

PDXNet Portal: Patient-Derived Xenograft model, data, workflow, and tool discovery

Running Title:

PDXNet Portal

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Conflict of Interest:

The University of Utah may choose to license PDX models developed in the Welm labs, which may result in tangible property royalties to Drs. Welm and members of their lab who developed the models. MTL is a founder and limited partner in StemMed Ltd. and a manager in StemMed Holdings, its general partner. He is a founder and equity stake holder in Tvardi Therapeutics Inc. Some PDX are exclusively licensed to StemMed Ltd. resulting in royalty income to MTL. Lacey Dobrolecki is a compensated employee of StemMed Ltd. The other authors declare no competing interest.

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1 **Abstract**

2 We created the PDX Network (PDXNet) Portal (<https://portal.pdxnetwork.org/>) to centralize
3 access to the National Cancer Institute-funded PDXNet consortium resources (i.e., PDX models,
4 sequencing data, treatment response data, and bioinformatics workflows), to facilitate
5 collaboration among researchers, and to make resources easily available for research. The portal
6 includes sections for resources, analysis results, metrics for PDXNet activities, data processing
7 protocols, and training materials for processing PDX data.

8 The initial portal release highlights PDXNet model and data resources, including 334 new models
9 across 33 cancer types. Tissue samples of these models were deposited in the NCI's Patient-
10 Derived Model Repository (PDMR) for public access. These models have 2,822 associated
11 sequencing files from 873 samples across 307 patients, which are hosted on the Cancer Genomics
12 Cloud powered by Seven Bridges and the NCI Cancer Data Service for long-term storage and
13 access with dbGaP permissions. The portal also includes results from standardized analysis
14 workflows on PDXNet sequencing files and PDMR data (2,594 samples from 463 patients across
15 78 disease types). These 15 analysis workflows for whole-exome and RNA-Seq data are freely
16 available, robust, validated, and standardized.

17 The model and data lists will grow substantially over the next two years and will be continuously
18 updated as new data are available. PDXNet models support multi-agent treatment studies,
19 determination of sensitivity and resistance mechanisms, and preclinical trials. The PDXNet portal
20 is a centralized location for these data and resources, which we expect to be of significant utility
21 for the cancer research community.

22 Introduction

23 Patient-Derived Xenograft (PDX) models are cancer models that support personalized medicine
24 research and preclinical and co-clinical trials¹⁻⁵. Specific PDX research areas include the study of
25 sensitivity and resistance mechanisms, evaluation of new treatment options, and the study of tumor
26 heterogeneity. The PDX research community is rapidly growing, with PDX-generated data being
27 the preferred support for proposing human clinical trials⁶. In 2017, the National Cancer Institute
28 (NCI) funded the PDX Development and Trial Centers (PDTC) research network (PDXNet,
29 pdxnetwork.org) consortium to accelerate PDX research by developing new PDX models across
30 cancer types, identifying new multi-agent treatments to bring forward into clinical trials,
31 generating complementary RNA-Seq and whole-exome sequencing data, and increasing the ethnic
32 diversity of publicly available PDX models.

33 PDXNet was also charged with developing collaborative research projects involving the 6 different
34 PDTCs to advance PDX science. Each of the PDTCs came into PDXNet with its own home-grown
35 data standards, data analytic pipelines and workflows. To facilitate collaboration, the disparate
36 processes and databases required harmonization at many different steps, so that data from centers
37 could be combined and analyzed efficiently. The harmonization goal was achieved through the
38 creation of the PDXNet portal and the analytical tools within it. The PDXNet portal resources
39 created by this effort enabled the successful completion of several collaborative research projects
40 ⁷⁻¹⁰ and are supporting many others.

41 In addition to facilitating PDXNet research, an additional benefit of the PDXNet Portal is to make
42 the PDXNet-generated data and workflows of the PDXNet Portal available as a public resource.
43 These data will support cancer research by increasing the quantity and diversity of PDX data
44 available and decreasing the effort required to analyze PDX sequencing data. We present the
45 PDXNet Portal as a utility for PDXNet data for the larger scientific community.

46 There are several existing public PDX resources that complement the PDXNet Portal. Launched
47 in 2012, the NCI Patient-Derived Model Patient Repository (PDMR)¹¹ collects and develops PDX
48 models and associated standardized sequencing data (RNA-Seq and whole-exome), with the goal
49 of supporting academic and industry research. The PDMR maintains a publicly available database
50 of models and an File Transfer Protocol (FTP) site for accessing sequencing data. Another resource
51 is PDXFinder¹². PDXFinder is an online resource that aims to harmonize internationally generated
52 PDX models and their associated metadata. PDXFinder is a collaboration between the European
53 Molecular Biology Laboratory's European Bioinformatics Institute (EMBL-EBI) and the Jackson
54 Laboratory. A key component of data harmonization in PDXFinder is the PDX minimal
55 information standard (PDX-MI)¹³, which allows for standardized PDX information exchange.
56 PDXFinder employs PDX-MI to support complex model searches that enable users to identify
57 model descriptions and subsequently link to model information and a request form. EuroPDX is a
58 consortium of eighteen non-profit cancer institutes that collaborate and coordinate PDX model
59 development and access to improve cancer patients' standard of care. Next, the EuroPDX Data
60 Portal (<https://dataportal.europdx.eu/>) is a resource that provides information about PDX models
61 generated by EuroPDX researchers and clinicians. Lastly, the Baylor College of Medicine PDX
62 Portal (<https://pdxportal.research.bcm.edu/>) provides access to breast cancer, leukemia, pediatric
63 liver cancer, pancreatic cancer, and sarcoma model collections.

64 The primary aim of the PDXNet Portal is to support the Cancer Moonshot¹⁴ model and data sharing
65 goals¹⁵. The PDXNet Portal facilitates the distribution of resources, complementary data analyses,
66 and developed tools. The resources generated include data collections and standardized
67 bioinformatics workflows. Complementary data analyses such as data quality control analyses that
68 support data-use are also available from the portal. Tools developed to support the use of the data
69 (e.g., workflow cost estimation) are also accessible. Integration with the NCI Cloud Resource, the
70 Cancer Genomics Cloud powered by Seven Bridges (CGC)¹⁶, allows approved researchers to
71 directly analyze PDXNet data or use developed workflows on private data. This manuscript details
72 the PDXNet portal features that provide a gateway for identifying and accessing resources
73 generated by the PDXNet community.

74 **Portal Design and Organization**

75 The PDXNet Portal is designed to support coordination with other resources, including the PDMR,
76 the CGC, and the NCI Cancer Data Service (CDS)¹⁷. Currently, the PDXNet portal references
77 PDMR model information, genomic, transcriptomic, and tumor volume response data used in
78 PDXNet research activities. The CGC serves as a PDXNet data staging area supporting data
79 harmonization, standardized data processing, and research activities. The PDXNet Portal supports
80 submission of sequencing data to the CDS to provide long-term research access to PDXNet data
81 resources. The CDS is part of the NCI Cancer Research Data Commons which aims to store data
82 resources generated by NCI-funded research. The CDS is available from across the NCI data
83 infrastructure through a dbGaP access mechanism. The PDXNet portal augments the dbGaP
84 submission process, through an administrative feature for generating data reports and through a
85 dbGaP submission tool written to support CDS submissions. The PDXNet Portal aims to use data
86 standards when they exist, supporting both the PDX-MI standard¹³ and the PDMR data
87 structures¹¹. These existing data structures allow for collaboration and information sharing with
88 existing PDX resources.

89 **Portal Features**

90 The PDXNet Portal is a publicly accessible website (<https://portal.pdxnetwork.org/>) with the
91 primary function of providing access to the PDXNet models and information on how to obtain
92 sequencing data. We extended the portal's primary mission to include additional resources,
93 including supporting access to the PDMR sequencing file data set, a PDXNet hematoxylin and
94 eosin stain image data set, and PDMR tumor volume data. Below, we describe the features and
95 sections of the Portal in detail.

96 **PDXNet Portal Landing Page**

97 The PDXNet Portal Landing page includes an overview and summary panel of contents (Figure
98 1). The Portal overview identifies the primary PDXNet funding sources and participants. In
99 summary, the NCI Cancer Therapy Evaluation Program (CTEP) funds four PDTCs and the
100 PDCCC, whereas the NCI Center to Reduce Cancer Health Disparities funds two PDTCs (see
101 Table 1 for additional details). The portal directs questions and requests for additional information
102 to the PDXNet website at <https://pdxnetwork.org>.

103 The data summary panel on the right side of the screen allows the reader to review model and data
104 summaries and the portal update timeline. The data summary panel lists the number of PDTCs
105 contributing data, the number of files uploaded by the PDTCs and available from the PDMR, the
106 total number of models, and the number of cancer types represented in those models. Tabs allow
107 the reader to review summary figures for PDX Models by cancer type and contributing PDTC,
108 sequencing files by experimental strategy, ancestry, and the Portal Update Timeline.

109 **Resources**

110 The PDXNet Portal resources section includes pages that describe models, data (genomic,
111 transcriptomic, and image), and analysis workflows made available on the CGC by the PDXNet
112 consortium. The CGC based analysis workflows are a significant resource developed by the
113 PDXNet community, allowing for reproducible and standardized analysis of PDX data⁸. The
114 resource section also highlights data mirrored from the PDMR sequencing data repository to the
115 CGC to support research activities. Lastly, we provide interactive plots and tables of sequencing
116 data information for the PDXNet and PDMR sequencing data sets on the CGC. The PDXNet portal
117 presents each resource (e.g., PDXNet, PDMR, workflows) on a separate page.

118 **PDXNet Models**

119 The PDXNet Portal Models tab summarizes verified model submissions to the PDMR made by
120 each PDTC (Supplement Figure 1). The PDXNet models are a primary consortium deliverable.
121 Each model submitted by a PDTC to the PDMR includes a completed model submission form that
122 details the general PDX information, model-specific information, and tissue implantation details.
123 Metadata are consistent with the PDX-MI and the PDMR data format. The metadata includes
124 model id information to facilitate search and cross referencing to related PDMR models.

125 To date, PDXNet researchers have submitted 334 models to the PDMR across 33 cancer types.
126 The most prevalent model cancer types include invasive breast carcinoma (30.8%, 103), melanoma
127 (20.1%, 67), adenocarcinoma – colon (12.3%, 41), and adenocarcinoma – pancreas (7.8%, 26).
128 See Table 2 for additional details.

129 **PDTC Sequencing Data**

130 The PDXNet Portal summarizes sequencing data submitted by the PDTCs for intraconsortium
131 sharing and for public sharing (Figure 2). The PDXNet Data Collection - PDTC tab presents the
132 core PDXNet sequencing data set. We processed submitted sequencing data with standardized
133 workflows (e.g., whole exome capture; additional) according to a written standard operating
134 procedure provided on the CGC. See the workflow section for description of the workflows used
135 for standardized processing.

