

Assessment proposed by the supervisor: Successful defense

Assessment proposed by the reviewer: Successful defense

Course of the defence:

Questions:

1. What are the differences between Repaired and Non-repaired libraries?
2. Do the differences, if any, contribute to the fluctuation of numbers in Repaired and Non-repaired haplotypes?
3. Does the data quality also influence the haplotype calling? How?
4. Why do we consider the unique counts only?
5. How do we identify the true artifacts from the sequencing errors?
6. What parameters do you use to assess the haplotype/ mutation quality?
7. Do we always apply the same parameters on the data regardless of the library perpetuation method?
8. Do we consider the distances between the mutations within the haplotype filtration steps?
9. What are the challenges of finding common haplotypes?
10. How does the comparison to COSMIC & gnomAD contribute to the conclusion?
11. How do we identify if a mutation is a CpG content?
12. What bars represent DNA lesions, and does the tool filter them efficiently? Justify your answer.

Score:

Assessment: ...Excellent.....

Date of defence: 20.10.2022

a. Prof. Irene Tiemann-Boege



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committee chairman