Supplemental Information

Figure I. Histogram showing the number of PLS regression models in which each spot occured.

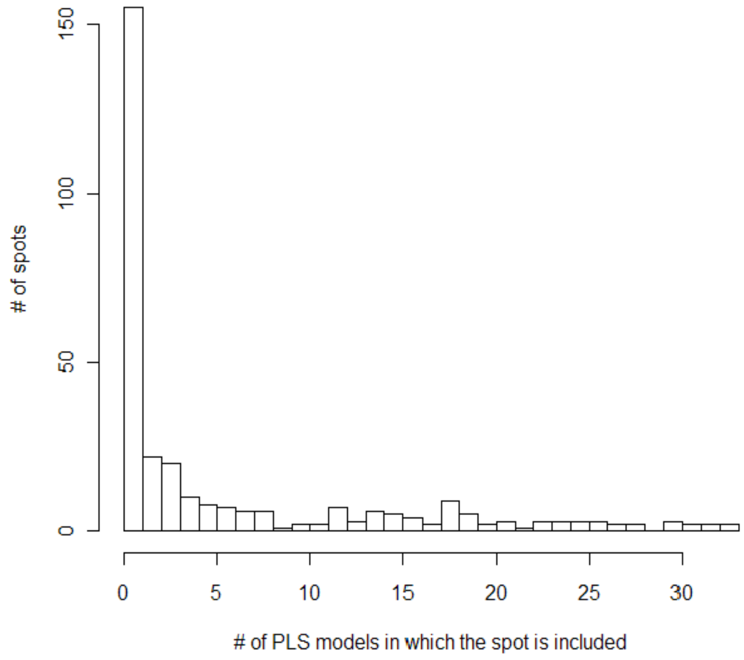


Figure II. Multidimensional scaling 2D embeddings using a similarity metric based on Kendall's correlation, before (left) and after variable selection (right), showing the relative similarity between samples. Samples are labeled with "A" (for "anesthesia") or "C" (for "crowded") and color-coded according to sampling time ("yellow", "orange" or "red", meaning t = 0 h, 6 h and 48 h, respectively).

