cBioPortal Beta Manual Test Cases

PRODUCTION URL: <http://www.cbioportal.org/>

BETA URL: <http://www.cbioportal.org/beta/>

**Quick Tests:**

|  |  |  |
| --- | --- | --- |
|  | Home Page: [[PRODUCTION](http://www.cbioportal.org)] [[BETA](http://www.cbioportal.org/beta)] | Verify query component renders. |
|  | Home Page: [[PRODUCTION](http://www.cbioportal.org)] [[BETA](http://www.cbioportal.org/beta)] | Verify Cancer Studies Plot in right nav renders |
|  | Basic Query: GBM TCGA Provisional, EGFR MDM2 MDM4 → Submit | Click on all tabs; verify that they render. |
|  | Modify Query, de-select “Mutations” | Click on all tabs, verify that they render and only copy number data is shown |
|  | Click Modify Query again | Verify that Mutations is still de-selected |
|  | Basic Query with OQL: TCGA Colorectal Cancer Nature, PIK3CA PTEN IGF2 - [[PRODUCTION](http://www.cbioportal.org/index.do?session_id=5a61ffea498eb8b3d563de36&show_samples=false&)] [[BETA](http://www.cbioportal.org/beta/index.do?session_id=5a61ffea498eb8b3d563de36&show_samples=false&)] | Click on all tabs, verify that they render. Verify that over-expression of IGF2 shows up in OncoPrint |
|  | Click Modify Query | Confirm all settings from query are present |
|  | Basic Pan Cancer Query: tcga provisional, EGFR | Click on all tabs, verify that they render |
|  | Modify Query, change Data Type Priority to “Only CNA” | Click on all tabs, verify that they render and only CNA data is shown |
|  | Click Modify Query again | Verify that “Only CNA” is still selected |
|  | Study View: [[PRODUCTION](http://www.cbioportal.org/study?id=gbm_tcga#summary)] [[BETA](http://www.cbioportal.org/beta/study?id=gbm_tcga#summary)] | Verify that page renders |
|  | Select Male patients and Query PTEN EGFR | Click on all tabs; verify that they render. |
|  | Click Modify Query | Verify the right study and samples were selected |
|  | Patient View: [[PRODUCTION](http://www.cbioportal.org/case.do#/patient?studyId=ucec_tcga_pub&caseId=TCGA-BK-A0CC)] [[BETA](http://www.cbioportal.org/beta/case.do#/patient?studyId=ucec_tcga_pub&caseId=TCGA-BK-A0CC)] | Verify that page renders |

**More Detailed Checks:**

|  |  |  |
| --- | --- | --- |
| [X] | Action | Expected Behavior |
|  | **Query page** |  |
|  | Go to home page | * Query interface appears * (169) studies shows up * First category is PanCancer Studies including MSK-IMPACT * When you mouse over the *Submit Query* button, you should see a slash icon |
|  | Search *tcga provisional* | * Only TCGA provisional studies shows up |
|  | Select all all listed studies | * All TCGA provisional studies selected |
|  | Type *EGFR* | * Submit *Query* is enabled |
|  | **Multi-study query** |  |
|  | Click *Submit Query* | * Multi-study results page shows up * 6 tabs: *OncoPrint, Cancer Types Summary, Expression, Mutations, Download, and Bookmark* * By default, for single gene and multi-study query, *Cancer Types Summary* is active * Click on each tab and make sure every tab loads up without error |
|  | Check header | Confirm header text exists and values are correct:  - “Modify Query” button  - “This combined study contains samples from 32 studies”  - “Gene Set / Pathway is altered in 531 (6.7%) of queried samples” |
|  | Hovering on the info icon | - Hovering on the info icon at the top should show all studies listed |
|  | Click a study name | - New tab should open with study view for the selected study |
|  | **Cancer Types Summary** | * Barchart of alteration frequency per study |
|  | Click Cancer Type Detailed | * Barchart of alteration frequency per cancer type detailed |
|  | Click *Cancer Type* | * Barchart of alteration frequency per cancer type |
|  | Hover over bars in chart | - Pop-up with detailed information should appear. Confirm that numbers are consistent with the y-axis |
|  | Click Customize | * Customize menu shows up |
