Supporting Information

Top-Down Mass Analysis of Protein Tyrosine Nitration: Comparison of Electron Capture Dissociation with 'Slow-Heating' Tandem Mass Spectrometry Methods

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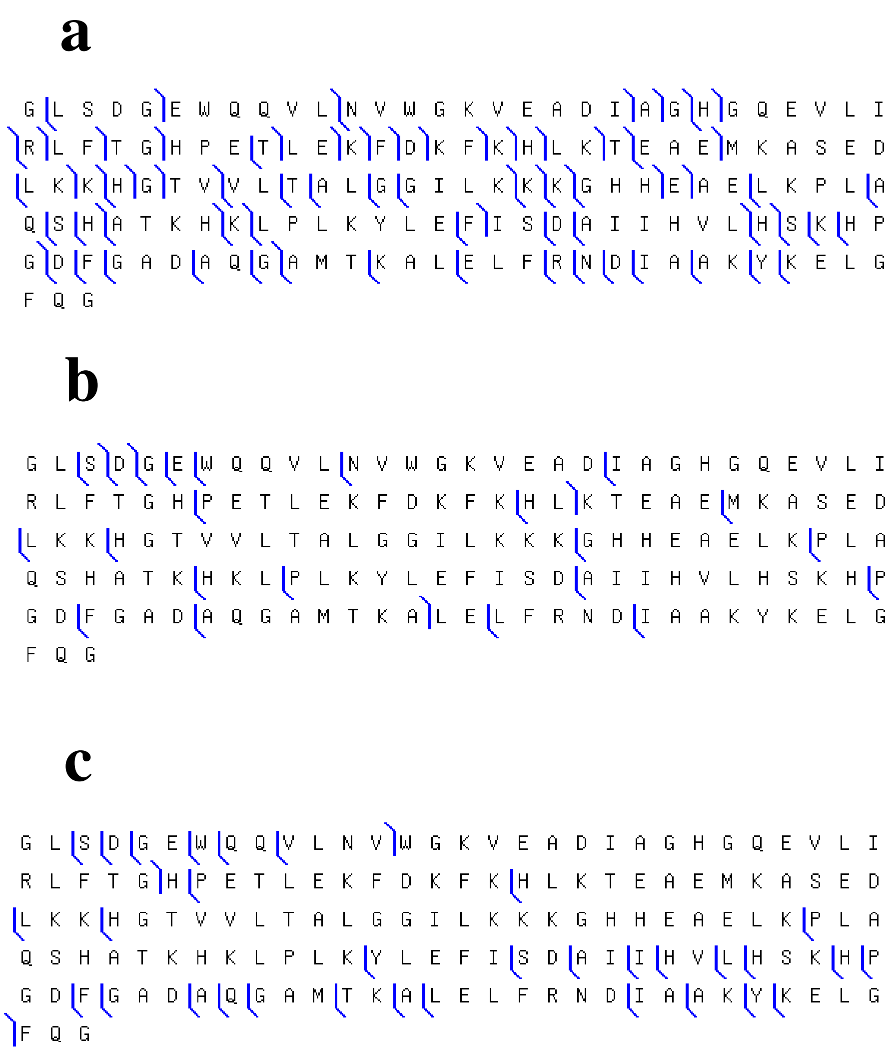

Figure S-1. Summary of fragment ions from the 20+ ions of unmodified myoglobin: (a) *c′* and *z*• ECD fragments, (b) IRMPD and (c) CID *b* and *y* fragments.