136 PDXNet researchers contributed 2,822 total sequencing files that include both whole-exome
137 (80.7%, 2,278) and RNA-Seq (19.3%, 544) data. Six institutional contributors submitted 873
138 samples from 307 patients. The sequencing sample types include PDX (51.6%, 1457), tumor (28.6,
139 808), normal (17%, 480), and blood (2.7%, 76). The most prevalent diseases represented among
140 the samples include breast (42.1%, 1,189), lung (12.8%, 362), pancreas (6.2%, 174), colon (5.8%,
141 164). Metadata provided by centers did not include disease information for 18.2% (515) samples
142 (see Table 3 for additional information).

143 **PDMR Sequencing Data**

144 The PDXNet Portal Model tab summarizes sequencing data transferred from the PDMR FTP
145 server to the CGC as of August 2020 (Supplement Figure 2). The PDMR generates whole-exome
146 and transcriptome sequencing data from models submitted according to tissue collection best
147 practices and model quality control practices¹¹. Molecular characterizations include whole-exome
148 sequencing and gene expression profiling. We processed the PDMR sequencing data with
149 standardized workflows as for the PDTC data.

150 The PDMR sequencing dataset on the CGC includes 9,492 paired-end sequencing files that include
151 both whole-exome (52.8%, 5,012) and RNA-Seq (47.2%, 4,480) data (See Supplement Table 4).
152 The data set includes 2,594 samples from 445 patients covering 34 disease types. The sequencing
153 sample types include PDX (82.7%, 7,846), primary tumor (5.7%, 542), normal germline (5.5%,
154 520), and organoid (3.2%, 304). The most prevalent diseases represented among the samples
155 include colon (21.1%, 2,002), head and neck (11.6%, 1,102), soft tissue neoplasm (10.1%, 958),
156 skin (8.7%, 828). Due to the size and cost associated with data transfers, synchronization between
157 the PDMR sequencing database and the CGC dataset is done periodically. The PDMR data
158 webpage has the most updated list of available PDMR sequencing data processed with
159 standardized PDXNet workflows.

160 **PDMR Image data**

161 The PDXNet Portal Image tab summarizes hematoxylin-eosin stain (H&E) image data provided
162 by the PDMR (Supplement Figure 3). The PDMR image data on the CGC includes 593 images
163 scanned from PDX (93.8%, 556) and primary tumors (6.2%, 37). The images correspond to 593
164 samples taken from 92 patients across 37 disease types. The PDX passages ranged from P0 to P6
165 with the top four passages corresponding to P1(41.4%, 225), P2 (24.1%, 131), P0 (22.8%, 124),
166 and P3 (8.3%, 45). The PDXNet Portal currently supports 43 metadata fields that data submitters
167 can populate upon submission (See Supplement Table 1 for the complete list).

168 **Interactive Data Explorers**

169 The PDXNet Portal data explorer allows users to interactively create summary tables from the
170 PDXNet and PDMR sequencing datasets (Supplement Figure 4). The interactive table supports 10
171 table and chart types including simple tables, bar charts, line charts, and heat maps (see Supplement
172 Table 1 for full list). Interactive tables also support 22 data summary options including count, sum,
173 average, and variance (see Supplement Table 2 for the full list). The user drags and drops from 20
174 metadata fields to the table type area to construct the table. Metadata field examples include
175 contributor, sample type, experimental strategy, and passage (see Supplement Table 3 for complete
176 list).

177 **PDXNet Workflows**

178 The PDXNet Portal Workflows tab summarizes analysis workflows developed by the PDXNet
179 community (Supplement Figure 5). We selected workflows for standard consortium-wide data
180 processing and public release from those submitted by each PDTC after benchmarking with
181 simulated and experimentally derived PDX data⁸. Since the initial public release, we have
182 restructured the workflows to efficiently process normal (tissue), tumor-only, and tumor-normal
183 data. These workflows are implemented on the CGC using the Common Workflow Language
184 (CWL)¹⁸ with Docker containerized tools, which allows for easy sharing and analysis
185 reproducibility. The PDXNet consortium developed a set of 15 workflows validated for processing

186 of both whole-exome and RNA-Seq data (Supplement Table 4). We are sharing these validated
187 and tested workflows with the broader community via the CGC Public Apps Gallery
188 (<https://cgc.sbggenomics.com/public/apps#q?search=pdx>). The use of CWL allows these
189 workflows to be portable to any CWL-compliant execution environment. The workflows
190 collectively facilitate the analysis of whole-exome or RNA-Seq data via mouse read
191 disambiguation, read alignment, variant calling or transcript quantification, and sample and cohort
192 level quality control. For whole-exome data, we also compute copy number variation (CNV),
193 tumor mutational burden (TMB), microsatellite instability (MSI), and homologous recombination
194 deficiency (HRD) during standardized processing. A full explanation of inputs, outputs, and data
195 processing steps for each workflow is provided on the CGC in the respective description section.

196 **Analysis**

197 The PDXNet Portal analysis section includes several metrics derived from primary data sources
198 and are described below in more detail. These results were generated from standard processing
199 analysis workflows or through PDXNet research activities⁸, and we provide these analyses to
200 support independent research by the broader research community.

201 **Ancestry Analysis**

202 The PDXNet Portal Ancestry Analysis page summarizes genetic ancestry analysis for datasets on
203 the portal (Supplement Figure 6). We compute ancestry with SNPweight¹⁹ using a reference
204 dataset generated from the 1000 Genomes Project Phase III²⁰. We classify each sample into one of
205 five categories, which correspond roughly to the concept of “continental ancestry.”²¹ These
206 categories include European (EUR), African (AFR), American (AMR), East Asia (EAS), and
207 South Asian (SAS). Samples that could not be confidently assigned to one of these categories are
208 labeled Mixed (MIX). On the left side of the page, ancestry data filters allow the user to select the
209 data contributors, ancestry, and disease type. Applying the selected filter to the data regenerates
210 the two summary figures. The first summary figure is a bar chart that shows the ancestry
211 distribution for the selected disease types. The second summary figure shows a pie chart with each
212 slice corresponding to the ancestry types chosen. Supplement Table 6 shows the summary of
213 ancestry estimation from PDX Models submitted to the PDMR.

214 **HRD-TMB-MSI Analysis**

215 The PDXNet Portal HRD-HSI-TMB analysis page allows the user to filter and summarize three
216 computational metrics generated from whole-exome sequencing data by PDXNet standardized
217 processing (Figure 3). The three computed metrics are Homologous Recombination Deficiency
218 (HRD), Tumor Mutational Burden (TMB), and Microsatellite Instability (MSI). HRD is computed
219 with ScarHRD²² for matched normal data. TMB is calculated as the number of coding mutations
220 that meet all quality criteria per Mb of the genome. Quality criteria are assessed using coverage,
221 allele frequency, mapping quality, and strand bias. Variants included in the calculation are somatic
222 and non-polymorphic, and are defined in SnpEff²³ as 'high' or 'moderate' functional impact. As
223 only a portion of the genome was sequenced, genome coverage (Mb) is calculated from the input
224 target coverage BED file. MSI is calculated with MANTIS²⁴ for samples with matched normal
225 data, and calculated with MSIsensor2²⁵ for tumor-only samples. For each metric, users can set data
226 filters for the visualizations. The data filters, on the left side of the page, allow the user to select
227 data contributor, sample type, experimental strategy, and disease type. Applying the selected filter
228 to the data generates a boxplot chart displaying the selected metrics for each disease type chosen
229 (Figure 3).

230 **Tumor Volume Analysis**

231 The PDXNet Portal Tumor Volume Analysis Page allows the user to visualize raw tumor volume
232 growth data provided by the PDMR (Figure 4). The filters enable the user to select contributor,
233 treatment, and disease type on the page's left side. Applying the selected filter to the data
234 regenerates the Tumor Volume and the Tumor Disease Types figure tabs. The currently available
235 volume data is from 75 models representing 30 disease types, which were treated with seven
236 possible agents (Supplement Table 7). The dataset has 17,920 volume measures from 89 treatment
237 studies. The Tumor Volume tab allows the user to choose plot level (Animal and Treatment Arm)
238 and plot pattern (multiple and combined), reorganizing the plots to correspond to select values.
239 The Tumor Disease type tab plots a disease pie chart based on user selection (Figure 4).

240 **Quality Control Analysis**

241 The PDXNet Portal QC Analysis page provides plots and tabular results for selected QC metrics
242 (Supplement Figure 7). The page displays QC metrics generated during the standardized data
243 processing procedure for each relevant data type. The page provides sub-tabs showing whole-
244 exome and RNA-Seq quality control metrics for a selected dataset PDXNet or PDMR. The whole-
245 exome tabs plot mean target coverage, percent target bases with greater than 20% coverage, and
246 percent duplication by data contributor. The RNA-Seq tabs plot percent usable bases, percent
247 ribosomal bases, and percent correct strand reads. The plotted metrics, along with additional QC
248 metrics are available in a table at the bottom of the page.

249 **Tools**

250 The PDXNet Portal tools section includes several Portal specific tools developed to support present
251 and future PDXNet and other independent general research activities.

252 **Workflow Cost prediction**

253 The Workflow cost prediction tool allows users to estimate the cost of processing their samples on
254 the CGC with the PDXNet workflows. This tool uses prediction models (gradient boosting trees²⁶)
255 generated from 7,000 workflow runs. The user can select either whole-exome or RNA-Seq
256 workflows and provide the number and optionally size of files to process. The calculator computes
257 the storage and computation cost for processing the user defined dataset. The estimated costs
258 assume the workflows were run on the CGC using spot instances. We expect the tool to allow
259 users to estimate data storage and computational cost for their own analyses allowing for
260 estimating grant budgets and budgeting lab expenses.

261 **PDX Minimum Information Metadata – Creation**

262 The generate metadata tab allows users to interactively generate a PDX minimum information
263 metadata sheet (PDX-MI). As described above, the PDXFinder working group developed the
264 PDX-MI as a standard for exchanging PDX information among institutions. The generate metadata
265 tab allows the user to create a PDX-MI spreadsheet by stepping through data entry dialog boxes.
266 The interface supports entry of patient information, treatment information, tumor information,
267 model, and sequencing metadata. The user downloads the spreadsheet upon data entry completion,
268 and no information is stored permanently on the PDXNet Portal site.

269 **PDX Minimum Information Metadata – Validation**

270 The validate metadata tab allows users to upload and validate a PDX-MI metadata spreadsheet.
271 The user can review uploaded contents at the bottom of the page. The validation verifies that

272 required metadata fields are present and that entries are valid. The validation feature generates a
273 summary of required fields that includes percent completed and most common data entry per field.
274 The validation feature reduces the amount of time necessary to review and check submitted PDX-
275 MI spreadsheets.