|  | * Type 100 in the *Min. # of Total cases* text field and enter | * Cancer types with 99 or fewer samples are hidden |
|  | * Slide *Min. % of Altered cases* to 5% | * Cancer types with alteration freq <5% are hidden |
|  | * Switch *Y-Axis Value* to *Absolute Counts* | * Absolute samples counts show up in y-axis; *Min. % of Altered cases cases* will be changed to *Min. # of Altered cases* and reset; *Min. # of Total cases* should remain |
|  | * Switch *Sort X Axis By* to *Alphabetically* | * Bars are sorted alphabetically by cancer type; neither slides should be reset. |
|  | * Uncheck *Show Genomic Alteration Types* | * All bars will be gray; legend is hidden |
|  | * Check *Show Genomic Alteration Types* | * All bars will be separated by alteration types; legend shows up |
|  | Click Customize again | - Customize menu disappears |
|  | Click Customize again, then use “X” to close customize menu | - Customize menu disappears |
|  | Click PNG button to download plot | - Downloaded plot should look identical to plot on website, including any customizations |
|  | Click SVG button to download plot | - Downloaded plot should look identical to plot on website, including any customizations  - Make sure SVG can be opened by Adobe Illustrator |
|  | Try the same customizations as when testing the customization menu and download those plots | - Downloaded plot should look identical to plot on website, including any customizations |
|  | **Modify Query** |  |
|  | Click **Modify Query** | The query form shows with the same query parameters selected |
|  | Add “ERBB2 ERBB3” in addition to EGFR and submit query | OncoPrint tab shows by default. Mutual Exclusivity Tab is now present. |
|  | **OncoPrint** |  |
|  | Click OncoPrint tab | * Showing “Loading Oncoprint data” * In a few seconds, OncoPrint shows up * Samples are ordered by alteration in EGFR first, and then ERBB2, and then ERBB3 * Alteration frequency: EGFR - 7%, ERBB2 - 6%, ERBB3 - 3% * The following alterations should exist      * *Study of origin* track should display and ordered alphabetically for the same alterations * Genetic Alteration legend show first and Study of origin * Heatmap menu should not show for multi-study queries |
|  | Add clinical tracks: *Mutation spectrum, Total mutations, Cancer type* | * Three clinical tracks show up |
|  | Hover over each track name | * Description of clinical track appears |
|  | Click the menu after ERBB2 and *move up* | * OncoPrint is re-ordered by ERBB2 first |
|  | Click the menu after *Cancer Type* track and *Sort by a-Z*, | * OncoPrint is ordered by Cancer Type alphabetically * within each cancer type, ordered by gene alterations |
|  | Click *Don’t sort track* | * Return to previous order |
|  | Click the menu after *Total mutations* track and *Sort by Z-a* | * OncoPrint is ordered by Total mutations descendantly |
|  | Click *Don’t sort track* | * Return to previous order |
|  | Go to menu -> Sort, check “Sort by case id (alphabetically)” | * OncoPrint is ordered by case id alphabetically |
|  | Check “Sort by data” | * Return to the previous order |
|  | Go to menu -> Mutation Color, check “cBioPortal>=10” and change 10 to 1 and enter | * All mutations will become putative driver |
|  | - Uncheck “cBioPortal >= 1” | * Return to previous colors after unchecking |
|  | - Click Hide VUS and then uncheck | * VUS hidden after Hide VUS |
|  | - Uncheck “Type”, and then recheck | - All mutations are listed as “Mutation” rather than missense/truncating/etc |
|  | - Uncheck “Putative drivers based on”, and then recheck | - There is no distinction for mutations between “putative driver” and “unknown significance” |
|  | Go to menu -> View and check/uncheck all boxes | * Behaves as expected |
|  | Test Download | * Files downloaded as expected |
|  | Test zooming | * Zooming as expected |
|  | Test minimap | * Minimap as expected |
