PCIG User Guide

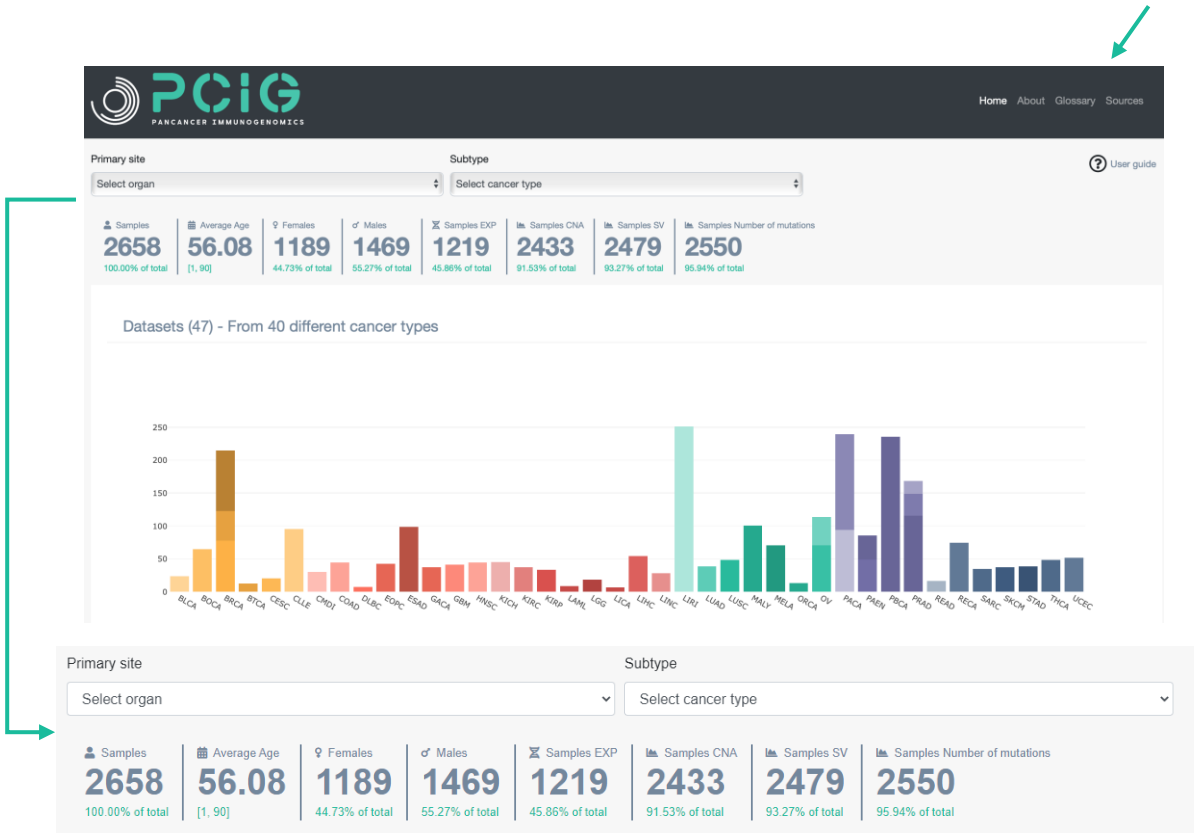
Welcome to PCIG, the PanCancer ImmunoGenomics tool!