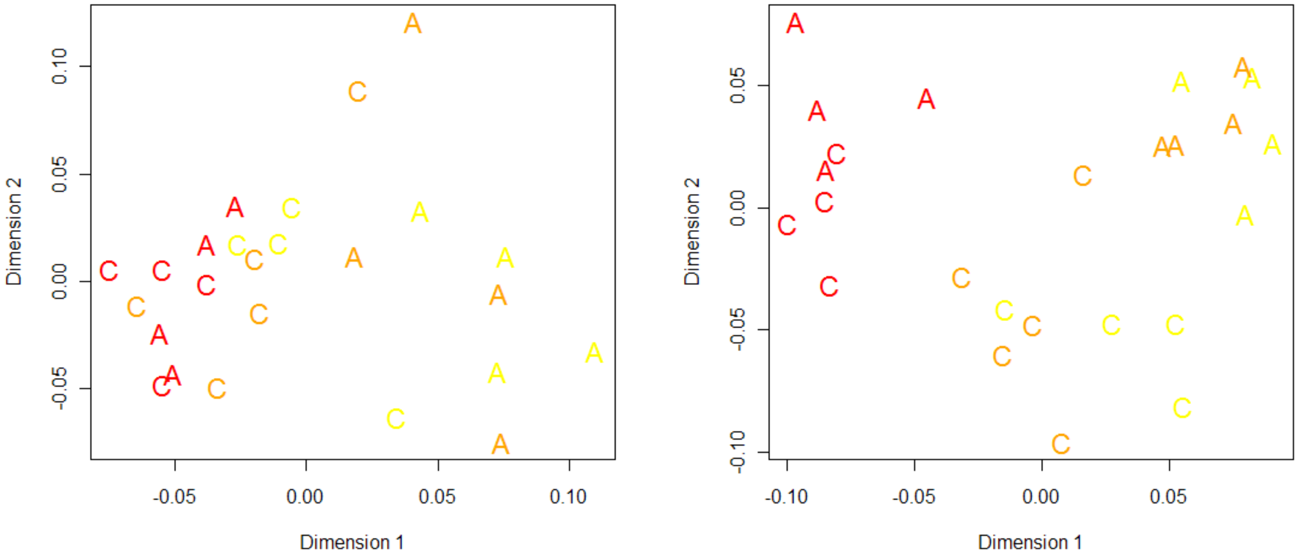


Figure III. Post-mortem profile of the muscle pH of gilthead seabream subjected to different harvesting conditions (previously published in Matos et al., 2010).

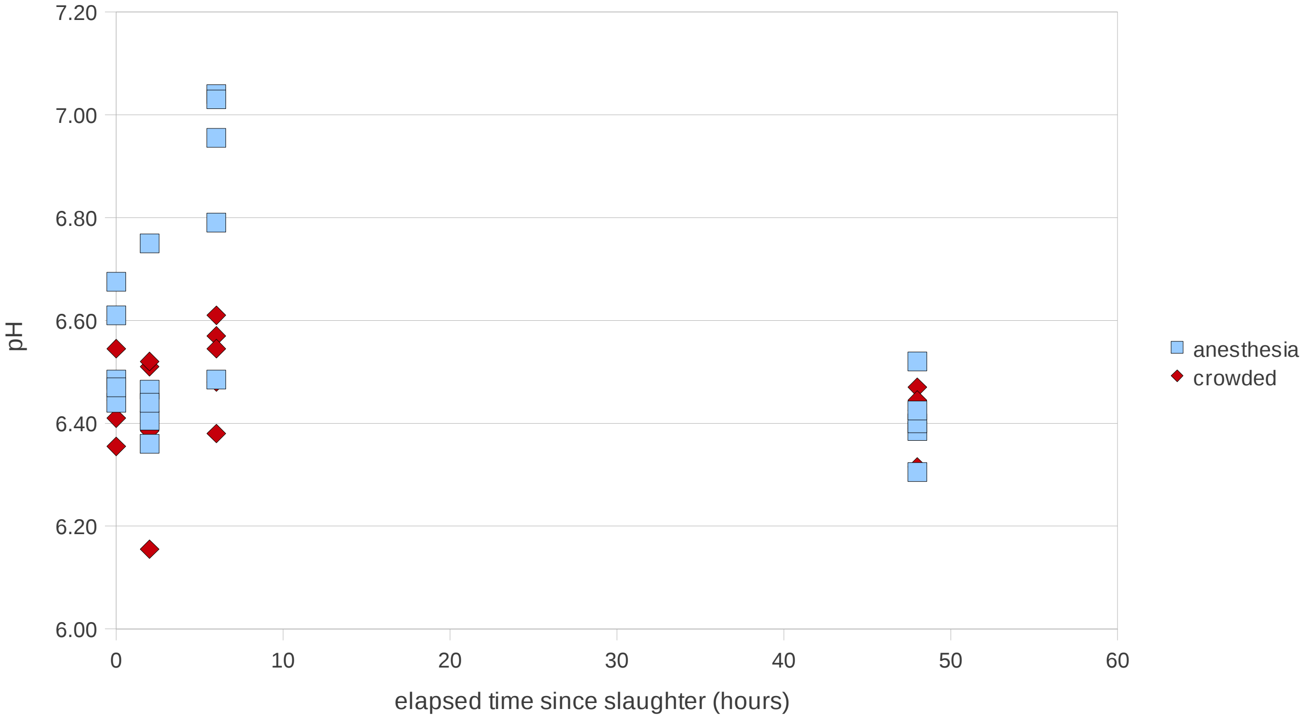


Figure IV. Scatterplots showing the relationship between measured muscle pH and the abundance of two specific protein spots. Samples are labeled with “A” (for “anesthesia”) or “C” (for “crowded”) and color-coded according to sampling time (“yellow”, “orange” or “red”, meaning t = 0 h, 6 h and 48 h, respectively).

