***Tumour Evolution Course***

1. Is the sequenced sample contaminated by normal cells? If so, what is percentage of normal cells in the sequencing reads?

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1. Is the tumor genome chromosomically unstable? What is the average number of alleles in the tumour cells?

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1. How many clones do compose the sequenced tumour?

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1. Do you detect any mutation In what fraction of the cells?
2. Are mutations giving resistance in the same clone or in different clones?

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**C. Annotation of somatic SNVs.**

1. Which are, if any, in your opinion the putative driver mutations? Why?

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Which are the clonal mutations in the list? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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1. How many cells carry the somatic SNV in the UTR of *KCNJ12?*

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**Tutorial II**

**A. Distribution of allelic frequencies of somatic and germline SNVs**

1. Why does mutations at 3.75% decrease in the “*non-silent*” dataset?

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1. Why do frequencies never reach 50%?

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**B. Distribution of allelic frequencies of somatic and germline SNVs after tumor content correction**

1. Ho many clones do you expect for the tumor?

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1. Are all mutations at 50% in the same clone or in different clones?

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