On the home page you can find the overview summary describing the main features for data found in PCIG:

- number of samples
- average age
- number of females and males
- number of samples with expression information
- number of samples with copy number alteration or structural variants
- number of mutations

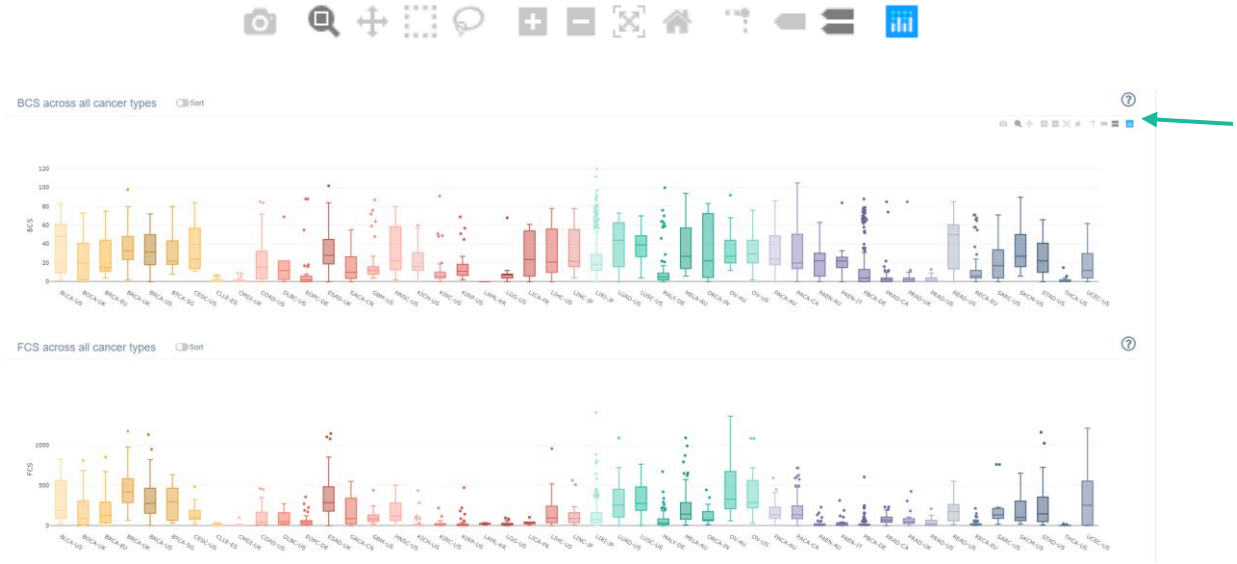
The percentages presented below numbers per feature correspond to a fraction out of the whole cohort in the PCIG database.

Next, the first plot presented displays the distribution of samples across all 47 cancer types.

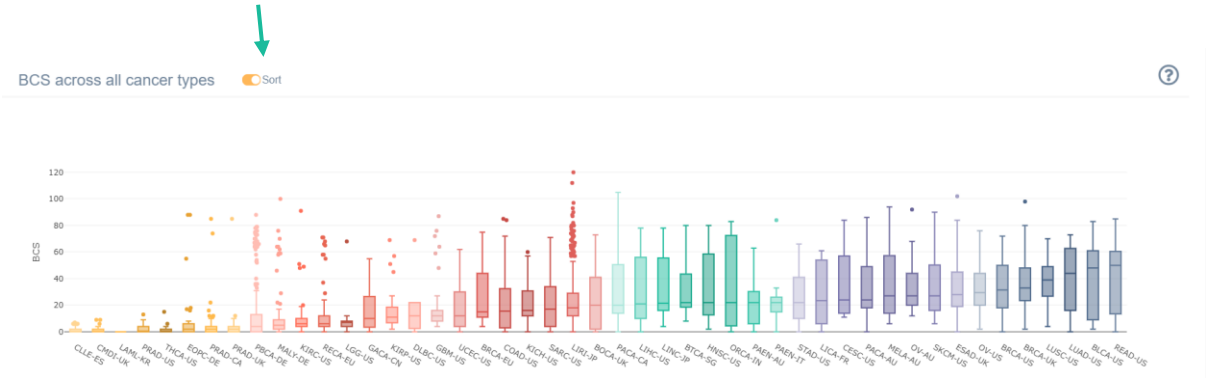


Scrolling down, users can find more plots showing different variables distribution across all cancer types (i.e. BCS, FCS, ESTIMATE Immune Score, ESTIMATE Stromal Score, MHC, CP, EC, SC, and Chemokine levels).

