



## OPPONENT'S REVIEW ON BACHELOR THESIS

**Name of the student:** Nina Nenin

**Thesis title:** Novel non-coding transcripts at imprinted loci in mammalian oocytes and embryos

**Supervisor:** Mgr. Lenka Gahurová, Ph.D

**Referee:** Mgr. Helena Hönig Mondeková, MSc

**Referee's affiliation:** Department of molecular biology and genetics

	Point scale <sup>1</sup>	Points
<b>(1) FORMAL REQUIREMENTS</b>		
<b>Extent of the thesis</b> (for bachelor theses min. 18 pages, for masters theses min. 25 pages), <b>balanced length of the thesis parts</b> (recommended length of the theoretical part is max. 1/3 of the total length), <b>logical structure of the thesis</b>	0-3	3
<b>Quality of the theoretical part (review)</b> (number and relevancy of the references, recency of the references)	0-3	3
<b>Accuracy in citing of the references</b> (presence of uncited sources, uniform style of the references, use of correct journal titles and abbreviations)	0-3	0
<b>Graphic layout of the text and of the figures/tables</b>	0-3	3
<b>Quality of the annotation</b>	0-3	2
<b>Language and stylistics, complying with the valid terminology</b>	0-3	3
<b>Accuracy and completeness of figures/tables legends</b> (clarity without reading the rest of the text, explanation of the symbols and labeling, indication of the units)	0-3	3
<b>Formal requirements – points in total</b>		17
<b>(2) PRACTICAL REQUIREMENTS</b>		
<b>Clarity and fulfillment of the aims</b>	0-3	3
<b>Ability to understand the results, their interpretation, and clarity of the results, discussion, and conclusions</b>	0-3	3
<b>Discussion quality – interpretation of the results and their discussion with the literature</b> (absence of discussion with the literature is not acceptable)	0-3	3
<b>Logic in the course of the experimental work</b>	0-3	3
<b>Completeness of the description of the used techniques</b>	0-3	3

<sup>1</sup> Mark as: 0-unsatisfactory, 1-satisfactory, 2-average, 3-excellent.

Experimental difficulty of the thesis, independence in experimental work	0-3	2
Quality of experimental data presentation	0-3	3
The use of up-to-date techniques	0-3	3
Contribution of the thesis to the knowledge in the field and possibility to publish the results (after eventual supplementary experiments)	0-3	2
Practical requirements – points in total		25
<b>POINTS IN TOTAL (MAX/AWARDED)</b>	<b>48</b>	<b>42</b>

### Comments of the reviewer on the student and the thesis:

The practical work of Nina Nenin was bioinformatical. She learned how to use up-to-date bioinformatical tools for RNA-seq analysis (including de novo transcript assembly). She also learned how to use R language and RStudio for data visualization and clustering.

The bachelor thesis has clear goals, the methodology and results are clearly written and easy to read. The introduction is focused on genomic imprinting in mammals and is rather detailed, it could have started with a broader introductory paragraph. The work itself is of adequate length and contains plenty of supplementary material from the analysis. There are some typos in the work which might have been removed while reading the work just one more time.

The only (but very irritating) thing to reproach is a bad citation practice used through the whole work.

### Suggestions and questions, to which the student has to answer during the defense.

#### Mistakes, which the students should avoid in the future:

Questions:

- 1) On page 6 in the introduction, you write: "After fertilization, beside the loss of DNA methylation, histone modifications transmitted from the gametes are also reprogrammed in the pre-implantation embryo.," Question: Do both gametes have histones?
- 2) I have some clarifying questions considering the methodology:
  - a. How did you deal with the fact, that some source datasets are strand specific and some not?
  - b. What was the cut-off value for trimming?
  - c. You were specifying the maximum and minimum values for soft-clipping per base (--sp) in mapping using Hisat2. What were these values? What are „default values“ in Hisat2?
  - d. Where did you obtain files with the annotations of individual TE classes elements for the transposable elements analysis?
  - e. In the methodology of sequence motif analysis, you specify 2000bp upstream and 500 bp downstream TSS as +2000/-500bp around the TSS. In the results you write it as -2000/+500 bp around the TSS. Is there any correct notation for this?
- 3) Questions considering the results:
  - a. What does the clustering analysis tell us? Is it reliable considering the variability of the source datasets? Have you considered different style of visualization of the results (Fig. 5a and 5b)? (For me, it is confusing when independent data for each

developmental stage are presented as a continuous line.)

- b. In the list of clustered transcripts (Tab. 2), there are 2987 transcripts all together. However, in the TE analysis, you analyse 2816 transcripts. What makes the difference? Also, in the methodology, you wrote it was analysed both for the clustered transcripts and for all the transcripts (including clustered and non-clustered transcripts). What were the results for all the transcripts?

**Mistakes:**

There are all mistakes in citing and referring that can be done in this work: missing references, incorrect citing and various citing and referring styles. I strongly recommend the student to use any citation manager in her future scientific work.

The annotation is more a description and summary of the work than the aim of the work.

**Conclusion:**

**In conclusion, I**

**r e c o m m e n d**

**the thesis for the defense and I suggest the grade excellent (1) .<sup>2</sup>**

In **České Budějovice** date **31.12.2019**

  
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signature

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<sup>2</sup> You can suggest a grade, which can be modified during the defense based on the presentation. However, if the reviewer is not present at the defense, the grade will not be counted. Grades: excellent (1). Very good (2), Good (3), Unsatisfactory/failed (4).