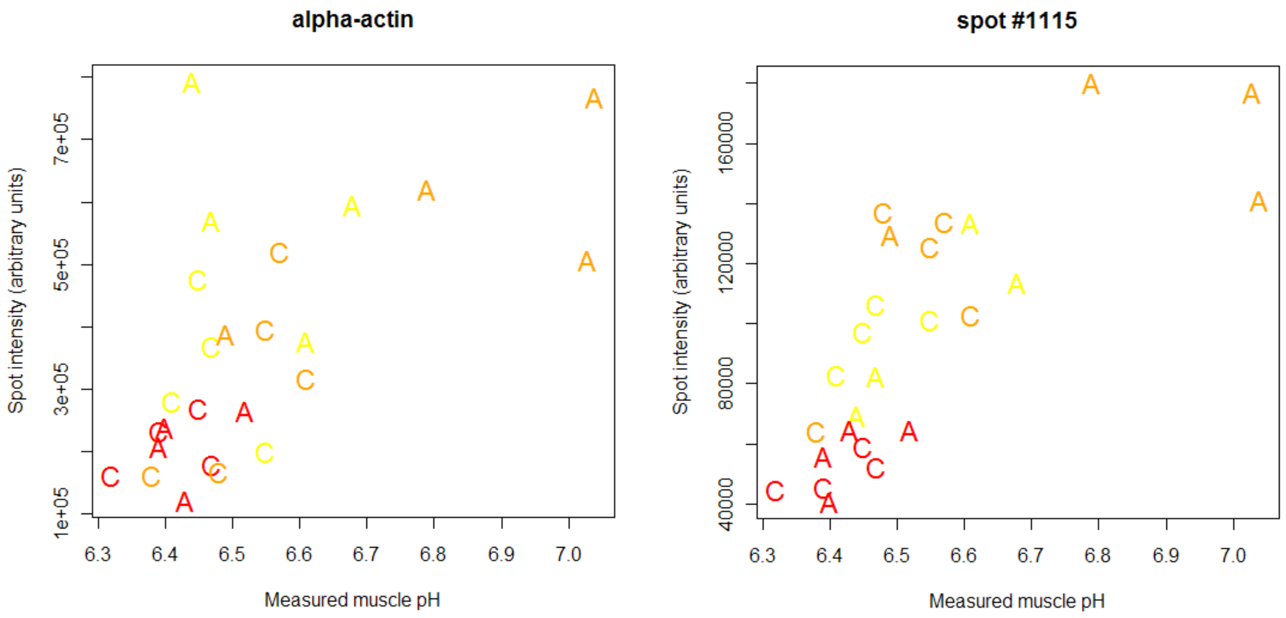


Figure V. Representative examples of obtained CBB-stained 2DE gels, showing how sarcoplasmic profiles evolve post-mortem (at 0h, 6h and 48h post-slaughter) for both experimental groups (“anesthesia” and “crowded”).

