http://imwg.myeloma.org/international-myeloma-working-group-imwg-criteria-for-the-diagnosis-of-multiple-myeloma/>

Plasma Cell Leukemia

- Peripheral blood absolute plasma cell count of at least $2.0 \times 10^9/L$ (2,000 cells/mm³)
- $\geq 20\%$ plasma cells in the peripheral differential white blood cell count.⁵

Solitary Plasmacytoma (in absence of bone marrow findings diagnostic for multiple myeloma or plasma cell leukemia)**Extramedullary:**

- No M-protein in serum and/or urine
- Extramedullary tumor of clonal plasma cells
- Normal bone marrow

- Normal skeletal survey
- No related organ or tissue impairment (end organ damage including bone lesions)

Bone Derived

- No M-protein in serum and/or urine
- Single area of bone destruction due to clonal plasma cells
- Bone marrow not consistent with multiple myeloma
- Normal skeletal survey (and MRI of spine and pelvis if done)
- No related organ or tissue impairment (no end organ damage other than solitary bone lesion)⁵

Note: if the recipient has greater than one plasmacytoma, but has not been diagnosed with another plasma cell disorder, select “other plasma cell disorder” and specify how many plasmacytomas are present and if each is bone derived or extramedullary.

Amyloidosis

Amyloidosis is the buildup of abnormally folded proteins in various tissues of the body. Affected tissues may include the kidneys, heart, liver, gastrointestinal tract, etc. In the most common type of amyloidosis, “AL amyloidosis,” light chains from antibodies function as the amyloid protein, building up within organs and disrupting organ function. Serum and urine tests are useful for evaluating amyloidosis, but a tissue biopsy is the best way to diagnose the condition.

Osteosclerotic myeloma/ POEMS Syndrome

POEMS syndrome is poorly understood, but generally refers to **p**olyneuropathy, **o**rganomegaly, **e**ndocrinopathy, **M** protein, and **s**kin changes. Diagnosis may be made using the presence of the major criteria and one minor criteria below:

Major Criteria (both of the following):

- Polyneuropathy
- Monoclonal plasmaproliferative disorder

Minor Criteria (at least one of the following):

- Sclerotic bone lesions⁶
- Castleman disease⁶
- Organomegaly (splenomegaly, hepatomegaly, lymphadenopathy)
- Edema (edema, pleural effusion, or ascites)
- Endocrinopathy (adrenal, thyroid⁷, pituitary, gonadal, parathyroid, pancreatic⁷)
- Skin changes (hyperpigmentation, hypertrichosis, plethora, hemangiomas, white nails)

- Papilledema

Light Chain Deposition Disease

Similar to amyloidosis, light chain deposition disease is characterized by the overproduction and deposition of light chains in organs throughout the body; however, the organ most often affected is the kidneys. Under microscopy, the pattern of deposition and the use of staining techniques help pathologists differentiate between amyloidosis and light chain deposition disease.⁸

⁵ The International Myeloma Working Group. Criteria for the classification of monoclonal gammopathies, multiple myeloma, and related disorders: a report of the international myeloma working group. *Brit J Haematol*. 2003;121(5):749-57.

⁶ Osteosclerotic lesion or Castleman disease is usually present.

⁷ Because of the high prevalence of diabetes mellitus and thyroid abnormalities, this diagnosis alone is not sufficient to meet this minor criterion. Dispenzieri A, Kyle RA, Lacy MQ, et al. POEMS syndrome: definitions and long-term outcome. *Blood*. 2003;101(7):2496-506.

⁸ UNC Kidney Center, University of North Carolina. Light Chain Deposition Disease. 5 Apr. 2013. Accessed at: <http://unckidneycenter.org/kidneyhealthlibrary/glomerular-disease/light-chain-deposition-disease>
Accessibility verified on January 30, 2017

For recipients diagnosed with more than one PCD, either sequentially or concurrently, ensure that all applicable questions are completed.

If the recipient's disease classification is one of the following, continue with question 400.

- Multiple myeloma – IgG
- Multiple myeloma – IgA
- Multiple myeloma – IgD
- Multiple myeloma – IgE
- Multiple myeloma – IgM (not Waldenstrom macroglobulinemia)
- Multiple myeloma – light chain only

If the recipient's disease classification is the following, continue with question 401.

- Amyloidosis

If the recipient's disease classification is the following, continue with question 402.

- Monoclonal gammopathy of renal significance (MGRS)

If the recipient's disease classification is the following, continue with question 405.

- Solitary plasmacytoma (no evidence of myeloma)

If the recipient's disease classification is the following, neither kappa nor lambda light chains will be present; therefore, continue with question 406.