|  | Hover over many samples/patients | - Pop-up should appear with appropriate information, properly formatted |
|  | While hovering, click on patient/sample ID | - Patient/sample view should open in a new tab (depending on if OncoPrint is showing data by patient or sample) |
|  | **Mutual Exclusivity** |  |
|  | Click Mutual Exclusivity tab | - Table should appear with all pairwise combinations of genes, sorted by p-Value. Above the table is a summary sentence. |
|  | Uncheck “Mutual exclusivity”. Then recheck. | - Nothing changes since in this query all gene pairs are co-occuring |
|  | Uncheck “Co-occurence”. Then recheck | - The table is empty |
|  | Check “Significant only”. Then uncheck. | - EGFR/ERBB2 row disappears, ERBB2/ERBB3 & EGFR/ERBB3 remain |
|  | Click on “Log Odds Ratio” column header | - Table sorts by Log Odds Ratio |
|  | Hover over all column headers | - Pop-up should appear |
|  | Click “Columns”, de-select a column | - Column should disappear from table |
|  | Click “Copy” button | - Try pasting into a document. Should paste with all data columns in the same sort order as on the site |
|  | Click “Download” button | - Open file, should have all data columns in the same sort order as on the site |
|  | **Expression** |  |
|  | Click Expression tab | * Each provisional study has a boxplot + scatter plot * The first gene EGFR is selected * RNA Seq V2 is selected * Sorted by Cancer Study and * “Log Scale” is checked and used in plot * “Show Mutations” is checked and mutations shown in plot * Samples are rendered based on different types of mutations as shown in legend * Y-axis label says “EGFR Expression RNA Seq V2 (log)” * X-axis is sorted in alphabetical order |
|  | Switch “Sort By” to “Median” | * X-axis is ordered by median expression per study |
|  | Uncheck “Log Scale” | - Data is no longer log-scaled  - Y-axis no longer includes “(log)” |
|  | Uncheck “Show Mutations” | * All samples are in one color and no more legend |
|  | Download PDF and SVG | * The downloaded files are exact the same as in plot |
|  | Download Data | * The downloaded file has the following columns: Sample Id, Cancer Study, Profile Name, Gene, Mutation, Value |
|  | Click “Select Studies” | - All studies should be selected |
|  | Toggle “Profile” to “RNA Seq” | - Plot updates to show AML & Stomach studies only  - Y-axis updates to “RNA Seq (log)” |
|  | Select gene *ERBB2* | * Plots for ERBB2 is loaded * Y-axis updates to say “ERBB2” rather than “EGFR” |
|  | **Mutations** |  |
|  | Click Mutations tab | - All three genes appear as options at the top, with EGFR selected  - Lollipop plot appears below that, with gene information & # of mutations by type to the right  - Mutations table loads, sorted by Annotation column |
|  | Hover over A289 in lollipop plot | - Tooltip should appear with “26 mutations AA Change: A289D/I/N/T/V” |
|  | Click on A289 in lollipop plot | - Mutations table below should filter to only show the 26 A289 mutations  - The selected lollipop should have an enlarged circle on top |
|  | Click “here” to reset all filters | - Mutations table shows all mutations |
|  | Click on “19 Truncating” to the right of the lollipop plot | - Lollipop plot should only show truncating lollipops (black)  - Mutations table should only list the 19 truncating mutations |
|  | Click “here” to reset all filters | - Lollipop plot & table show all mutations again |
|  | Use slider to change y-axis limit to 5 | - Lollipop plot y-axis changes, top value is now >=5 and many lollipops max out at that value |
|  | Use box to enter 26 as the new y-axis max | - Lollipop plot y-axis goes to 26 |
|  | Click SVG & PDF buttons | - Downloads should look exactly the same |
|  | Customize plot in some way (e.g. select Truncating mutations), then download again | - Downloads should reflect the customization |
|  | Click Legend button | - Legend appears |