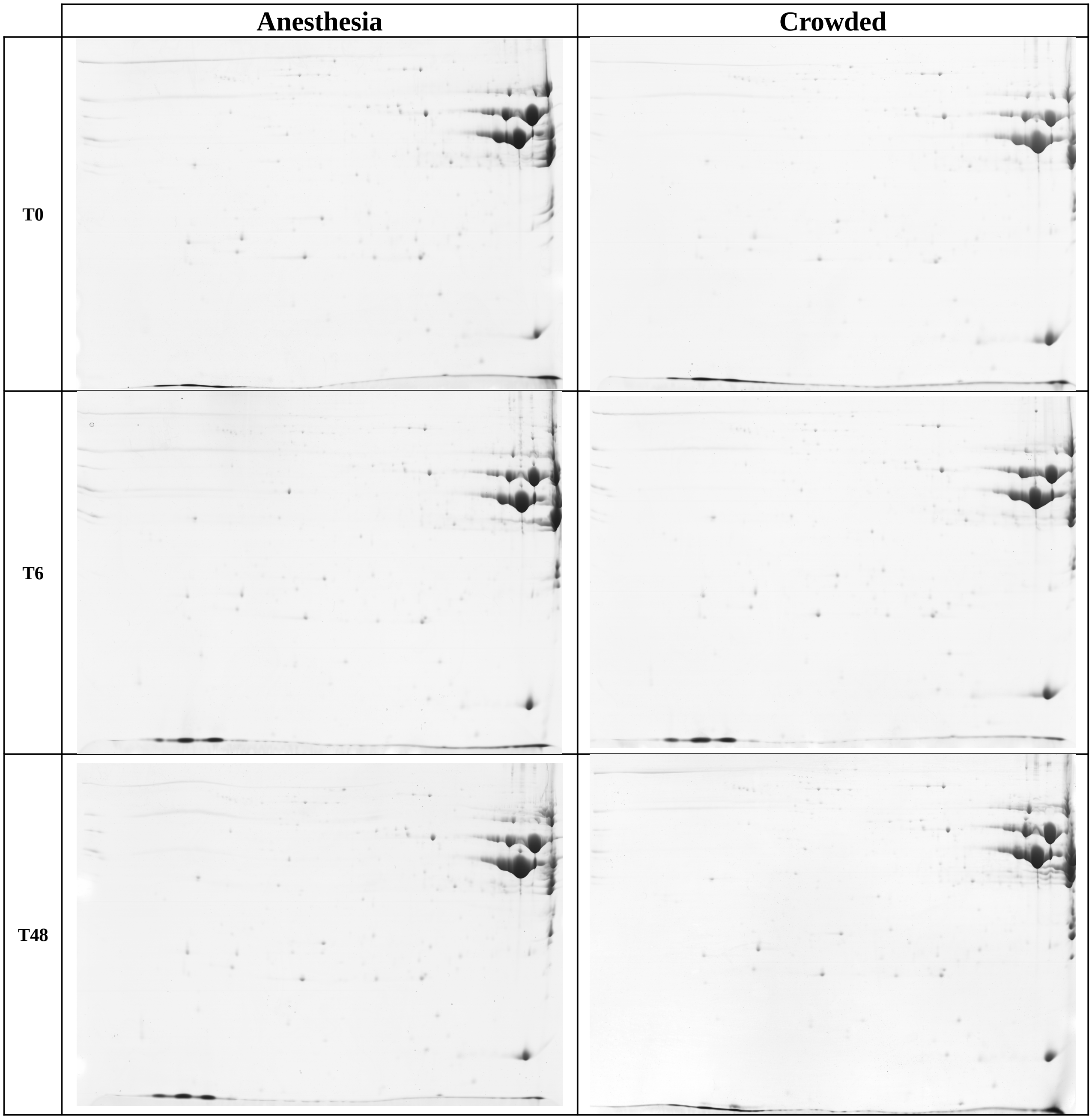


Figure VIa. Time profiles of protein abundance for spots reliably identified by MS. Mean values and standard deviations for each subgroup are reported. Green color denotes “anesthesia” group and red color denotes “crowded” group.

