

Comparing the omics landscapes of HEK293 and CHO for improved bioproduction

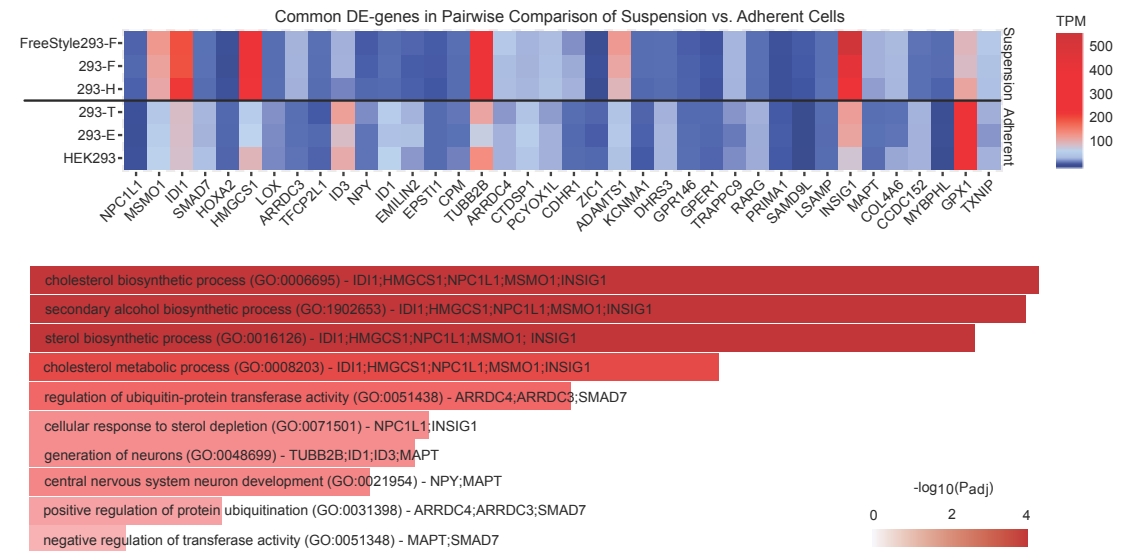
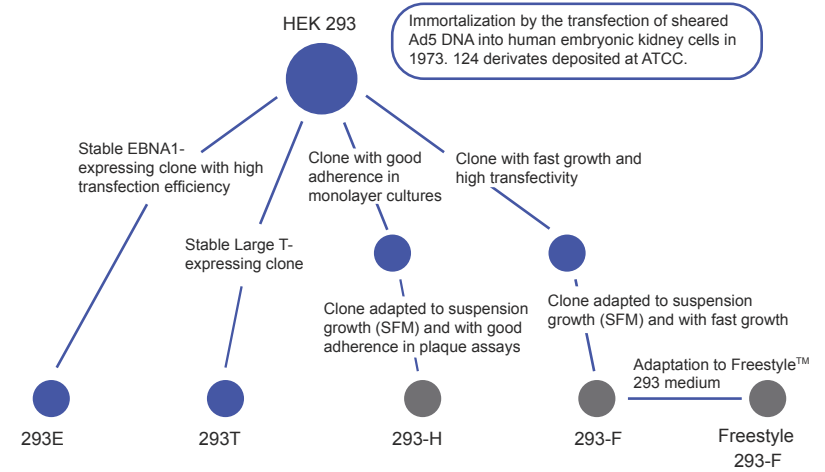
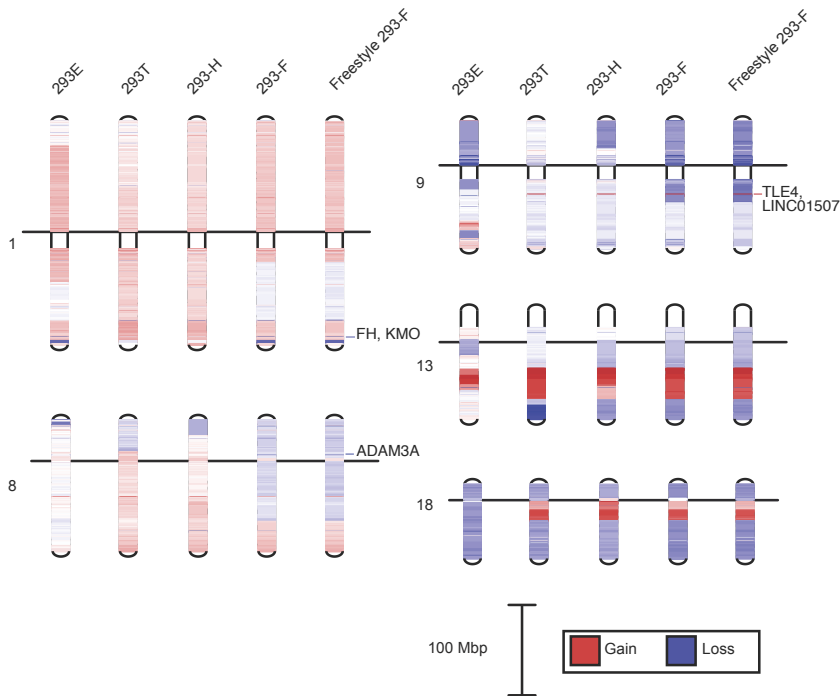
Mapping differences between industrially relevant HEK293 strains and learning lessons from the divergence in secretory pathways between HEK293 and CHO