|  | Click Legend button again | - Legend disappears |
|  | Hover over a domain | - Tooltip appears with description of domain |
|  | Click “PFAM” link in tooltip | - New tab opens to PFAM page for domain |
|  | Click “Mutation Aligner” link in tooltip | - New tab opens to MutationAligner page for domain |
|  | Click UniProt link | - New tab opens to UniProt page for EGFR |
|  | Click Transcript link | - New tab opens to ensembl page for EGFR transcript |
|  | Hover over (i) after “Somatic Mutation Frequency: 3.2%” | - Tooltip appears |
|  | Click “View 3D Structure” | - 3D Structure appears |
|  | Pan/zoom/rotate structure, click buttons, etc | - Verify appropriate responses |
|  | Test expand, minimize and close buttons | - Window expands, minimizes and closes appropriately |
|  | View Mutations table | - Above table should be “305 Mutations (page 1 of 13)  - Visible columns should be: *Study, Sample ID, Cancer Type, Protein Change, Annotation, Mutation Type, Copy #, COSMIC, Allele Freq (T), # Mut in Sample*  - Text below table should be “Showing 1-25 of 305 Mutations”  - Left arrow should be greyed out with a slash icon when you hover  - Show more and right arrow should be clickable |
|  | Click “Show more” twice | - Table should 50 and then 100 mutations |
|  | Click right arrow three times | - Mutations table updates  - Right arrow is greyed out when there are no more mutations |
|  | Click “Reset” | - Table shows 25 mutations again |
|  | Click link in Study column | - New tab opens to study view for the selected study |
|  | Click link in Sample ID column | - New tab opens to patient view for selected sample |
|  | Hover over OncoKB icon | - OncoKB tooltip appears for the correct mutation |
|  | - Click “Levels” | - Information about OncoKB levels appears |
|  | - Click “OncoKB” | - New tab opens to OncoKB page for the gene |
|  | - Click “Biological Effect” | - Content changes to references |
|  | - Click “Feedback” | - Feedback form appears |
|  | Hover over CIViC icon | - CIViC tooltip appears for the correct mutation |
|  | - Click “EGFR” | - New tab opens to CIViC page for EGFR |
|  | - Click on mutation | - New tab opens to CIViC content for mutation |
|  | Hover over MyCancerGenome icon | - Tooltip appears with link to MyCancerGenome |
|  | - Click link | - New tab opens to MyCancerGenome for the appropriate mutation/cancer type |
|  | Hover over hotspot icon | - Tooltip appears with description of hotspot analysis |
|  | - Click link to paper | - New tab opens to PubMed page for Chang et al |
|  | - Click link to website | - New tab opens to cancerhotspots.org |
|  | Click on column header to sort | - Verify that mutations sort according to the data in the column you selected |
|  | Click “Columns”, add “Functional Impact” column | - Verify that data loads |
|  | Hover over Functional Impact header & values, click on links | - Verify that tooltips appear and links work |
|  | Type “lung” into search box | -Verify that table & lollipop plot update. L858R should be the more frequent mutation now. |
|  | Hover over L858R in lollipop plot | - L858R rows in mutations table should be highlighted |
|  | Click “copy” button, paste into excel | - Verify data pastes properly formatted |
|  | Click “download” button | - Open, verify data is properly formatted |
|  | **Download** |  |
|  | Click Download tab | The following sections should appear in order, with content  - “The following are downloadable data files (click to download)” followed by links  - “Contents below can be copied and pasted into Excel”  - “Frequency of Gene Alteration”  - “Type of Genetic alterations across all cases”  - “Cases affected”  - “Case matrix” |
|  | Click all links | Verify that files download and are properly formatted |
|  | Look at “Frequency of Gene Alteration” | - Should look like this: |