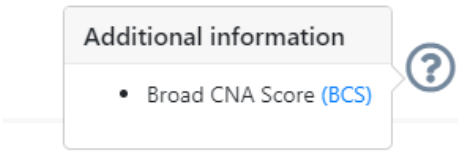
All plots are interactive. When hovering over them, different annotations for data features are displayed, along with function buttons to download, zoom into, or toggle images.



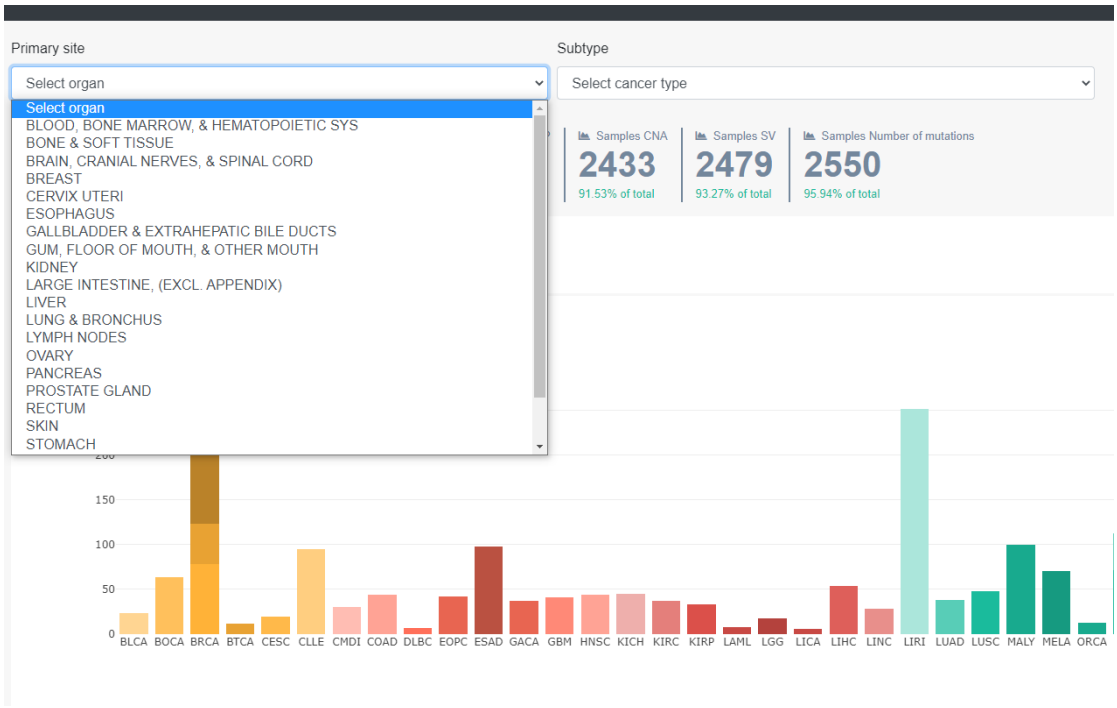
By default, plots are ordered alphabetically by cancer type, but they can also be sorted by feature value with this slider:



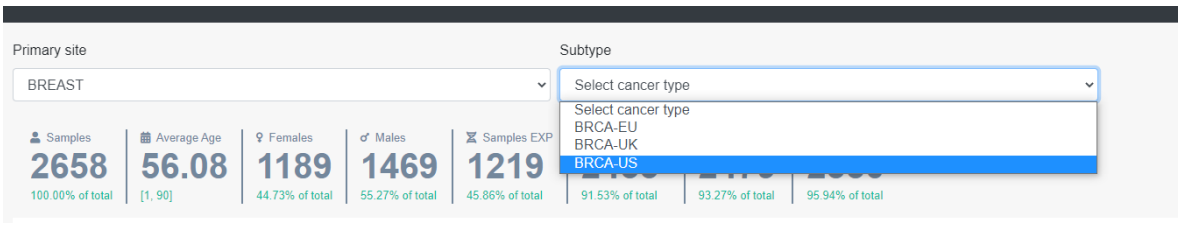
Across the application, users will find several question mark buttons with additional information and links to the glossary.