276 **Implementation**

277 The backend of the PDXNet Portal is an R-Shiny app hosted on a cloud-based server. The portal
278 uses the PDMR and PDX-MI metadata standards. The PDMR and PDX-MI standards allow us to
279 harmonize data across sources, quickly import data from the PDMR and other data sources, and
280 exchange information with other PDX related portals. We also collect additional metadata required
281 to facilitate computation on the CGC, including omics-related information. We use the Cancer
282 Therapy Evaluation Program (CTEP) disease classification to standardize disease entries although
283 we initially accepted institutionally-defined disease classification. In the cases where a standard
284 does not exist; we collect sufficient metadata required to display and process the data source. For
285 example, we take a minimalistic approach to managing tumor volume and H&E image data.
286 Several PDXNet teams are working towards the development of best practices for these data types.
287 Until these best practices are published, we will evolve these operational standards to support
288 harmonization and analysis.

289 The PDXNet Portal team updates information on the portal semi-automatically using the same
290 data model as the PDMR, allowing PDXNet to sync with PDMR model information. The PDMR
291 provides regular updates to PDXNet on PDTs model submissions to update the PDX Model's
292 page. We receive sequencing data upload updates from the PDTs and the PDMR, and we have
293 developed scripts for extracting PDXNet standardized processing results, allowing for quality
294 control information and computational metrics to be tabulated for semi-automated PDXNet Portal
295 updates. The PDXNet Portal source code will not be made publicly available for security reasons.
296 Future PDXNet Portal versions will support controlled access sign-in to provide links to controlled
297 files.

298 **Data Availability**

299 Each PDXNet Portal data tab allows users to download metadata. Data for smaller data types such
300 as tumor volume data and computed metrics (ex. HRD and TMB) can be downloaded directly
301 from the portal. For larger data types, please request data from the PDXNet Portal's Contact page.
302 We will coordinate with PDTs to make data available either directly or through dbGaP as
303 required by the PDXNet data sharing agreement.

304 **Discussion**

305 The PDXNet Portal is a vital component of the PDXNet consortium. The portal establishes a
306 mechanism for public discovery of consortium-generated resources including models, data, and
307 workflows. The portal allows researchers to examine the data, models, and metadata using
308 integrated query features. These portal capabilities facilitate cancer data discovery, a core goal of
309 the NCI Cancer Moonshot program. Additionally, the PDXNet Portal allows the consortium to
310 manage data analysis projects by clarifying which data are available, their source, their quality,
311 and their suitability for research projects and scientific questions. Within the PDXNet consortium,
312 the PDXNet Portal functions as a centralized source of information for the status of the available

313 models. The standardized sequence processing, quality control, and computation of common
314 metrics (e.g., MSI, TMB, HRD, and genetic ancestry) further enhance data analysis, model use,
315 prioritization of future models and data collection.

316 Enhancement of collaboration between researchers is a main objective of the PDXNet Portal. To
317 accomplish this, we are integrating the PDXNet Portal and PDXNet data with existing NCI, NIH,
318 and NCBI infrastructure. All data visible on the PDXNet Portal will also be available through the
319 Cancer Data Service (CDS)¹⁷ through dbGaP²⁷ access. Accessing PDXNet data on the Cancer
320 Genomics Cloud²⁸ allows users to perform sophisticated analyses utilizing cloud computing within
321 an integrated bioinformatics ecosystem. By co-locating data and analysis, as well as integrating
322 data management, this infrastructure can decrease the time required for researchers to perform
323 analyses.

324 For large consortia such as PDXNet, metadata and secondary data types are often just as important
325 as sequencing data for supporting impactful research. Examples of these additional data types
326 include high-resolution images and tumor volume/drug response data. These data extend the types
327 of problems researchers can address. We expect that the portal's image and tumor volume
328 functionality will expand as these datasets grow. Future iterations of the portal will include
329 interactive exploration across data types allowing users to address complex research problems.

330 PDX models are widely used in cancer research, but there remain challenges in standards for data
331 submission, access, and quality. The PDXNet Portal reflects PDXNet activities to implement such
332 standards not only for sequencing data but also metadata and secondary data types. Another
333 consideration requiring careful implementation is to balance data security versus ease of use. The
334 PDXNet Portal will grow with new data and features as the PDXNet consortium continues to
335 generate new models. Consequently, standardized processing and batch effects are of increasing
336 concern for downstream analyses. To ensure that researchers have confidence in the data quality,
337 we will continue to share the informative metrics computed by the standardized PDXNet quality
338 control workflows.

339 Several key features are the focus for the next iteration of the PDXNet Portal. These include tools
340 to search for commonly found genomic variants (ex. SNPs, INDELS, and copy number variations)
341 within models, diseases and genes of interest, and interactive exploration of gene expression data.
342 These tools would enable researchers to perform meaningful analyses directly from the portal and
343 more rapidly realize value from PDXNet data. Visualization and analysis of associated data,
344 including imaging and tumor volume/drug response data, will also be a focus. These data types
345 have the potential for high impact, particularly given the innovation in large scale data
346 visualization techniques in many fields.

347 Further development of links between the PDXNet Portal and NCI computational infrastructure
348 will benefit researchers as well. Moving large quantities of data is time-consuming and can be
349 expensive. Enabling researchers to perform their analysis where the data is already present lowers
350 the entry barrier into the computational analysis of PDX model data. To facilitate these links, we
351 envision users will be able to create cohorts for analysis using the PDXNet Portal and transferring
352 that selection to the Cancer Genomics Cloud or other computational platform, where they will be
353 able to easily take advantage of well-developed computational infrastructure.

354 We will extend PDXNet Portal capabilities as the size and complexity of PDXNet datasets grow.
355 These enhancements will allow the research community to quickly find and evaluate PDXNet
356 resources to supplement their research studies. We will continue to improve the PDXNet Portal
357 value by collaborating with related PDX initiatives, including the PDMR, PDXFinder, and
358 EuroPDX. Such collaborations will demonstrate how to effectively conduct studies across
359 institutions, providing examples for the broader research community in how to optimize their PDX
360 studies with respect to the public PDX models and datasets that are becoming increasingly
361 available.

362 **Acknowledgments**

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364 sequencing data generation.

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437 democratized - A new paradigm in large-scale computational research. *Cancer Research*
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439

440 **Table 1. PDXNet Development and Trial Centers (PDTC) and the PDX Data Commons
441 and Coordinating Center (PDCCC)**

PDXNet	
PDX Development and Trials Centers (PDTC)	
HCI-BCM*	Huntsman Cancer Institute and Baylor College of Medicine
MDACC	MD Anderson Cancer Center
WUSTL*	Washington University at St. Louis
WISTAR*	Wistar Institute and MD Anderson Cancer Center
BCM&	Baylor College of Medicine
UCDAVIS&	The University of California at Davis
PDX Data Commons and Coordinating Center	
JAX-SB*&	Jackson Laboratory and Seven Bridges

* NCI Cancer Therapy Evaluation Program Funding

& NCI Center to Reduce Cancer Health Disparities Funding

444 **Table 2. PDX models generated by PDX Development and Trials Centers**

	HCI-BCM	MDACC	WUSTL	Wistar	UC Davis	BCM	Totals
Breast	78	12	2	0	0	16	108
Head and Neck	0	0	2	0	0	0	2
Digestive/Gastrointestinal	0	50	44	0	3	0	97
Endocrine and Neuroendocrine	0	2	0	0	0	0	2
Musculoskeletal	0	1	4	0	0	0	5
Respiratory/Thoracic	0	30	1	0	2	0	33
Skin	0	3	2	63	0	0	68
Genitourinary	0	0	5	0	10	0	15
Gynecologic	0	3	0	0	0	0	3
Unknown Primary	0	0	0	1	0	0	1
total	78	101	60	64	15	16	334

HCI-BCM: Huntsman Cancer Institute and Baylor College of Medicine, *MDACC*: MD Anderson Cancer Center, *WUSTL*: Washington University at St. Louis, *Wistar*: The Wistar Institute, *UC Davis*: University of California Davis, *BCM*: Baylor College of Medicine

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447 **Table 3. Sequencing data files generated by PDX Development and Trial Centers**