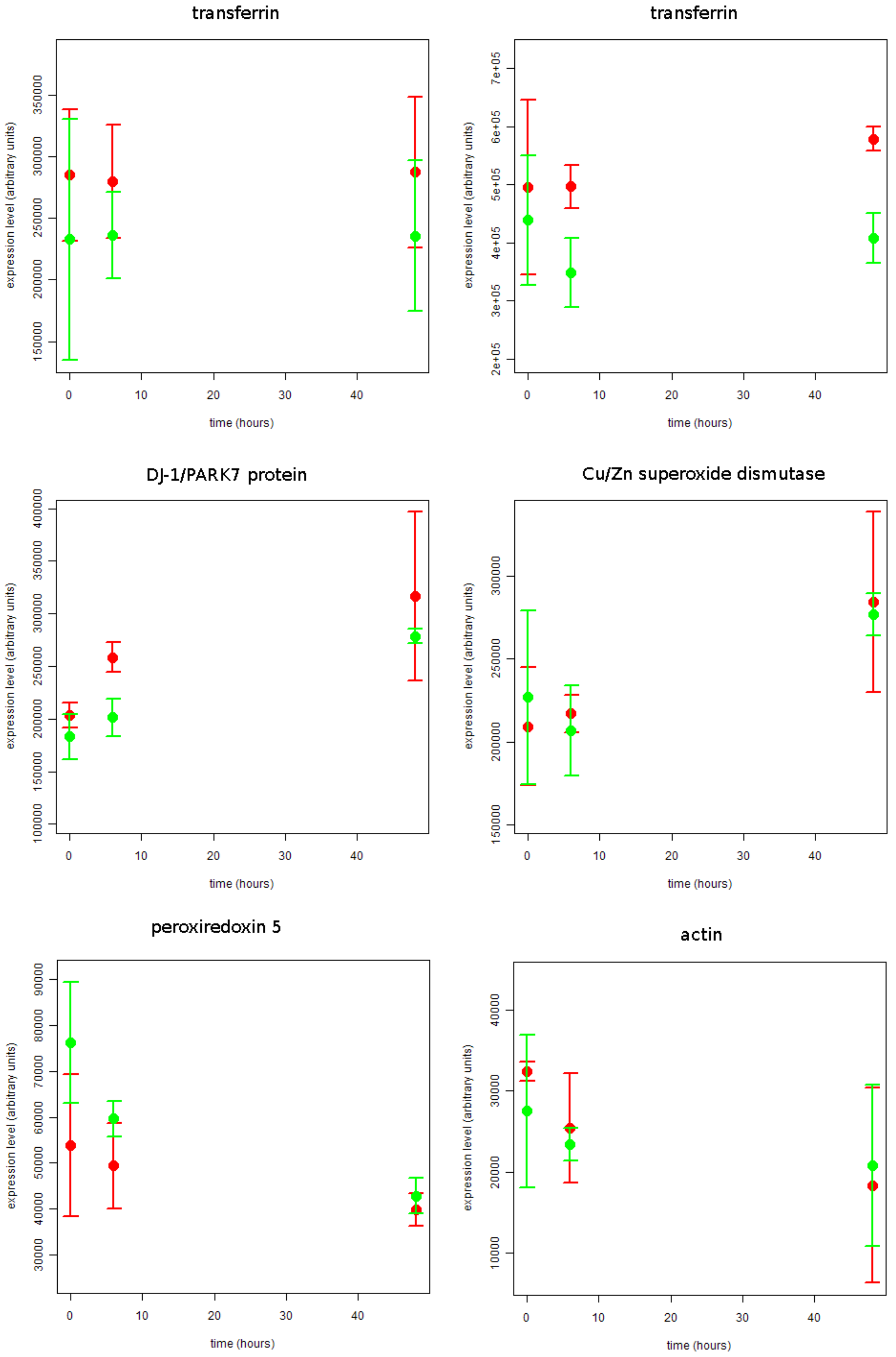


Figure VIb. Time profiles of protein abundance for spots reliably identified by MS. Mean values and standard deviations for each subgroup are reported. Green color denotes “anesthesia” group and red color denotes “crowded” group.

