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Dear colleagues,

Just a brief update regarding the comparisons between the incomplete genomes from our Swiss strains (mentioned during the last call) and the outbreak-strains reported from Western France: our bioinformaticians found common individual mutations, but overall large differences, excluding similarity of the strains.

Kind regards

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Division of Infectious Diseases & Hospital Epidemiology

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Task Force COVID-19 University Hospital Basel

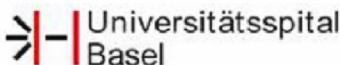
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