- Multiple myeloma – non-secretory

If the recipient's disease classification is one of the following, continue with question 408.

- Plasma cell leukemia
- Smoldering myeloma
- Osteosclerotic myeloma/POEMS syndrome

If the recipient's disease classification is the following, continue with question 399.

- Other Plasma Cell Disorder

Question 400: Specify heavy and/or light chain type: (check all that apply)

Indicate the heavy and / or light chain type for the recipient's disease and continue to question 406. This question allows for more than one response, if applicable.

Question 401: Specify Amyloidosis classification:

Specify the amyloidosis classification as one of the following and continue to question 408:

- AL amyloidosis (light-chain amyloidosis): This is the most common type of amyloidosis where the abnormally folded protein is the light chain component of an immunoglobulin. Misfolded proteins can deposit in the nervous system, heart, kidneys, or digestive tract; however they can often affect more than one organ.⁹
- AH amyloidosis (heavy-chain amyloidosis): This is a rare type of amyloidosis where the abnormally folded protein is the heavy chain component of an immunoglobulin.¹⁰
- AHL amyloidosis (heavy- and light-chain amyloidosis): This is a rare type of amyloidosis where the abnormally folded protein is composed of fragments of both the Ig heavy chain and light chain.¹⁰

fn9. "AL Amyloidosis." Amyloidosis Foundation, <http://amyloidosis.org/facts/al/>.

¹⁰ Nasr, S. H. (2013). The diagnosis and characteristics of renal heavy-chain and heavy/light-chain

amyloidosis and their comparison with renal light-chain amyloidosis. *Kidney International*, 83(3), 463–470. <https://doi.org/10.1038/ki.2012.414>

Question 402: Select monoclonal gammopathy of renal significance (MGRS) classification:

Specify the monoclonal gammopathy of renal significance (MGRS) classification. If the classification reported is “monoclonal immunoglobulin deposition disease (MIDD),” report the MIDD subtype in question 403. For all other classifications, continue to question 404.

Question 403: Select monoclonal immunoglobulin deposition disease (MIDD) subtype:

Specify the monoclonal immunoglobulin deposition disease (MIDD) as one of the following and continue to question 404:

- Light chain deposition disease (LCDD)
- Light and heavy chain deposition disease (LHCDD)
- Heavy chain deposition disease (HCDD)

Question 404: Was documentation submitted to the CIBMTR? (e.g. pathology report)

Indicate if a pathology report is attached to support the MGRS classification reported in questions 398-399 and continue with question 408. For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 405: Solitary plasmacytoma was:

Indicate if the solitary plasmacytoma was “bone derived” or “extramedullary.” Refer to the Plasma Cell Characteristics above for additional information regarding the characteristics of each type.

Question 406: What was the Durie-Salmon staging (at diagnosis)?

Indicate Durie-Salmon staging at diagnosis and continue with question 407. If the Durie-Salmon stage is not documented in the medical record, use the table below to determine the appropriate stage.

If the Durie-Salmon stage is unknown and cannot be determined using the table below, select “unknown” and continue with question 408.

Question 407: What was the Durie-Salmon sub classification (at diagnosis)?

Indicate the Durie-Salmon sub classification at diagnosis and continue with question 264. If the Durie-Salmon sub classification is not documented in the medical record, use the criteria below to determine the appropriate sub classification.

A: Relatively normal renal function (serum creatinine <2.0 mg/dL)

B: Abnormal renal function (serum creatinine ≥2.0 mg/dL)

Durie-Salmon Staging System for Multiple Myeloma⁸

Stage	Criteria
I	All of the following: <ul style="list-style-type: none"> • Hemoglobin > 10 g/dL • Serum calcium normal (< 10.5 mg/dL) • On radiograph, normal bone structure or solitary bone plasmacytoma only • Low M-component production rate (IgG < 5 g/dL, IgA < 3 g/dL), Urinary light chain M-component on electrophoresis (< 4 g/24 hr)
II	Fitting neither stage I nor stage III
III	One or more of the following: <ul style="list-style-type: none"> • Hemoglobin < 8.5 g/dL • Serum calcium > 12 mg/dL • Advanced lytic bone lesions (three or more lytic lesions) • High M-component product rate (IgG > 7 g/dL, IgA > 5 g/dL), Urinary light chain M-component on electrophoresis (> 12 g/24 hr)
Sub-classification	(either A or B) A: Relatively normal renal function (serum creatinine < 2.0 mg/dL) B: Abnormal renal function (serum creatinine ≥ 2.0 mg/dL)

⁸ Adapted from Durie BG, Salmon SE: A clinical staging system for multiple myeloma: Correlation of measured myeloma cell mass with presenting clinical features, response to treatment, and survival. *Cancer*. 1975;36:842-54.