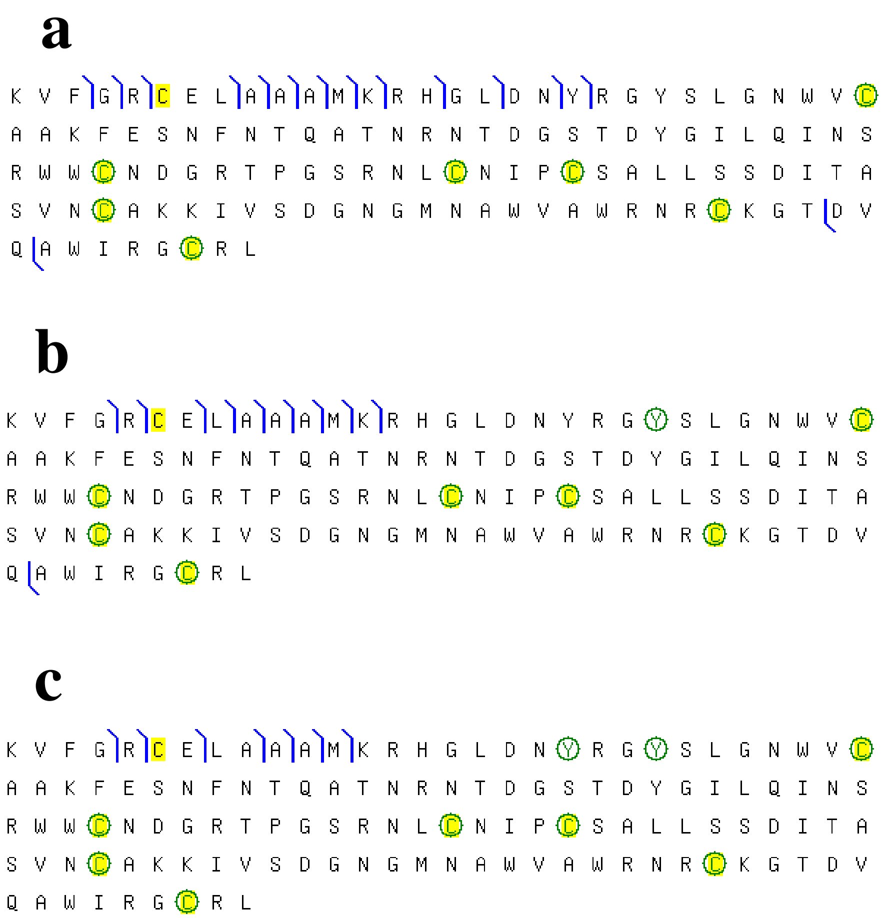

Figure S-2. Summary of ECD fragments (*c′* and *z*• ions) from the 10+ ions of non-reduced (a) unmodified (b) mono- and (c) bis-nitrated lysozyme. Mass shift -1 Da is assumed for circled cysteine residues (see text in the main manuscript). Nitrated tyrosine residues are circled.