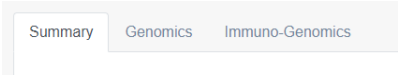
To filter the data by specific cancer type, users can select between multiple ‘Primary site’ options on the left dropdown menu.

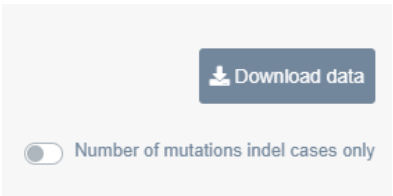


Then, the Subtype filter will be ready to select the sample subtypes available for the selected Primary Site.



Once ‘Primary site’ and ‘Subtype’ filters are set, the following tabs will be displayed: **Summary**, **Genomics,** and **Immuno-Genomics**.





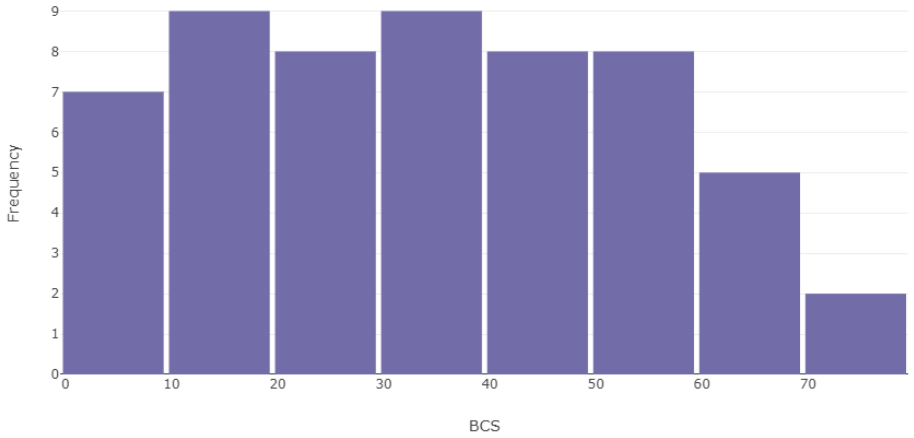
At the top-left corner there are two buttons. The first one is used to download all the data displayed and used for the currently selected cancer type. The second one enables seeing all the analysis just for the indel mutation cases.

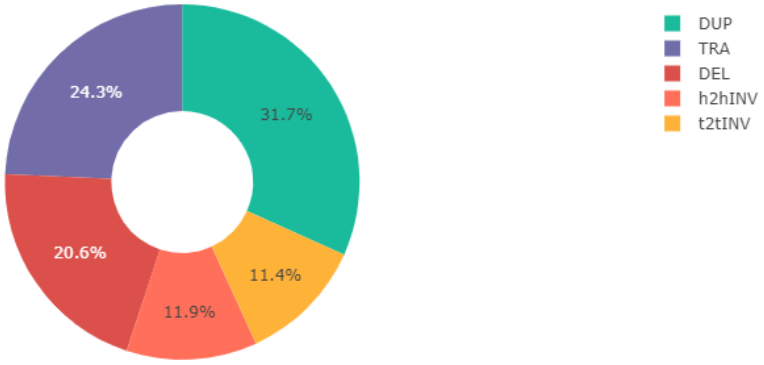
Summary tab presents the distribution of all the variables used in the tool.

