

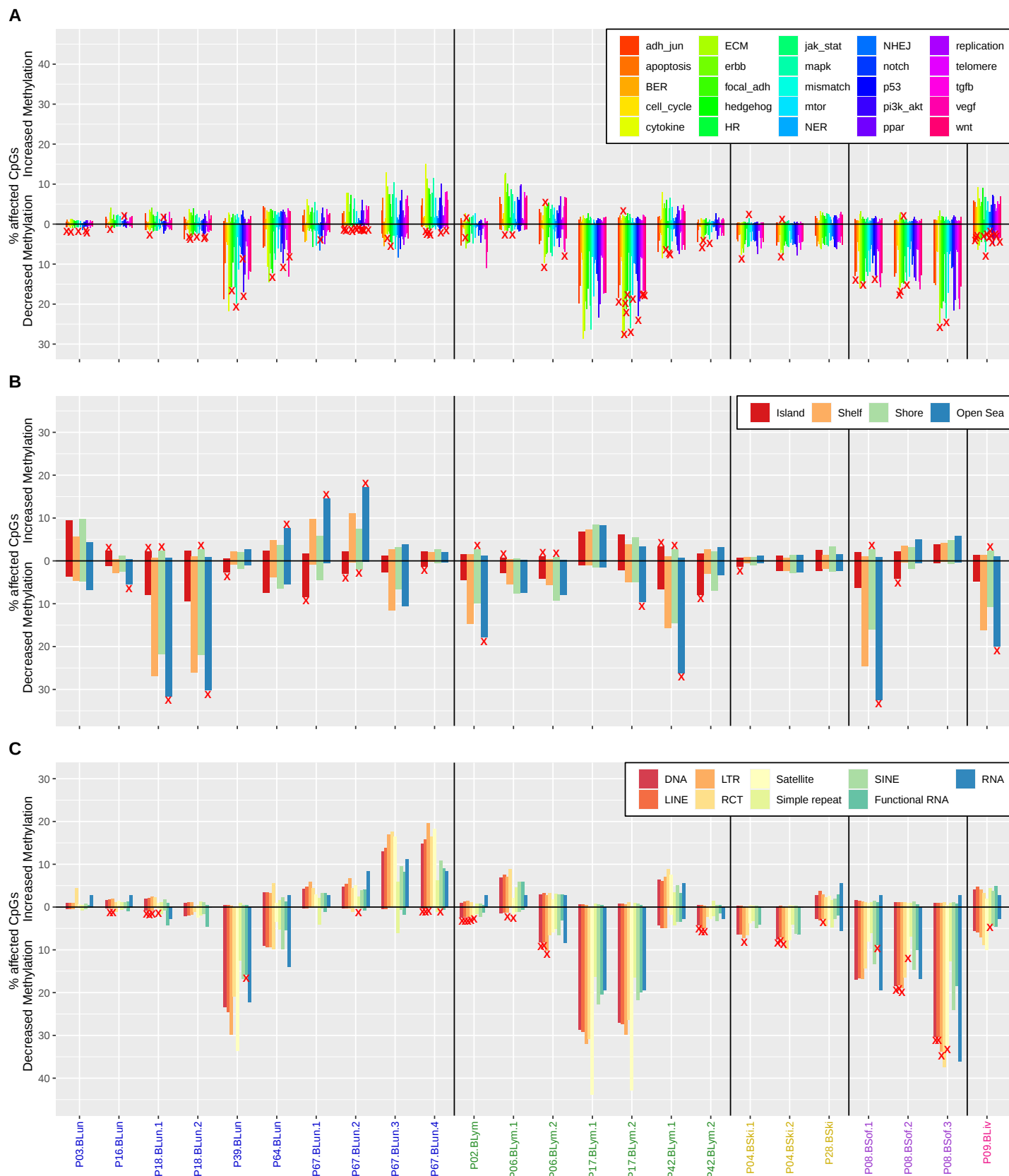


Figure S2: Patient-specific overview of differentially methylated CpGs predicted by the HMM-approach located in signaling pathway genes (A), CpG island categories (B), and transposon families (C). Significant enrichment of a category is marked with a red 'x' (FDR-adjusted p-value < 0.05). The patient-specific metastases pairs are sorted by the tissue in which the extracranial metastasis occurred (x-axis) with brain vs. lung (blue), brain vs. lymph node (green), brain vs. skin (yellow), brain vs. soft tissue (purple) and brain vs. liver (pink).