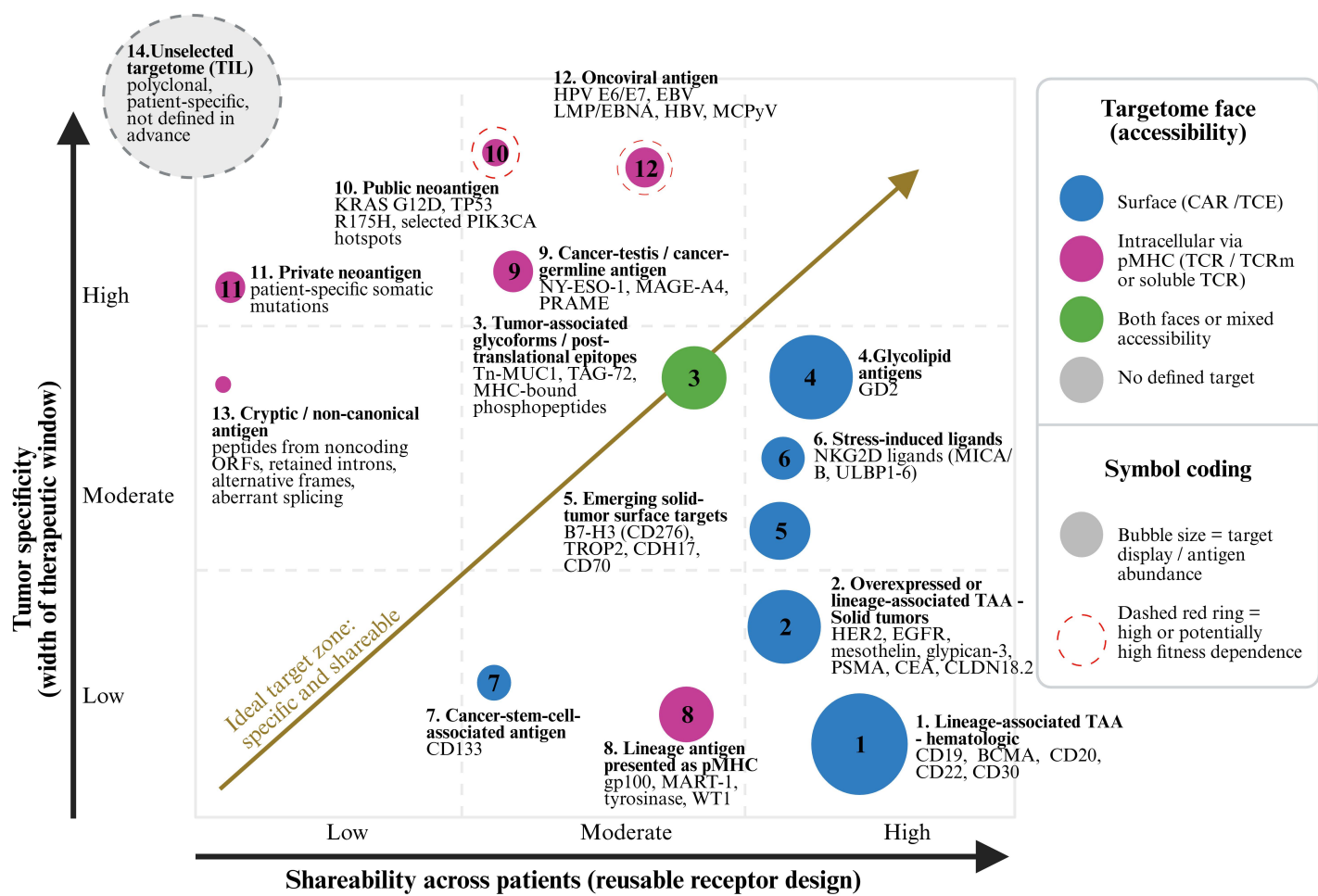


Supplementary Figure 1



Supplementary Figure 1. The antigen-class landscape of the tumor targetome. Schematic representation of the fourteen antigen classes compared in Table 2; numbering follows the order of the table rows. Each class is positioned by shareability across patients (horizontal axis), which determines whether a single receptor design can be reused, and by tumor specificity (vertical axis), which sets the width of the therapeutic window. Symbol size indicates target display — surface antigen density for CAR targets and pMHC abundance for TCR targets — and a dashed red ring marks classes in which loss of the target is expected, or may be expected, to impose a fitness cost on the tumor. Color denotes the face of the targetome on which a class is accessible, and therefore the receptor class best suited to engage it: surface (CAR or T-cell engager), intracellular via peptide–MHC (TCR, TCR-mimic antibody, or soluble TCR), or both. Tumor-infiltrating lymphocyte therapy (class 14) is shown outside the plot area because no target is selected in advance. Notably, the upper-right region, in which high specificity, high shareability, and high target display would coincide, is unoccupied; this trade-off, rather than the merit of any single class, is the central constraint on target selection. Positions are qualitative and context-dependent, and individual targets within a class may deviate from the position of the class.