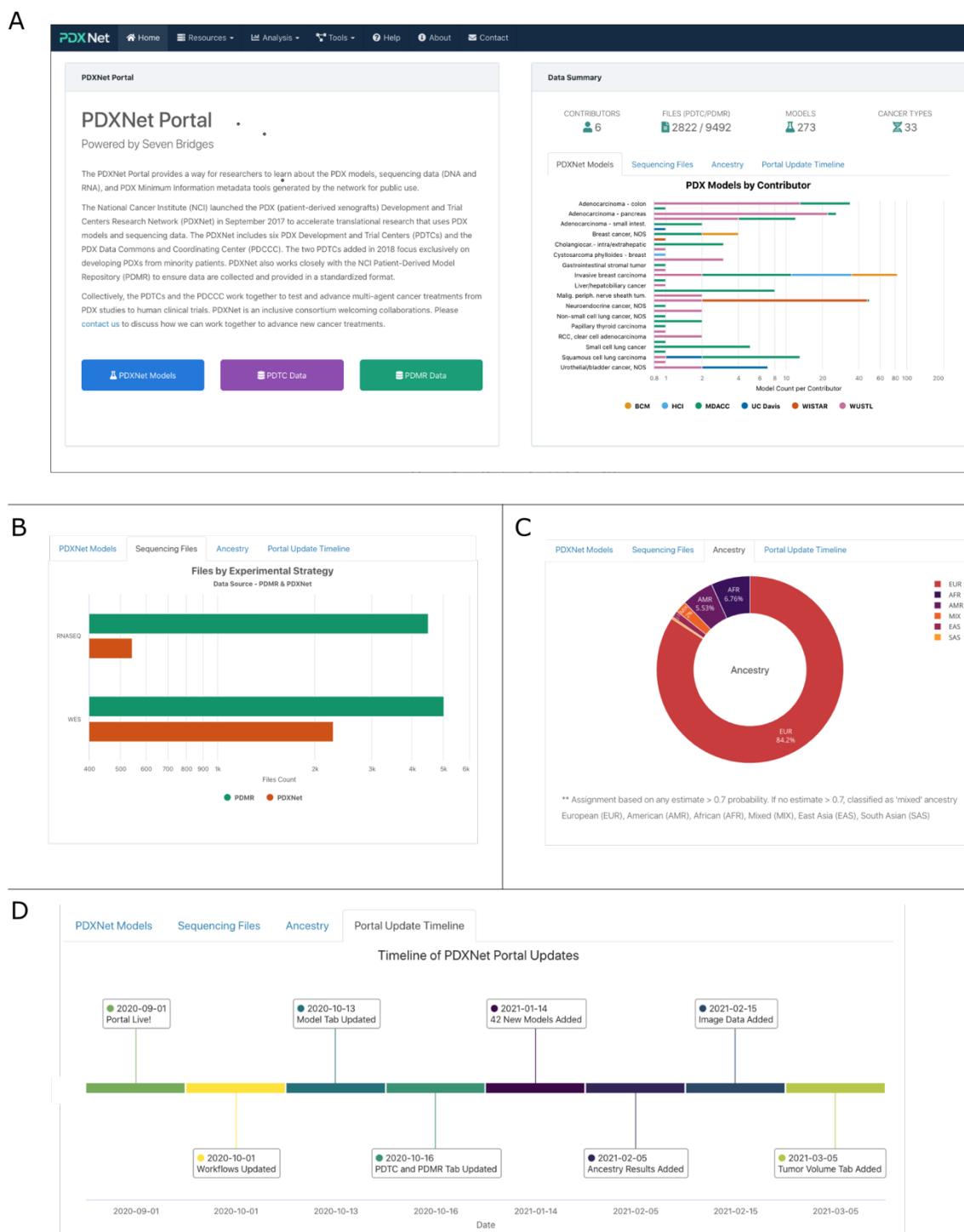
	Overall N=2822	BCM-HCI N= 1099	MDACC N=418	UC Davis N=48	WISTAR N= 382	WUSTL N= 875
Experimental Strategy n(%)						
RNA-Seq	544 (19%)	102 (9%)	6 (1%)	32 (67%)	144(38%)	260(30%)
WES	2,278 (81%)	997 (91%)	412 (99%)	16 (33%)	238(62%)	615(70%)
Disease Type, n(%)						
Bladder	100(3.5%)	2(<0.2%)	0(0%)	48(100%)	0(0%)	50(5.7%)
Blood	84(3.0%)	0(0%)	84(20%)	0(0%)	0(0%)	0(0%)
Bone	8(0.3%)	0(0%)	0(0%)	0(0%)	0(0%)	8(0.9%)
Breast	1189(42%)	985(90%)	0(0%)	0(0%)	0(0%)	204(23%)
Colon	164(5.8%)	4(0.4%)	0(0%)	0(0%)	0(0%)	160(18%)
Gastrointestinal	22(0.8%)	0(0%)	0(0%)	0(0%)	0(0%)	22(2.5%)
Head and Neck	26(0.9%)	2(<0.2%)	0(0%)	0(0%)	0(0%)	24(2.7%)
Kidney	58(2.1%)	0(0%)	0(0%)	0(0%)	0(0%)	58(6.6%)
Lung	362(13%)	0(0%)	320(77%)	0(0%)	0(0%)	42(4.8%)
Neuroendocrinial	2(<0.1%)	0(0%)	2(0.5%)	0(0%)	0(0%)	0(0%)
Ovarian	8(0.3%)	0(0%)	0(0%)	0(0%)	0(0%)	8(0.9%)
Pancreas	174(6.2%)	0(0%)	0(0%)	0(0%)	0(0%)	174(20%)
Rectum	22(0.8%)	0(0%)	0(0%)	0(0%)	0(0%)	22(2.5%)
Skin	32(1.1%)	0(0%)	0(0%)	0(0%)	0(0%)	32(3.7%)
Soft Tissue Neoplasm	56(2.0%)	0(0%)	0(0%)	0(0%)	0(0%)	56(6.4%)
Unknown	515(18%)	106(10%)	12(2.9%)	0(0%)	382(100%)	15(1.7%)
Sample Type, n(%)						
Normal	481(17%)	121(11%)	142(34%)	0(0%)	0(0%)	218(25%)
PDX	1,497(52%)	594(54%)	146(35%)	0(0%)	202(53%)	515(59%)
Tumor	884(31%)	384(35%)	130(31%)	48(100)	180(47%)	142(16%)

HCI-BCM: Huntsman Cancer Institute and Baylor College of Medicine, *MDACC*: MD Anderson Cancer Center, *WUSTL*: Washington University at St. Louis, *Wistar*: The Wistar Institute, *UC Davis*: University of California Davis, *BCM*: Baylor College of Medicine

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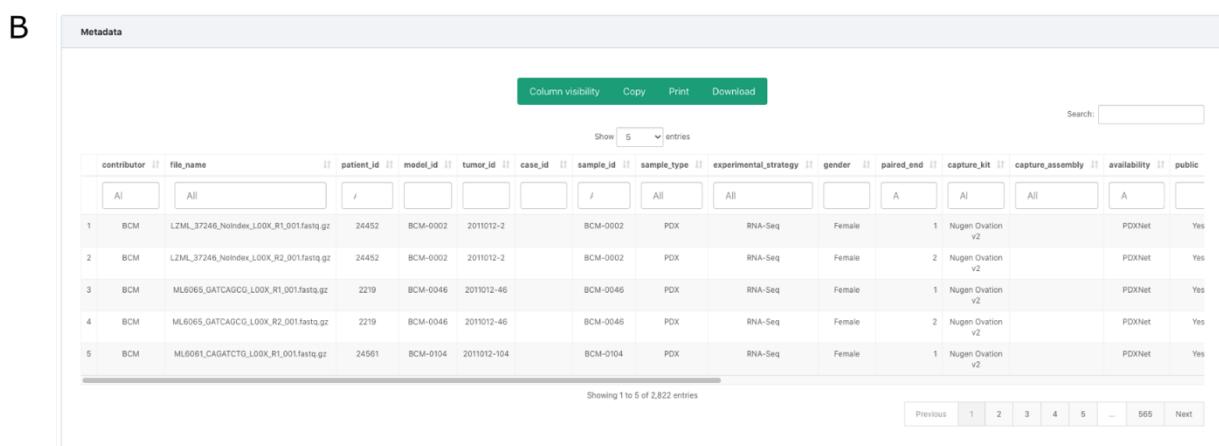
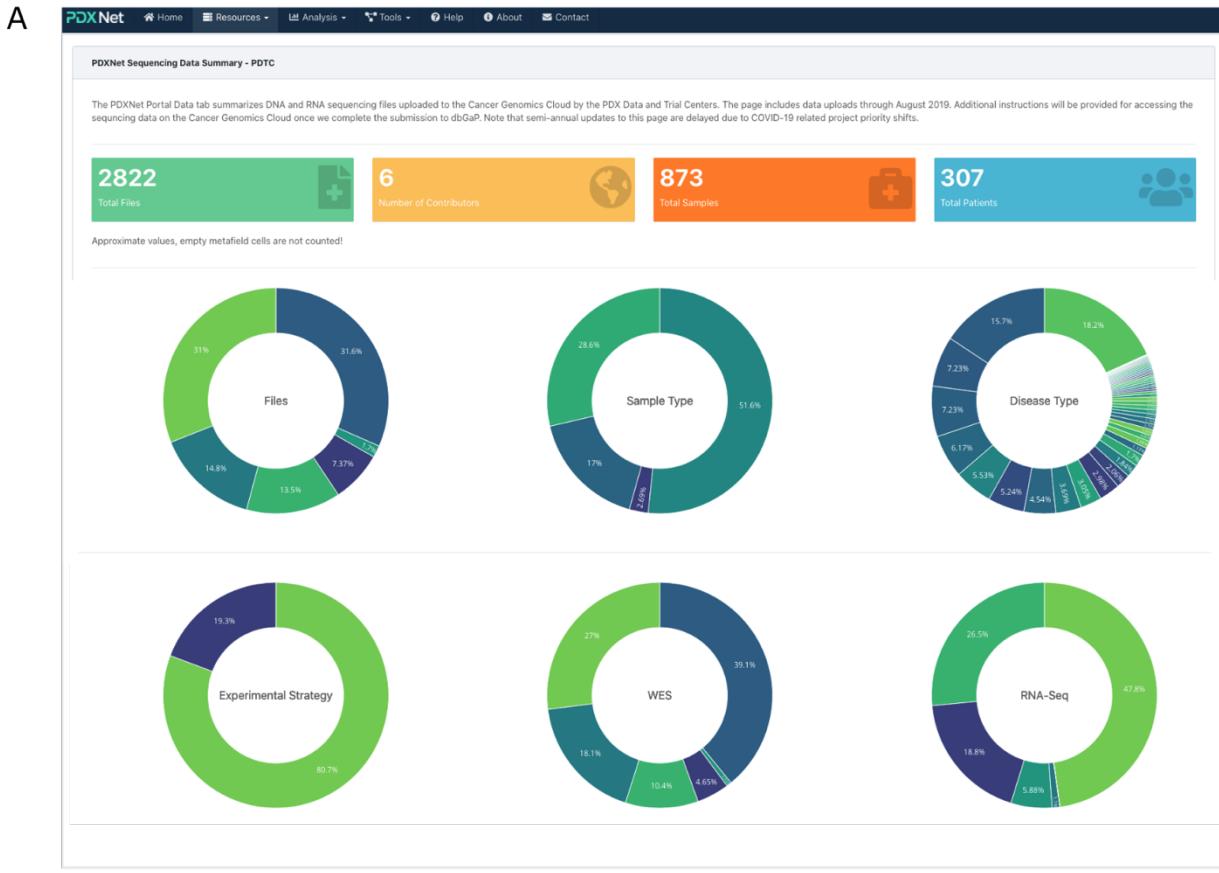
450 Figures

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453 **Figure 1. PDXNet Portal Landing Page**