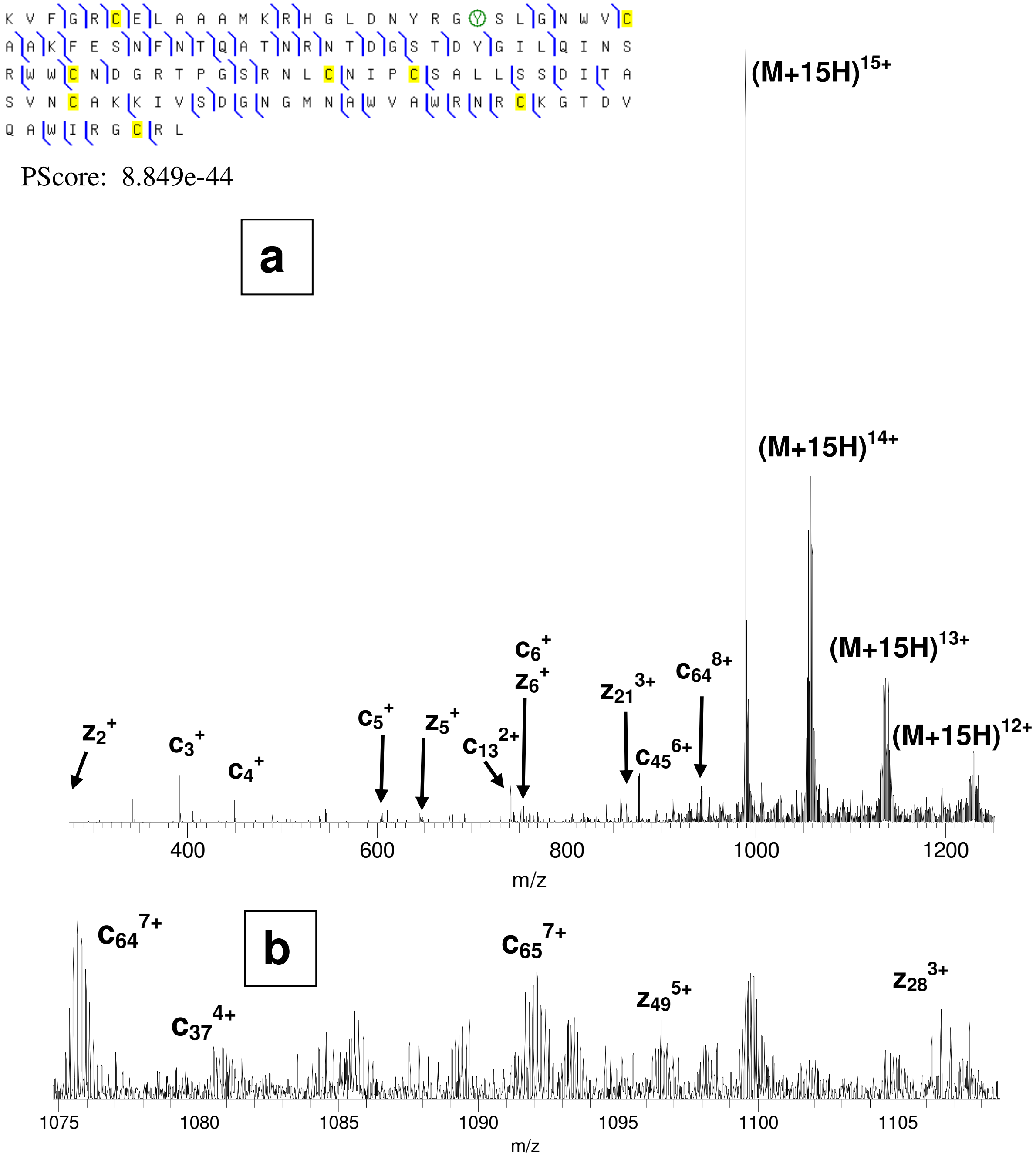

Figure S-3. ECD MS/MS spectra and fragment summary of the 15+ charge state of reduced mono-nitrated lysozyme (a) over the range of all m/z values where the fragments were found and (b) zoom-in between m/z = 1075 - 1108 with isotopic distributions of some of the fragments.

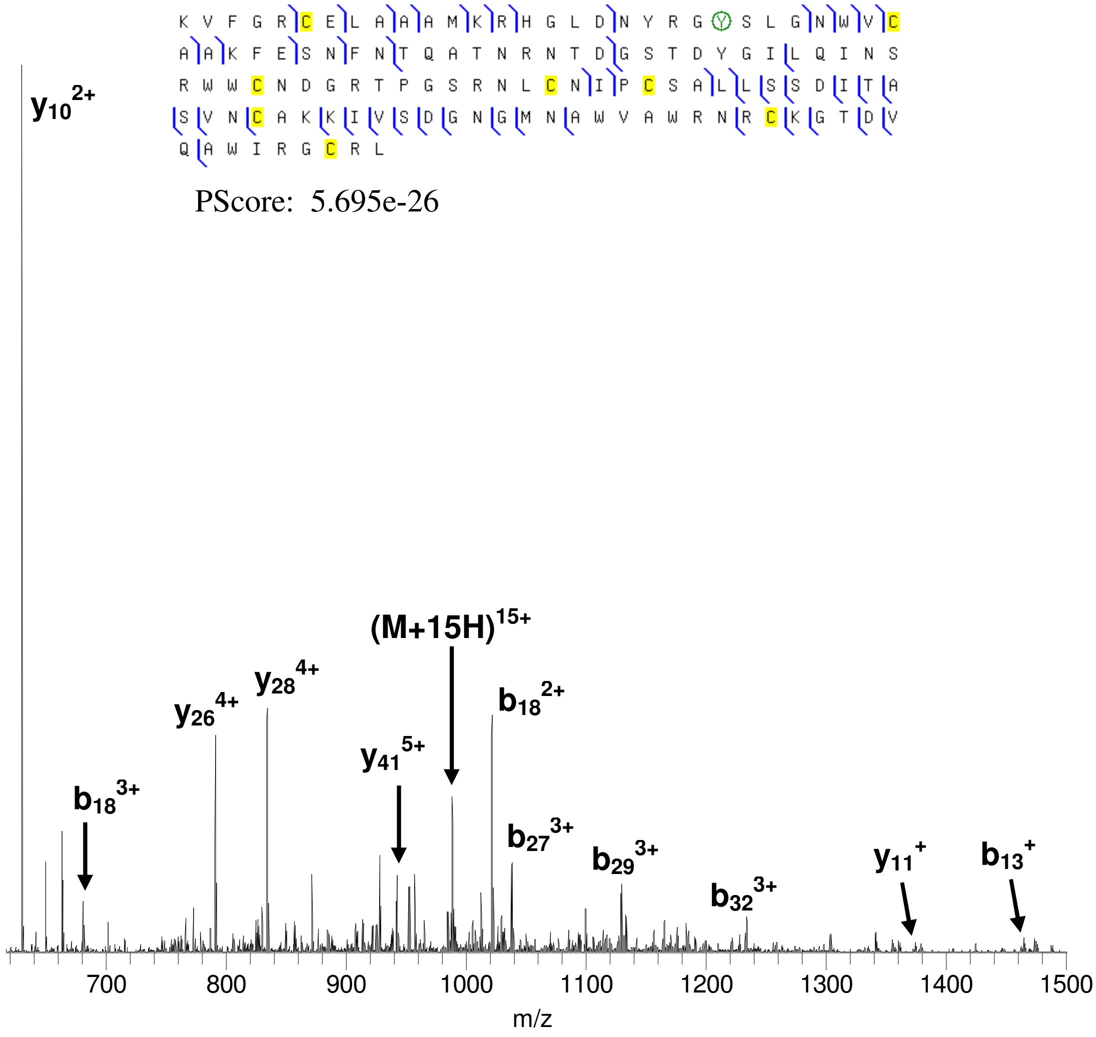

Figure S-4. IRMPD MS/MS spectra and fragment summary of the 15+ charge state of reduced mono-nitrated lysozyme.