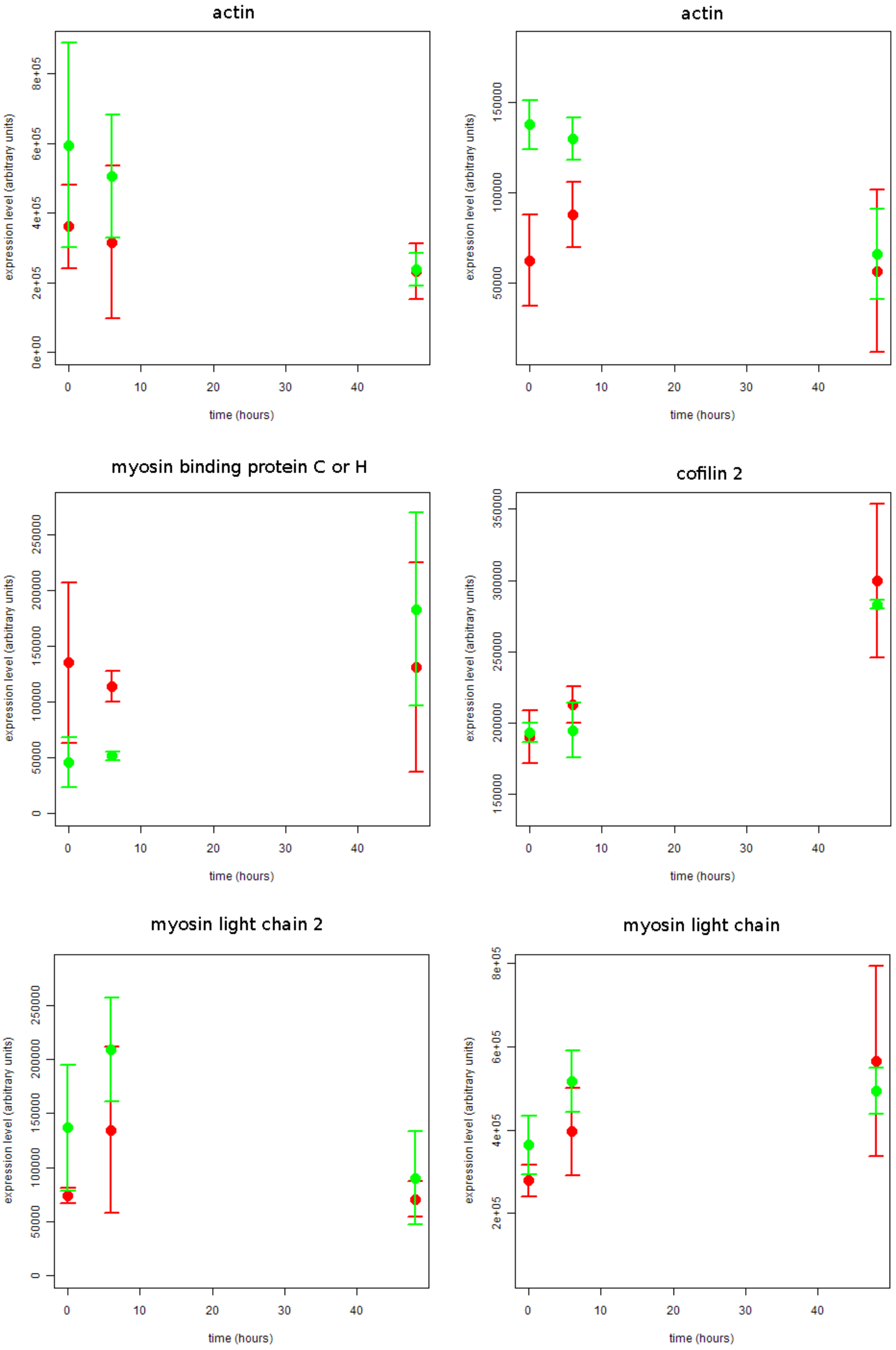


Figure VIc. Time profiles of protein abundance for spots reliably identified by MS. Mean values and standard deviations for each subgroup are reported. Green color denotes “anesthesia” group and red color denotes “crowded” group.

