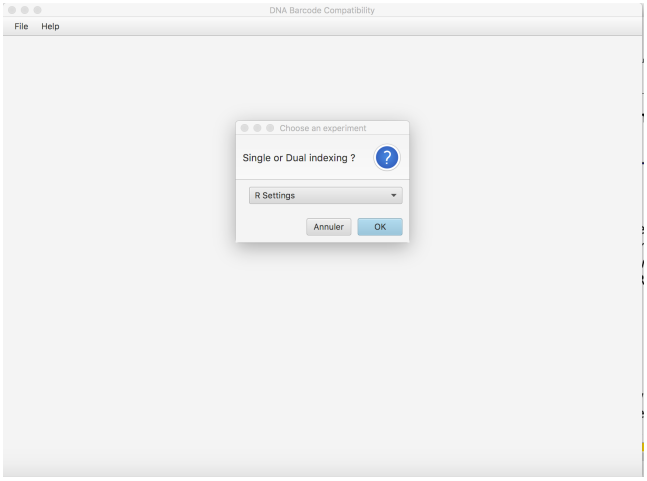
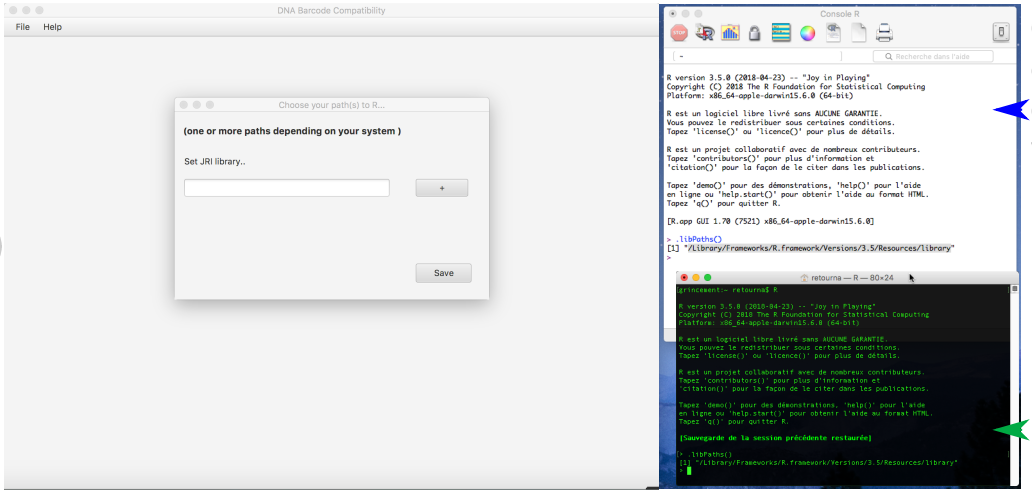
Configure the DNABarcodeCompatibility interface to enable the communication with the R environment

1



When you **first** start the DNABarcodeCompatibility user graphical interface, a window pops up, please select R Settings to set the library paths.

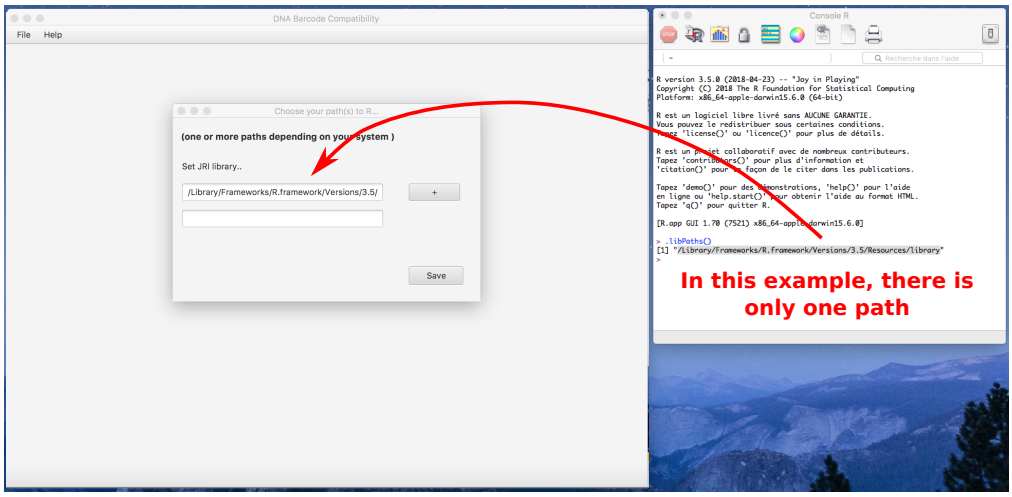
2



On Windows and MacOSx, clicking the R application opens an R console in which to type in **.libPaths()** to list all possible library paths.

