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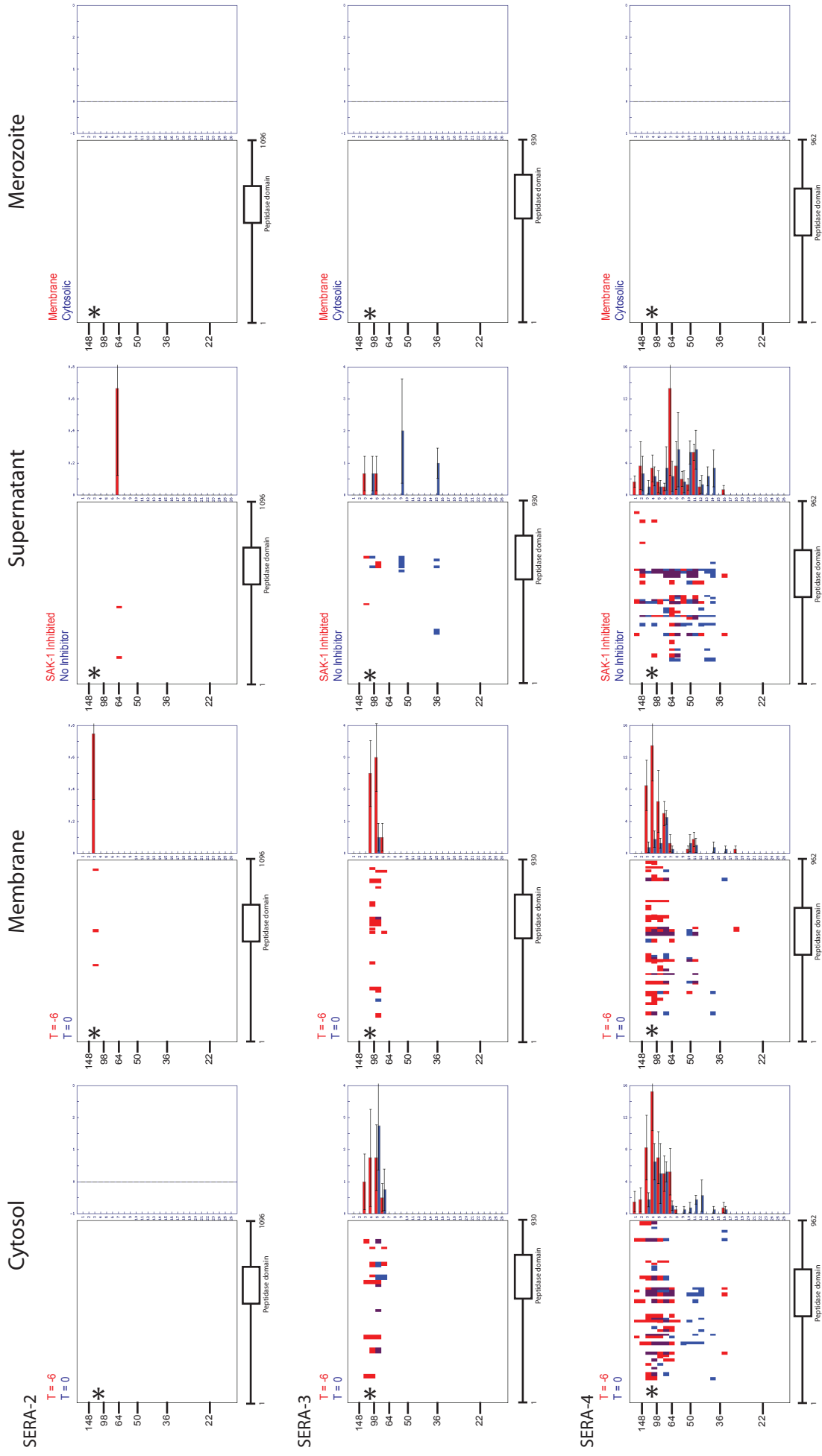
Bowyer, PW; Simon, GM; Cravatt, BF; Bogyo, M (2011) Global profiling of proteolysis during rupture of *Plasmodium falciparum* from the host erythrocyte. *Molecular & cellular proteomics* , 10 (5). M110.001636. ISSN 1535-9476

