



**Supplementary Figure 5.** Overlap between significantly differentially expressed genes ( $\log_2$  fold change  $> 2$  and  $p$ -value adjusted for false discovery rate using the Benjamini-Hochberg procedure, with an FDR  $< 0.05$ , in tumors expressing *PRDM9* within each cancer type. The blue histogram represents the number of differentially expressed genes in each cancer type, and the top histogram represents the number of differentially expressed genes shared with cancer types represented in the dotted map. The median number of differentially expressed genes associated with *PRDM9* expression across cancer types was 122.5, with the lowest being 3 (Renal cell cancer) and the highest being 808 (Liver hepatocellular carcinoma).