PMI Frequently Asked Questions

General Questions

Will Groups receive a central patient ID?

- There will be a Screening Protocol Participant ID and a Treatment Protocol Patient ID. There will not be a central Patient ID.

What is the mechanism for transfer of the three separate fields the protocol ID, cohort ID, and stratum ID to Groups randonode? What set up is needed on Group side?

- Groups will need to collect the screening protocol name, cohort, and stratum fields on the Treatment Protocol Eligibility Checklist (EC). These fields will be provided on the PMI Standard EC Template; this template will be available in the caDSR II and should be used to create the needed protocol-specific ECs. There will a validation check in OPEN that will verify that the enrolling site is being assigned to the treatment protocol for that location. The PMI Project team will provide a one-page document how to set up your RandoNode.

For crossovers from cohort 1 to cohort 2 (Group study EAY191-N2) are patients expected to submit PMI Off Treatment standard form and go back to central study?

- N2 is not a crossover, it is a reassignment because the cohorts are based on prior drug exposure. Participants with progressive disease on regimen 2 on Cohort 1 are eligible to enroll to cohort 2 if they can be re assigned. A participant who enrolls on cohort 2 over WILL take a slot and be evaluated separately.

How long will it take for the patient to be able to come down the pipeline to re-enter our study as cohort 2 candidate? EAY191-N2 study will have a second eligibility checklist in OPEN for these patients.

- The reassignment will take 24 or less hours depending on what time the reassignment was completed. N2 is not considered a crossover. For crossovers, they are immediate. Crossovers were implemented as a Step 2 on the Treatment Protocols. The PMI Off Treatment Standard Form should NOT be completed for crossover, the patient should be registered to Step 2 on the Treatment protocol.

The sequence of events would be:

- [Site] Register patient to Screening protocol Step 1 in MATCHbox assigns to N4 and sends it back to OPEN.
- [Site] Register patient to N4 Treatment protocol Cohort 1 Step 1 in OPEN (Single agent regimen).
- Patient progresses.
- [Site] Register patient to N4 Treatment protocol Cohort 2 in OPEN on Treatment protocol Step 2 to Crossover. (Multi agent regimen.)
- [Site] Complete PMI Off Treatment Standard Form for N4 when treatment on N4 is completed.
- [Site] Perform one of the below
    - Register patient for Screening protocol Step 1 in OPEN to get a new treatment assignment for said patient, OR
    - Complete the PMI Off Study Standard Form for the Screening protocol.

If yes to above, how will patients on EAY191-N2 that discontinue treatment for reasons other than progression, go into Follow up, have a progression, proceed to crossover to cohort 2? How will that be handled since PMI Off Treatment form was submitted with a reason other than progression? Also, what about those to progressed but do not want to consent to cross over to cohort 2?

- The crossover is immediate. You cannot crossover or be reassigned if there is an AE of the single agent. Cannot be reassigned to a dual agent therapy if you had an AE on the single agent.

If patients need to go through central study when crossing from cohort 1 to 2, how is crossover from treatment 1 to treatment 2 within the same cohort handled like we have in NRG study EAY191-N4? At what point PMI Off Treatment standard form needs to be submitted?

- Crossover is for disease-based cohorts and going from cohort 1 to cohort 2 is for drug exposure-based cohorts. The latter requires reassignment. For crossover, once they have enrolled to the first step and gotten their treatment assignment and patient progresses, they are eligible for a crossover.
- They would:
    - Enroll to step 2 on the treatment protocol
    - Assign a crossover treatment

OIDs should be abbreviations of the form, is there any way to keep this in mind in the future and for any forms that aren't finalized yet?

- Westat can change the Form OID in Rave once they have the ALS from caDSR. Moving forward for PMI forms, the form OIDs will be abbreviated. Current ones will not be changed.

What's the quickesThe treatment regimens are just associated with the drug, but it is not specific to the dose level (as is with the TACs).t way to get a form builder account for NCIs new system?

- The best thing to do is to contact caDSR.RA@mail.nih.gov so we can respond and assist. Everyone that had a Form Builder account in the old system has one in the new system, but we will need to work with them to make sure they can sign on and request curation if needed.

Where (what folder) does this EC template need to be in? Can it be in the Enrollment Folder with the other enrollment forms (Demography, Step Information, and Treatment Assignment)?

- The EC template can be placed in the enrollment folder.

For the ineligible status, is there a new field to use to ensure proper set up?

- This test case is now optional.

What is the form OID for the EC template?

- Form OID will be part of their form build in caDSR II.

How are the permissible values for the Cohort and Stratum CDEs added for each treatment trial? Are we responsible for submitting a request to the CBIIT curation team or will these be added in another way to ensure screening trial and treatment trial groups are using the same permissible values?

- Cohort and Stratum are being populated in OPEN through a group lookup window that is being populated with the Cohort and stratum that was assigned to the patient at screening.
- No curation activities are required or should be managed for the Cohort & Stratum CDEs/ fields. These are non-enumerated fields that should be used as already specified on the PMI EC Template.

