

**Supplemental Table S1.** Distribution of deduced peptide sequences of TriFLCDS with proteome data of *Arabidopsis*, rice, and sorghum hierarchically clustered by threshold of amino acid identity. Ath, Osa and Sbi are corresponding to the modeled proteome dataset of *Arabidopsis* from TAIR (v. 7), rice from RAP-DB (v. 2) and sorghum from JGI (v.1.4) respectively.

Sequence type	Identity (%)							
	100	90	80	70	60	50	40	30
	No. of clusters							
TriFLCDS and Ath and Osa and Sbi	9	419	1,178	1,573	1,771	1,911	1,939	1,916
TaCDS and (Ath or Osa or Sbi)	2	383	1,640	2,514	2,851	2,823	2,714	2,179
HvCDS and (Ath or Osa or Sbi)	7	401	1,119	1,560	1,703	1,654	1,563	1,253
TaCDS	7,865	4,929	3,278	2,136	1,520	1,161	912	690
HvCDS	6,018	3,334	2,176	1,468	1,042	804	647	528
TaCDS or HvCDS	94	1,173	618	307	186	108	61	24
Total with TriFLCDS-specific	13,977	9,436	6,072	3,911	2,748	2,073	1,620	1,242
Total with TriFLCDS	13,995	10,639	10,009	9,558	9,073	8,461	7,836	6,590
Ath or Osa or Sbi	116,868	104,812	90,448	76,251	63,105	50,632	38,915	24,147
Total	130,863	115,451	100,457	85,809	72,178	59,093	46,751	30,737