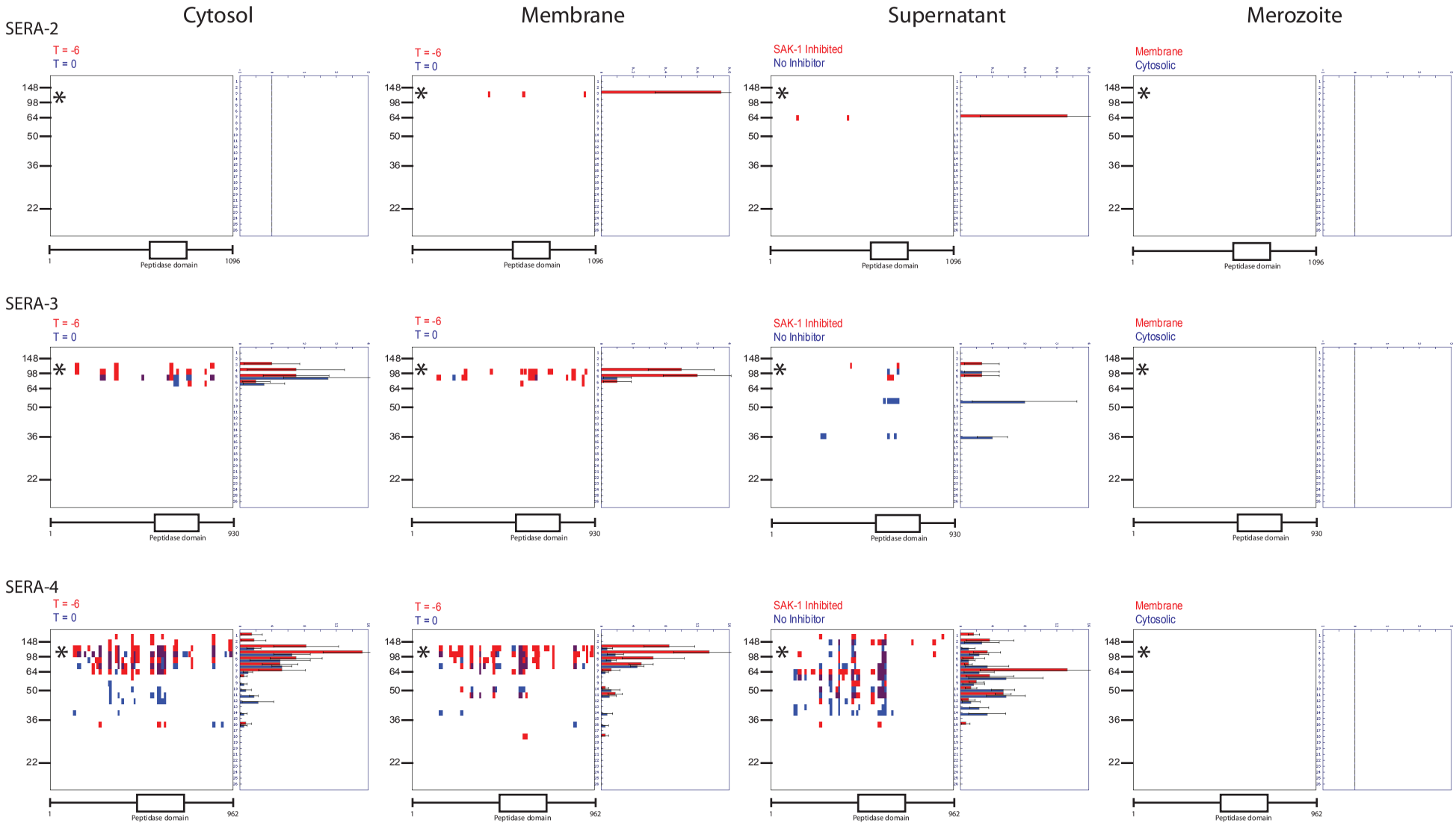
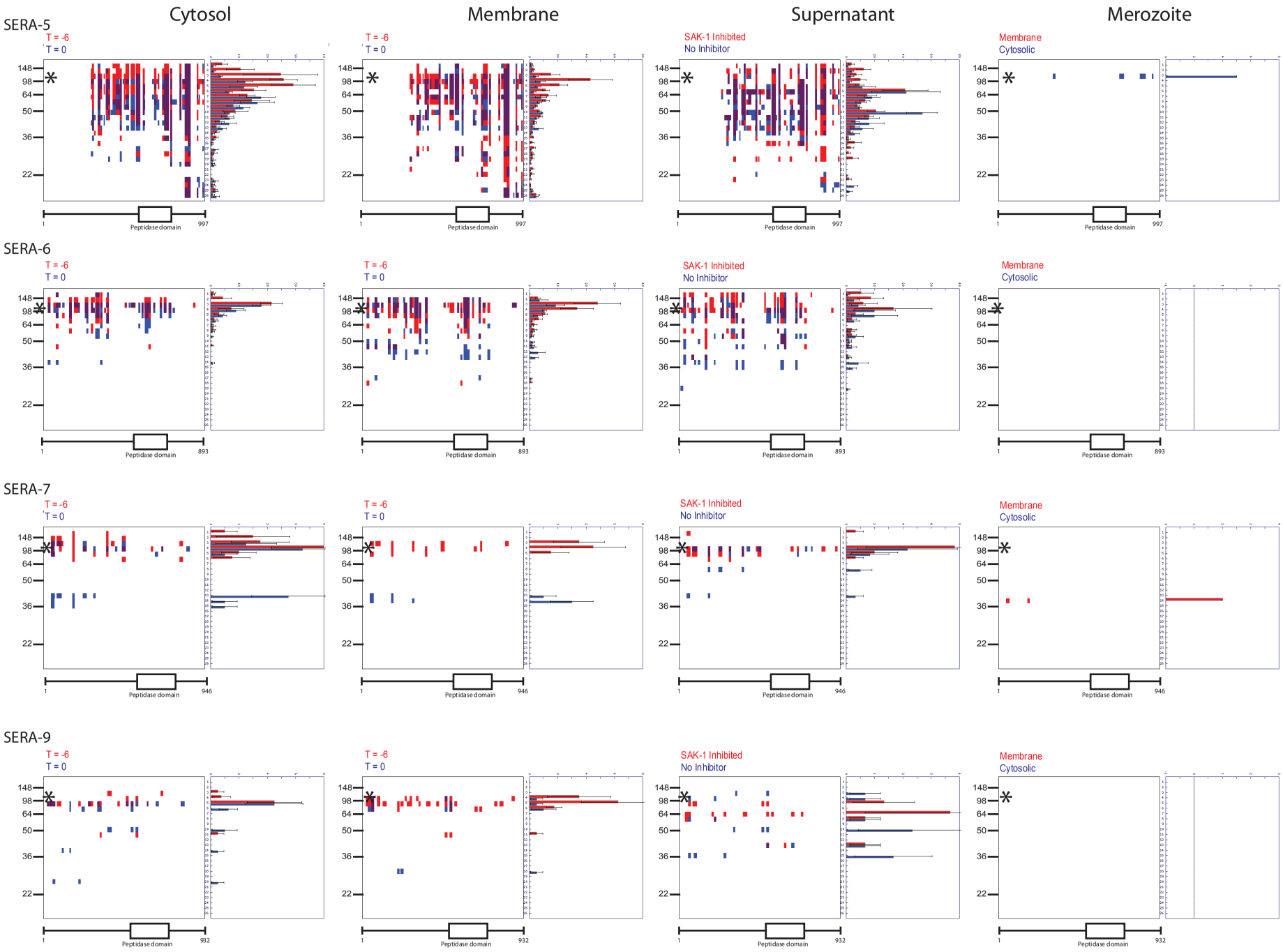
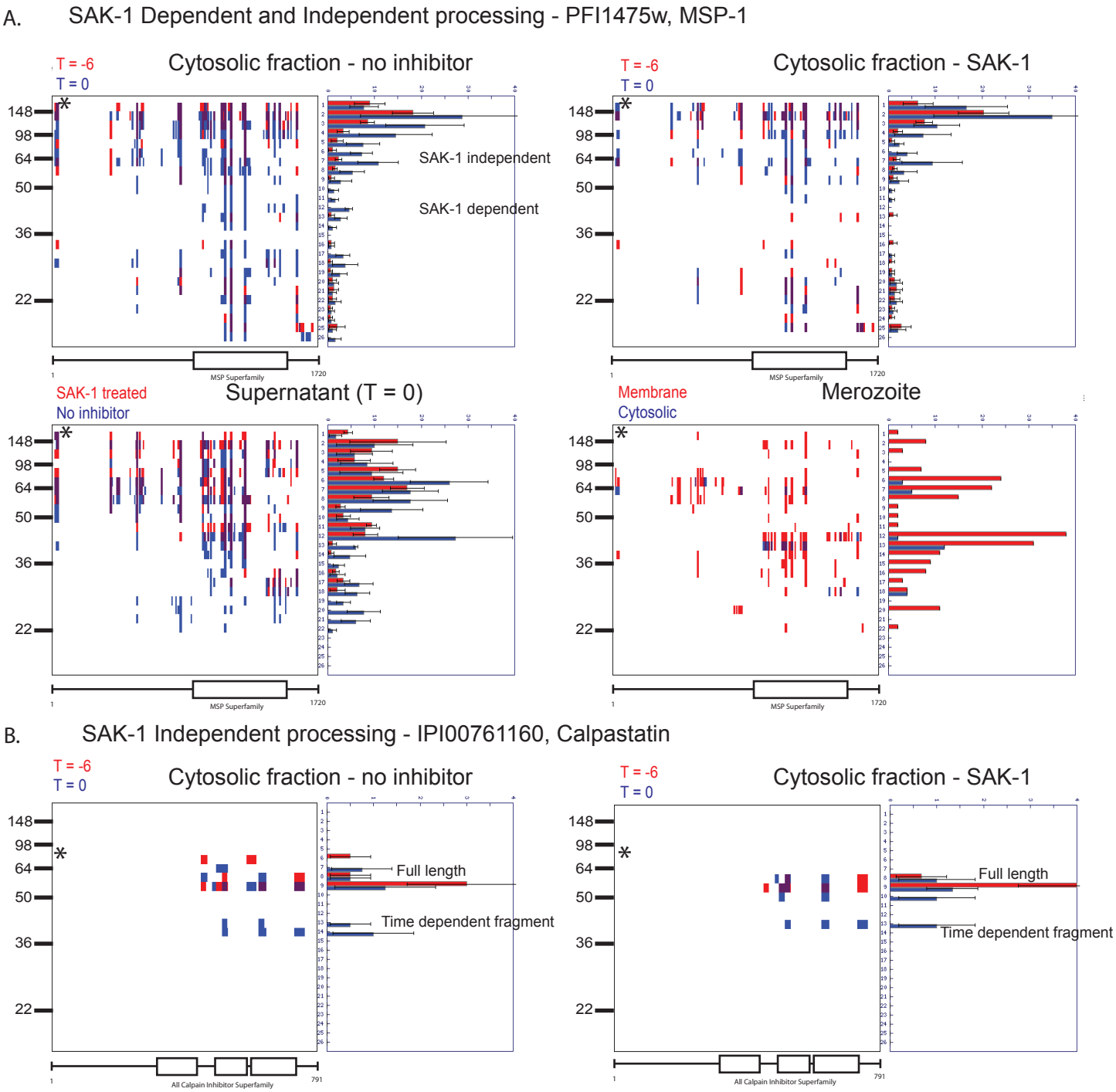


Supplemental Figure 1. Proteolytic maturation of the SERA proteins. Peptographs of the SERA proteins identified in the PROTOMAP dataset. Samples for each SERA protein in the cytosolic, membrane, supernatant and merozoite fractions are shown. These compare T= 0 (blue) to T= -6 (red) for the cytosol / membrane fractions, SAK-1 treated (red) and untreated (blue) for the supernatant and membrane (red) and cytosol (blue) for the purified merozoite fraction. Note that only SERA-5 and SERA-7 peptides were detected in the merozoite samples.

Supplemental Figure 1 Continued





Supplemental Figure 2. A. Processing of MSP-1. Peptographs of MSP-1 for the cytosolic fraction (upper) for normal (left) and SAK-1 treated (right) samples. Note the time dependent, DPAP3 independent processing event in both (bands 6-9) as well as the DPAP3 dependent processing (right, bands 12-13 and 17-19). The processing is also observed in the supernatant fractions which directly compare MSP-1 processing in the supernatant for the control (blue) and SAK-1 treated (red) experiments. The peptograph derived from purified merozoites (bottom right) is shown for comparison. B. SAK-1 Independent processing of Calpastatin. Peptographs from the cytsolic fraction are shown for mammalian calpastatin. The processed fraction is present in both the SAK-1 and untreated samples. * identifies predicted size of full-length proteins (PFI1475w – 195.7 kDa, IPI00761160 – 84.9 kDa)