Why are prior treatment fields included for this trial when these are all treatment naive patients? Are you expecting them to enter prior treatment for other cancers if they've had any?

- On Tier 1, all participants must be treatment naïve. There are even in protocols for Tier 1, patients can have taken some therapy as long as it's a minimal dose.

In the A3 schema there is an indication that there should be a max of 6 pts enrolled to cohort 4 for a given histology. How will this be handled in the screening trial and in terms of managing/capping enrollment to cohort 4?

- This will be handled in MATCHbox. No assignments will be generated for Histology once maximum is reached.

What happens/what is the process when the site leaves the DLAP Scenario ID blank? What happens/what is the process when there's a blank DLAP Scenario ID under Physician's choice?

- The site user may not have a scenario ID so they don't have to populate it. Field is required on the EC form but may be left blank by the site in the event that the data has not yet been entered and confirmed in DLAP. There is no correlation between Physicians choice or DLAP.

Is it correct that two Off Treatment forms aren't needed for a crossover?

- The Off Treatment from does not need to be completed for a Crossover.

The CDE 10948385 is being used to capture the ICD code for Screening and is a text string. Would 6154743 be better as that has a dictionary associated with it that represents the ICD-O-3 topography codes you mentioned?

We are asking so we don't collect a different data element on the treatment form then what is being collected on the screening form and this would allow Alliance to monitor the rates as well and if we need to do some collapsing of a set of codes to a broader class of "histology/type of cancer" we would be able to evaluate that as we go.

- The fields on the screening protocol are integrated with the disease service. We will consider this option at a future timepoint, but you will have access in MATCHbox to view this data in real-time and export that data.

What is the proposed process if a patient does not consent to banked specimens.? How will each Group relay that information to the NCI so that they do not expect banking material from that patient?

- Groups can have the consent question in OPEN. With this we are also looking into the creation of a custom report to relay information to NCI.

We have consensus that the format you described below would be acceptable, though some concerns/questions have been raised: Can you confirm this method would require updates to the OPEN Checklist to add a field? Can you confirm that sites would only need to "pick" from the list once, after which their selection would be parsed out to populate both the code and name fields.

- No new fields should be needed. We are planning on concatenating like the prior therapy field, just that there might be some updates needed to the CDEs to accommodate the full value.

With regards to Regimen, can you please confirm if the Regimens presented in the schematic are equivalent to TACs in OPEN? Or are these PMI specific treatment codes.

- The treatment regimens are just associated with the drug, but it is not specific to the dose level (as is with the TACs).

We are working to develop our Eligibility Checklist for EAY191-C1, and would like to confirm how to accommodate the OPEN required 'Stratification' Module which contains stratum and treatment assignment with the 'Treatment Module 2' on the PMI EC?
Can the module name be revised on the LPO's EC? We would like to change the module name to stratification to support the standard messaging to OPEN from our Randonode.

- The module name is tied into the integration and there are dependencies on the drop down and suggestions. This would be a global change and impact all groups and would push timelines.

We are planning on using ALS Version 7.0 for EAY191-C1 and want to confirm if that is acceptable?

- Groups can use 7.0, but will need to migrate to 7.1 or 7.2 when 7.2 comes out.

ComboMATCH Questions

Our studies have a planned follow up after the treatment completion and PMI Off Treatment forms. These will be used to roll out follow up folders in Rave. Will NRG receive information that a patient is assigned to a different ComboMATCH protocol, and will we receive notification our follow up should be stopped?

- No, the Groups will not receive information that the patient is assigned to a different ComboMATCH protocol. MATCHbox will send an email notification to the enrolling site when assignment is confirmed for a patient. Also, no email notification will be sent to the groups if a patient goes off treatment, or if a patient is reregistered and assigned to another protocol.

Does NRG need to share data from our ComboMATCH studies? Is there a mechanism for that and in what format our data needs to be?

- As long as the Group returns the treatment arm that matches what is in the protocol. For treatment assignment, Groups can send assignment name. However, for OPEN you need the codes. This information will be added to the Randonode document.

What is the max number of steps to build into ComboMATCH. Has this been determined already?

- NCI still currently working on re-registration requirements.

We are in the process of writing specifications for folder rollout for the ComboMATCH Screening protocol in Rave. The assumption is that we need to build multiple Steps into Rave. I have reviewed all the materials, including the test plans and instructions for generating OPEN Checklists, and it appears that there is no plan to have the ability to enter Step 2 registrations in the Screening Study at Go Live. Is this correct?

- Yes, this is correct. Step 2 is only for re-registration.

We are finishing out study builds for our ComboMATCH treatment trial (EAY191-S3) and our MyeloMATCH treatment trial (MM1YA-S01) and I would like to confirm the correct arm names and/or Treatment Assignment Codes. Can you please provide the correct names and codes for these two trials?

