

Table S3. List of optimized MRM transitions used for relative quantitation analysis of TGM2, EEF2, SELENBP1 and LUM with isotope-labeled internal standards.

Peptide Sequence	NAT Precursor <i>m/z</i>	NAT Fragment <i>m/z</i>	SIS Precursor <i>m/z</i>	SIS Fragment <i>m/z</i>	Collison Energy	Fragment Ion	Retention Time Segment (in min)	Dwell Time (in ms)	Protein ID
YSGC®LTESNLIK	692.8	804.5	696.9	812.7	24	y7	0-12	17	TGM2
YSGC®LTESNLIK	692.8	917.6	696.9	925.8	24	y8	0-12	17	TGM2
SEGTYC®C®GPVSVR	736.3	934.7	741.4	944.6	33	y8	0-12	17	TGM2
SEGTYC®C®GPVSVR	736.3	614.5	741.4	624.3	24	y6	0-12	17	TGM2
EGIPALDNFLDKL	722.8	573.5	726.4	576.8	23	y10⁺⁺	15-45	25	EEF2
EGIPALDNFLDKL	722.8	186.8	726.4	186.8	29	b2	15-45	25	EEF2
TFC®QLILDPIFK	747.8	504.2	752	512.3	29	y4	15-45	25	EEF2
TFC®QLILDPIFK	747.8	845.9	752	853.6	25	y7	15-45	25	EEF2
LILPSIISR	549.9	759.5	554.9	769.5	24	y7	12-15	25	SELENBP1
LILPSIISR	549.9	227.0	554.9	227.0	20	b2	12-15	25	SELENBP1
HEIIQTLQMK	620.9	266.9	624.9	266.9	28	b2	0-12	17	SELENBP1
HEIIQTLQMK	620.9	362.0	624.9	362.0	33	b3-H ₂ O	0-12	17	SELENBP1
NNQIDHIDEK	613.3	257.9	617.3	265.9	24	y2-H₂O	0-12	17	LUM
NNQIDHIDEK	613.3	275.9	617.3	283.9	27	y2	0-12	17	LUM
SLEYLDLSFNQMSK	838.1	841.4	842.1	849.5	25	y7	12-15	25	LUM
SLEYLDLSFNQMSK	838.1	1069.6	842.1	1077.8	23	y9	12-15	25	LUM

NAT is endogenous proteotypic tryptic peptide.

SIS is stable isotope labeled peptide labeled on C-terminal amino acid, giving mass shift of +8 Da (from ¹³C₆¹⁵N₂-lysine), +10 Da (from ¹³C₆¹⁵N₄-arginine), and +7 Da (from ¹³C₆¹⁵N-leucine) compared to non-labeled counterpart (NAT).

C® is carbamidomethylated cysteine.

Bolded fragment ion indicates quantifier ion, and the other fragment ion for each peptide is qualifier ion.