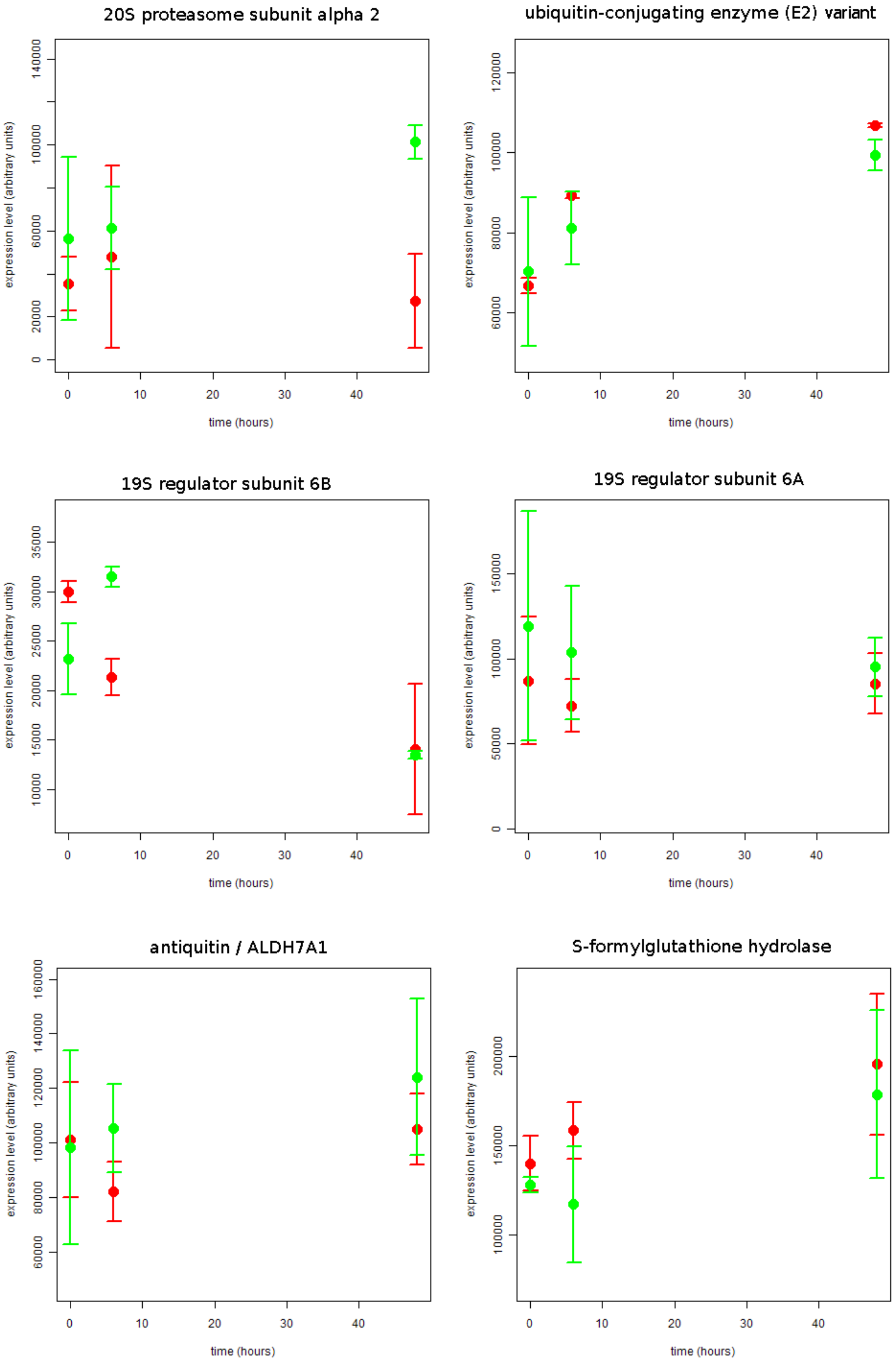
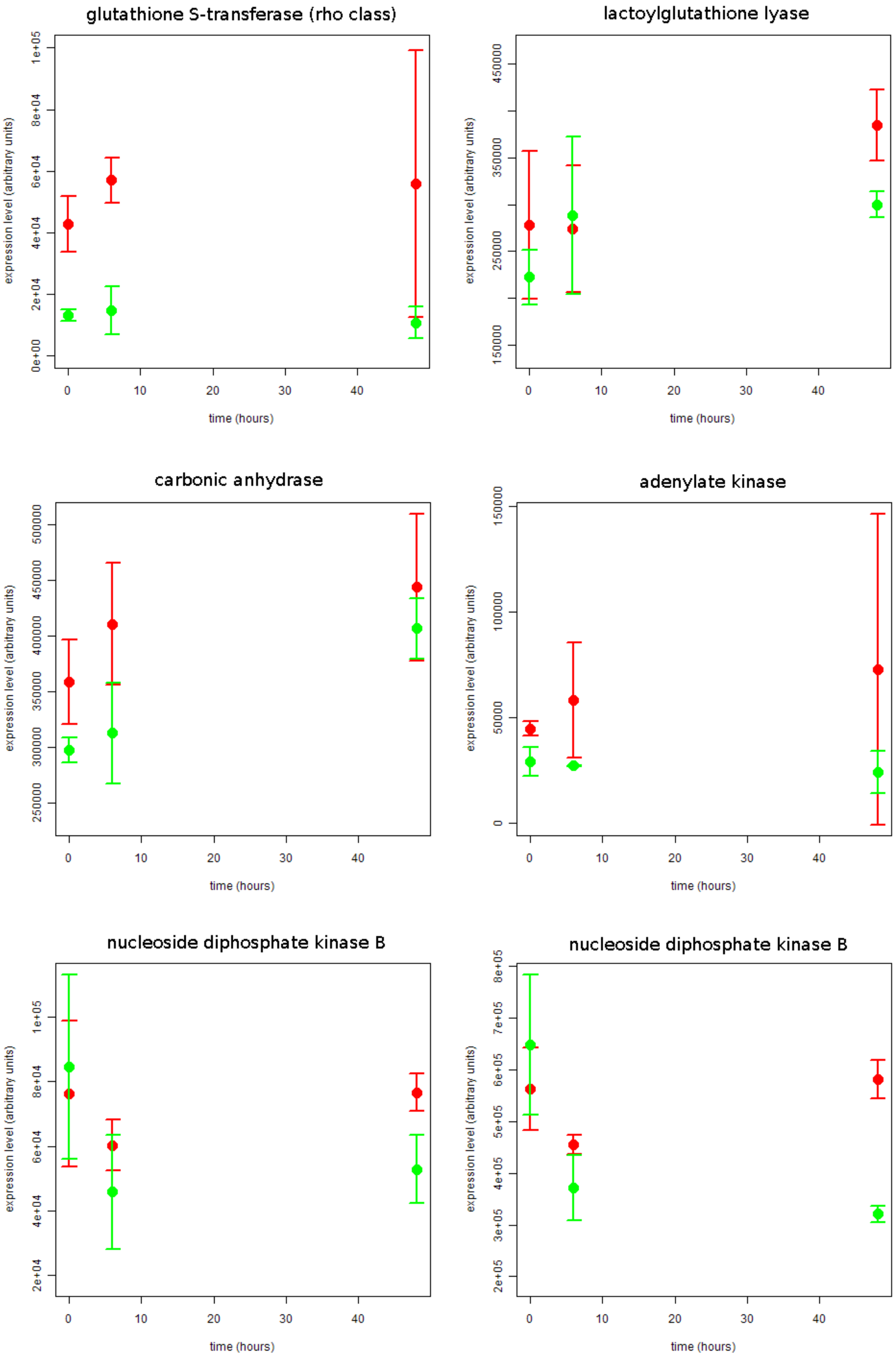


Figure VId. Time profiles of protein abundance for spots reliably identified by MS. Mean values and standard deviations for each subgroup are reported. Green color denotes “anesthesia” group and red color denotes “crowded” group.



glutathione S-transferase (rho class)

lactoylglutathione lyase

carbonic anhydrase

adenylate kinase

nucleoside diphosphate kinase B

nucleoside diphosphate kinase B

Figure VIe. Time profiles of protein abundance for spots reliably identified by MS. Mean values and standard deviations for each subgroup are reported. Green color denotes “anesthesia” group and red color denotes “crowded” group.