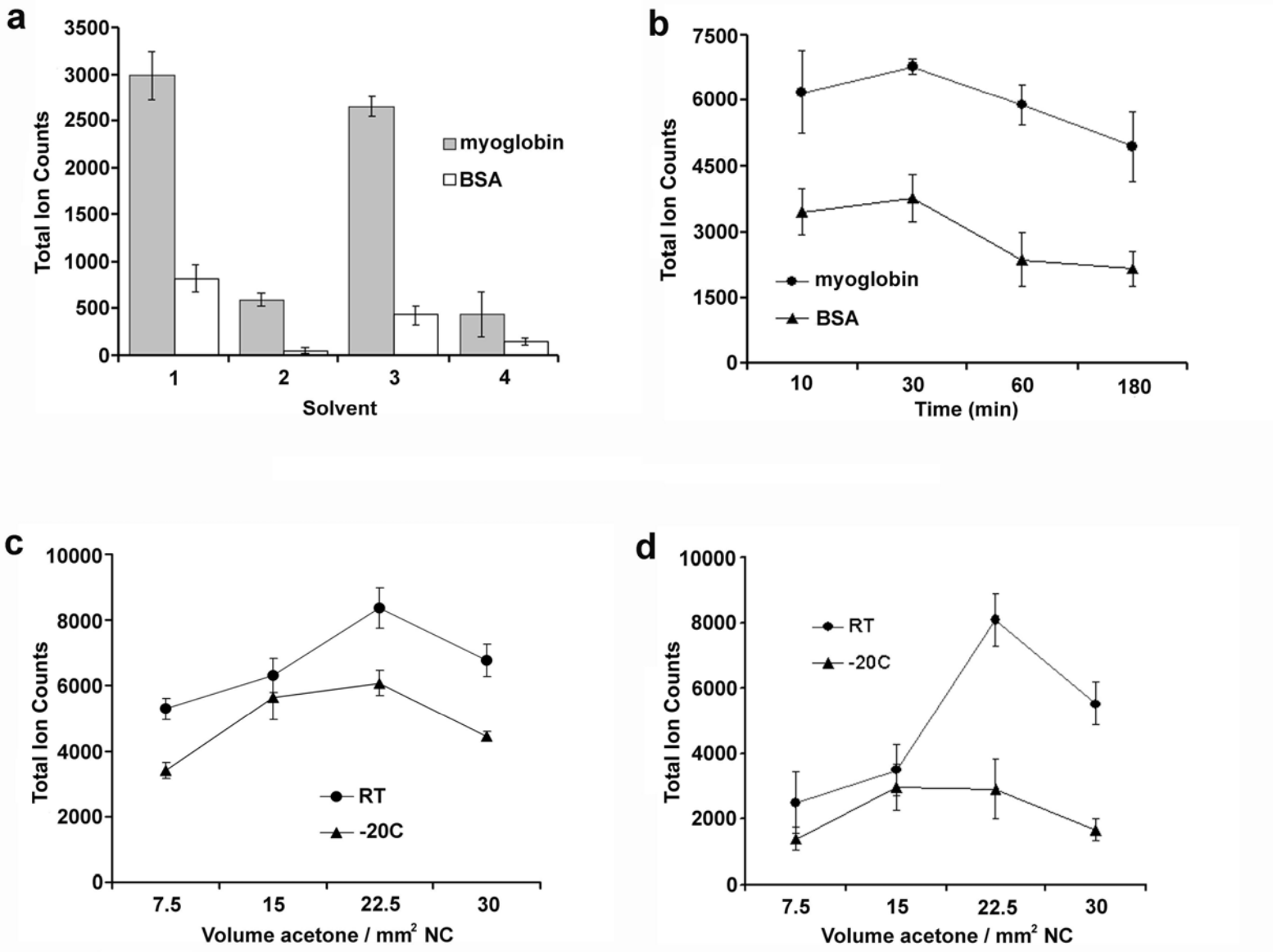
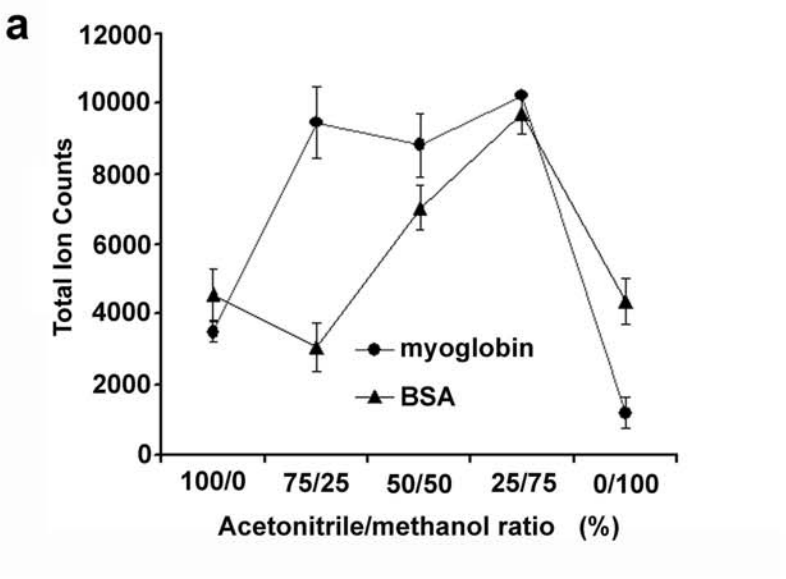
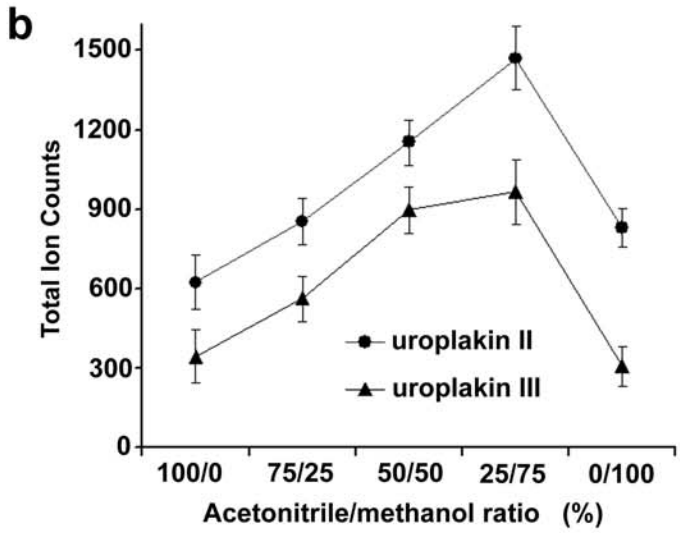