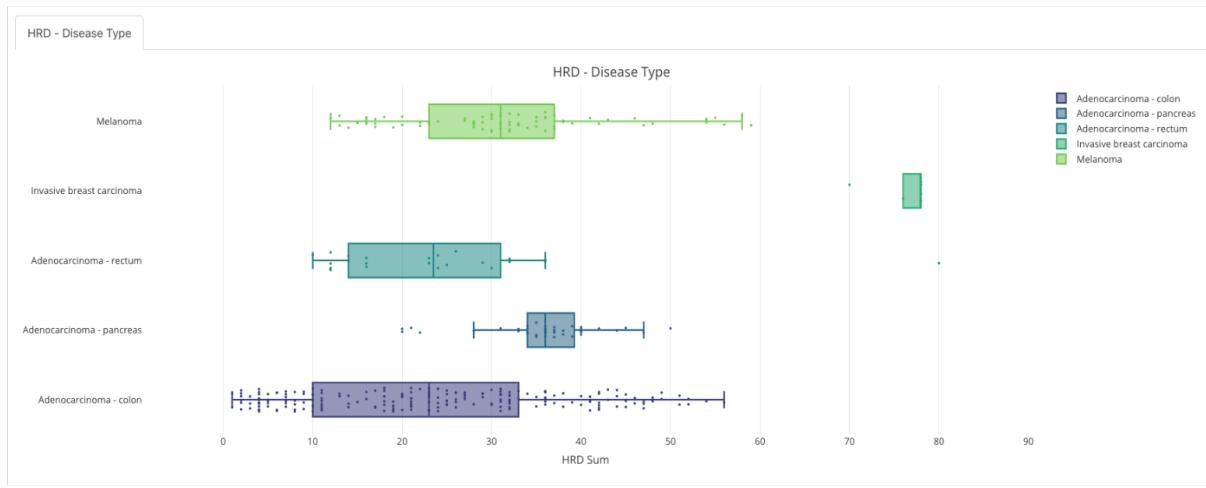


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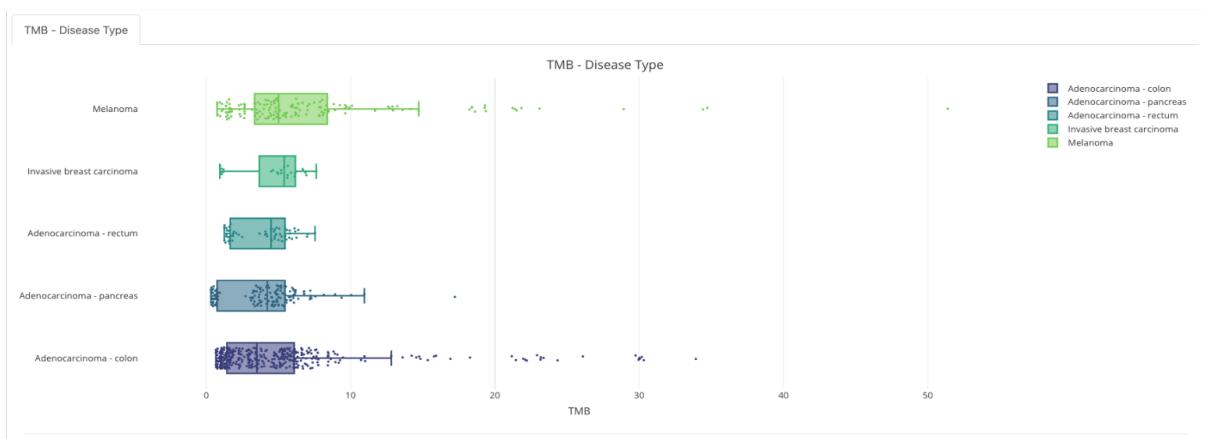
455 **Figure 2. PDXNet sequencing data page on the PDXNet portal**

456

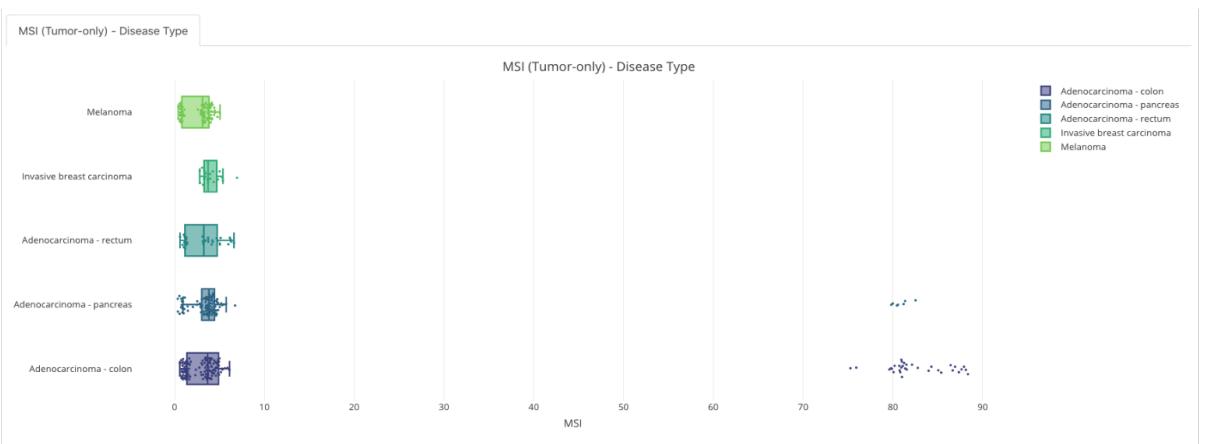
A



B

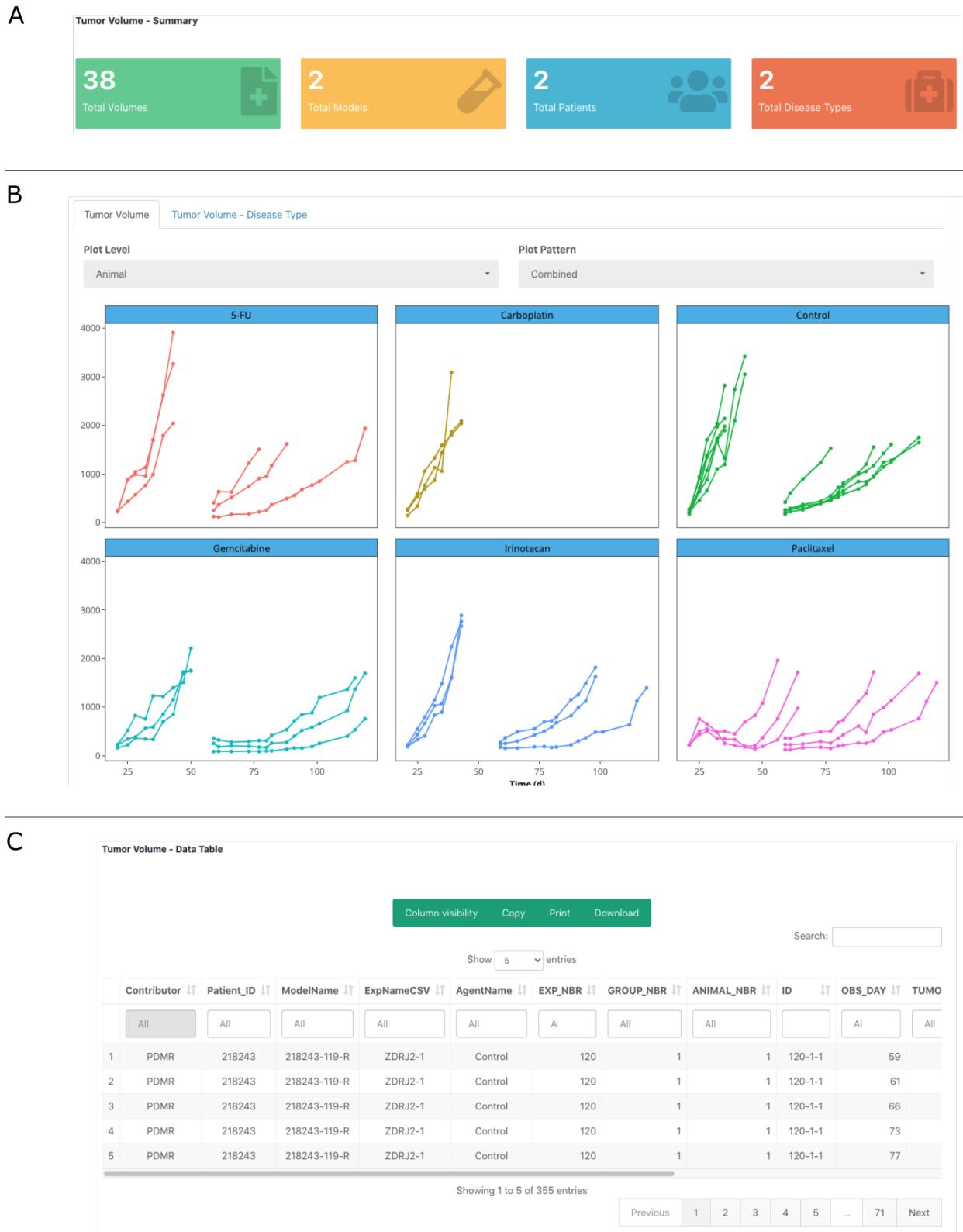


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Figure 3. Examples figures generated from the HRD-TMB-MSI page on the PDXNet Portal



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Figure 4. Tumor volume data page on the PDXNet Portal

462

463 **Figure Legend**

464 **Figure 1. PDXNet Portal Landing Page**

465 Views from the PDXNet Portal Landing Page. **(A)** The initial PDXNet Portal Landing Page. **(B)**
466 Experimental strategies (whole-exome and RNA-Seq) for the PDXNet (green) and PDMR (red)
467 sequencing datasets. **(C)** Computed ancestry in a pie chart. Ancestry is classified in the following
468 categories: European (EUR-Red), African (AFR-Blue), American (AMR-Purple), Mixed (MIX-
469 Orange), East Asian (EAS-Light Purple), South Asian (SAS-Yellow). **(D)** Major portal updates in
470 a timeline starting in September of 2019 through March 2021.

471 **Figure 2. PDXNet sequencing data page on the PDXNet Portal**

472 Components of the PDXNet sequencing data page. (A) Panel shows summary statistics including
473 number of sequencing files (green), contributors (yellow), total samples (orange), and total patients
474 (blue). Also, shown are donut plots for contributors, sample types, disease type, experimental
475 strategy, WES contributors, and RNA-Seq contributors. (B) Panel shows metadata for the PDXNet
476 sequencing data in a spreadsheet format. The interface supports searching and sorting metadata.
477 Users can copy, print, and download metadata into accessible formats.

478 **Figure 3. Examples figures generated from the HRD-TMB-MSI page on the PDXNet 479 Portal**

480 Plots generated on the PDXNet Portal HRD-TMB-MSI page **(A)** Plot of Homologous
481 Recombination Deficiency (HRD) computed from sequencing data provided by PDXNet
482 researchers. The plot shows HRD by disease type **(B)** Plot of Tumor Mutational Burden (TMB)
483 computed from sequencing data provided by PDXNet researchers. The plot shows TMB by disease
484 type. **(C)** Plot of TMB computed from sequencing data provided by PDXNet researchers, by
485 disease type.