Question 408: Did the recipient have a preceding or concurrent plasma cell disorder?

Indicate if the recipient had a concurrent or preceding plasma cell disorder. Many recipients progress to symptomatic myeloma from a preceding condition or have a concurrent plasma cell disorder, such as amyloidosis.

Example 1. If a recipient has smoldering myeloma (asymptomatic) and then develops symptomatic multiple myeloma, “multiple myeloma” should be reported as the primary diagnosis in question 398 and “smoldering myeloma” should be reported in question 409.

Example 2. If a recipient has smoldering myeloma (asymptomatic) and amyloidosis, “amyloidosis” should be reported as the primary diagnosis in question 398 and “smoldering myeloma” should be reported in question 409.

Example 3. If the recipient has symptomatic multiple myeloma and amyloidosis, “multiple myeloma” should be reported as the primary diagnosis in question 398 and “amyloidosis” should be reported as a concurrent diagnosis in question 409.

Questions 409-410: Specify preceding / concurrent disorder:

Indicate the preceding or concurrent disorder. See the Plasma Cell Characteristics information above for

descriptions of disease and the previous question for examples of situations with preceding or concurrent disorders. If the recipient has a preceding or concurrent plasma cell disorder that is not listed, select “other plasma cell disorder (PCD)” and specify the type in question 410.

Question 411: Date of diagnosis or preceding / concurrent disorder:

Report the date the recipient was first diagnosed with the preceding or concurrent plasma cell disorder. Enter the date the blood/urine was collected for the laboratory evaluations (e.g., serum/urine protein electrophoresis [SPEP/UPEP, respectively], or serum/urine immunofixation) or enter the date of the first pathological diagnosis (e.g., bone marrow biopsy, plasmacytoma, tissue). Enter the date the sample was collected for examination.

If the exact date is not known, use the process described for reporting partial or unknown dates in General Instructions, Guidelines for Completing Forms.

Copy questions 409-411 to report more than one concurrent or preceding disorder.



Assessments at diagnosis: Questions 412 – 441 refer to the labs and assessments performed at diagnosis of the primary disease for transplant.

Question 412-413: Serum β 2 microglobulin:

At the time of plasma cell disorder diagnosis, an elevated β 2 microglobulin protein may indicate a poorer prognosis. Indicate whether the β 2 microglobulin protein was “known” or “unknown” at the time of plasma cell disorder diagnosis. If this value was “known,” report the value and unit of measure documented on the laboratory report in question 413. If “unknown,” continue with question 414.

Questions 414-415: Serum albumin:

Indicate whether the serum albumin was “known” or “unknown” at the time of plasma cell disorder diagnosis. If “known,” report the value and unit of measure documented on the laboratory report. If “unknown,” continue with question 416.

Questions 416-417: Stage at Diagnosis: I.S.S.

Report the recipient’s ISS stage of myeloma at diagnosis.

I.S.S. Staging System for Multiple Myeloma¹¹

Stage	Description
Stage I	Serum β 2-microglobulin < 3.5 mg/L and serum albumin \geq 3.5 g/dL

Stage II	Serum β 2-microglobulin < 3.5 mg/L and serum albumin < 3.5 g/dL OR Serum β 2-microglobulin 3.5 to <5.5 mg/dL irrespective of serum albumin level
Stage III	Serum β 2-microglobulin \geq 5.5 mg/L irrespective of serum albumin level

¹¹ Greipp, P. R., San Miguel, J., Durie, B. G., Crowley, J. J., Barlogie, B., Bladé, J., ... & Westin, J. (2005). International staging system for multiple myeloma. *Journal of Clinical Oncology*, 23(15), 3412-3420.

Questions 418-419: Stage at Diagnosis: R – I.S.S.

The Revised International Staging System (R-ISS) includes variables included in the original ISS (serum beta-2 microglobulin and serum albumin), while also including the additional prognostic information obtained from serum LDH and high-risk chromosomal abnormalities detected by interphase fluorescent in situ hybridization (iFISH) after CD138 plasma cell purification.¹² High risk chromosomal abnormalities identified by iFISH include:

- Deletion 17p / 17p-
- t(14;4)
- t(14;16)

Report the recipient's R-ISS stage of myeloma at diagnosis

R-I.S.S. Staging System for Multiple Myeloma¹²

Stage	Description
Stage I	ISS stage I and standard-risk chromosomal abnormalities identified by iFISH and normal LDH
Stage II	Not R-ISS stage I or III
Stage III	ISS stage III and either high-risk chromosomal abnormalities identified by iFISH or high LDH

¹² Palumbo, A. et al (2015). Revised International Staging System for Multiple Myeloma: A Report From International Myeloma Working Group. *J Clin Oncol*, 33(26), 2863-9. doi: 10.1200/JCO.2015.61.