Alternatively, on Linux and MacOSx, run R within a terminal and type in **.libPaths()**

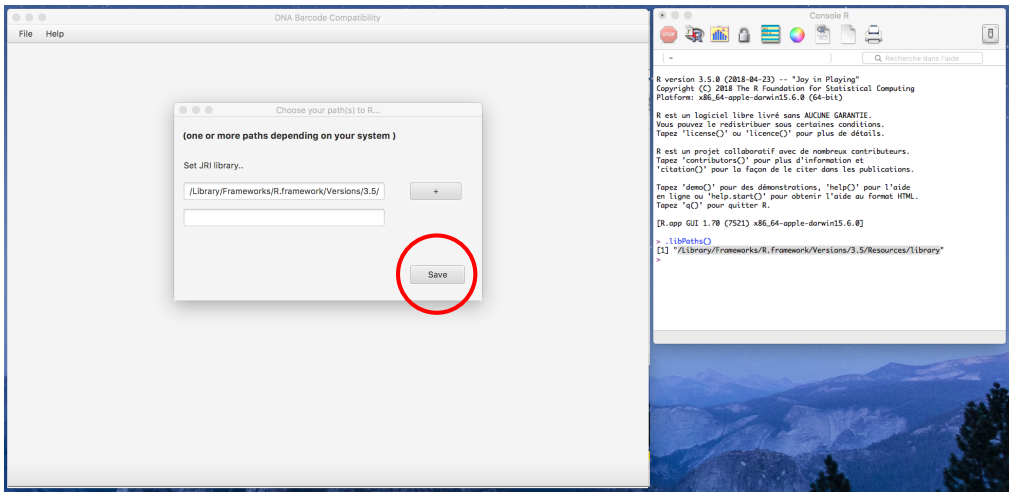
3



Copy and paste one-by-one all paths **without quotes** into each empty field of the pop up window

In this pop up window, you can add en empty field by clicking on the "+" icon.

