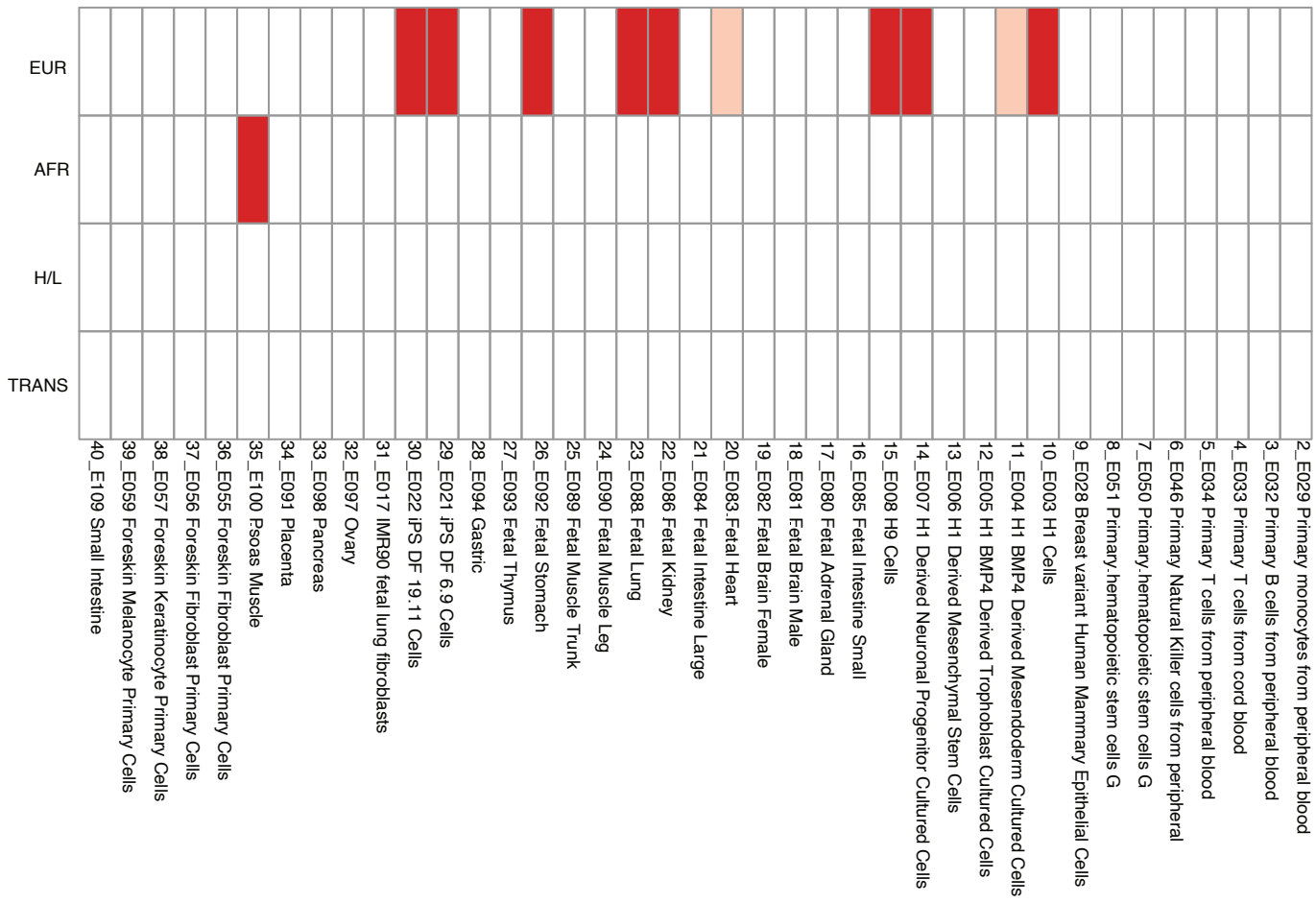


■ q-value < 0.01
■ 0.01 < q-value < 0.05

Results using top 1000 probes for each ethnicity from Breeze et al eGFR EWAS 2021 (analysed using eFORGE Consolidated erc data)



Lack of diversity in chromatin mapping samples may affect EWAS data interpretation: Heatmap showing eFORGE DNase I hotspot analysis results for top significant differentially methylated positions (DMPs) from estimated glomerular filtration rate (eGFR) EWAS analysis on European Americans (EA, top, different tissues including kidney enriched), African Americans (AA, second from top), Hispanic/Latinos (H/L, 3rd from top), and a combination of EA, AA and H/L (transethnic analysis, bottom). X axis lists different biosamples used in the eFORGE analysis; Y axis indicates eFORGE – log10 p-value for overlap enrichment of the DMP set for DNase-seq data across different tissue samples (black dots indicate significant samples, non-significant samples in pink and blue). No enriched tissues are detected for AA, H/L or transethnic analyses, despite a full array background CpG panel and proximity filtering of sites that present high DNAm correlation. This lack of enriched tissues may reflect a lack of epigenetic data in AA and H/L, among other causes.