Autophagy and Tumor Database

Tutorial

Contents

1 Introduction

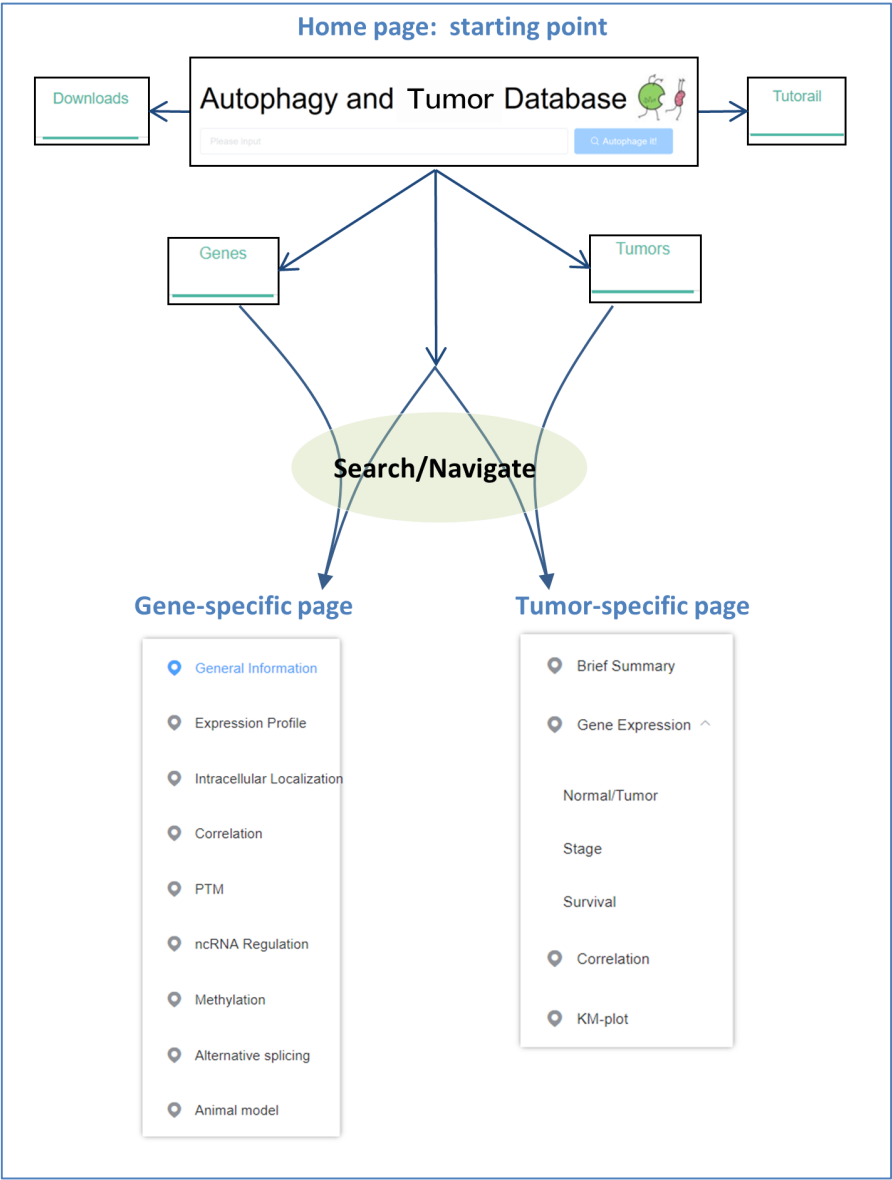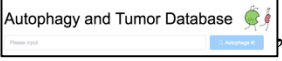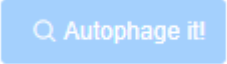The structure of *Autophagy Archive* website is shown in Figure 1.

Figure 1 The structure of the website

2 Search/Navigate

Search fileds were provided in three pages.

They are homepage [Autophagy and Tumor Database], Genes page [Genes] and Tumors page [Tumors].

