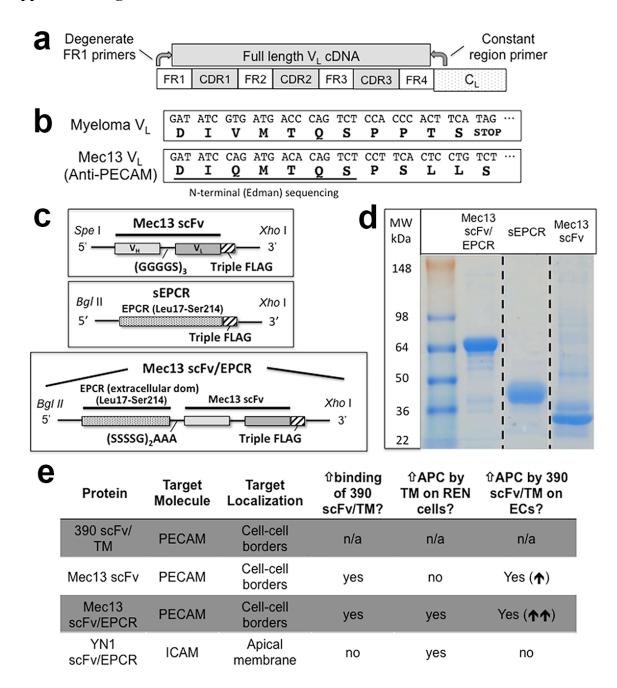
## **Supplemental Figure 1:**



Supplemental Figure 1. Cloning, assembly, and purification of Mec13 scFv, sEPCR, and Mec13 scFv/EPCR fusion protein. (a) The typical approach to PCR cloning of variable heavy and light chain regions ( $V_H$  and  $V_L$ ) utilizes degenerate 5' primers corresponding to the beginning of the FR1 region and a 3' primer corresponding to the start of the constant region. (b) In the case of the Mec13 hybridoma, the typical approach amplified only the myeloma  $V_L$ , which is nearly identical to the PECAM-specific  $V_L$  at the N-terminus of FR1 region. N-terminal (Edman) sequencing was used to identify a one amino acid difference (Gln vs. Val). Degenerate primers were synthesized and paired with the 3' constant region primer, enabling amplification of a full-length cDNA for the Mec13  $V_L$ . (c) Assembly of  $V_H$  and  $V_L$  sequences into Mec13 scFv and Mec13 scFv/EPCR constructs. (d) SDS PAGE gel electrophoresis of Mec13 scFv, soluble EPCR, and Mec13 scFv/EPCR fusion protein shows relative size and purity. (e) Summary of key fusion proteins and scFv's, their surface targets, and their effects.