**Table S1.** Parameters of the nanoHPLC separation method employed in the nanoLC-QqTOF-MS-based proteomics experiments.

|  |  |  |
| --- | --- | --- |
| **Parameter** | **Settings** | |
| Method parameters | |  |
| Injection volume | 2 μL |  |
| Injection mode | sample loading pressure 217.5 bar |  |
| Column temperature | 45⁰C |  |
| Eluents | |  |
| Solvent A | 0.1% (v/v) aq. formic acid |  |
| Solvent B | 0.1% (v/v) formic acid in acetonitrile |  |
| Elution regimen | Time (min) | % B |
|  | 0 | 2 |
|  | 20 | 40 |
|  | 20,5 | 85 |
|  | 35,9 | 85 |
|  | 37,9 | 2 |
|  | 40 | 2 |
| Trap Column | Thermo Trap Cartridge 5mm |  |
| Volume | 0.148 μL |  |
| Equilibration pressure | 217.5 bar |  |
| Estimated equilibration time | 0.65 min |  |
| Equilibration volume (×10) | 1.48 μL |  |
| Separation Column | Bruker FORTY |  |
| Volume | 0.742 μL |  |
| Equilibration pressure | 600.0 bar |  |
| Estimated equilibration time | 7.91 min |  |
| Equilibration volume (×4) | 2.97 μL |  |

**Table S2.** Instrument settings applied for ESI-QqTOF-MS DDA experiments employed in the nanoHPLC-QqTOF-MS-based proteomics experiments.

|  |  |
| --- | --- |
| **Parameter** | **Settings** |
| MS conditions | |
| Ionization mode | Positive |
| Mass to charge ratio (*m/z*) range | 150 – 2200 |
| Spectra rate | 2 Hz |
| End plate offset | 500 V |
| Capillary voltage | 4500 V |
| Nebulizer | 1.5 bar |
| Dry temperature | 200°C |
| Dry gas | 2.0 l/min |
| MS/MS conditions | |
| Scan mode | Auto MS/MS |
| Fragmentation type | Collision-induced dissociation |
| Isolation width | 2 – 3 |
| MS/MS spectra acquisition | 8 – 32 Hz |
| Threshold (per 1000 sum.) | 250 cts |
| Cycle time | 3 sec |
| Collision energy | from 23 eV (m/z 300) to 65 eV (m/z 1300) |
| Scan mode | Auto MS/MS |

**Table S3.** PEAKS Studio 10.6 parameters for database search settings.

|  |  |
| --- | --- |
| **Database search settings** | |
| Analysis program | PEAKS Studio 10.6 build 20201221 |
| Parent mass error tolerance: | 10.0 ppm |
| Fragment mass error tolerance: | 0.05 Da |
| Precursor mass search type: | Monoisotopic |
| Protease | Trypsin |
| Missed cleavage sites | 2 |
| FDR | 2 |
| Fixed modifications: | Carbamidomethylation: 57.02 |
| Variable modifications | Oxidation (M): 15.99 |
|  | Acetylation (Protein N-term): 42.01 |
|  | Deamidation (NQ): 0.98 |
| S-nitrosylation: 28.99 |
| Max variable PTM per peptide | 2 |
| Filter charge | 1 – 7 |