Presenter: Magdalena Malm, Ph.D., Researcher, KTH Royal Institute of Technology
mamalm@kth.se; <https://rocklab.se/>

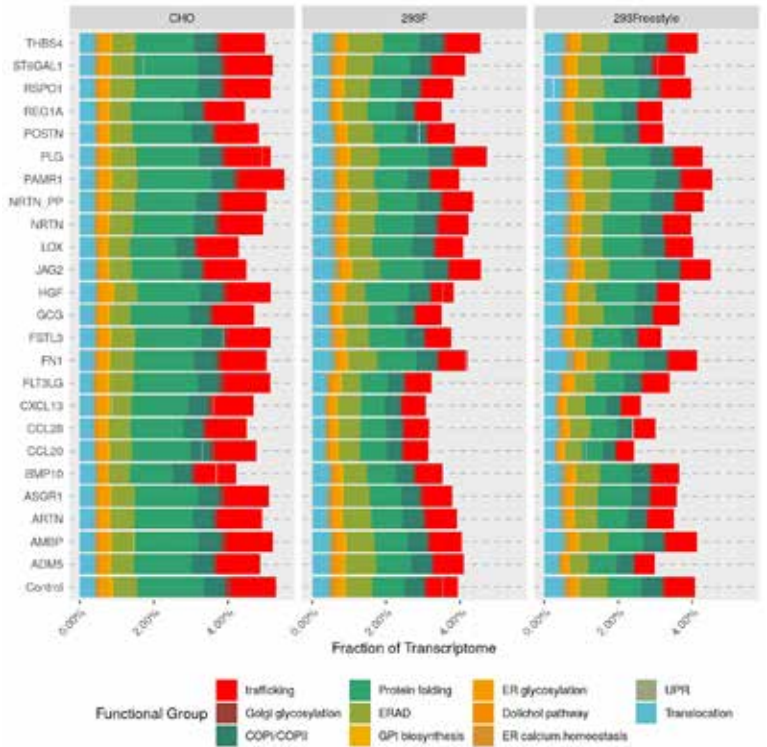
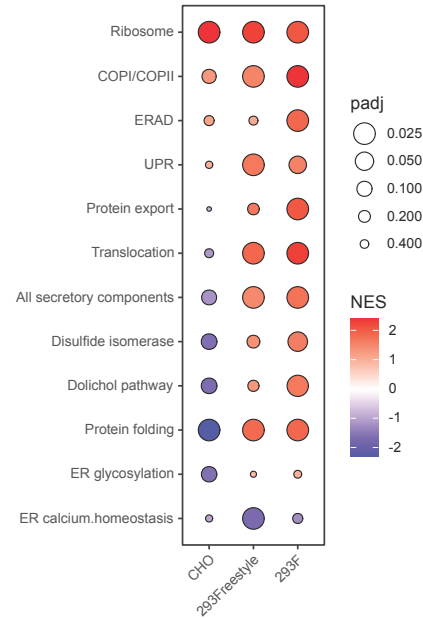
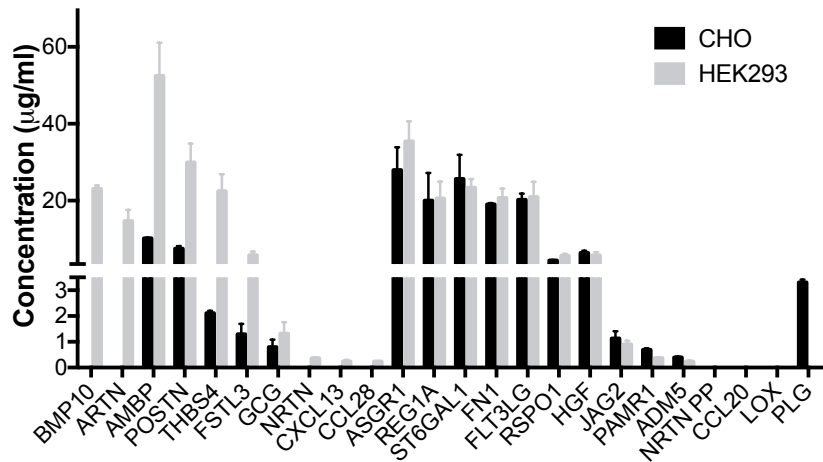
PI: Prof. Johan Rockberg, KTH Royal Institute of Technology



