1   **Supplemental Figure S5**

Mascot ID score: 44.1 m/z=763.8658; RT=23.652   Mascot ID score: 44.1 m/z=763.8658; RT=23.65

CSN1
^{236}GERD**S**QTQAILT**K**^{248}

Mascot ID score: 35.7 m/z=693.3164; RT=21.02   Mascot ID score: 35.7 m/z=693.3164; RT=21.08

CSN1
^{468}**S**PPREG**S**QGEL**T**PANS**S**QSR^{486}

Mascot ID score: 39.6 m/z=936.3377; RT=18.94   Mascot ID score: 39.6 m/z=936.3376; RT=18.93

CSN3
^{407}**S**MGSQEDD**S**GNKP**SSYS**^{423}

Mascot ID score: 81.3 m/z=713.3624; RT=30.48   Mascot ID score: 81.3 m/z=713.3624; RT=30.51

CSN8
^{166}KPVAGALDV**S**FNK^{178}
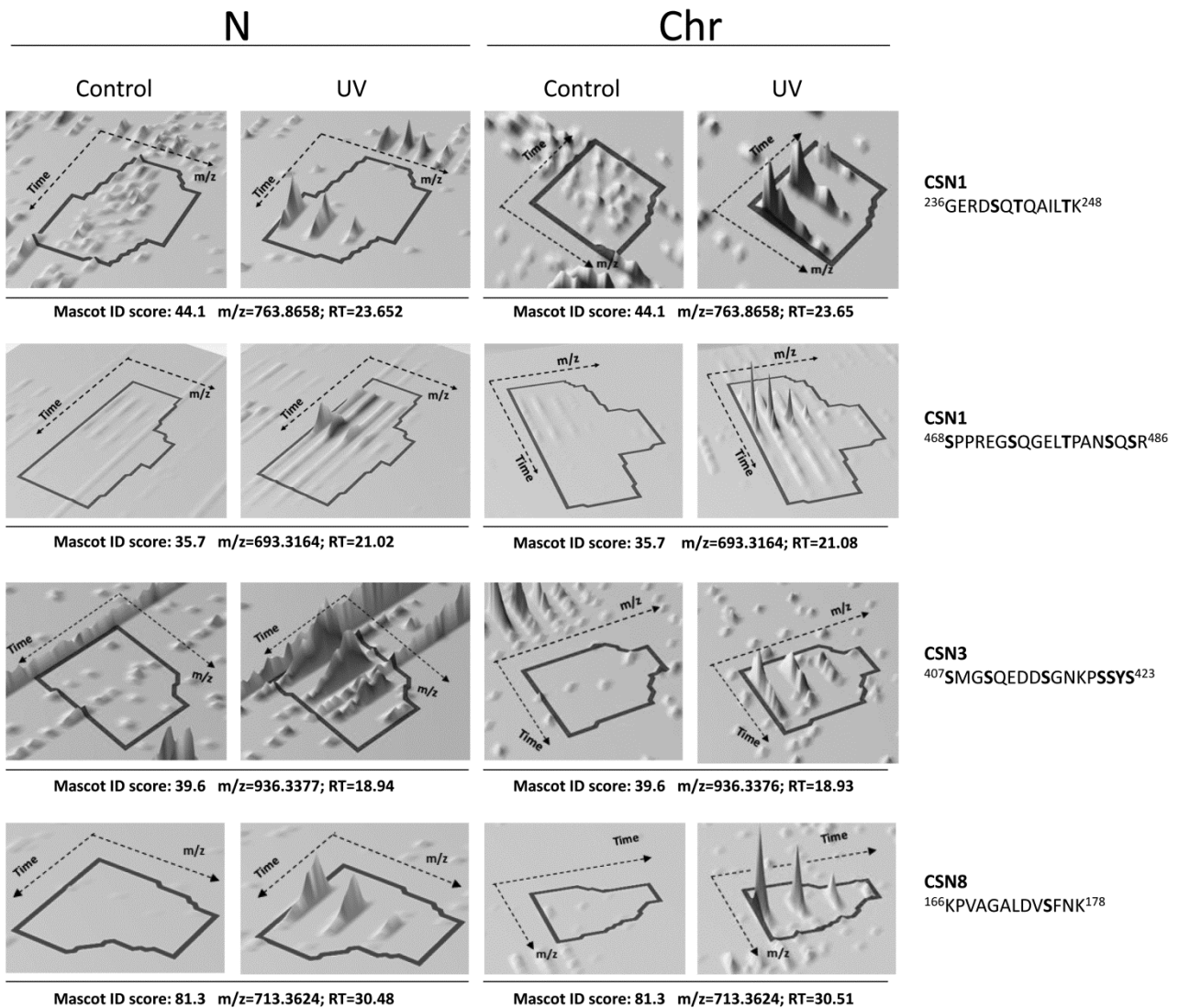
2

3   **FIG S5. Representative raw intensities of the UV-upregulated CSN phosphopeptides.** Raw data

4   were analyzed by the TransOmics software, which aligns the data and performs peak detection.

5   Examples of the phosphopeptide peak intensities, detected in control and UV irradiated samples, in

6   the nucleoplasmic (N) and chromatin (Chr) fractions are shown. Since the data was acquired on a

7   high-resolution mass spectrometer, each peptide is represented by a cluster of peaks (indicated by a

8   line that surrounds the cluster), which are the different isotopes of corresponding peptide. The

9   quantitative differences between the samples can be clearly seen when comparing the control and

10   UV samples. The most probable phosphorylation site on each peptide, as calculated by the Mascot

11   software, is highlighted in bold.