Questions 420-422: Plasma cells in blood by flow cytometry:

Indicate if plasma cells in the blood by flow cytometry was “known” or “unknown” at the time of diagnosis. If “known,” report the percentage of plasma cells detected in the blood by flow cytometry documented on the flow cytometry report in question 421 and the absolute number documented on the flow cytometry report in question 422.

If only the percentage of plasma cells in the blood detected by flow cytometry is available, multiply the percentage of plasma cells by the white blood count (WBC) to determine the absolute number of plasma

cells.

If “unknown,” continue with question 423.

Questions 423-425: Plasma cells in blood by morphologic assessment:

Indicate if plasma cells in the blood by morphologic assessment was “known” or “unknown” at the time of diagnosis. If “known,” report the percentage of plasma cells detected in the blood by morphologic assessment documented on the laboratory report in question 424 and the absolute number documented on the laboratory report in question 425.

If only the percentage of plasma cells is available, multiply the percentage of plasma cells by the white blood count (WBC) to determine the absolute number of plasma cells.

If “unknown,” continue with question 426.

Questions 426-427: LDH:

Indicate whether the LDH (lactate dehydrogenase) level was “known” or “unknown” at the time of plasma cell disorder diagnosis. If “known,” report the value and unit of measure documented on the laboratory report in question 427 and continue with question 428. If “unknown,” continue with question 429.

Question 428: Upper limit of normal for LDH:

Indicate the upper limit of normal for LDH value and the unit of measure used at your institution.

Question 429: Were cytogenetics tested (conventional or FISH)? (at diagnosis)

Cytogenetic analysis is the study of chromosomes. Cytogenetic assessment involves testing blood or bone marrow for the presence of a known chromosomal abnormality which reflects the recipient’s disease. Testing methods you may see include conventional chromosome analysis (karyotyping) or fluorescence in situ hybridization (FISH). For more information about cytogenetic testing and terminology, see [Appendix C](#).

Karyotyping is performed by culturing cells (growing cells under controlled conditions) until they reach the dividing phase. Techniques are then performed to visualize the chromosomes during cell division so that various bands and reconfigurations can be seen. Banding pattern differentiation and chromosomal reconfiguration demonstrate evidence of disease.

FISH is a sensitive technique that assesses a large number of cells. This technique uses special probes that recognize and bind to fragments of DNA. These probes are mixed with cells from the recipient’s blood or bone marrow. A fluorescent “tag” is then used to visualize the binding of the probe to the diseased cells.

Indicate whether cytogenetic studies were performed at diagnosis. If cytogenetic studies were performed at diagnosis, check “Yes” and go to question 430. If cytogenetic studies were not obtained at diagnosis or it is not known whether chromosome studies were performed, indicate “No” or “Unknown” respectively and go to

question 442.

Questions 430-431: Were cytogenetics tested via FISH? (at diagnosis)

If FISH studies were performed at diagnosis, report “Yes” for question 430 and indicate whether clonal abnormalities were detected in question 431. If multiple FISH assessments were performed, report “Abnormalities Identified” if any testing showed clonal abnormalities at diagnosis. If FISH studies were not performed at diagnosis, report “No” for question 430 and go to question 436. Examples of this include: no FISH study performed or all FISH samples were inadequate.

Report chromosomal microarrays / chromosomal genomic arrays as FISH assessments.



Question 432 is disabled and cannot be answered at this time.

Questions 432-434: Specify cytogenetic abnormalities (FISH) (at diagnosis)

Report the ISCN compatible string if applicable in question 432, then continue with question 433.

Select all cytogenetic abnormalities identified by FISH assessments at diagnosis in questions 433-434.

If a clonal abnormality is detected, but not listed as an option in question 433, select “Other abnormality” and specify the abnormality in question 434. If multiple “Other abnormalities” were detected, report “see attachment” in question 434 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 435: Was documentation submitted to the CIBMTR? (e.g. FISH report)

Indicate if a FISH report is attached to support the cytogenetic findings reported in questions 433-434. For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Questions 436-437: Were cytogenetics tested via karyotyping? (at diagnosis)

If karyotyping studies were performed at diagnosis, report “Yes” for question 436 and indicate whether clonal abnormalities were detected in question 437. If multiple karyotyping assessments were performed, report “Abnormalities Identified” if any testing showed clonal abnormalities at diagnosis. If karyotyping studies were not performed at diagnosis, report “No” for question 436 and go to question 442. Examples of this include: no karyotyping performed or all karyotyping samples were inadequate.



