Computational approaches to scrutinize results from spatial proteomics of operable pancreatic cancer and neighboring tissue

Juho Pirhonen^{1,2§}, <u>Ábel Szkalisity</u>^{1,2§}, Jaana Hagström^{3,4}, Yonghyo Kim^{5,6,10}, Ede Migh⁷, Mária Kovács⁷, Maarit Hölttä^{1,2}, Johan Peränen^{1,8}, Hanna Seppänen^{9,10,11}, Caj Haglund^{9,11}, Jeovanis Gil^{5,6,10}, Melinda Rezeli^{5,6}, Johan Malm¹², Peter Horvath^{7,13,14}, György Markó-Varga⁵, Pauli Puolakkainen^{9,11}, Elina Ikonen^{1,2} §Co-First authors





• Neoplastic parenchyma has lost normal pancreatic functions

- However, it's metabolically more active than surrounding neoplastic stroma
- Adjacent parenchyma harbors most of the significance for survival
- It shares features of neoplastic tissues and healthy controls
- Increased transcriptional complexity is associated with bad prognosis in pancreatic cancer

