

In "An evaluation of pool-sequencing transcriptome-based exon capture for population genomics in non-model species", Deleury *et al.* propose a new method to generate a transcriptome-based exon capture suitable for large scale population genomics studies at the computational levels by mapping directly to the transcriptome and cost efficient by the use of pool-sequencing. They illustrate the different step on *Harmonia axyridis*. They also create a new method to identify intron-exon boundaries, method available through github.

I would recommend the paper after some revisions.

My comments are listed below.

#### General comments:

The authors performed a lot of different steps to generate the data used for the benchmark. Nonetheless, because of the amount of steps, the reader can be lost in the different filtering and the data used. A flowchart could help to understand and to follow the text, as well as the stating what are the data used in the paper, we can be lost between the draft genome of *Harmonia axyridis*, the *de novo* transcriptome of *H. axyridis* and the use of other species.

#### Specific comments:

line 52: 'even in after, the in should be removed.'

Figure 1: We cannot see the 'Individuals only', probably because it is too small compared to the other two. Maybe another representation is needed, otherwise, we don't know where the 'Individuals only' are.

Figure 2: The arrow in the text of the figure should be removed, they didn't add anything and are confusing. The figure is also a bit unclear and it is difficult to read and understand which text is referring to which panel. Maybe a figure with the panels on the left and the text on the right will be better.

line 446: Is the use of the word 'private' here mean specific? Is it classically used? If not, the word specific should be used instead, here and after.

line 459: IEB will be better written in full letters because it seems that it is the first time the acronym is used in the Result part.

line 462: IEB will be better written in full letters in the title.

line 548-574: The two paragraphs say the same thing. It is, I think a mistake. One should be chosen.

#### Comment on IEB\_finder:

I was able to run the first step, i.e. Step 1 : collect\_CDS\_infos.pl, but for the second step (Mapping genomic reads on CDS sequences), there is no 'genomicReads.fq' file to test the tool.