In the homepage [Autophagy and Tumor Database], when typing in your interested entity, the website autocomplete your search terms (Figure 2). Both the gene names and the tumor names will be matched. Select the interested entity, clink on the *Autophagy it!* [Q Autophage it!] button, the website goes forward.
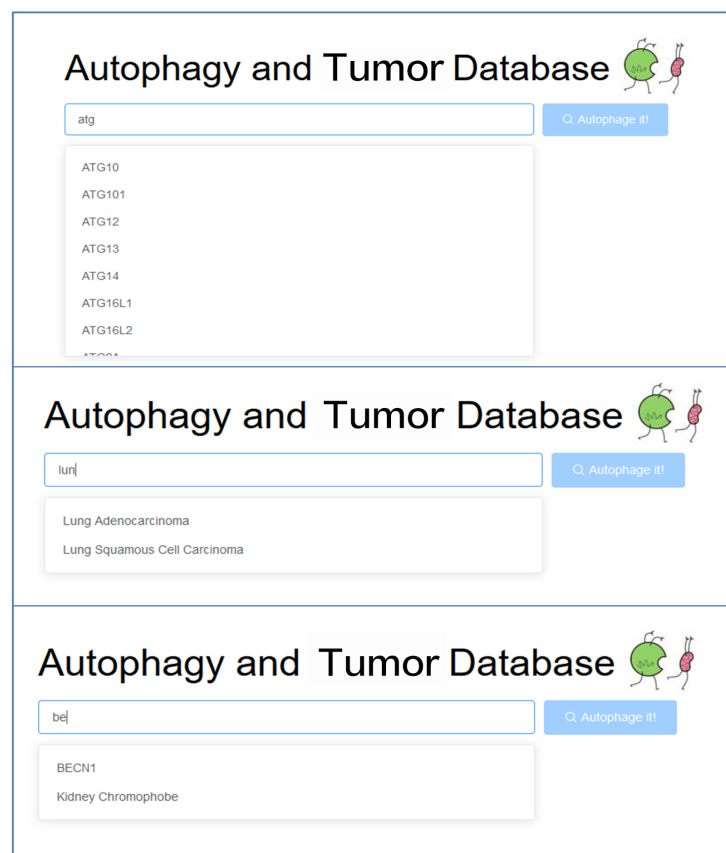

Figure 2 Auto-completion in the search box

In the Genes page `Genes`, *Illustration*, *Search* and *Dropdown list* offer three entrances to a gene-specific page. *Illustration* allows a visual selection for interested genes. By clicking on the ovals, the website will navigate to the targeted page (see "3 Gene-specific page"). *Search* works the same as shown in the Figure 1. *Dropdown list* listed all the included genes.

In the Tumors page `Tumors`, *Illustration*, *Search* and *Dropdown list* offer three entrances to a tumor-specific page (see "4 Tumor-specific page"). They work similarly in the Genes page.

Caution: Only several tumors or genes are displayed in the illustration. For more information, please browse by *Search* OR *Dropdown list.*

3 Gene-specific page

In a gene-specific page, the following information was displayed: General Information, Expression Profile, Intracellular Localization, Correlation, PTM, ncRNA Regulation, Methylation, Alternative splicing, Animal model. Let's take **BCL2** as the interested gene.

Correlation shows the correlation coefficients between the expression of BCL2 and the expression of microRNAs, transcription factors and lncRNAs. To get more precise results, one can select tumors, range of correlation coefficients and ranges of p values in the Filter (Figure 3). The colors of the cells indicates the values of correlation coefficients. Hovering the mouse on the cells, the name of the miRNA appears (Figure 4). On clicking the cells, a scatter plot will be drawn (Figure 5).
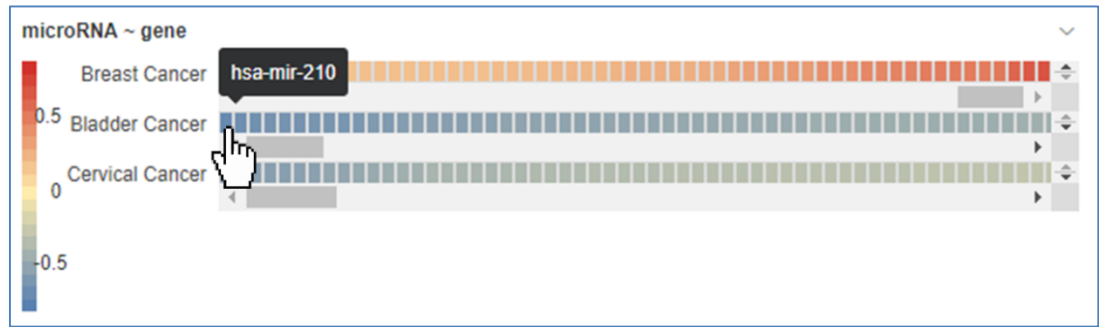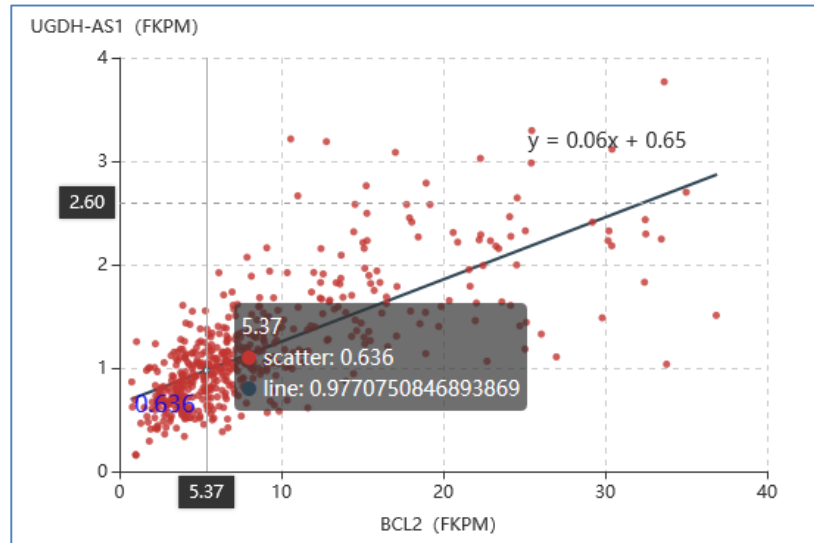
Figure 3