Question 438 is disabled and cannot be answered at this time.

Questions 438-440: Specify cytogenetic abnormalities (karyotyping) (at diagnosis)

Report the ISCN compatible string if applicable in question 438, then continue with question 439.

Select all cytogenetic abnormalities identified by karyotyping assessments at diagnosis by checking all abnormalities that apply in question 439.

If a clonal abnormality is detected, but not listed as an option in question 439, select “Other abnormality” and specify the abnormality in question 440. If multiple “Other abnormalities” were detected, report “see attachment” in question 440 and attach the final report(s) for any other abnormalities detected. For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 441: Was documentation submitted to the CIBMTR? (e.g. karyotyping report)

Indicate if a karyotyping report is attached to support the cytogenetic findings reported in questions 439-440.

For further instructions on how to attach documents in FormsNet3SM, refer to the Training Guide.

Question 442: What was the disease status?

Indicate the disease status of the PCD at the last evaluation prior to the start of the preparative regimen. See the Multiple Myeloma Response Criteria section for multiple myeloma and solitary plasmacytoma disease status definitions. See Plasma Cell Leukemia Response Criteria for plasma cell leukemia disease status definitions.

This question will not be enabled if the primary disease for transplant is monoclonal gammopathy of renal significance (MGRS).

Question 443: Date Assessed:

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen. Report the date the blood / urine was collected for the laboratory evaluations (e.g., SPEP / UPEP, serum / urine immunofixation) or report the date the bone marrow was collected for pathological evaluation. Date of radiographic study (PET, MRI, CT) may be used **if** the same radiographic study had previously been obtained and **only** in limited circumstances (e.g., plasmacytomas, lytic lesions).

If the exact date is not known, use the process for reporting partial or unknown dates as described in General Instructions, [General Guidelines for Completing Forms](#).

Question 444: Specify amyloidosis hematologic response (for Amyloid patients only)

Indicate the disease status of amyloidosis at the last evaluation prior to the start of the preparative regimen. See the Amyloidosis Response Criteria section for disease status definitions.

If therapy was not given to treat amyloidosis, report “Unknown.”

Question 445: Date assessed:

Enter the date of the most recent assessment of disease status prior to the start of the preparative regimen. Report the date the blood / urine was collected for the laboratory evaluations (e.g., free light chain ratio, serum / urine immunofixation) or report the date the bone marrow was collected for pathological evaluation.

If the exact date is not known, use the process for reporting partial or unknown dates as described in General Instructions, [General Guidelines for Completing Forms](#).

Last modified: Aug 19, 2020

Q446-447: Solid Tumors

Question 446-447: Specify the solid tumor classification:

Indicate the solid tumor disease classification at the time of diagnosis. Germ cell tumors that originate in the ovary or testes should be reported as ovarian or testicular, respectively. If the subtype is not listed, report as "Other solid tumor" and specify the reported malignancy in question 447. If a certain disease becomes a common indication for HCT, the CIBMTR will add the disease as a separate category.

Last modified: May 09, 2020

Q448-449: Severe Aplastic Anemia

Questions 448-449: Specify the severe aplastic anemia classification:

Indicate the severe aplastic anemia disease classification at diagnosis. If the subtype is not listed, report as “other acquired cytopenic syndrome” and specify the reported disease in question 449. If a certain disease becomes a common indication for HCT, the CIBMTR will add the disease as a separate category.

Last modified: May 09, 2020

Q450-483: Inherited Abnormalities of Erythrocyte Differentiation or Function

Questions 450-452: Specify the inherited abnormalities of erythrocyte differentiation or function classification

Indicate the inherited abnormalities of erythrocyte differentiation or function disease classification at diagnosis. If the subtype is not listed, report as “other constitutional anemia” and specify the reported disease in question 451 or “other hemoglobinopathy” and specify the reported disease in question 452. If a certain disease becomes a common indication for HCT, the CIBMTR will add the disease as a separate category.

Question 453: Did the recipient receive a gene therapy to treat the inherited abnormalities of erythrocyte differentiation or function (sickle cell, sickle thalassemia, and beta thalassemia major only):

Indicate if the recipient received a gene therapy to treat the inherited abnormalities of erythrocyte differentiation or function. If the recipient received a gene therapy, indicate “yes.” If inherited abnormalities of erythrocyte differentiation or function is reported as sickle cell, sickle thalassemia, or beta thalassemia continue with question 454. If “yes” is selected for this question, Cellular Therapy Product (4003) Form and Cellular Therapy Infusion (4006) Form should also be completed.