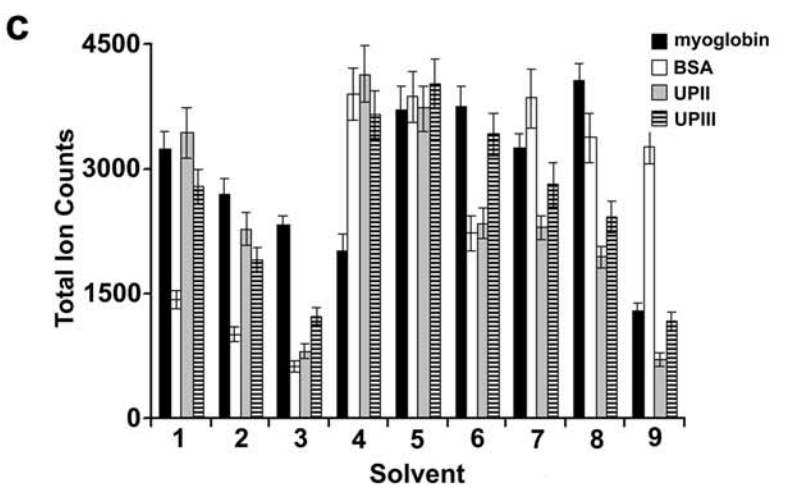
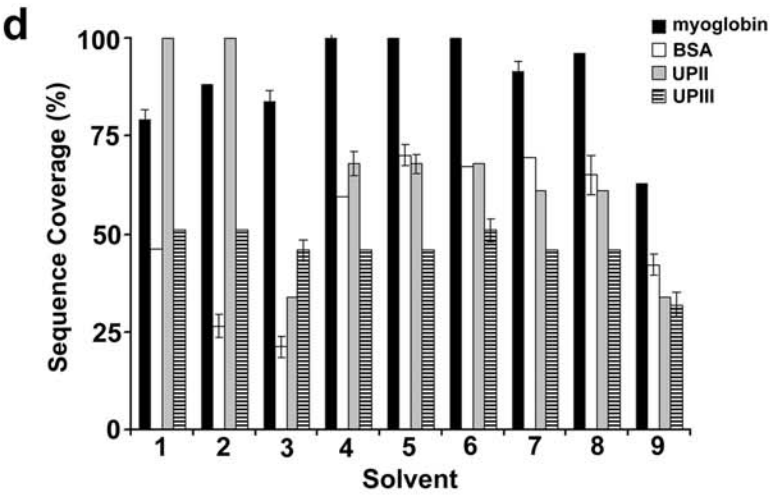