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#### Usage Guidelines

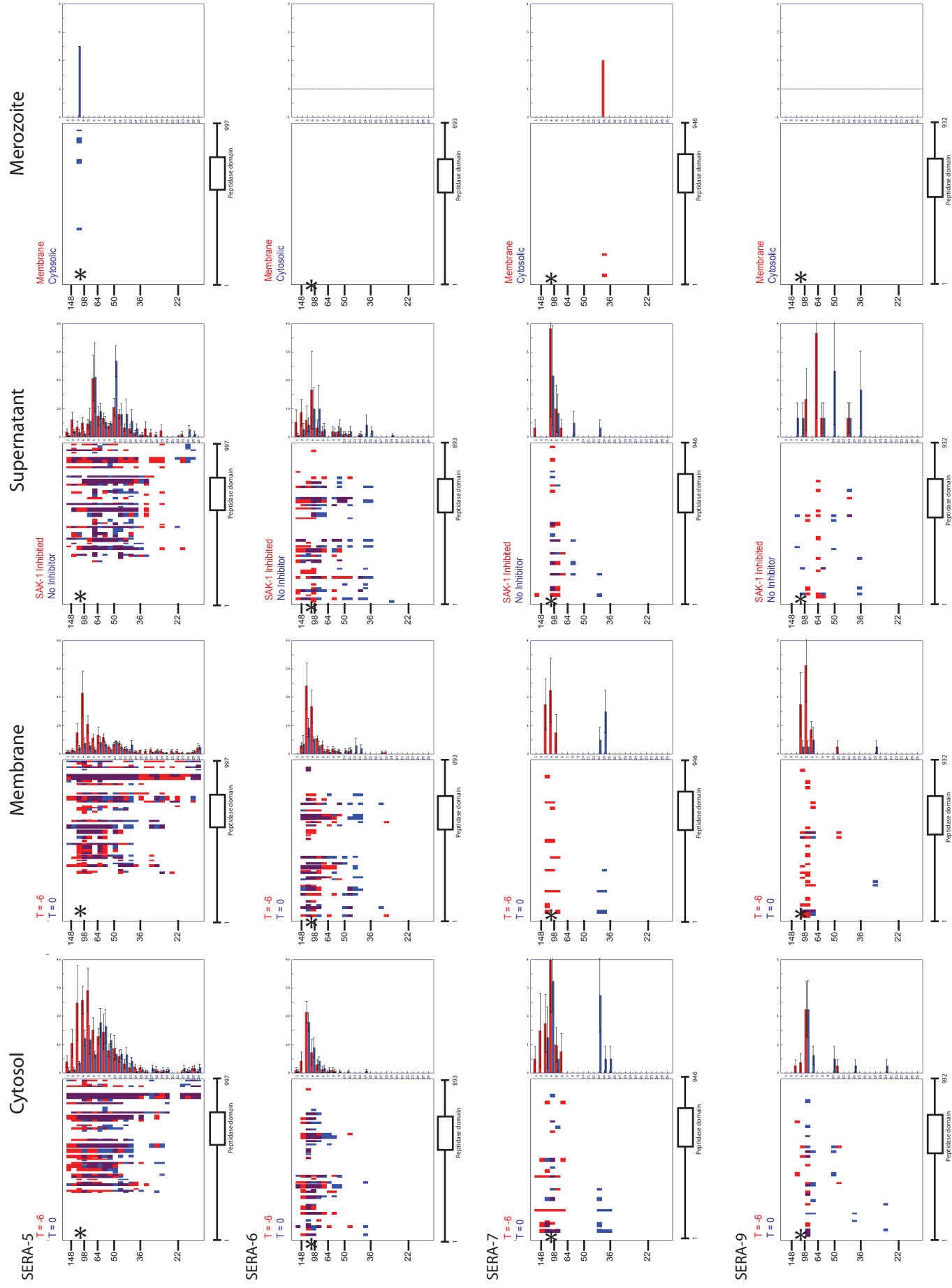
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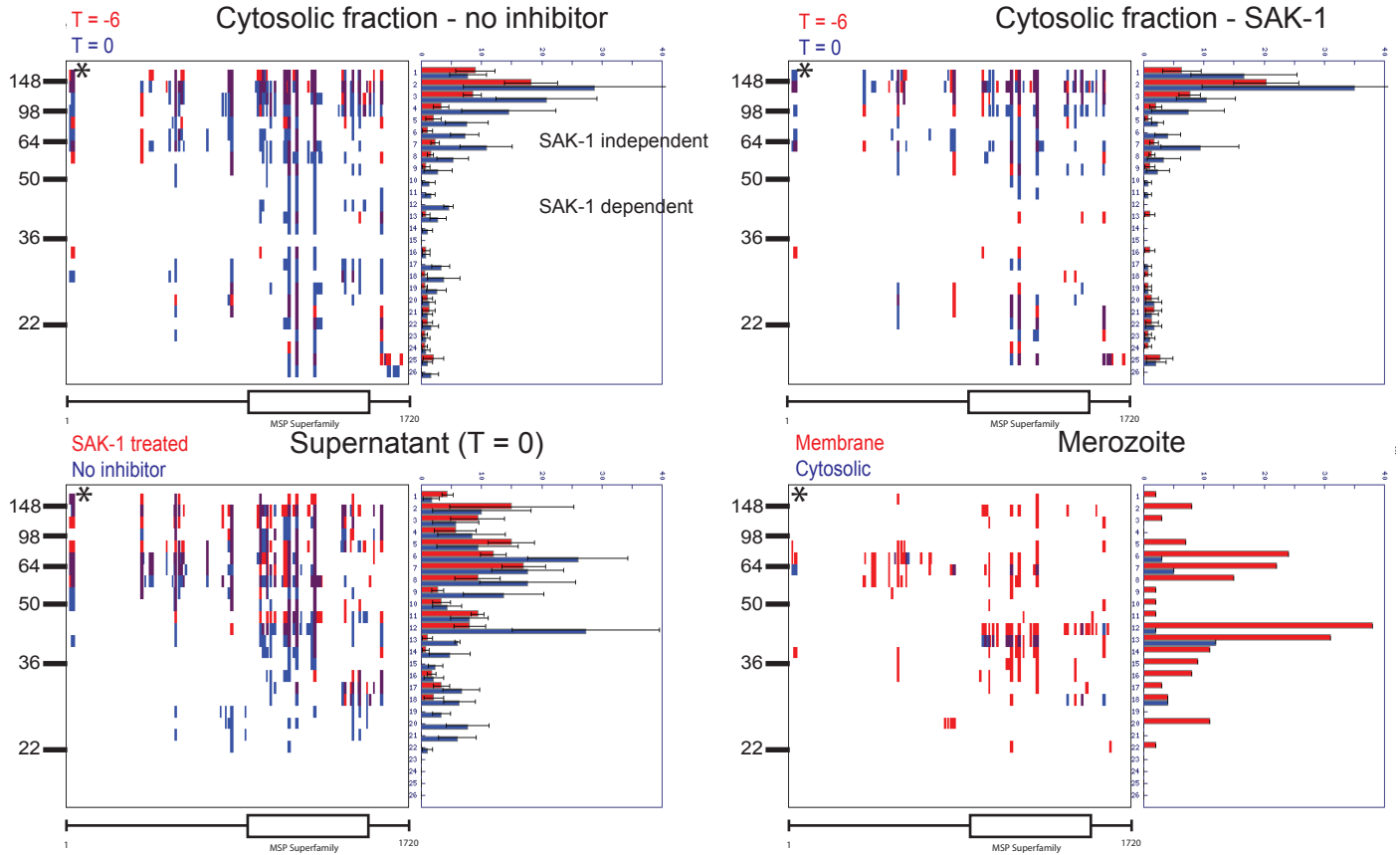