If the recipient did not receive a gene therapy indicate “No.” If inherited abnormalities of erythrocyte differentiation or function is reported as sickle cell, sickle thalassemia, or beta thalassemia continue with question 454, otherwise submit the form.

Question 454: Was tricuspid regurgitant jet velocity (TRJV) measured by Echocardiography pre-HCT (sickle cell, sickle thalassemia and beta thalassemia major only):

Tricuspid regurgitant jet velocity (TRJV) measurements are used in determining the pulmonary artery pressure for recipients with sickle cell and other hemolytic disorders.

An elevated TRJV is an indication of pulmonary hypertension a condition common in adults with hemolytic diseases. TRJV can be determined by echocardiography (ECHO), this information is typically documented in the echocardiogram report.

Report “Yes” and go to question 455 if an echocardiogram was performed prior to the start of the preparative regimen / infusion to measure TRJV. Report “No” and go to question 457 if an echocardiogram was not performed to measure TRJV. If “unknown,” continue with question 457.

Questions 455-456: TRJV Measurement:

Questions 455-456 refer to the echocardiogram scan used to answer question 454. Report whether the TRJV measurement is known. This information is typically documented in the echocardiogram report. Consult the appropriate transplant physician if the results are unclear. If “known,” report the measurement in question 456. Otherwise, report “Unknown” for question 455 and go to question 457.

Question 457: Was liver iron content (LIC) tested within 6 months prior to infusion (sickle cell, sickle thalassemia and beta thalassemia major only):

Transfusions for hemolytic diseases such as sickle cell can often lead to iron build up or accumulation in the liver and other target organs. Liver iron content (LIC) is commonly used to measure total iron storage for recipients at risk for hemosiderosis. LIC is a more sensitive method of testing for measuring the level of iron in the liver. Common methods include but are not limited to: liver biopsy, T2*MRI and FerriScan.

Report “Yes” and go to question 458 if LIC testing was performed within 6 months prior to infusion. If LIC testing was not performed within 6 months prior to infusion report “No” and continue to question 460.

Question 458: Liver Iron Content

Report the liver iron content measurement in question 458 and continue with question 459. This will typically be documented in the report of the method used to estimate LIC.

Question 459: Method used to estimate LIC:

LIC may be tested using different techniques including but not limited to biopsy, FerriScan or MRI.

Report the method used to determine the LIC. Indicate “Other” if the method is not listed as an option.



Questions 460-483 should be answered for Beta Thalassemia Major ONLY.

Question 460: Is the recipient red blood cell dependent? (requiring transfusion to maintain HGB >7g/dl):

Questions 460-483 will only be answered for recipients with Beta thalassemia major, if this form is being completed for any other inherited abnormalities of erythrocyte differentiation, submit the form.

Report “Yes” and go to question 461 if the recipient is red blood cell dependent. Report “No” and go to question 468 if the recipient does not require blood cell transfusions to maintain HGB >7g/dl.

Question 461: Year of first transfusion (since diagnosis):

Indicate the year of the first transfusion since diagnosis in question 461 then continue with question 462. If the year is unknown report the year of diagnosis.

Question 462: Was iron chelation therapy given at any time since diagnosis?

Iron chelation therapy is commonly used for recipients with Thalassemia to prevent or reduce iron overload. Iron chelation therapy is the removal of excess iron from the body using drugs such as Deferrioxamine (Desferal) or Deferasirox (Jadenu, Exjade).

Select “Yes” if iron chelation therapy was given at any time since diagnosis and continue with question 463. If iron chelation therapy was not given or it is unknown whether iron chelation therapy was given, select “no”

or “unknown” and continue with question 468.

Question 463: Did iron chelation therapy meet the following criteria: initiated within 18 months of the first transfusion and administered for at least 5 days / week (either oral or parenteral iron chelation medication)?

If iron chelation therapy was given as specified above select “Yes” and continue with question 466. If iron chelation therapy was given but does not meet the specified criteria, select “No” and continue with question 464. If iron chelation therapy was given but administration details are unavailable, select “Unknown” and continue with question 466.

Questions 464-465: Specify reason criteria was not met:

Indicate the reason criteria was not met for question 463 and continue with question 466. If the reason is not listed report as “Other” and specify the reason criteria was not met in question 465.

Questions 466-467: Year iron chelation therapy started:

If the date iron chelation therapy was started is known, report “Known” and indicate the date in question 467. If the start date of iron chelation therapy is unknown, report “Unknown” and continue with question 468.

Question 468: Did the recipient have hepatomegaly (>= 2cm below costal margin):

Hepatomegaly is an enlargement of the liver. Indicate “yes” if hepatomegaly was present at the time of the most recent evaluation prior to infusion and continue with question 469. Indicate “no” if hepatomegaly was not present and “unknown” if it is not possible to determine the presence or absence of hepatomegaly at the most recent evaluation prior to infusion and continue with question 470.

