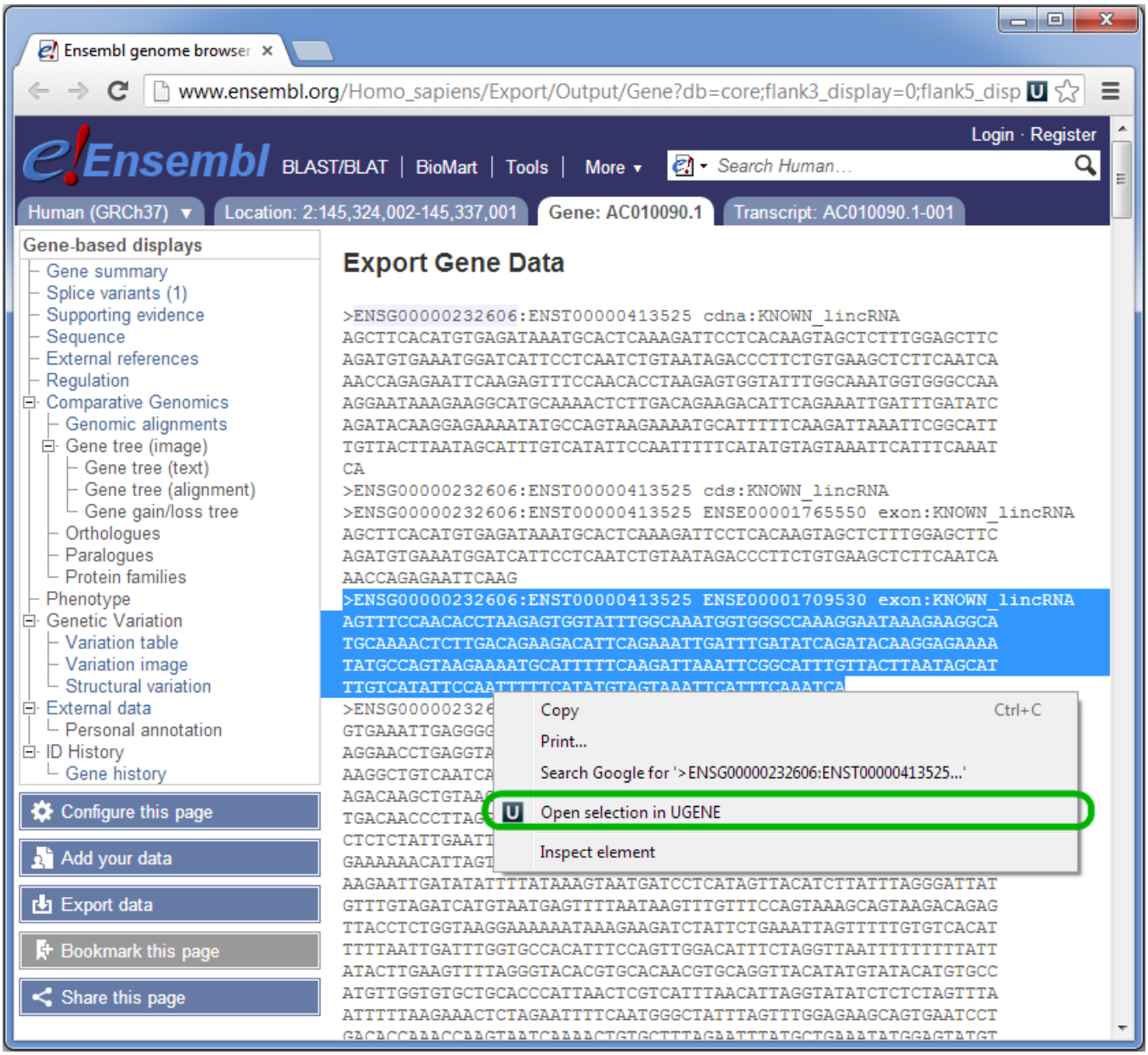
Opening selected data in UGENE

Imagine that you have browsed for required data (e.g. a sequence with annotations) and opened, for example, an html view for the data in a web browser. Now you would like to open the data in UGENE to analyze them in more detail. Or, alternatively, maybe you would like to analyze a certain sequence part.

In this case you select the required data in the web browser window. the *Open selected in UGENE* item should now appear in the context menu:



The selected data will be opened in UGENE.