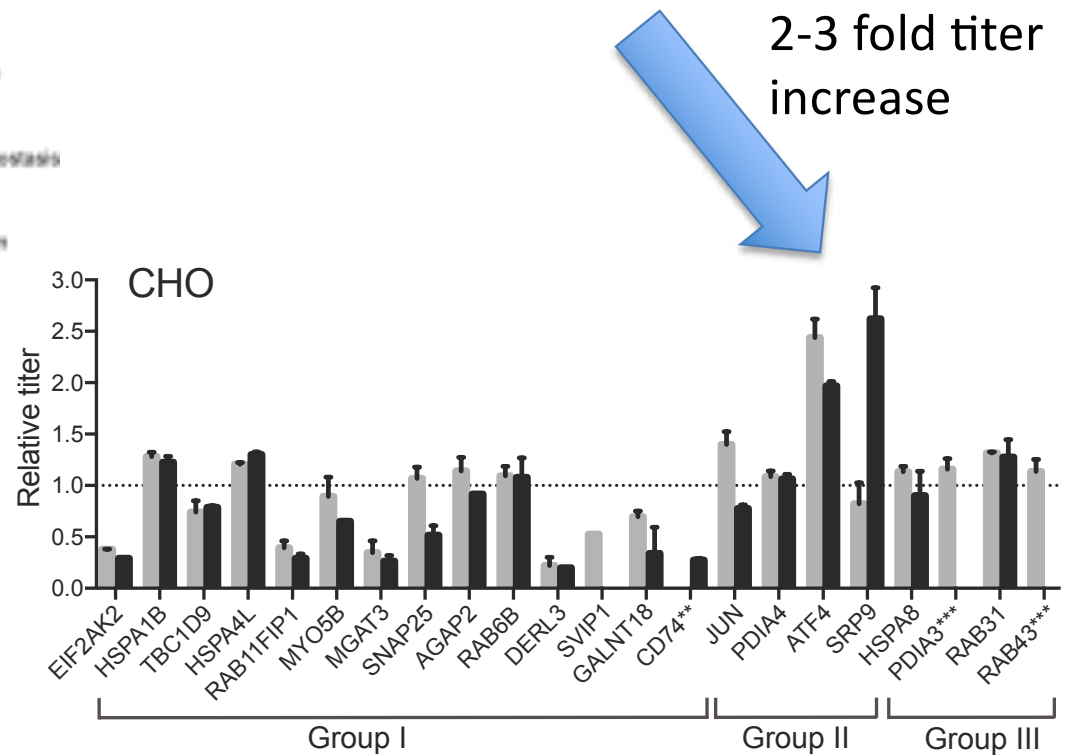
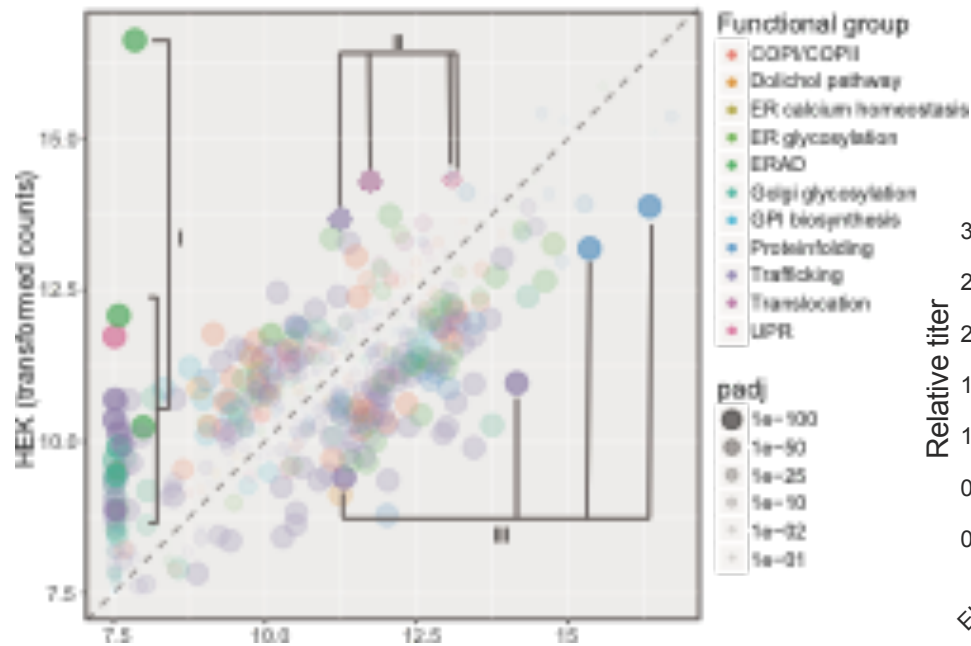
Six industrially relevant HEK293 cell lines show genomic and transcriptomic divergences