486 **Figure 4. Tumor volume data page on the PDXNet Portal**

487 Components of the PDXNet tumor volume page. The figure shows a filtered dataset. **(A)** Panel
488 shows summary statistics including number tumor volume datasets (green), number of models in
489 the selected dataset (yellow), total number of patients (blue), and total number of diseases
490 represented (red). **(B)** Panel shows the tumor volume data organized by the treatment arm. The
491 user can control plot level (animal or treatment arm) and plot pattern (multiple or combined)

492 **Supplementary Materials**

493

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495

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529

530

531 **PDXNet Member Contribution**

532

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534 AW, BDD, BW, CJB, CXP, DAD, FMB, JD, JM, JHC, JR, GW, LCC, LD, MD, MH,
535 MSC, MTW, NM, PNR, SK, SL, TW, YAE

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538 XYW

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540 AS, CF, DAD, JG, JHC, MWL, SK

541 **Portal Integration Planning**

542 SK, MWL, DAD, JG, MR, SLS, SS, JHC

543 **Writing Manuscript**

544 SK, MWL, DAD, JG, JHC

545

546

547 **Supplementary Tables**

548 **Supplementary Table 1. Metadata associated with Hematoxylin and eosin (H&E) Images**
549 **on the PDXNet Portal.**

Hematoxylin and Eosin (H&E) Image Metadata	
Age	Percent stromal content
Cell annotation available?	Percent tumor content
Contributor	Primary cancer site
CTEP Code	Proteomics
Diagnosis Subtype	Race
Disease Type	Regional annotation available?
Engraftment site	RNA-Seq/ Exp array
Ethnicity	Sample ID
Gender	Sample Type
Histology	SNP array
Image file name	Stain
Is information of this model already in CGC?	Staining/scanning method available?
Magnification	Thumbnail
Metastatic site	Treatment
Model ID	Treatment information in patient tumor
Mouse strain	Treatment information in PDX tumor
Note	Tumor Biomarkers
Original Species	Tumor differentiation
Other pathology notes	Tumor Grade
Passage	Tumor Stage
Patient ID	WES/Mutations
Percent necrotic content	

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552 **Supplementary Table 2. Supportive interactive table options on the PDXNet portal**

**Supported Interactive
Tables and Charts**

Area Chart
Col Heatmap
Horizontal Bar Chart
Horizontal Stacked Bar Chart
Line Chart
Row Heatmap
Scatter Chart
Table
Table Bar Chart
Treemap

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557 **Supplementary Table 3. Data summary options available through interactive tables on the
558 PDXNet Portal**

Interactive Table Data Summary Options

Average	Median
Count	Minimum
Count as fraction of column	Sample variance
Count as fraction of row	Standard deviation
Count as fraction of total	Sum
Count unique values	Sum as fraction of column
First	Sum as fraction of row
Integer sum	sum as fraction of total
Last	sum over sum
List unique values	80% lower bound
maximum	80% upper bound

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561 **Supplementary Table 4. PDXNet metadata fields available on the Interactive Table**
562 **Explorer on the PDXNet Portal**

**PDXNet Metadata Fields Available on the
Interactive Table Explorer**

Access Level	File size
Availability	Gender
Capture Assembly	Investigations
Capture Kit	Is FFPE
Case id	Model id
Comments	Paired End
Contributor	Patient id
Created Date and time	Platform
Data Category	Public
Data Format	Sample ID
Data Type	Sample type
experimental strategy	Tumor id
File name	

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564

565 **Supplementary Table 5. Patient-derived model repository sequencing data processed with**
566 **standardized PDXNet workflows referenced on the PDXNet Portal**

Sample Type, n(%)	Overall	RNA-Seq	WES
	N=9492	N=4480	N=5012
Normal	520(5.5%)	0(0%)	520(10%)
Organoid	304(3.2%)	152(3.4%)	152(3.0%)
PDC	276(2.8%)	124(2.8%)	152(3.0)
PDX	7846(83%)	3930(88%)	3916(78%)
Tumor	542(5.7)	274(6.1%)	268(5.3%)
unknown	4(<0.1%)	0(0%)	4(<0.1%)

567

568 **Supplementary Table 6. Standardized PDXNet bioinformatics workflows linked to the**
569 **PDXNet Portal**

Workflow Description

RNA-Seq

Prepare Multi-sample Data

PDX RNA Expression Estimation Workflow

PDX RNA Expression Estimation Workflow (Single End)

RNA Expression Estimation Workflow Patient Tumor

RNA Expression Workflow Patient Tumor (Single End)

Whole Exome Sequence

PDX WES CNV (Xenome) Tumor-Normal Workflows

PDX WES Tumor-Normal (Xenome) with Variant Calling, CNV Estimation, TMB, MSI, and HRD Scores

PDX WES Tumor-Only (Xenome) with Variant Calling, MSI, and TMB Scores

WES Tumor-Normal with Variant Calling, CNV Estimation, TMB, MSI, and HRD Scores

WES Tumor-Only with Variant Calling, MSI, and TMB Scores

WES Tumor-Only from BAM (Variant, MSI, TMB)

WES Tumor-Normal from BAM(Variant, CNV, HRD, MSI, TMB)

SNP Array

SNP Array Tumor-Only Workflow for Illumina Infinium Omni 2.5 Exome-8 (Version 1.4) Snp Array

Quality

PDX WES Sample QC

PDX Sample QC

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571

572 **Supplementary Table 7. Summary of computed ancestry for PDXNet Models**

	Contributors				# of Patients
	HCI-BCM	MDACC	PDMR	WUSTL	
AFR	10	3	8	3	24
Adenocarcinoma - colon			4		4
Adenocarcinoma - pancreas				2	2
Adenocarcinoma - rectum			1		1
Invasive breast carcinoma	10				10
Lung Adenocarcinoma		3	2		5
Melanoma			1	1	2
AMR	18	2			20
Invasive breast carcinoma	18				18
Lung Adenocarcinoma		2			2
EAS			1		1
Adenocarcinoma - colon			1		1
EUR	8	30	158	24	220
Adenocarcinoma - colon			72	7	79
Adenocarcinoma - pancreas			24	13	37
Adenocarcinoma - rectum			14	1	15
Invasive breast carcinoma	8		10	2	20
Lung Adenocarcinoma		30	14	1	45
Melanoma			24		24
MIX	1	2	3		6
Adenocarcinoma - colon			1		1
Adenocarcinoma - pancreas			1		1
Invasive breast carcinoma	1				1
Lung Adenocarcinoma		2	1		3
# of Patients	37	37	170	27	271

HCI-BCM: Huntsman Cancer Center, MDACC: MD Anderson Cancer Center, PDMR: Patient-Derived Model Repository, WUSTL: Washington University at St. Louis

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574

575 **Supplementary Table 8. Summary of PDMR tumor volume dataset on the PDXNet portal**
576 **shown by disease type and treatment**

Disease	Control	Treatment							Total
		5-FU	Carboplatin	Erlotinib	Gemcitabine	Irinotecan	Paclitaxel	Vemurafenib	
Colon	13	10	10	7	11	11	11	7	81
Lung	13	9	10	8	10	10	10	8	78
Pancreas	12	11	1	9	11	11	11	7	82
Skin	9	7	1	3	7	6	7	3	48
Bladder	7	5	1	3	5	6	6	4	42
Head and Neck	10	5	1	4	6	6	6	3	45
Kidney	2	2		1	2	2	2	1	14
Ovarian	1	1	1		1	1	1		6
Uterine	4	4	1	1	4	4	4	1	26
Gastric	1	1	1	1	1	1	1	1	8
Soft Tissue Neoplasm	9	8	3	2	9	9	9	1	54
Endocrine	1	1	3	1	1	1	1		7
Bone	1	1	1		1		1		5
CNS	3	3	1	2	3	3	3	2	22
Rectum	1	1	1		1	1	1		6
Grand Total	87	69	36	42	73	72	74	38	524

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578

579 **Graphical User Interface Screenshots**

580 **Resources**

581

A



B

Model Submissions													
Column visibility Copy Print Download													
Show <input type="button" value="5"/> entries													
PDXSource	Contributor	ContributorPDX.ID	PDMR.Patient.ID	Gender	CTEP.SDCCode	CTEP.SDCDescription	DiagnosisSubtype	Disease.BodyLocation	Age.atDiagnosis	Date.ofDiagnosis	Has.KnownMetastaticDisease	Grade.StageInformation	Pati
1 PDXNet Consortium Members	MDACC	BB174	K42829	Female	10009951	Adenocarcinoma - colon	adenocarcinoma of sigmoid colon	Digestive/Gastrointestinal	48	42790	Yes	Stage	GII Stage c me Pari Chir Lyn
2 PDXNet Consortium Members	MDACC	BB175	K30337	Female	10009951	Adenocarcinoma - colon	adenocarcinoma	Digestive/Gastrointestinal	26	42500	Yes	Stage	GII Stage diff LC me Perit
3 PDXNet Consortium Members	MDACC	BB176	K45526	Female	10009951	Adenocarcinoma - colon	Lynch syndrome, mucinous and signet ring cell adenocarcinoma	Digestive/Gastrointestinal	41	42132	Not reported	TNM (Pathological)	GII pT1 diff LC me Live
4 PDXNet Consortium Members	MDACC	BB182	K75568	Female	10009951	Adenocarcinoma - colon	poorly differentiated mucinous and signet ring cell adenocarcinoma	Digestive/Gastrointestinal	54	42644	Yes	Stage, TNM	GII Stage LC me

