Background
Hepatocellular carcinoma (HCC) is a primary type of liver cancer that ranks as the fourth most leading cause of cancer-related deaths worldwide. Treatment options including ablation and chemo-therapies are not always efficient to eliminate advanced HCC. Immunotherapies have general low response rates in advanced HCC patients, indicating that new approaches are needed in order to improve the current clinical responses.

Our main objective is to identify mutations that can be clinically relevant targets for T cell immunotherapy in HCC patients.

Results
The top ranking somatic mutations identified respectively for the three patients, are shown on Table 1. Among those, we identified ‘hot-spot’ mutations in driver oncogenes such as the CTNNB1 and highly frequent HCC associated genes including the PIK3CA, CDKN2A and KMT2C.

For each frequent HLA allele such as A*01, A*02, A*03, B*47 and C*03 we identified peptides with high predicted binding affinity (figure 2).

Conclusions
Main findings:
- Identification of hot-spot mutations in driver oncogenes and highly frequent HCC associated genes.
- Potential high affinity binders for frequently expressed HLA class I alleles.

These data are increasing the likelihood of identifying T cell receptors that can be used for T cell-based immunotherapy broadly in a high number of cancer patients. The immunological testing of these mutations and the identification of specific T cell receptors is ongoing.

References
Figure 1 was made in BioRender (BioRender.com)

Table 1. Top ranking somatic mutations identified by Illumina Trusight Oncology 500 platform. Driver oncogenes in which ‘hot-spot’ mutations identified are underlined and pointed with asterisk (*).