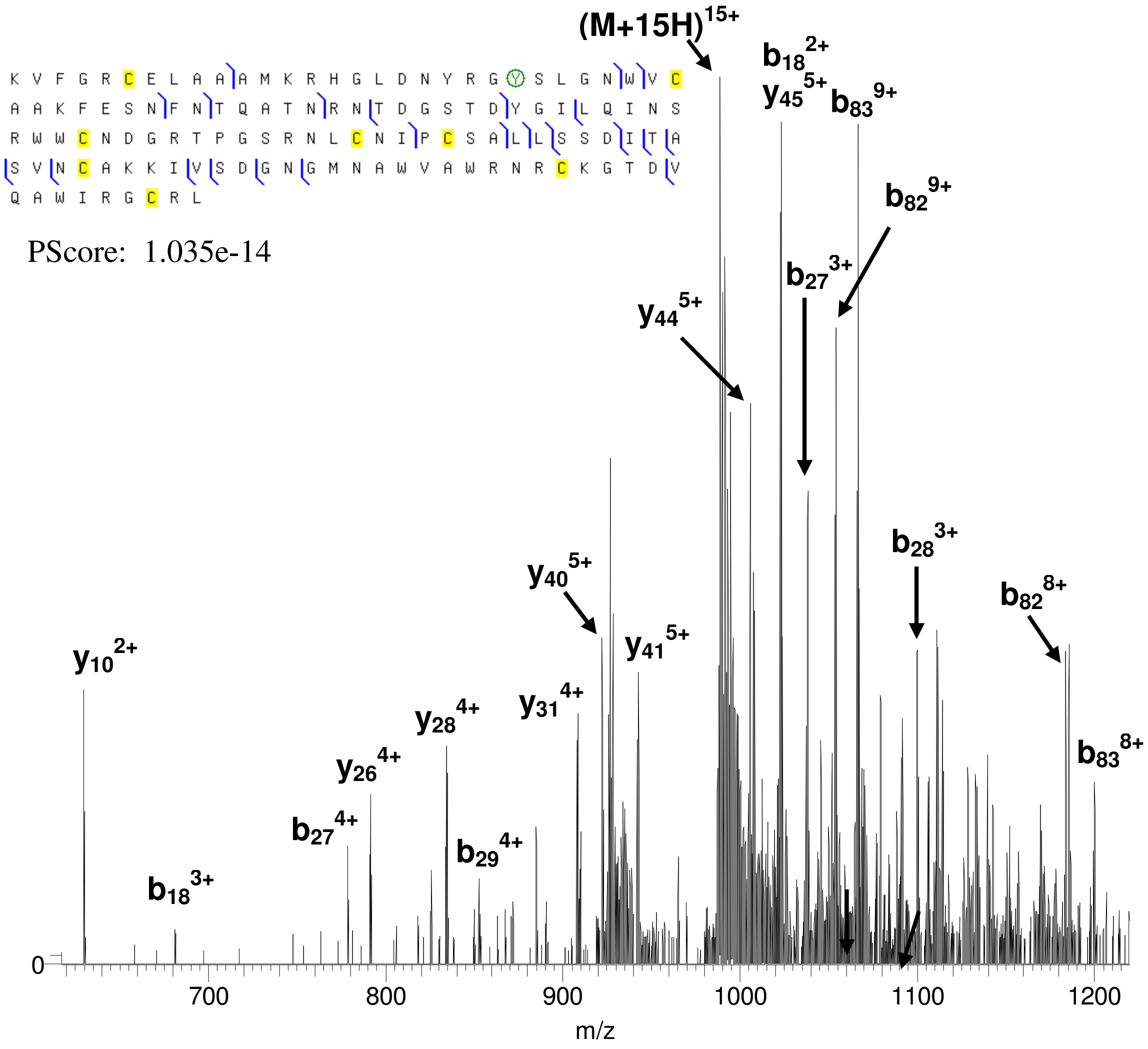

Figure S-5. CID MS/MS spectra and fragment summary of the 15+ charge state of reduced mono-nitrated lysozyme.