Legends for supplementary files

Deletion of Cysteine Cathepsins B or L Yields Differential Impacts on Murine Skin Proteome and Degradome**.**

Tholen et al.

Supplementary File 1: MS/MS spectra of dimethylated (naturally unmodified) N-termini identified in the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin (replicate 1).

Supplementary File 2: MS/MS spectra of dimethylated (naturally unmodified) N-termini identified in the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin (replicate 2).

Supplementary File 3: MS/MS spectra of dimethylated (naturally unmodified) N-termini identified in the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin (replicate 1).

Supplementary File 4: MS/MS spectra of dimethylated (naturally unmodified) N-termini identified in the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin (replicate 2).

Supplementary File 5: MS/MS spectra of acetylated N-termini identified in the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin (replicate 1).

Supplementary File 6: MS/MS spectra of acetylated N-termini identified in the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin (replicate 2).

Supplementary File 7: MS/MS spectra of acetylated N-termini identified in the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin (replicate 1).

Supplementary File 8: MS/MS spectra of acetylated N-termini identified in the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin (replicate 2).

Table S1: List of all identified and quantified proteins in the quantitative proteome comparison of wild-type and *Ctsb*$^{-/-}$ skin (replicate 1). *Ctsb quantification by LC-MS/MS is due to chromatographic background in the *Ctsb*$^{-/-}$ sample.

Table S2: List of all identified and quantified proteins in the quantitative proteome comparison of wild-type and *Ctsb*$^{-/-}$ skin (replicate 2). *Ctsb quantification by LC-MS/MS is due to chromatographic background in the *Ctsb*$^{-/-}$ sample.

Table S3: List of all identified and quantified proteins in the quantitative proteome comparison of wild-type and *Ctsl*$^{-/-}$ skin (replicate 1). *Ctsl quantification by LC-MS/MS is due to chromatographic background in the Ctsl$^{-/-}$ sample.

Table S4: List of all identified and quantified proteins in the quantitative proteome comparison of wild-type and *Ctsl*$^{-/-}$ skin (replicate 2). *Ctsl quantification by LC-MS/MS is due to chromatographic background in the *Ctsl*$^{-/-}$ sample.

Table S5: List of all identified and quantified proteins in both replicates of the quantitative proteome comparison of wild-type and *Ctsb*$^{-/-}$ skin lysates. *Ctsb quantification by LC-MS/MS is due to chromatographic background in the *Ctsb*$^{-/-}$ sample.

Table S6: List of all identified and quantified proteins in both replicates of the quantitative proteome comparison of wild-type and *Ctsl*$^{-/-}$ skin lysates. *Ctsl quantification by LC-MS/MS is due to chromatographic background in the *Ctsl*$^{-/-}$ sample.

Table S7: Dimethylated (naturally unmodified) N-termini identified in the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin (replicate 1). This is a comprehensive, non redundant listing. Up to two potential protein IDs per peptide are stated. Prime-site sequences of proteineous cleavage sites were determined experimentally. The corresponding non-prime sequences are derived bioinformatically by database searches. Modifications are lysine and N-terminal dimethylation (light formaldehyde + 28.03 Da; heavy formaldehyde + 34.06 Da) and cysteine carboxyamidomethylation(+ 57.02 Da).

Table S8: Dimethylated (naturally unmodified) N-termini identified in the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin (replicate 2). This is a comprehensive, non redundant listing. Up to two potential protein IDs per peptide are stated. Prime-site sequences of proteineous cleavage sites were determined experimentally. The corresponding non-prime sequences are derived bioinformatically by database searches. Modifications are lysine and N-terminal dimethylation (light formaldehyde + 28.03 Da; heavy formaldehyde + 34.06 Da) and cysteine carboxyamidomethylation(+ 57.02 Da).

Table S9: Dimethylated (naturally unmodified) N-termini identified in both replicates of the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin. This is a comprehensive, non redundant listing displaying those dimethylated (naturally unmodified) N-termini that occur in both replicates.

Table S10: Dimethylated (naturally unmodified) N-termini identified in the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin (replicate 1). This is a comprehensive, non redundant listing. Up to two potential protein IDs per peptide are stated. Prime-site sequences of proteineous cleavage sites were determined experimentally. The corresponding non-prime sequences are derived bioinformatically by database searches. Modifications are lysine and N-terminal dimethylation (light formaldehyde + 28.03 Da; heavy formaldehyde + 34.06 Da) and cysteine carboxyamidomethylation(+ 57.02 Da).

Table S11: Dimethylated (naturally unmodified) N-termini identified in the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin (replicate 2). This is a comprehensive, non redundant listing. Up to two potential protein IDs per peptide are stated. Prime-site sequences of proteineous cleavage sites were determined experimentally. The corresponding non-prime sequences are derived bioinformatically by database searches. Modifications are lysine and N-terminal dimethylation (light formaldehyde + 28.03 Da; heavy formaldehyde + 34.06 Da) and cysteine carboxyamidomethylation(+ 57.02 Da).

Table S12: Dimethylated (naturally unmodified) N-termini identified in both replicates of the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin. This is a comprehensive, non redundant listing displaying those dimethylated (naturally unmodified) N-termini that occur in both replicates.

Table S13: Ranking of dimethylated (naturally unmodified) N-termini reduce in the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin.

Table S14: Ranking of dimethylated (naturally unmodified) N-termini reduced in the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin.

Table S15: Acetylated N-termini identified in the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin (replicate 1). Up to two potential protein IDs per peptide are stated. Prime-site sequences of proteineous cleavage sites were determined experimentally. The corresponding non-prime sequences are derived bioinformatically by database searches. Modifications are lysine and N-terminal dimethylation (light formaldehyde + 28.03 Da; heavy formaldehyde + 34.06 Da), cysteine carboxyamidomethylation (+ 57.02 Da) and N-terminal acetylation (+ 42.01 Da).

Table S16: Acetylated N-termini identified in the TAILS experiment comparing wild-type and *Ctsb*$^{-/-}$ skin (replicate 2). Up to two potential protein IDs per peptide are stated. Prime-site sequences of proteineous cleavage sites were determined experimentally. The corresponding non-prime sequences are derived bioinformatically by database searches. Modifications are lysine and N-terminal dimethylation (light formaldehyde + 28.03 Da; heavy formaldehyde + 34.06 Da), cysteine carboxyamidomethylation (+ 57.02 Da) and N-terminal acetylation (+ 42.01 Da).

Table S17: Acetylated N-termini identified in the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin (replicate 1). Up to two potential protein IDs per peptide are stated. Prime-site sequences of proteineous cleavage sites were determined experimentally. The corresponding non-prime sequences are derived bioinformatically by database searches. Modifications are lysine and N-terminal dimethylation (light formaldehyde + 28.03 Da; heavy formaldehyde + 34.06 Da), cysteine carboxyamidomethylation (+ 57.02 Da) and N-terminal acetylation (+ 42.01 Da).

Table S18: Acetylated N-termini identified in the TAILS experiment comparing wild-type and *Ctsl*$^{-/-}$ skin (replicate 2). Up to two potential protein IDs per peptide are stated. Prime-site sequences of proteineous cleavage sites were determined experimentally. The corresponding non-prime sequences are derived bioinformatically by database searches. Modifications are lysine and N-terminal dimethylation (light formaldehyde + 28.03 Da; heavy formaldehyde + 34.06 Da), cysteine carboxyamidomethylation (+ 57.02 Da) and N-terminal acetylation (+ 42.01 Da).