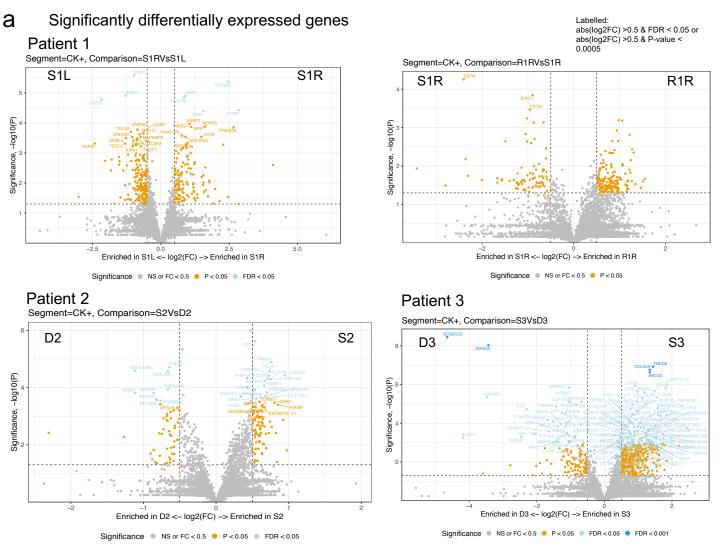
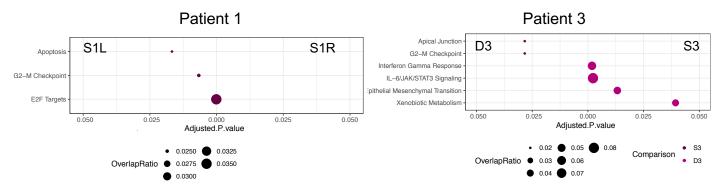
Supplementary Figure S7. Differential expression profiling of tumour biopsies from spatially resolved CK+ segments of Patients 1-3



b Significantly upregulated Hallmark gene sets (MSigDB)



Supplementary Figure S7. Differential expression profiling of tumour biopsies from spatially resolved CK+ segments of patients 1-3. a) Significantly differentially expressed genes (DEGs) in each comparison were identified based on mean expression level from different ROIs. DEGs were labelled (abs(log2FC) >0.5 & FDR < 0.05 or abs(log2FC) >0.5 & P-value < 0.0005) and colour-coded according to the figure legend of each Volcano plot. b) The dot plots report significantly upregulated gene sets (MSigDB Hallmark 2020) for DEGs identified in each comparison. Position corresponds to the adjusted p-value on x axis, size indicates the overlap ratio with the corresponding gene set and colour-based on biopsy. For patient 1, the dots to left of 0 report gene sets enriched in the left breast from surgery biopsy (S1L) and to the right of 0 report gene sets enriched in the right breast (S1R). Similarly, for patient 3 dots to the left of 0 correspond to gene sets enriched in diagnostic biopsy (D3) and to the right are those that were enriched in surgical biopsy (S3).