Figure 4

Figure 5

In Alternative splicing, select a tumor on the right, [Tumor filter ▾] [submit]

click "submit". A boxplot follows (Figure 6).

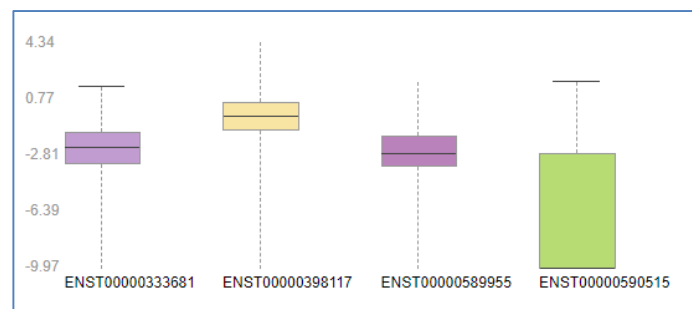Figure 6

4 Tumor-specific page

In a tumor-specific page, the following information was displayed: Brief Summary, Gene Expression (Normal/Tumor, Stage, Survival), Correlation, KM-plot. Let's take **Breast Cancer** as the interested cancer.

Correlation works similarly as that in "3 Gene-specific page".

In KM-plot, this website provides customized survival analysis with sub-population selection, data source selection and cut-off points selection. Datasets available include TCGA (Figure 7) and series from GEO.
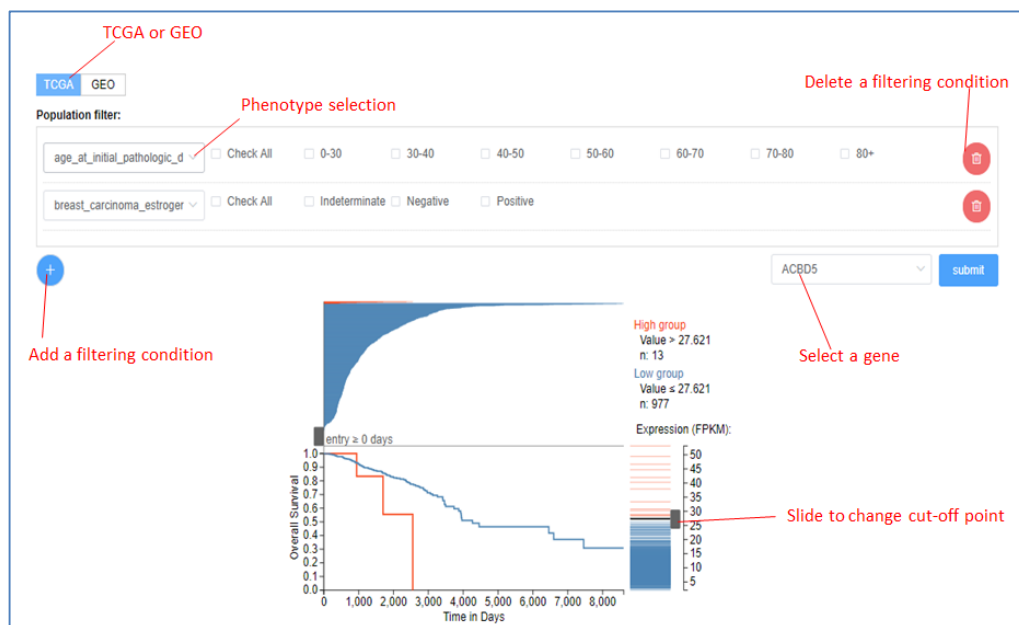

Figure 7