Supplemental Fig. 1
(a) Optimization of the solvent used for precipitation of the proteins/peptides and dissolution of the NC. 1 = acetone, 2 = ethanol, 3 = acetonitrile, 4 = methanol; (b) Optimization of the precipitation time; (c) Optimization of the temperature and the volume of acetone for myoglobin; (d) Optimization of the temperature and the volume of acetone for BSA.



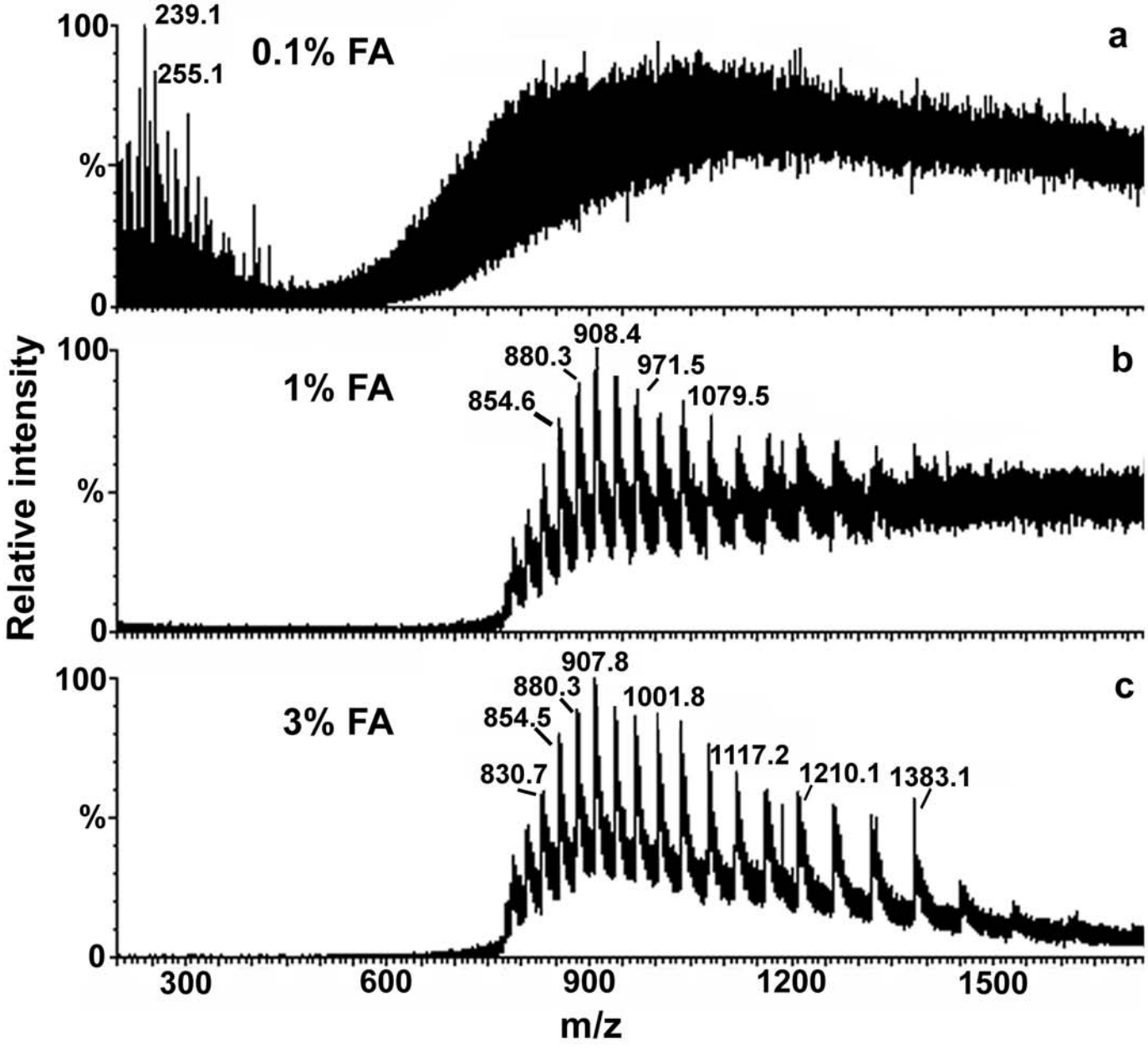




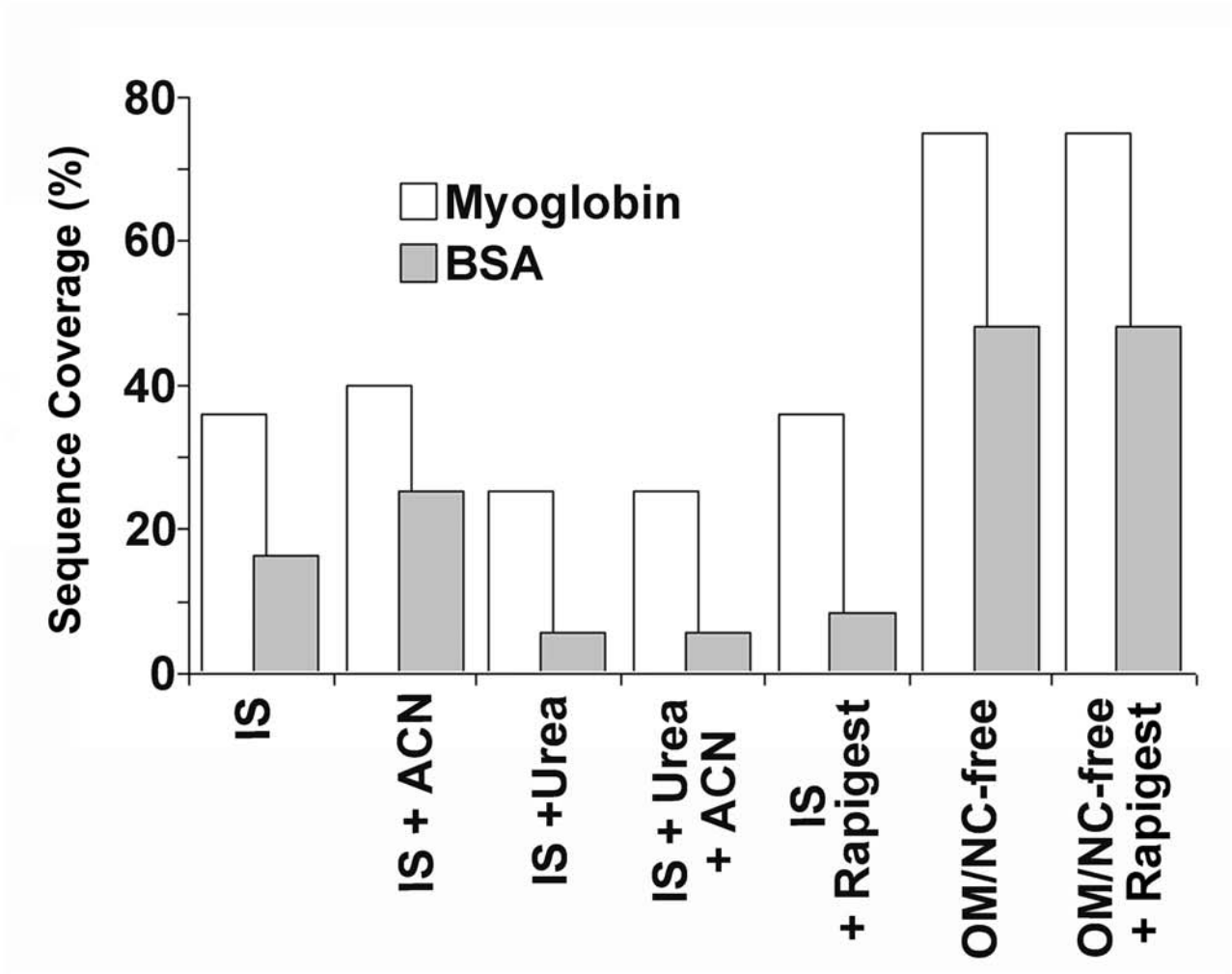


Supplemental Fig. 2

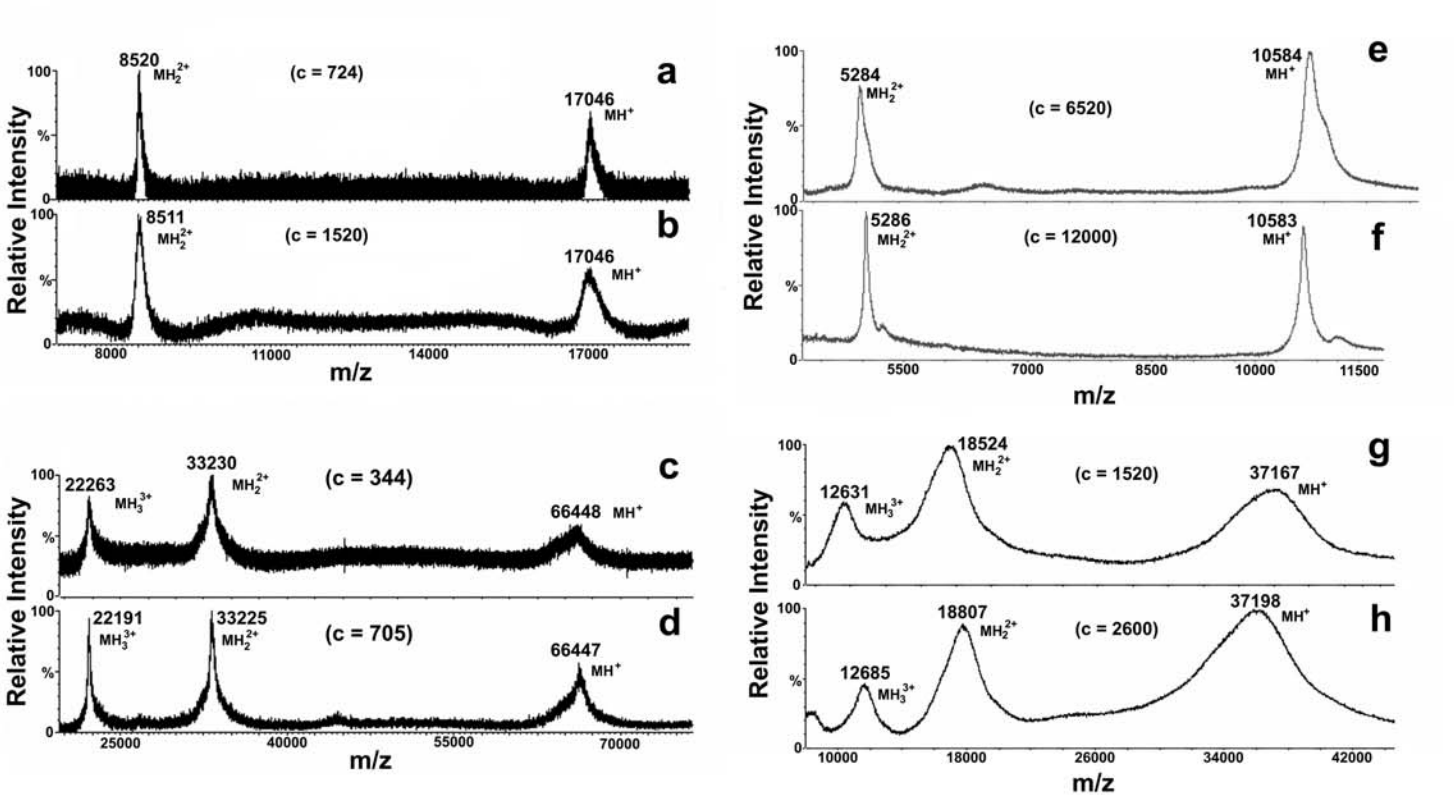
(a) Optimization of the MALDI matrix solution for intact soluble proteins; (b) Optimization of the