Supporting Information Table S2. **Peptides used for absolute protein quantification.**

ID[1]	TC[2]	Name	Peptide sequence	Precursor m/z[3]	Transition m/z	CE[4]
Medtr7g086300	TC106598	Methionine synthase (MetS)	SFDLLSLL[HeavyL]PK	570.34	244.17	23
				570.34	790.55	23
			SFDLLSLLPK	566.83	244.17	23
				566.83	783.53	23
Several isoforms	Several isoforms	S-adenosyl-methionine synthetase (SAMS)	TIFHL[HeavyL]NPSGR	574.82	416.22	23
				574.82	787.43	23
			TIFHLNPSGR	571.31	416.22	23
				571.31	780.41	23
Medtr7g011230	TC127299	Cystathionine gamma-synthase	IFIETVL[HeavyL]PK	533.83	244.17	21
				533.83	693.42	21
			IFIETVLPK	530.33	244.17	21
				530.33	686.41	21
contig_8476_2	TC101953	Cystathionine beta-lyase	GLTEDL[HeavyL]VR	455.26	509.32	19
				455.26	638.36	19
			GLTEDLVR	451.75	502.30	19
				451.75	631.34	19
Medtr7g079080	TC104383	ACC synthase (ACS)	HGENSPYF[HeavyF]DGWK	723.83	825.40	28
				723.83	922.45	28
			HGENSPYFDGWK	718.82	815.37	28
				718.82	912.42	28
Medtr6g092620	TC108709	ACC oxidase (ACO)	WIEI[HeavyI]PPSK	488.78	331.20	20
				488.78	677.39	20
			WIEIPPSK	485.27	331.20	20
				485.27	428.25	20

[1] IDs retrieved from the International Medicago Genome Annotation Group (IMGAG) Mt3.5 v4

[2] Tentative Consensus (TC) sequences retrieved from the Dana Farber Cancer Institute (DFCI) *Medicago truncatula* Gene Index release 8.0 database.

[3] m/z, mass-to-charge ratio

[4] Collision energy