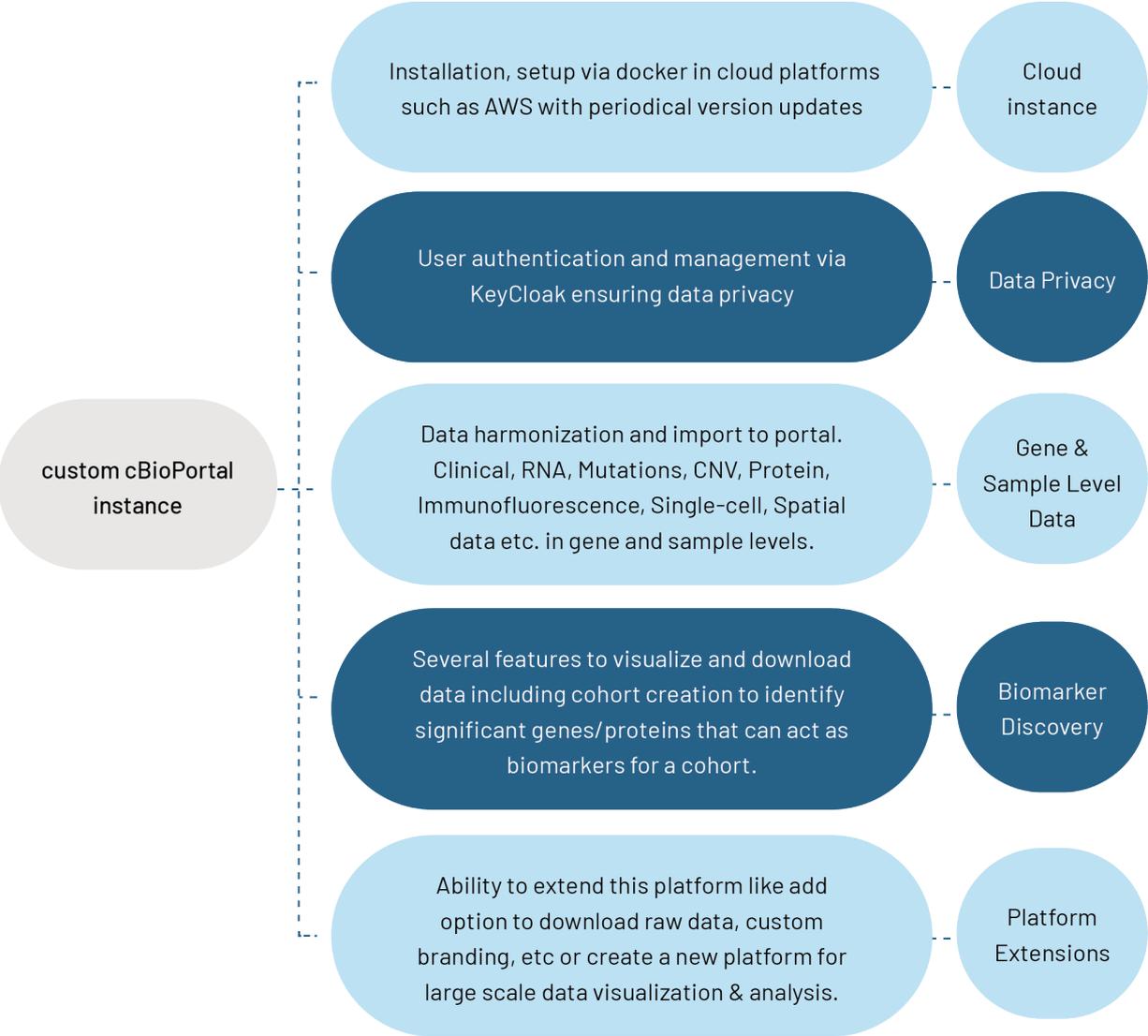


# Visualization and Analysis of Large Scale Genomics Data:

End-to-End solutions with customizations  
using cBioPortal

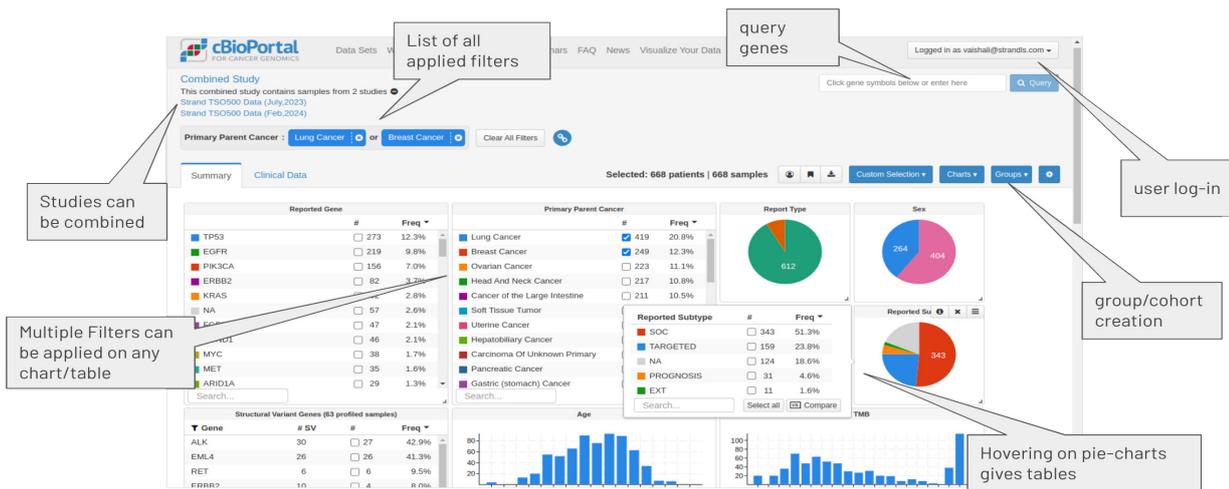


# cBioPortal Capabilities and Extensions