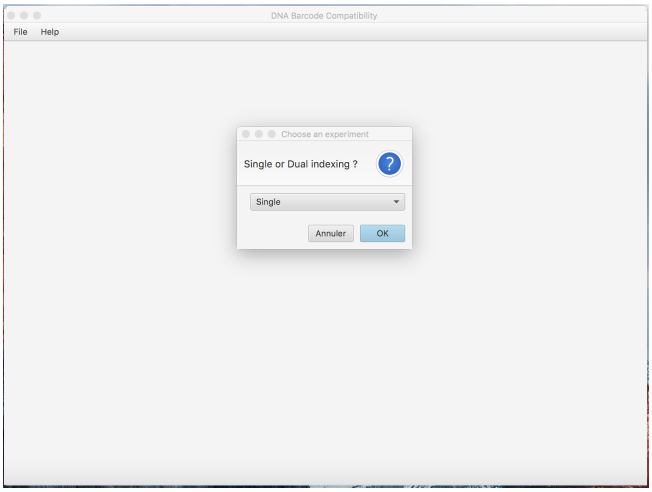
4

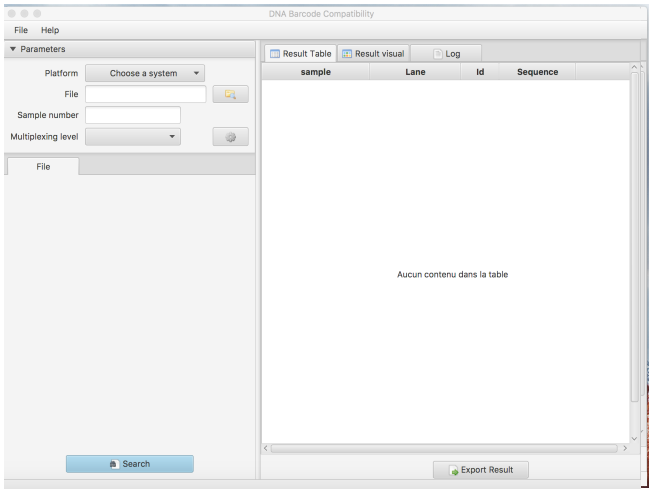


Click the save button and then close the pop up explicitly

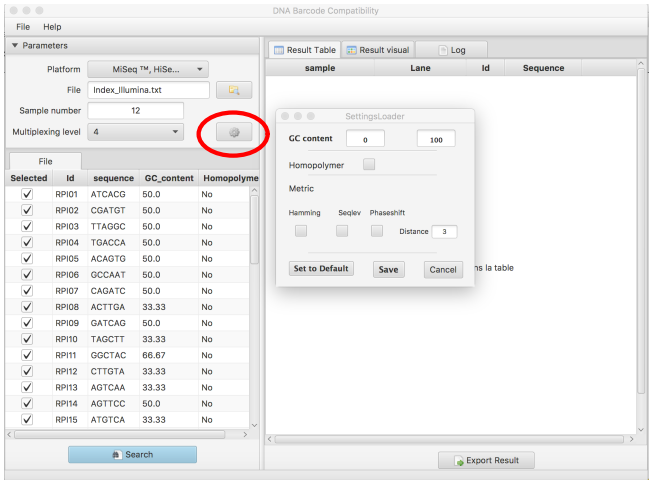
Design a single barcoding multiplex experiment

1





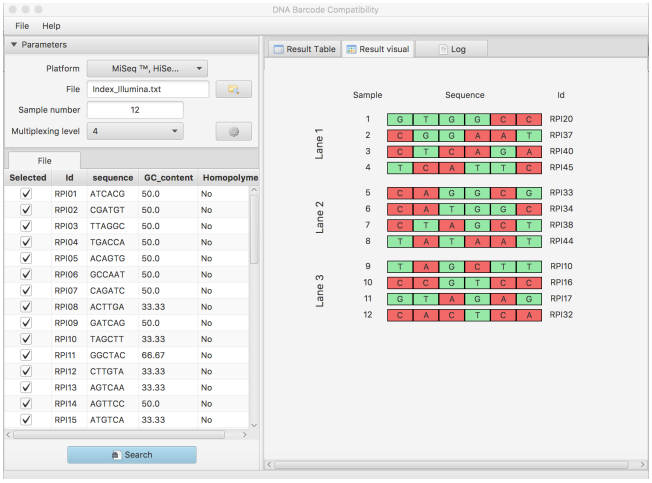
2



. Select the sequencer platform
. Load the "Index_Illumina.txt" file
. Fill in the sample number field
. Select the multiplex level
. Add other constraints in the setting loader

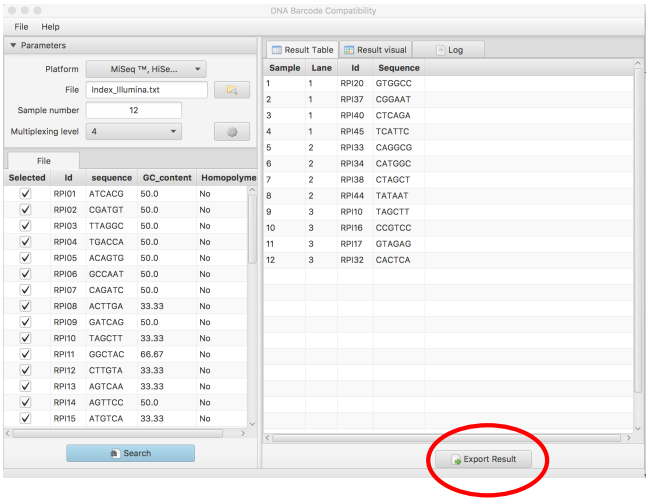
. Click the Search button

3



Click on the "Result Visual" panel to visualise how barcoded samples are distributed among lanes of flow cells