MALDI matrix solution for membrane proteins; (c) Effect of the MALDI matrix solution on total MALDI-TOF MS ion counts for digested proteins; (d) Effect of various MALDI matrix solvents on sequence coverage of digested proteins by MALDI-TOF MS. (c, d) 1 = 75:25 methanol-acetonitrile, 2 = 50:50 methanol-acetonitrile, 3 = 25:75 methanol-acetonitrile, 4 = 75:25 acetonitrile-water, 5 = 50:50 acetonitrile-water, 6 = 25-75 acetonitrile-water, 7 = 75:25 methanol-water, 8 = 50:50 methanol-water, 9 = 25:75 methanol-water.



Supplemental Fig. 3
Effect of formic acid (FA) concentration on the MS signal of intact carbonic anhydrase II analyzed by direct infusion-ESI-Q-TOF MS. (a) 0.1% FA; (b) 1% FA; (c) 3% FA.



Supplemental Fig. 4
Protein coverage obtained for myoglobin and BSA after various digestion methods. (IS) in-solution; (ACN) acetonitrile; (OM/NC-free) On-membrane digestion followed by removal of the NC.



Supplemental Fig. 5

Comparison of the (a, c, e, g) previously published method for molecular weight determination of intact electroblotted proteins onto NC by direct dissolution in the MALDI matrix solution with the (b, d, f, h) new NC-free approach. (a, b) 200 fmol myoglobin; (c, d) 1 pmol BSA; (e, f) 10 pmol UPII; (g, h) 3 pmol UPIII.