Question 469: Liver size as measured below the costal margin at most recent evaluation prior to infusion:

Specify the number of centimeters the liver is below the right costal margin.

Question 470: Was a liver biopsy performed at any time since diagnosis?

Evaluation of liver tissue may be necessary to determine the extent of the disease. Indicate if a liver biopsy was performed at any time since diagnosis. If “yes,” continue with question 471. If “no,” continue with question 477.

Questions 471-472: Date assessed:

If the date of the liver biopsy is known, report “Known” and indicate the date in question 472. If the date of the liver biopsy is unavailable report “Unknown” and continue with question 473.

Question 473: Liver cirrhosis:

Select “present” if the biopsy showed characteristics of live cirrhosis. Select “absent” if the biopsy was negative for liver cirrhosis. Select “unknown” if the results of the evaluation were unknown or inconclusive.

Continue with question 474.

Question 474: Bridging fibrosis:

Select “present” if the biopsy showed characteristics of bridging fibrosis. Select “absent” if the biopsy was negative for bridging fibrosis. Select “unknown” if the results of the evaluation were unknown or inconclusive. Continue with question 475.

Question 475: Chronic hepatitis:

Select “present” if the biopsy showed characteristics of chronic hepatitis. Select “absent” if the biopsy was negative for chronic hepatitis. Select “unknown” if the results of the evaluation were unknown or inconclusive. Continue with question 476.

Question 476: Was documentation submitted to the CIBMTR? (e.g., liver biopsy):

Indicate whether a liver biopsy is attached to support / clarify the center’s responses to questions 468-475. For further instructions on how to attach documents in FormsNet3SM, refer to the [Training Guide](#) Training Guide AE.pdf#page=25.

Question 477: Is there evidence of abnormal cardiac iron deposition on MRI of the heart at time of infusion?

A cardiac MRI may be performed to assess cardiac iron disposition. Indicate “yes” if cardiac MRI shows evidence of abnormal cardiac iron deposition at the time of infusion. Select “no” if there is no evidence of abnormal cardiac iron disposition at the time of infusion.

Question 478: Did the patient have a splenectomy at any time prior to infusion?:

Destruction of platelets in the spleen is thought to play an important role in thrombocytopenia because corrections of platelet count and size have been reported after splenectomy. Select “yes” if the recipient underwent a splenectomy after diagnosis but prior to the preparative regimen. If the recipient did not have a splenectomy report “no”, if it is unknown whether a splenectomy was performed report “unknown”.

Questions 479-480: Serum Iron

A serum iron test is used to determine how much iron is in the serum. If the serum iron level is lower than normal, it indicates the body’s iron stores are low (iron deficiency). If the serum iron level is higher than normal it could indicate hemochromatosis, a condition that causes the body to store too much iron.

Indicate whether the serum iron was “known” or “unknown” at the last evaluation prior to the start of the preparative regimen. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 480. If “unknown,” continue with question 481.

Questions 481-482: Total iron binding capacity (TIBC):

TIBC is a test used to gauge the total amount of iron in the blood. It is often measured in micrograms per deciliter (mcg/dL) or micromoles per liter (micromol/L). Indicate whether TIBC was “known” or “unknown” at the last evaluation prior to the start of the preparative regimen. If “known,” report the laboratory count and unit of measure documented on the laboratory report in question 482. If “unknown,” continue with question 483.

Question 483: Was the serum bilirubin less than two times the upper limit of normal?

Report “yes” if the recipient’s serum bilirubin was less than two times the upper limit of normal at the last evaluation prior to the start of the preparative regimen. Report “no” if the recipient’s serum bilirubin was not less than two times the upper limit of normal at the last evaluation prior to the start of the preparative regimen. If serum bilirubin was not evaluated at the last evaluation prior to the start of the preparative regimen, report “unknown”.

Last modified: May 09, 2020

Q484-491: Disorders of Immune System

Questions 484-487: Specify disorder of immune system classification:

Indicate the disorder of the immune system's disease classification at diagnosis. If the subtype is not listed, report as "other SCID", "other immunodeficiency" or "other pigmentary dilution disorder" and specify the reported disease in question 485, 486 or 487. If a certain disease becomes a common indication for HCT, the CIBMTR will add the disease as a separate category.

Question 488: Did the recipient have an active or recent infection with a viral pathogen within 60 days of HCT?