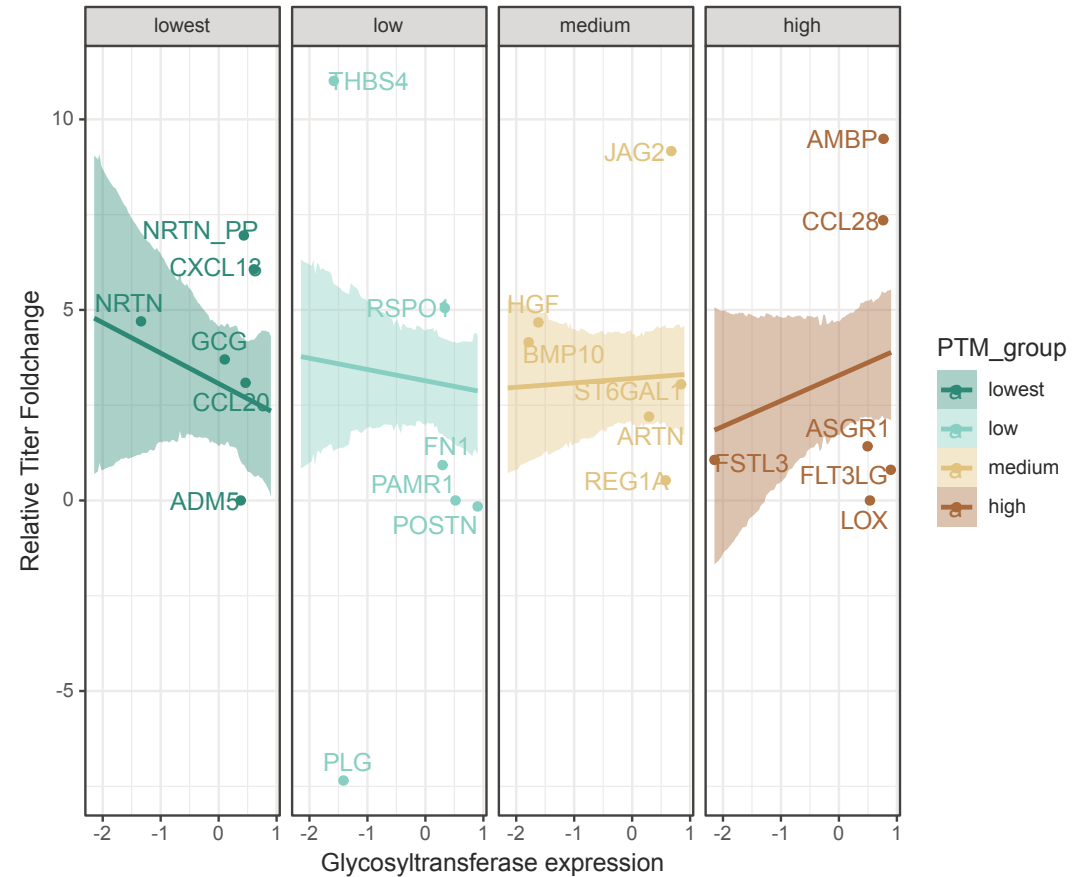
The secretory pathway utilization is different in HEK293 and CHO cell lines during expression of difficult-to-express proteins



Co-expression of highly abundant HEK293 secretory pathway components can boost bioproduction in CHO



Heavily glycosylated proteins benefit from higher activation of glycosyltransferases in HEK293 compared to CHO



HEK293 transcriptomic mapping enables identification of secretory pathway bottlenecks in CHO

