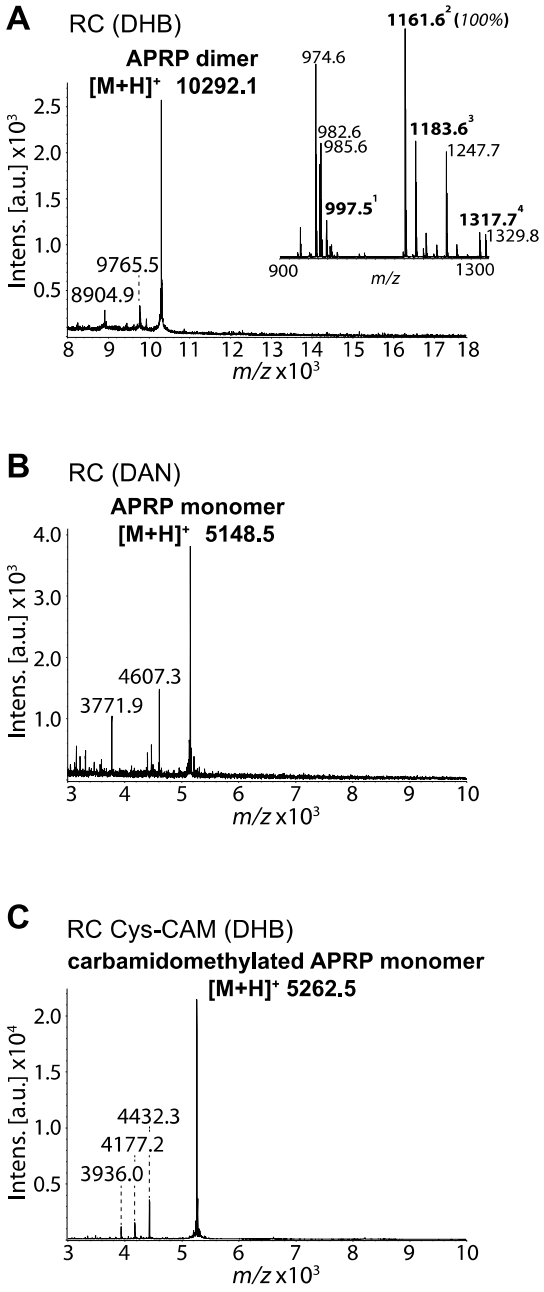


**Figure S1** Mass spectrometry characterization of APRP dimers and monomers. MALDI-TOF mass spectra in positive reflectron mode from single *Drosophila* RC preparations before (**A**) and after (**B**) reduction of disulfide bonds. (**C**) Carbamidomethylated APRP monomer in a pooled extract of 20 RCs. (**A**) Direct tissue profiling of a single RC showed mass matches for all known AKH products in the mass range *m/z* 900-1300 (inset, 1 pQLTFSPDWa, 997.5 $[M+Na]^+$; 2 pQLTFSPDWGK-OH, 1161.6 $[M+H]^+$, 3 1183.6 $[M+Na]^+$; 4 pQLTFSPDWGKR-OH, 1317.7 $[M+H]^+$). The ion signal recorded at *m/z* 10292.1 matched a putative APRP dimer. (**B**) Reduction of cysteine bonds by direct profiling of a single RC with DAN matrix revealed a mass match for a possible APRP monomer (*m/z* 5148.5) and confirmed a dimeric structure. The ion signal was not recorded prior to reduction of disulfide bonds. (**C**) Carbamidomethylation of cysteines resulted in a mass shift of *m/z* +114 and confirmed the presence of two cysteines. Subsequent fragmentation of the precursor ion *m/z* 5262.5 confirmed the predicted APRP monomer sequence (see Fig. S2). All ion signals are labeled with monoisotopic masses. Cys-CAM, carbamidomethylation of cysteines.