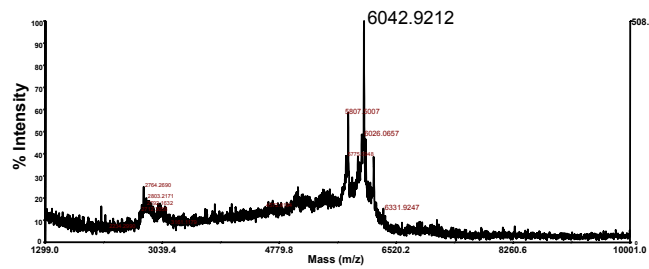


Supplemental Figure 4:

Comparison of MALDI-TOF analysis, of undigested (Panel A) and digested (Panel B) MT-enriched fraction, separated by size exclusion chromatography, from HCEsv cells extract. Panel A: The spectra of undigested MTs revealed 3 peaks, of which the main peak exhibited an experimental molecular mass of 6042.92, very close to the theoretical molecular mass of 6042.16 assigned to the human MT2A. Panel B: Spectra of digested MTs. The MS spectra obtained was searched against the Swiss-Prot protein database using the online program Mascot. The mass tolerance was set at 100 ppm for peptide TOF-MS. Other parameters were typically set as follows: i) taxonomy, Homo sapiens; ii) trypsin digestion up to 6 miss cleavages; and iii) variable modification including acetyl (N-term) and oxidation (Met). This peptide mass mapping analysis identified the MT-2A with the highest sequence coverage (65%) and a Score of 52.

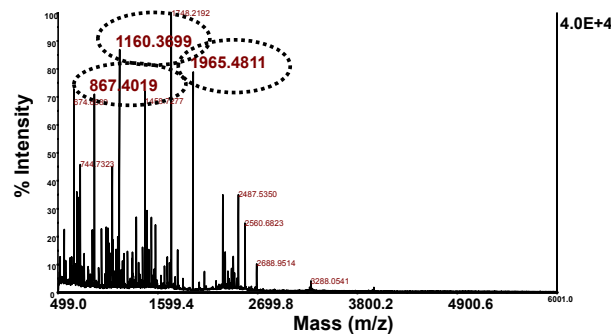
A) MALDI-TOF (undigested MT-enriched fraction)



MT-2A

Taxonomi identifier	9606 [NCBI]
Molecular formula	C ₂₂₅ H ₃₈₄ N ₇₁ O ₈₃ S ₂₁
Molecular weight (theoretical)	6042.16
Molecular weight (experimental)	60429.212

B) MALDI-TOF (digested MT-enriched fraction)



Match to MT-2A Human (Score 52)

Observed	Mr(expt)	Mr(calc)	Delta	Peptide Sequence
1965,48	1964,47	1964,65	-0,18	.(acetyl)MDPNCSAAGDSCTCAGSCK.C
1160,37	1159,36	1159,40	-0,03	K.SCCSCCPVGCAK.C
867,40	866,39	866,34	0,05	K.CAQGCICK.G Acetyl (N-term)