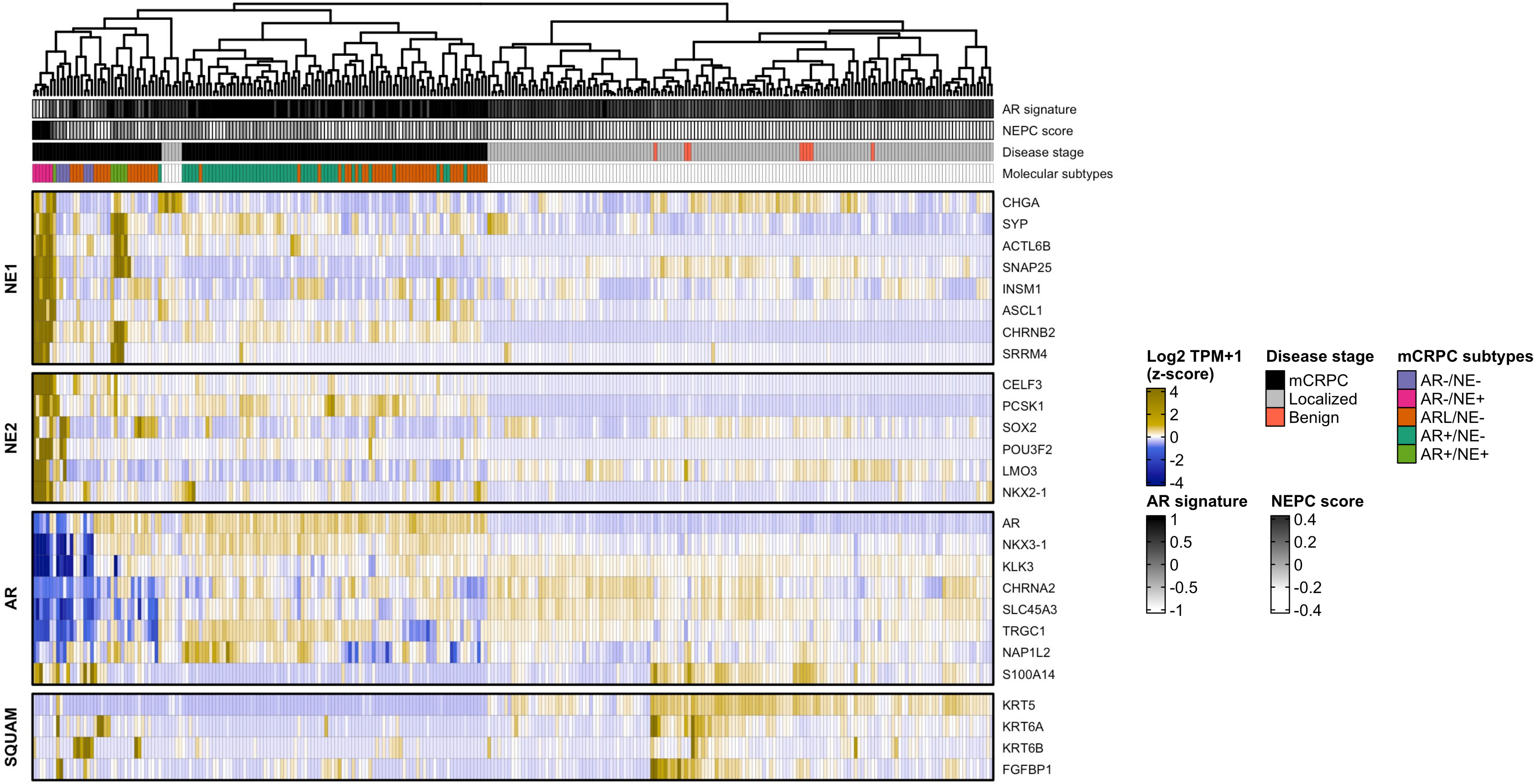
Supplementary Figure 2.



Supplementary Figure 2. Hierarchical clustering analyses of benign, localized, and mCRPC tumors representing the expression of neuroendocrine marker genes (NE), androgen-related genes (AR), and genes related to squamous (SQUAM) differentiation.

Heatmap showing gene expression levels Log2 TPM+1 (z-score) of genes in NE1, NE2, AR and SQUAM gene panels in 8 benign (in red), 148 localized (in gray) and 210 mCRPC (in black) tumors using hierarchical clustering analyses. Column distances were calculated using Pearson's method.