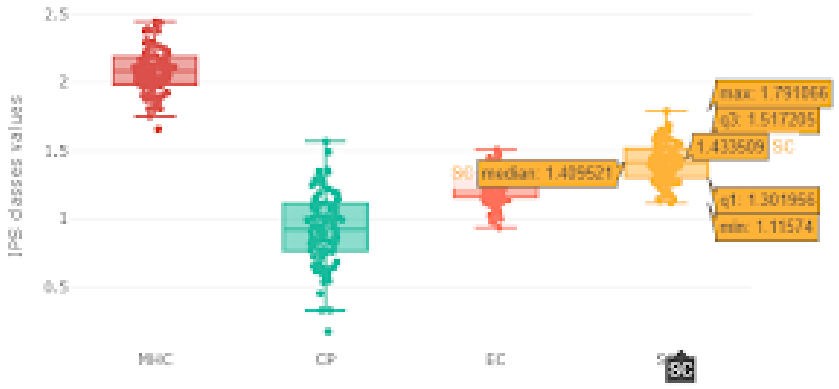
- CNA scores distribution with the respective statistical test
- Number of mutations distribution

- Structural variants distributions
- Structural variants effects
- ESTIMATE scores (ImmuneScore and StromalScore) distribution
- ImmunophenoScore distribution

Different plots were used to show these distributions, such as bar plots, doughnut plots and boxplots.

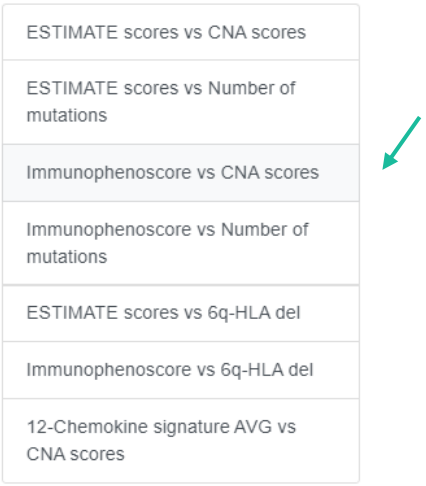






In the Genomics tab, the following correlation analyses and distribution plots are displayed:

- CNA scores vs Number of mutations
- CNA scores vs Chromothripsis



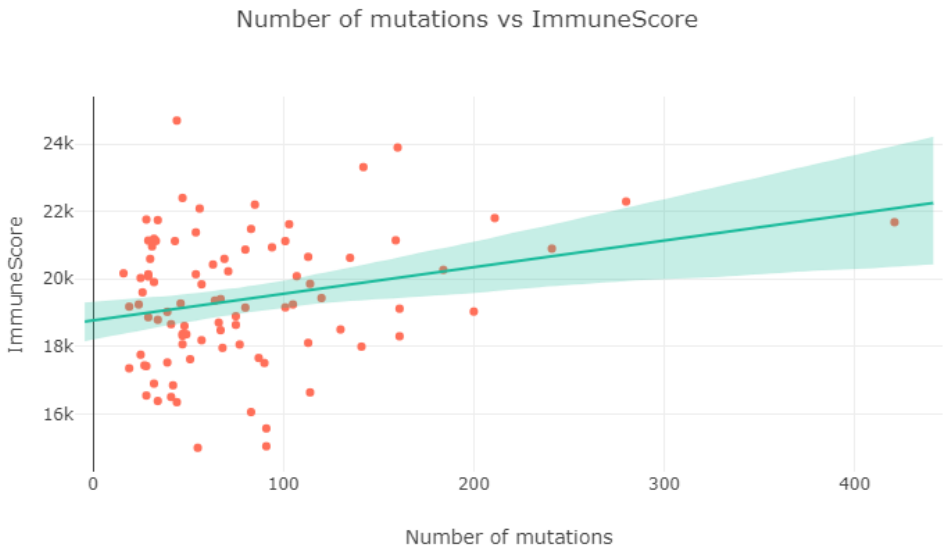
Finally, the Immuno-Genomics tab presents the following plots and correlation summaries:

- Estimate scores vs CNA scores
- Estimate scores vs Number of mutations
- Immunophrenoscore vs CNA scores
- Immunophrenoscore vs Number of mutations
- ESTIMATE scores vs 6q-HLA del
- Immunophrenoscore vs 6q-HLA del
- 12-Chemokine signature AVG vs CNA scores

Using the navigation menu, one can navigate directly to the analysis of your choice.