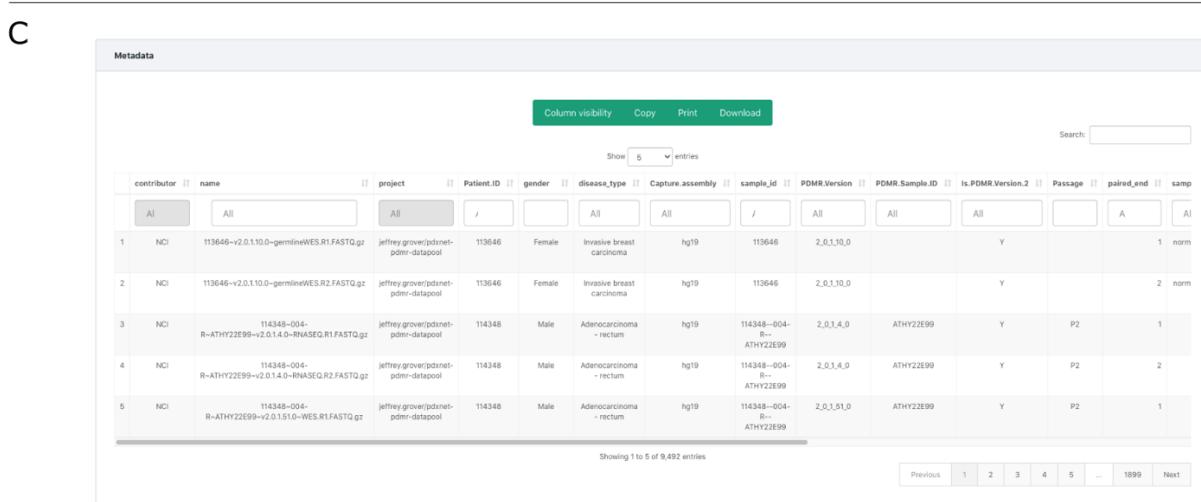
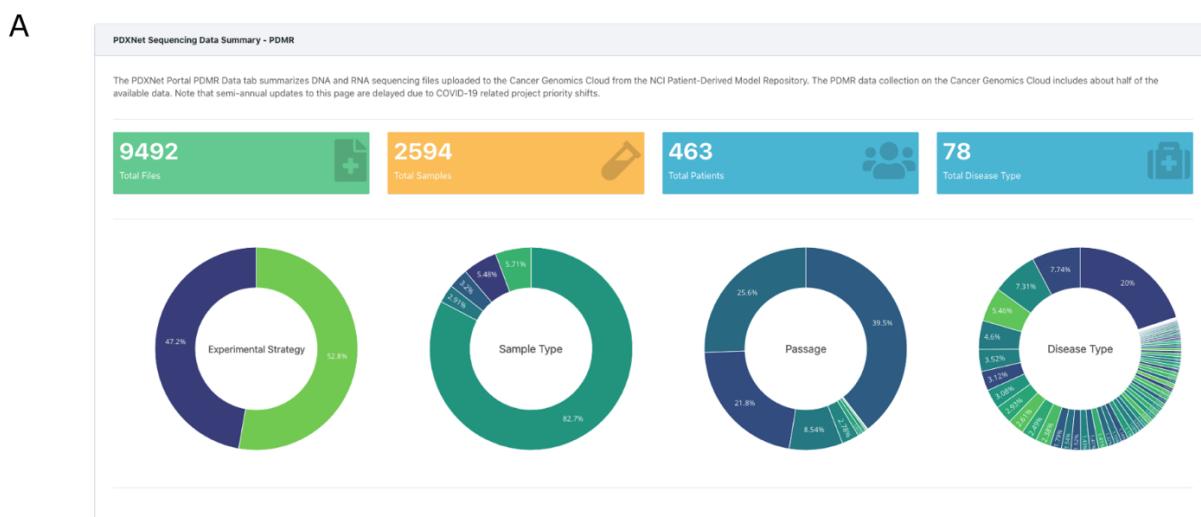
582 **Supplement Figure 1. PDX models generated by PDXNet researchers shown on the PDXNet**

583 **Portal**

584

585 Figure shows components of the PDXNet Model sequencing data page in separate panels **(A)** Panel
586 shows summary statistics including number of total models (blue), number of contributors
587 (yellow), and number of cancer types (orange). Also, shown are donut plots for contributors and
588 cancer types. Below the donut plots is a chart showing the number of models generated since
589 January 2019. **(B)** Panel shows metadata for the PDXNet PDX models in a spreadsheet format.
590 The interface supports searching and sorting metadata. Users can copy, print, and download
591 metadata into accessible formats.

592

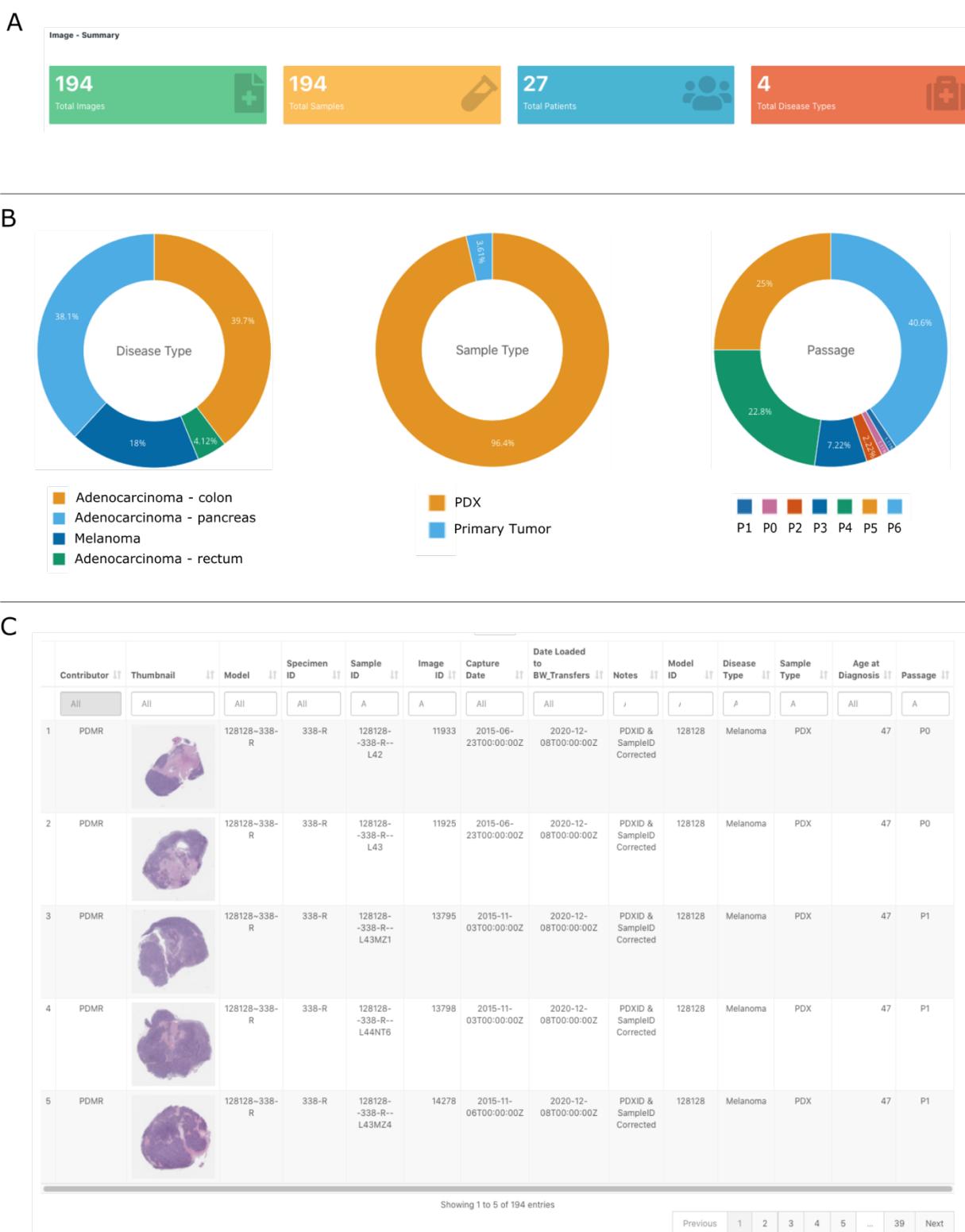


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Supplement Figure 2. Patient Derived Model Repository (PDMR) sequencing data listed on the PDXNet portal

596 Figure shows components of the PDMR sequencing data page in separate panels **(A)** Panel shows
597 summary statistics including number of sequencing files (green), contributors (yellow), total
598 samples (orange), and total patients (blue). Also, shown are donut plots for contributors, sample
599 types, disease type, experimental strategy, WES contributors, and RNA-Seq contributors. **(B)**
600 Panel shows age from PDMR patients on a bar chart. **(C)** Panel shows metadata for the PDMR
601 sequencing data in a spreadsheet format. The interface supports searching and sorting metadata.
602 Users can copy, print, and download metadata into accessible formats.
603

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Supplement Figure 3. Patient-Derived Model Repository (PDMR) image page on the PDXNet Portal

608 Figure shows components of the PDMR image data page in separate panels **(A)** Panel shows
609 summary statistics including number of images (green), contributors (yellow), total patients (blue),
610 and total disease types (red). **(B)** Panel B shows donut plots for disease type, sample type, and
611 passage. **(C)** Panel shows metadata for the PDMR image data in a spreadsheet format. The
612 interface supports searching and sorting metadata. Users can copy, print, and download metadata
613 into accessible formats.

614

Interactive Exploration

The PDXNet Portal Interactive tab allows users to interactively create tables from the list of DNA and RNA sequencing file uploaded to the Cancer Genomics Cloud by the PDX Data and Trial Centers. The page includes data uploads through August 2019.

Pivot Tables

PDML Files PDTC Files

Table Count experimental_strategy

contributor	sample_type	experimental_strategy	RNA-Seq	WES	Totals	
BCM	PDX		102	106	208	
HCI	Normal			120	120	
	PDX		386	386		
	Tumor		384	384		
MDACC	Normal		142	142		
WISTAR	PDX		6	140	146	
	Tumor			130	130	
	blood			76	76	
UC Davis	Normal		218	218		
	PDX		144	58	202	
	Tumor			104	104	
WUSTL	Normal		260	255	515	
	PDX			142	142	
	Tumor					
	Totals		544	2,278	2,822	

615

616 **Supplement Figure 4. Interactive data explorer page on the PDXNet Portal**

617 Figure shows the interactive exploration page on the PDXNet portal. The user can interactively
618 create a pivot table with either the metadata from the PDXNet sequencing data or the PDML
619 sequencing data. Constructing the table involves dragging and dropping table fields on the left side
620 to the table area (green) on the right side of the screen.
621

PDX Workflows

The PDX Coordination Center implemented standardized data processing workflows for all data uploaded by PDXNet researchers to the Cancer Genomics Cloud. The workflows are implemented in Common Workflow Language in order to facilitate portability. Links to individual workflows can be found below. Please go to the Cancer Genomics Cloud public apps gallery to see an up-to-date list of available PDX workflows.

⑤ PDX WES CNV (Xenome) Tumor-Normal Workflow

This Whole Exome Sequencing (WES) Tumor-Normal workflow identifies copy number variants from a human exome experiment by primarily using the Broad Institutes best-practices workflow for alignment and the Sequenza R package to estimate genome wide copy number.

⑤ PDX WES Tumor-Normal (Xenome) with Variant Calling, CNV estimation, TMB, MSI, and HRD scores

This Whole Exome Sequencing (WES) tumor-normal workflow first uses the Broad Institutes best-practices workflow for read alignment, and then analyzes those data in several ways. Identifies variants from a human exome experiment with GATK-4 MuTect2 for variant calling. Estimates genome wide copy number with the Sequenza R package. Calculates tumor mutation burden (TMB) score using filtered variants. Calculates microsatellite instability (MSI) status using Mantis. Calculates Homologous recombination deficiency (HRD) score using scarHRD with output from Sequenza.

⑤ PDX WES Tumor-Only (Xenome) with Variant Calling, MSI, and TMB scores

This Whole Exome Sequencing (WES) tumor-normal workflow first uses the Broad Institutes best-practices workflow for read alignment, and then analyzes those data in several ways. Identifies variants from a human exome experiment with GATK-4 MuTect2 for variant calling. Calculates microsatellite instability (MSI) status using MSIensor2. Calculates tumor mutation burden (TMB) score using filtered variants.