- MATCHBox the IDs are below, and they give both stratification and randomization. List of codes has been sent.
  - EAY191-S3
  - MM1YA-01

MeyloMATCH Questions

Why are the topography, morphology, and grade fields all required? They are mostly not applicable to the disease for this trial, especially grade. Seems like that would be "N/A" for all patients. If they must enter topography and morphology, can we at least narrow down the lists to the few things that are applicable?

- SWOG can decide if they want to collect these questions on their MM Screening Protocol EC form in the caDSR II during form build activities. This field will be marked as optional in OPEN: If data is present, it will be pushed.
- The 'Morphology' field is required for the MyeloMATCH protocols, specifically "9860/3"; SWOG can default the value for this field in OPEN.

OPEN/Rave Questions

It seems none of us at SWOG have the right Rave roles to upload the central study ALS. It says we can't create a new Project in Architect without creating them in iMedidata first, like we do when we build a new study. Can you find out what RAVE role CTSU uses to upload central study ALS?

- Going forward Central Study xGlobal CFs-Matchbox will be used for PMI trials, and if it is created in iMedidata it will allow you to invite users and restrict access for PMI central study via iMedidata. SAE integration central study is also in iMedidata
- Regarding your question about permission to create Project directly in Rave, the user should be assigned a Security Role that has 'Create' Action flag checked for Architect Project in Core Configuration.

How will the screening ID, cohort, and stratum fields be validated on the treatment trial OPEN forms to ensure the correct responses were entered? Will these be auto filled on the form in some way, or will there be an edit check that needs to be configured for these fields?

- Configured group look up windows based on the screening patient ID that was entered.
- For crossover – Step 2. In OPEN they would need to create a step 2 enrollment or enter patient ID of step 1 of the treatment protocol.

We also wanted to verify which form these fields (Screening protocol ID, Screening participant ID, Cohort, Stratum) were expected to be populated in Rave. Alliance does not currently use the Eligibility Checklist form in Rave so we want to make sure we understand where these fields are expected. I believe Shauna Hillman has been working with others regarding some Rave questions, but I wanted to note we still need this information from the OPEN form processing side as well. We need to make a code change on our end to send this information to Rave so we need this information as soon as possible to be ready by the OEWG deadline.

- Groups are expected to populate the screening protocol ID, screening participant ID cohort and stratum fields in Rave.

Will we be receiving an ALS for the Rave Eligibility Checklist Form? This is a new form for Alliance.

- There is no ALS for the Rave EC Template. We are using our normal EC template process. The form is built in caDSR II based on our template and that will provide you the form OID.
- The four fields you will need for that form are:
  - Screening Protocol ID
  - Screening Participant ID

- Cohort
- Stratum

What data will be entered in OPEN for a new assignment? How will we get that data into Rave? I assume there's a template form that we'll need to build out so the data can be pushed into our Rave instance.

- The PMI Project team will address reassignment questions at a future meeting since reassignment was not part of the Phase 1 release.

How is the step information form going to look for a reassessment vs a new assignment? Will a logline still be added showing that specimens were analyzed but that the decision was that they should stay on their current treatment trial? Is a logline added every time they submit something in OPEN or only in some cases?

- A notification will be sent that a treatment is complete, and the patient is eligible for a new tier assignment.
- Every new step in OPEN will result in a log line in Rave. If they get reassigned, they have a log line added. No additional new log lines based on updates or events, only mapped with STEP.

Will our data management staff have access to the EAY191 Source Documents being uploaded to OPEN? Typically, we have sites upload Path Reports into Rave, however if EA will have access to the Path Reports uploaded to OPEN we could reduce burden on sites and eliminate duplicate data entry.

- Access can be given in OPEN to view the reports, however you will need to view the report patient by patient.

After the initial paper-based process, it sounds like there will be Precision Medicine Specimen Tracking Forms and the other specimen-related forms submitted via Rave (listed below). Should these forms be part of our study build or will they exist in a different Rave "instance"?

- **Samples Tracking and Manifest Form**
- **Local Pathology Group Information Form**
- **CLIA Laboratory Specimen Submission Form**
- **MyeloMATCH Generic Specimen Submission Form**
- **Pathology Group Form**

- MM Generic Specimen submission form will not be part of the Rave study build; this is a place paper form for the STFM which will be part of the study build in the future.
- The Below forms are targeted to be added to the PMI Screening Protocol as part of Phase II activities.
  - PMI STMF
  - PMI Pathology Group Form
  - PMI CLIA Submission Form

How is our Randonode supposed to be pushed into OPEN?

- A Randonode setup document was provided to explain how RandoNode is supposed to push into OPEN with the initial release.

We are wondering if our data management staff will have access to the EAY191 Source Docs being uploaded into OPEN by sites. Typically, we have sites upload Path Reports into Rave, however if we willl have access to the Path Reports uploaded to OPEN we could reduce burden on sites and eliminate duplicate data entry.

- Groups can go in and download documents on a patient-by-patient basis. Unfortunately, Mass patient downloads are not available.