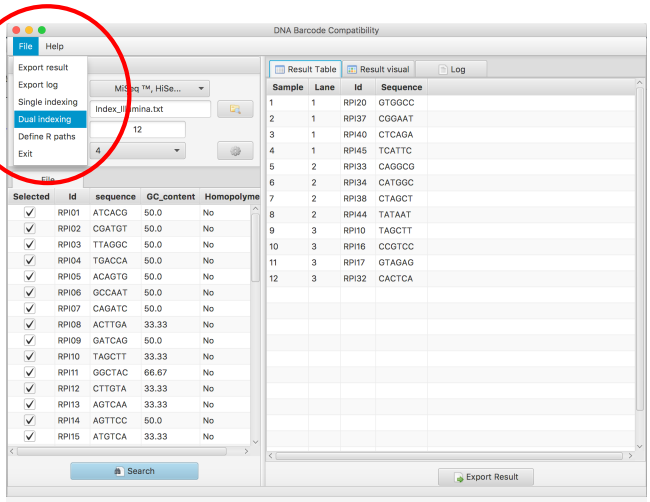
4

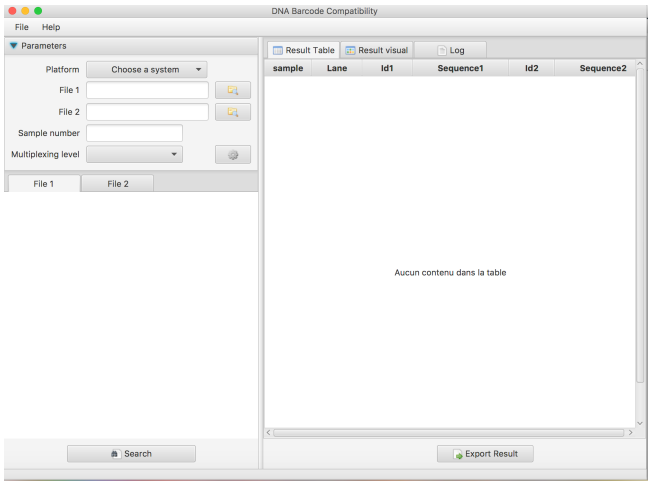


Click on the "Result Table" panel and click on "Export Result" to save the results

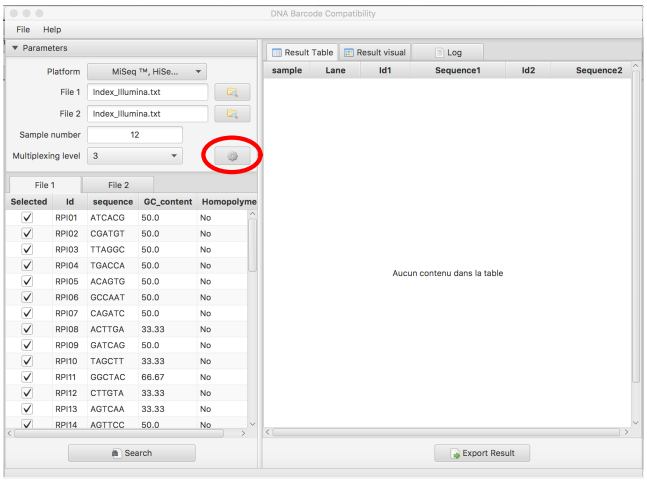
Design a dual barcoding multiplex experiment

1





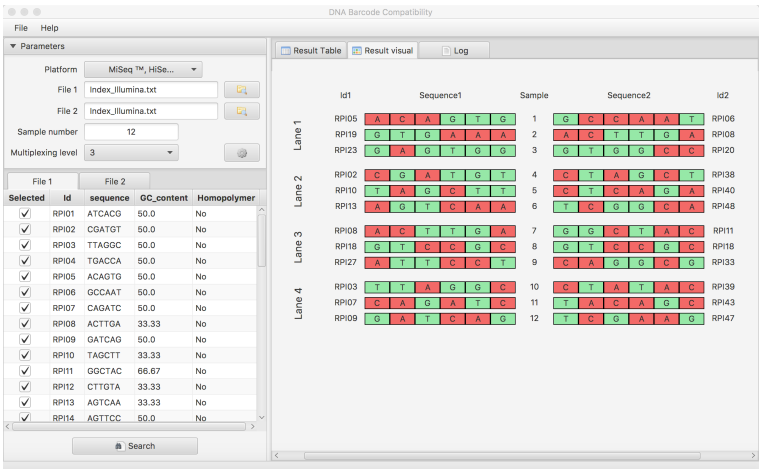
2



. Select the platform
. Load the "index_Illumina.txt" file
. Fill in the sample number field
. Select the multiplex level
. Add other constraints in the setting loader

. Click the search button

3



Click on the "Result Visual" panel to visualise how barcoded samples are distributed among lanes of flow cells

Click on the "Result Table" panel and click on "Export Result" to save the results