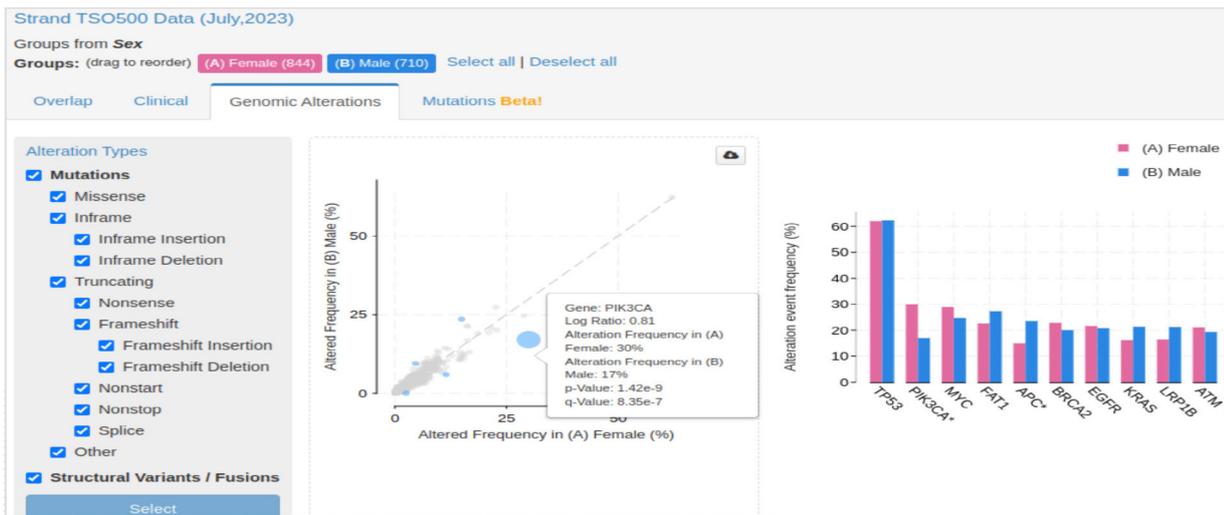
Strand has collaborated with organizations to set up, harmonize, and import genomics data into a custom cBioPortal instance and also possesses the capabilities to create a new platform tailored to specific needs.

