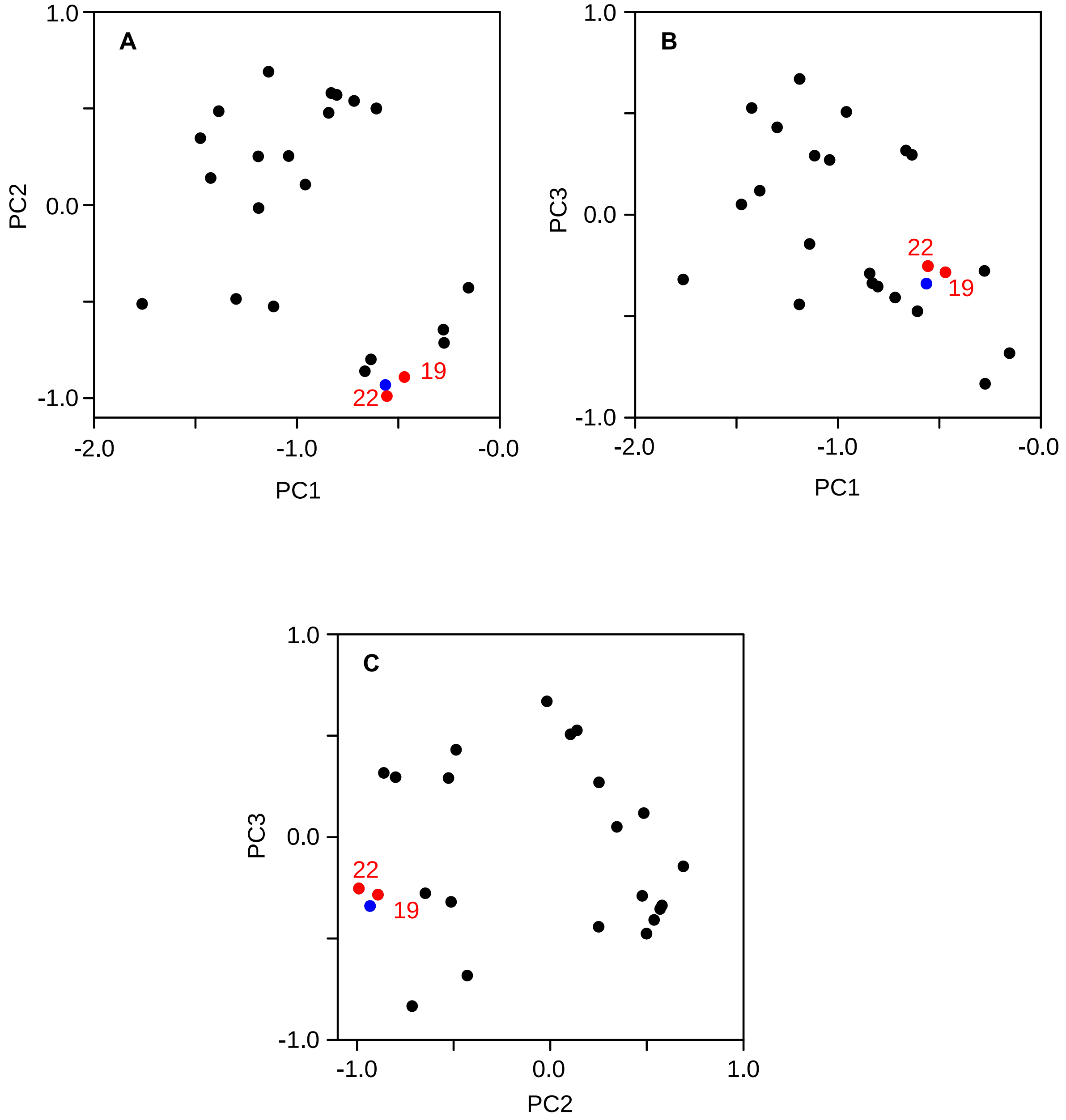
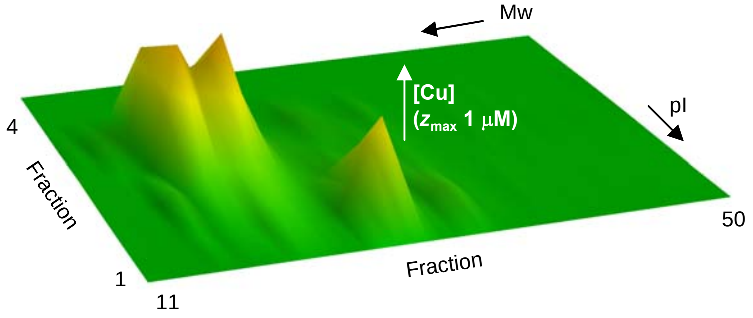
Supplementary Fig. 1. Correlation between the concentration of copper in p1 (*blue*) and the abundance of individual proteins quantified following SDS PAGE by scanning gels and integrating the areas under peaks. Proteins 19 (subsequently CueP) and 22 (*red*) are the best correlating proteins in all statistical analyses. Principal component analyses using components 1 and 2 (*A*), 1 and 3 (*B*) and 2 and 3 (*C*) are shown. Principal component analysis using all three components is shown in Fig. 3*D*.



Supplementary Fig. 2. The distribution of protein bound periplasmic copper in *S.* Typhimurium Δ*cueP*. Periplasmic extracts were resolved by two-dimensional anion exchange (*pI*) into 1ml fractions and size exclusion (*Mr*) chromatography into 0.5 ml fractions and analyzed for metals by inductively coupled plasma-mass spectrometry; the full profile for copper is shown.



Supplementary Fig. 3. A mutant lacking CueP has an increased copper load. Copper contents of wild-type *S.* Typhimurium (*WT*) and Δ*cueP* grown in M9 minimal medium in the presence of 25 µM added copper. Metal contents are shown as atoms cell^{-1} (*black*) or atoms mg^{-1} cellular protein (*gray*).