US #	User story	Acceptance criteria
01	As a clinician, I want to get a list of all withdrawn patients.	Given I am on the Participant tab and have permission to view this When I apply the filter "Withdrawn = Yes" Then I see a complete list of all withdrawn patients And I only see non-identifiable patient IDs And I see the withdrawal date and governance status And I understand immediately that these records are not available for research use
02	As a clinician/curation scientist, I want to retrieve patients with multiple tumours that underwent WGS.	Given I am on the Participant tab When I filter for "Sample count ≥ 2" and "WGS = Yes" Then I see a list of patients with at least two sequenced tumours And each patient displays all associated biosample IDs and sequencing dates And I can immediately recognise which tumours correspond to relapse, progression, or new event
03	As a clinician, I want to identify ZERO2 patients with IDH1/IDH2 mutations relative to all CNS tumours.	Given I am viewing Participant When I select CNS cancer category from the filter And I filter by "Study = ZERO2" and "Mutation = xxx" Then I see the number of ZERO2 patients with these mutations And I see all the patient with CNS tumour in ZERO2 study with xx
04	As a clinician/curation scientist, I want methylation classes and scores across all tumours.	Given I am using Patient search Then each biosample patient in my results shows methylation class and score

		And I see confidence levels or QC flags when applicable And I can filter results to focus on a specific class or score range
05	As a curation scientist, I want to retrieve all samples with a specific variant so I can understand variant frequency across cancer types.	Given I have permission to see this, I enter a variant (HGVS, genomic position, or VRS ID) When I run the participant search Then I see all participant + samples containing that variant And I see diagnosis and sample metadata alongside each match And I can immediately filter results by cancer type or study
06	Get all samples with reportable variants of a specific type (SNV, CNV, etc)	Given I have permission to see reportables When I apply SNV filter Then I see all samples with SNV-type reportable variants
07	Search full analysis set by any ID	-
08	As a curation scientist, I want to retrieve samples with a specific combination of mutations	-
09	As a curation scientist, I want to see samples with reportable germline mutations	-
10	Get RNA expression for a subset of genes	-
11	Count patients who have done WGS	Given I am on the participants page When I apply WGS filter Then I only see participants who have done WGS

12	Get samples with both WGS and RNA	-
13	Samples with PDX or HTS data	-
14	Samples with specific tumour profile (TMB, mutsig, z-score)	-
15	NTRK3 + IHC + response rate	-
16	Associate a single sample with all its IDs	-
17	Samples with specific class importance (VOUS3.8)	-
18	As a user, I want to view the state of data loading for each sample so I can understand progress and identify issues quickly.	-
19	As a user, I want metrics describing pipeline timing so I can understand operational performance.	Scenario: Viewing study monitoring data Given I have permission to view this data & I've logged in as a CCI user When I select "Study monitoring" tab Then I see Turn Around Time graph And I can filter by "From X event" -> "To X event", yearly or quarterly metric or a specific date range
20	As a user, I want to see the number of patients enrolled per study.	Scenario: Viewing study enrollment counts Given I have permission to view this data When I select "Study monitoring" tab Then I see the number of patients enrolled per study And I can filter by year or patient characteristics And I immediately see which studies have the largest cohorts
21	As a researcher I want to see all PDX models for a specific	Scenario: Viewing PDX models

	cancer type.	Given I have permission to view this data When I select view all cancer types button Then I see a tree map allowing me to select specific cancer type I'm looking for And I can apply this filter And I immediately see how many PDX models available, who the contributors are, how it was validated.