|  | Look at “Type of Genetic alterations across all cases” | - Should look like this: |
|  | Look at “Cases affected” | - Should look like this: |
|  | Look at “Case matrix” | - Should look like this: |
|  | **Bookmark** |  |
|  | Click on Bookmark tab | - Should look like this: |
|  | Click each link | - Verify that links work |
|  |  |  |
|  |  |  |
|  | **Single-study query** |  |
|  | Modify Query -> Deselect All studies -> Select Breast TCGA provisional and submit query | * OncoPrint show up with other tabs: *Cancer Types Summary, Mutual Exclusivity, Plots, Mutations, Co-Expression, Enrichments, Survival, Network, CN Segments, Download, Bookmark* |
|  | **OncoPrint** |  |
|  | Click OncoPrint tab | * Showing “Loading Oncoprint data” * In a few seconds, OncoPrint shows up * Samples are ordered by alteration in EGFR first, and then ERBB2, and then ERBB3 * Alteration frequency: EGFR - 2.7%, ERBB2 - 14%, ERBB3 - 2% * The following alterations should exist      * Heatmap menu should be present |
|  | Add clinical tracks: *Mutation spectrum, Total mutations, Cancer Type Detailed*  *-* Hover over each track name | * Three clinical tracks show up * Description of clinical track appears |
|  | Click the menu after ERBB2 and *move up*  - Click and drag on ERBB2 to put it back where it was | * OncoPrint is re-ordered by ERBB2 first   - OncoPrint is re-ordered by EGFR first |
|  | Click the menu after *Cancer Type Detailed* track and *Sort by a-Z*,  Then click *Don’t sort track* | * OncoPrint is ordered by Cancer Type alphabetically * within each cancer type, ordered by gene alterations * Return to previous order after click *Don’t sort track* |
|  | Click the menu after *Total mutations* track and *Sort by Z-a*,  Then click *Don’t sort track* | * OncoPrint is ordered by Total mutations descendantly * Return to previous order after click Don’t sort track |
|  | Go to menu -> Sort, check “Sort by case id (alphabetically)”  - Then check “Sort by data” | * OncoPrint is ordered by case id alphabetically * Return to the previous order |
|  | Go to menu -> Mutation Color, check “cBioPortal>=10” and change 10 to 1 and enter  - Uncheck “cBioPortal >= 1”  - Click Hide VUS and then uncheck  - Uncheck “Type”, and then recheck  - Uncheck “Putative drivers based on”, and then recheck | * All mutations will become putative driver * Return to previous colors after unchecking * VUS hidden after Hide VUS   - All mutations are listed as “Mutation” rather than missense/truncating/etc  - There is no distinction for mutations between “putative driver” and “unknown significance” |
|  | Go to menu -> View and check/uncheck all boxes | * Behaves as expected |
|  | Test Download | * Files downloaded as expected |
|  | Test zooming | * Zooming as expected |
|  | Test minimap | * Minimap as expected |
|  | Hover over many samples/patients  - Click on patient/sample ID | - Pop-up should appear with appropriate information, properly formatted  - Patient/sample view should open in a new tab (depending on if OncoPrint is showing data by patient or sample) |
|  | **Cancer Types Summary** |  |
|  |  |  |
|  | **Mutual Exclusivity** |  |
|  |  |  |
|  | **Plots** |  |
|  |  |  |
|  | **Mutations** |  |
|  |  |  |
|  | **Co-Expression** |  |
|  |  |  |
|  | **Enrichments** |  |
|  |  |  |
|  | **Survival** |  |
|  | Click on the Survival tab | * Both overall and disease free survival KM plots should show |
|  | Mouse over on + | * Tooltip show up: patient id, survival estimate, time of last observation |
|  | Mouse over on drop | * Tooltip show up: patient id, survival estimate, time of death / replaps |
|  | Click on SVG, PNG, Data | * Download working as expected |
|  | **Network** |  |
|  |  |  |
|  | **CN Segments** |  |
|  |  |  |
|  | **Download** |  |
|  |  |  |
|  | **OQL** |  |
|  |  |  |
|  | **Patient View** |  |
|  |  |  |
|  | **Study View** |  |
|  |  |  |
|  |  |  |