February 16, 2026

Dear HOPP SEP students,

Please read and answer the questionnaire before the class. If you have any questions about them, we will discuss them during the class.

1) As part of your project you are interested in modelling mutations that frequently occur in cancer patients. For this purpose, you are reviewing MSK-IMPACT clinical sequencing results using the cBioPortal platform*. One of the genes that most commonly is found to be mutated in this dataset is TP53, a known tumor suppressor gene. What are the characteristics of these types of genes?
    a. In cancer patients, inactivating mutations are the most frequent type of mutations occurring in tumor suppressors genes.
    b. Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like promoter methylation.
    c. Loss of tumor suppressors decreases the likelihood of malignant transformation.
    d. Mutation in tumor suppressors genes can only be somatic, and they don't occur as germline mutations.

2) After acknowledging the importance of TP53 as a tumor suppressor, you are interested in understanding the effect of other tumor suppressors. Which of the following genes is not a tumor suppressor?
    a. RB, a gene involved in controlling the pass through a cell cycle checkpoint.
    b. APC, a gene involved in downregulating the expression of beta-catenin, a known proto-oncogene.
    c. BRCA, a gene responsible for the reparation of DNA.
    d. RAS, a gene involved in promoting cell growth.

Describe the differences between:

- DNA mutation vs DNA methylation:

- Gene promoter vs gene exon:

- Somatic testing vs Germline testing:

- Oncogene vs Tumor suppressor gene:

*To explore the frequency of tumor mutations using the publicly available sequencing data from MSK-IMPACT, go to cBioPortal (MSK, Nat Med 2017):
https://www.cbioportal.org/study/summary?id=msk_impact_2017