**Supplemental Figure 1.** Proteolytic maturation of the SERA proteins identified in the PROTOMAP dataset. Samples for each SERA protein in the cytosolic, membrane, supernatant and merozoite fractions are shown. These compare T=0 (blue) to T=-6 (red) for the cytosol / membrane fractions, SAK-1 treated (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.

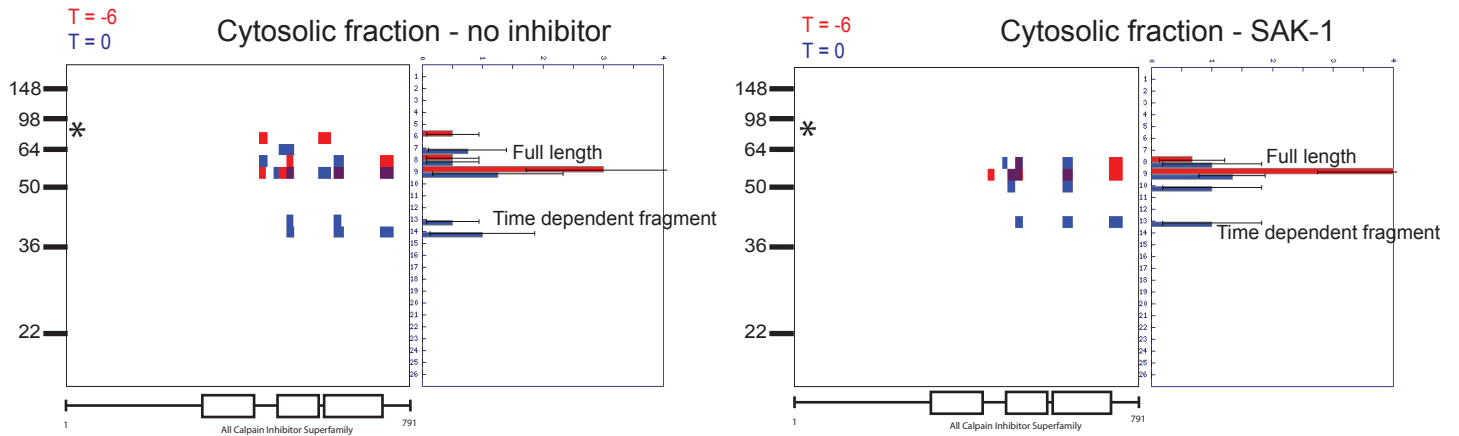
# Supplemental Figure 1 Continued



A. SAK-1 Dependent and Independent processing - PFI1475w, MSP-1



B. SAK-1 Independent processing - IPI00761160, Calpastatin



**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 cytosolic 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)