⑤ PDX WES Sample QC

This Whole Exome Sequencing (WES) tumor-normal workflow first uses the Broad Institutes best-practices workflow for read alignment, and outputs sample QC metric files. Note: This workflow utilizes the tool Xenome to removed mouse-reads from the raw-read data. Xenome uses host and graft reference sequences to characterize the set of all possible k-mers according to whether they belong to: only the graft (and not the host), only the host (and not the graft), both references, neither reference, and marginal assignments. This workflow uses all reads classified as human-only. Step1: SBG Split Pair by Metadata. Step2: Alignment and Target Coverage. Step3: Indexing BAM files (Samtools index BAM). Step4: Somelet Extract.

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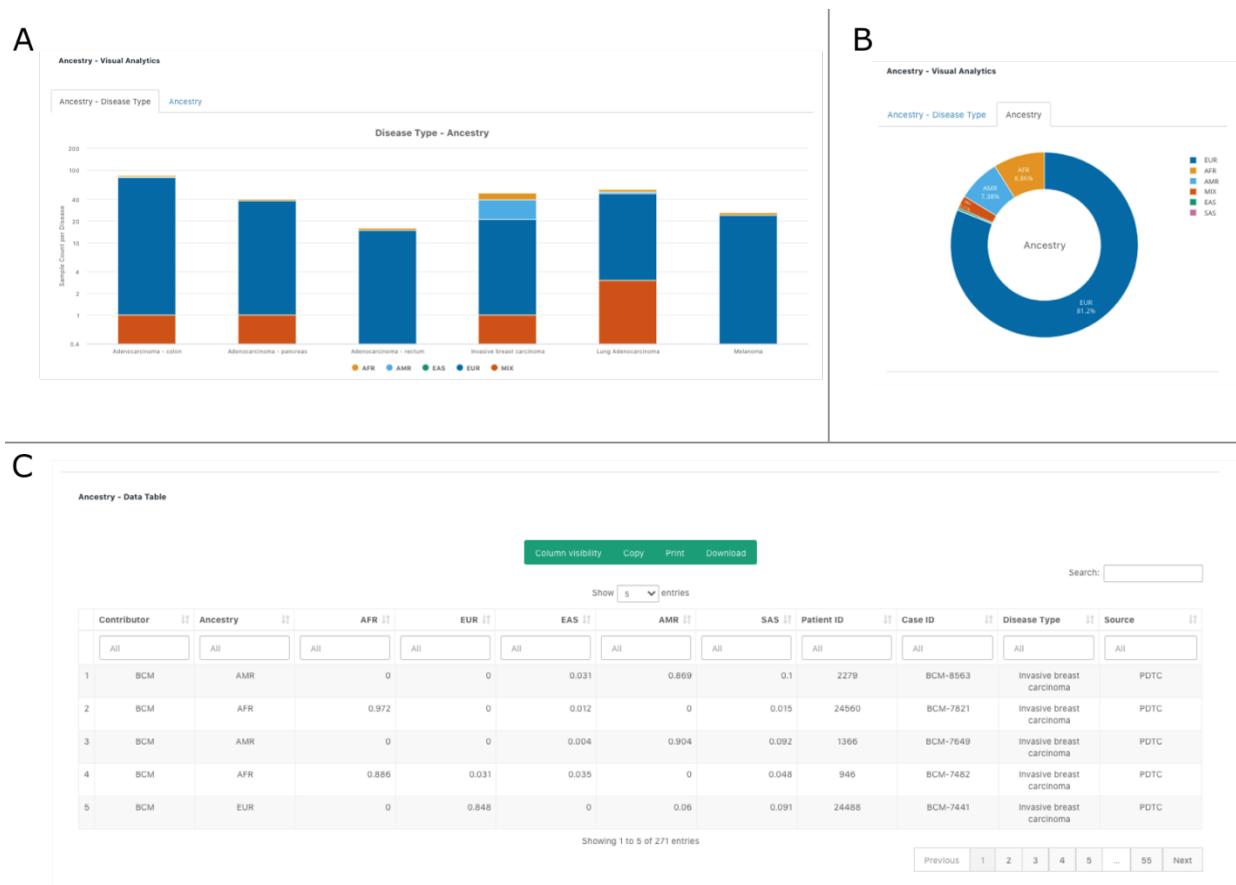
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Supplement Figure 5. Standardized PDXNet processing workflows shown on the PDXNet Portal

625 Figure shows a section of the workflow page on the PDXNet portal. The page includes brief
626 descriptions of standardized workflows created to process RNA-Seq, whole exome, and to a lesser
627 extent array data. The page includes links to comprehensive workflow documentation on the
628 Cancer Genomics Cloud Public Apps Gallery; where the workflows are made publicly available.
629

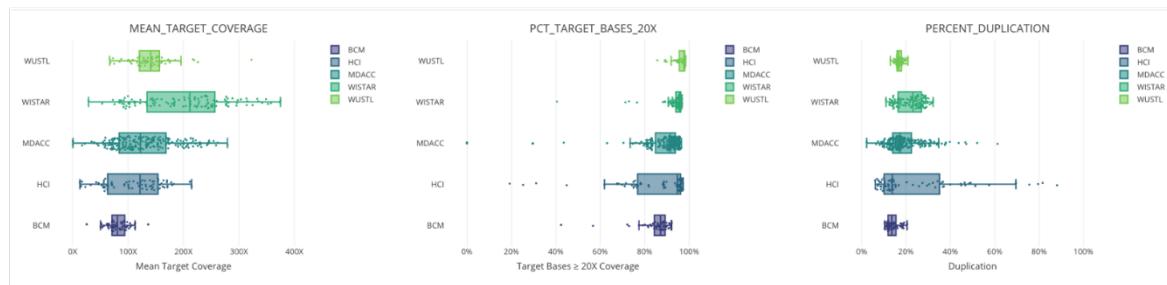


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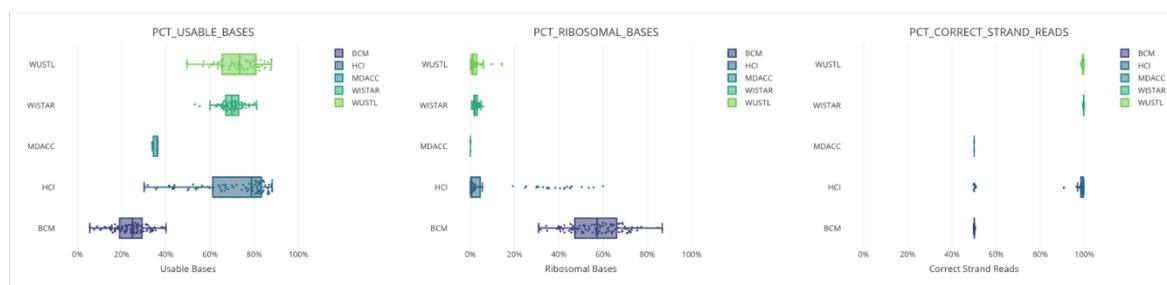
Supplement Figure 6. Ancestry information computed from sequencing data shown on the PDXNet Portal

633 Figure shows plots generated on the ancestry data page of the PDXNet portal **(A)** Panel A shows
634 a stacked bar chart with each bar corresponding to a user selected disease. Each bar shows the
635 ancestry composition of available samples by color. The ancestry algorithm classifies samples as
636 African (AFR), American (AMR), East Asian (EAS), South Asian (SAS), and Mixed (MIX). **(B)**
637 Panel shows computed ancestry in a pie chart. Ancestry is classified in the following categories:
638 European(EUR), African(AFR), American(AMR), Mixed(MIX), East Asian(EAS), South
639 Asian(SAS). **(C)** Panel shows ancestry metadata for the processed sequencing data in a spreadsheet
640 format. The interface supports searching and sorting metadata. Users can copy, print, and
641 download metadata into accessible formats.

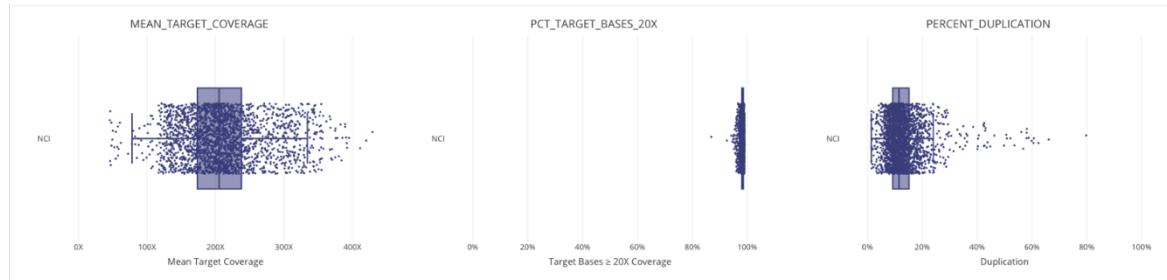
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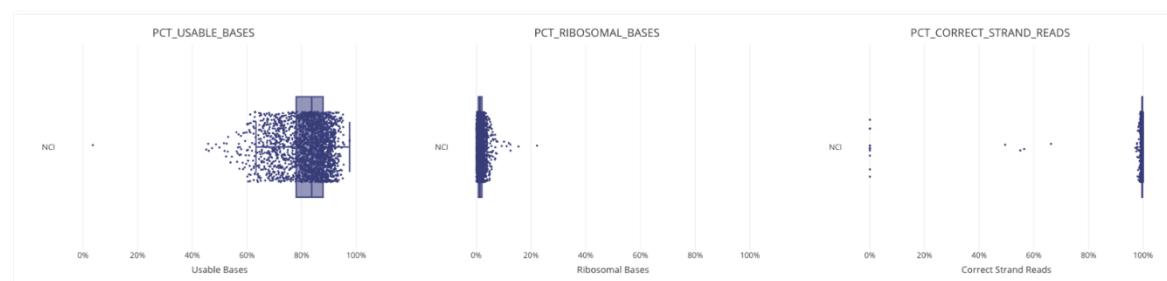
B



C



D



642

643 **Supplement Figure 7. Sequencing quality control plots examples generated on the PDXNet**
644 **Portal**

645 Figure shows sequencing data QC figures generated on the quality control page of the PDXNet
646 Portal (A) Plot shows mean target coverage, percent target coverage at 20x, and percent duplication

647 as box plots with data for each PDX Development and Trial Center presented as a different box
648 plot. (B) Plot shows percent usable basis, percent ribosomal basis, and percent correct strand reads
649 as box plots with data for each PDX Development and Trial Center presented as a different box
650 plot. (C) Plot shows mean target coverage, percent target coverage at 20x, and percent duplication
651 as box plots generated from PDMR data. (D) Plot shows percent usable basis, percent ribosomal
652 basis, and percent correct strand reads as box plots generated from PDMR data.
653

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