## Study Summary View



A glimpse of the study summary view featuring Strand's TSO500 data from over 2000 patients.

## cBioPortal: Differential Genomic Alterations View



Cohort creation and comparison of male and female samples in the TSO500 dataset.

- All alteration types present in the data are selected. A specific type can also be selected.
- The scatter plot compares the alternate allele frequencies, with blue dots representing significant genes/ biomarkers.
- The bar chart displays the top 10 genes with the highest alternate allele frequencies in the selected cohorts.

## cBioPortal: Differential Genomic Alterations View

Gene	Cytoband	(A) Female	(B) Male	Co-occurrence Pattern	Log2 Ratio	p-Value	q-Value	Enriched in
PIK3CA	3q26.32	253 (29.98%)	121 (17.04%)		0.81	1.42e-9	8.35e-7	(A) Female
VTCN1	1p13.1-p12	21 (2.49%)	0 (0.00%)		>10	2.414e-6	7.097e-4	(A) Female
APC	5q22.2	126 (14.93%)	167 (23.52%)		-0.66	1.106e-5	2.167e-3	(B) Male
CCNE1	19q12	97 (11.49%)	42 (5.92%)		0.96	7.137e-5	0.0105	(A) Female
FGFR4	5q35.2	39 (4.62%)	67 (9.44%)		-1.03	1.311e-4	0.0154	(B) Male
ATRX	Xq21.1	57 (6.75%)	22 (3.10%)		1.12	6.662e-4	0.0653	(A) Female
PTPRS	19p13.3	34 (4.03%)	55 (7.75%)		-0.94	1.221e-3	0.0912	(B) Male

- The scatter plot and bar charts show the summarized view, and a detailed view can be seen in the Alterations table.
- Option to filter on 'Significant only' retains genes with a Benjamini-Hochberg corrected q-value of less than 0.01.
- Cohort comparisons to get the differential view are applicable to other data types as well, such as clinical, RNA expression, protein expression, copy number, methylation, etc.

## cBioPortal: Querying genes - OncoPrint view



- OncoPrint enables the visualization of the type of alterations present in the samples for the queried genes.
- For example, in this image, the three top-reported genes for lung cancer samples have been queried.
- Any type of clinical attributes, such as age, tumor content percentage, etc., can be added to this view to observe associated trends.

## cBioPortal: Querying genes - Mutations (Lollipop) view



- The protein change and the location of the mutation in the queried gene's protein structure, along with annotations from different sources such as OncoKb, can be visualized in this lollipop plot.
- Further details are available in the table, where the columns are customizable and downloadable.



We were very impressed with the quality of work and timeliness; you're definitely our go-to for bioinformatics consulting

- Director, Bioinformatics, Illumina



We were immensely impressed by Strand's ability to rapidly recruit a substantially sized clinical cohort of cancer patients, and to design and run a complex liquid biopsy panel on samples drawn from the cohort, all in roughly a year's time.

- Dr. Nishant Agarwal  
Chief of Otolaryngology-Head and Neck surgery and  
director of Head and Neck Surgical Oncology,  
University of Chicago.



We have been using the StrandOmics pipeline to analyze and generate a report for our clinical cancer panels for over three years now. I would highly recommend using it to analyze data generated from clinical cancer NGS panels and the outputted clinical report provided after analysis.

- Senior Scientist/ Medical laboratory director for NY State,  
Prim Bio Research Institute



24<sup>+</sup>

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