Viral infections are caused by exposure to a new virus or reactivation of a dormant virus already present in the body. The most common viral infections are due to HSV (Herpes Simplex Virus), and CMV (Cytomegalovirus). Report "yes" if the recipient had an active or recent infection with a viral pathogen within 60 days of HCT and continue with question 489. If the recipient did not have an active or recent infection with a viral pathogen report "no" and continue to question 490.

Question 489: Specify the viral pathogen (check all that apply):

Specify any viral pathogens causing infection reported in question 488.

Question 490: Has the recipient ever been infected with PCP/PJP:

PCP Pneumocystis is a common fungal infection commonly affecting the lungs. Indicate if the recipient has ever been infected with PCP/PJP.

Question 491: Does the recipient have GVHD due to maternal cell engraftment pre-HCT? (SCID only):

Recipients with SCID often have presence of maternal T lymphocytes (T cells) in the circulation. This is a complication that results from maternal-fetal transfusion and the failure in SCID patients to recognize and to reject foreign cells, allowing maternal T cells to engraft. This is also known as maternal engraftment. This engraftment can induce graft-versus-host disease (GVHD).

Report "yes" if the recipient has a history of or current manifestations of GVHD due to maternal cell engraftment at the last evaluation prior to the preparative regimen and continue to signature line.

If the recipient does not have GVHD due to maternal cell engraftment pre-HCT, report "no" and submit the form.

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Q492-493: Inherited Abnormalities of Platelets

Questions 492-493: Specify inherited abnormalities of platelets classification:

Indicate the inherited abnormalities of platelets disease classification at diagnosis. If the subtype is not listed, report as “other inherited platelet abnormality” and specify the reported disease in question 493. If a certain disease becomes a common indication for HCT, the CIBMTR will add the disease as a separate category.

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Q494-496: Inherited Disorders of Metabolism

Questions 494-495: Specify inherited abnormalities of metabolism classification:

Indicate the inherited abnormalities of metabolism disease classification at diagnosis. If the subtype is not listed, report as “other inherited metabolic disorder” and specify the reported disease in question 495. If a certain disease becomes a common indication for HCT, the CIBMTR will add the disease as a separate category.

Question 496: Report the Loes composite score (Adrenoleukodystrophy (ALD) only):

The Loes composite score is often used to assess disease/progression for recipients with ALD. The Loes composite score is a rating from 0-34, this signifies the severity of abnormalities detected in the brain after evaluation of MRI. Report the Loes composite score in question 496, if the score is unknown, check with a transplant physician to determine this value.

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Q497-501: Histiocytic Disorders

Questions 497-498: Specify the histiocytic disorder classification:

Indicate the histiocytic disorder disease classification at diagnosis. If the subtype is not listed, report as "other histiocytic disorder" and specify the reported disease in question 498. If a certain disease becomes a common indication for HCT, the CIBMTR will add the disease as a separate category.

Question 499: Did the recipient have an active or recent infection with a viral pathogen within 60 days of HCT? Hemophagocytic lymphohistiocytosis (HLH) only:

Viral infections are caused by exposure to a new virus or reactivation of a dormant virus already present in the body. The most common viral infections are due to HSV (Herpes Simplex Virus), and CMV (Cytomegalovirus). Report "yes" if the recipient had an active or recent infection with a viral pathogen within 60 days of HCT and continue with question 500. If the recipient did not have an active or recent infection with a viral pathogen report "no" and go to question 501.

Question 500: Specify the viral pathogen (check all that apply):

Specify any viral pathogens causing infection reported in question 500.

Question 501: Has the recipient ever been infected with PCP/PJP:

PCP Pneumocystis is a common fungal infection commonly affecting the lungs. Indicate if the recipient has ever been infected with PCP/PJP.

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Q502-505: Autoimmune Diseases

Questions 502-505: Specify autoimmune disease classification

Indicate the autoimmune disease classification at diagnosis. If the subtype is not listed, report as “other autoimmune disease “other autoimmune cytopenia,” or “other autoimmune bowl disorder,” and specify the reported disease. If a certain disease becomes a common indication for HCT, the CIBMTR will add the disease as a separate category.

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Q506-507: Tolerance Induction Associated with Solid Organ Transplant

Questions 506-507: Specify transplanted organ: (check all that apply):

In an effort to achieve organ tolerance and potentially avoid long term systemic immunosuppression, a recipient may receive an infusion of cells prior to a subsequent solid organ transplant. Indicate the transplanted organ, if organ is not listed, report as “other organ” and specify in question 507.

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Q508: Other Disease

Question 508: Specify other disease:

Before using this category, check with a transplant physician to determine whether the disease can be classified as one of the listed options in the Disease Classification questions. An example of another disease is dystrophic epidermolysis bullosa (DEB).

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