Two types of plots are presented to explain correlation analysis:

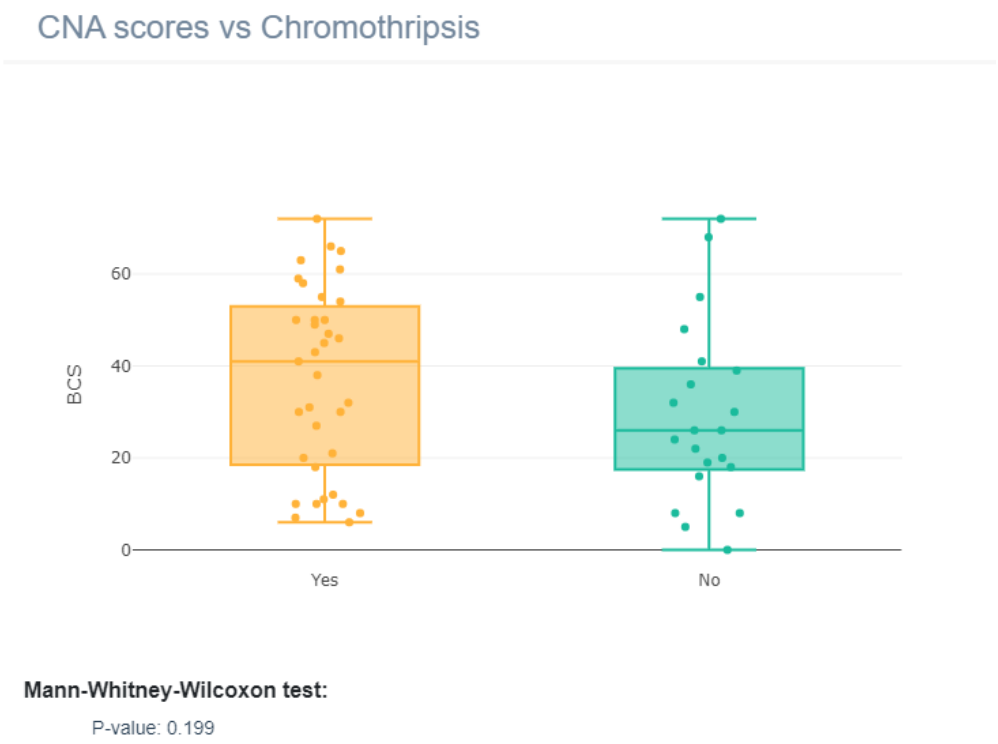
- Quantitative variables are presented using scatter plots along with regression lines and confidence intervals associated. Results for Spearman's correlation test and associated p-values are displayed underneath each plot.



Spearman test:

P-value: 0.099
Correlation coefficient: 0.174

- Qualitative variables are presented by using boxplots. In these cases, Mann-Withney-Wilcoxon test associated p-values are shown.



Finally, in the immuno-genomics tab, the user can find two tables listing all the correlations for different Immunophenoscore and Chemokine signatures. These tables can be filtered and downloaded in multiple and different formats.

Correlations summary

IPS	BCS		FCS	
	p-value	cor. coef.	p-value	cor. coef.
b2m	0.654	-0.061	0.899	0.017
tap1	0.926	-0.013	0.175	0.184
tap2	0.933	0.011	0.031	0.289
hla_a	0.293	-0.143	0.643	0.063
hla_b	0.574	-0.077	0.346	0.128
hla_c	0.292	-0.143	0.782	-0.038
hla_dpa1	0.527	-0.086	0.706	-0.051
hla_dpb1	0.766	-0.041	0.910	-0.015
hla_e	0.884	-0.020	0.128	0.206
hla_f	0.528	-0.086	0.226	0.164

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