Supporting information

Table S1 Inter-correlation coefficients between biological triplicates

	293_1F_2mm	293_6F_2mm	294_1F_2mm
293_1F_2mm	**1.00**	**0.96**	**0.91**
293_6F_2mm	**0.96**	**1.00**	**0.94**
294_1F_2mm	**0.91**	**0.94**	**1.00**
	293_7S_2mm	294_9S_2mm	294_6S_2mm
293_7S_2mm	**1.00**	**0.92**	**0.94**
294_9S_2mm	**0.92**	**1.00**	**0.98**
294_6S_2mm	**0.94**	**0.98**	**1.00**
	293_1F_1.5mm	293_6F_1.5mm	ms8F_1.5mm
293_1F_1.5mm	1.00	0.86	0.78
293_6F_1.5mm	0.86	1.00	0.79
ms8F_1.5mm	0.78	0.79	1.00
	293_7S_1.5mm	294_9S_1.5mm	294_6S_1.5mm
293_7S_1.5mm	1.00	0.84	0.93
294_9S_1.5mm	0.84	1.00	0.89
294_6S_1.5mm	0.93	0.89	1.00

F: fertile; S: sterile.

Table S2 Intra-correlation coefficients among technical triplicates

	F 2 mm			S 2 mm			F 1.5 mm			S 1.5 mm		
Sample Designation	293_1	293_6	294_1	293_7	294_9	294_6	293_1	293_6	ms8F	293_7	294_9	294_6
Correlation run 1 to 2	0.82	0.88	0.85	0.87	0.95	0.94	0.88	0.88	0.94	0.86	0.89	0.91
Correlation run 2 to 3	0.90	0.90	0.85	0.90	0.96	0.93	0.93	0.88	0.91	0.87	0.85	0.91
Correlation run 1 to 3	0.82	0.89	0.91	0.89	0.93	0.96	0.89	0.85	0.93	0.86	0.86	0.91
Average	0.84	0.89	0.87	0.89	0.95	0.94	0.90	0.87	0.93	0.86	0.87	0.91
SD(±)	0.05	0.01	0.03	0.02	0.01	0.01	0.03	0.02	0.02	0.01	0.02	0.00

F: fertile; S: sterile.

Table S3 Criteria for data filtration*

Peptide FDR	Protein FDR	Number of assigned peptides	Minimum number of times spectra counted	Number of unique proteins	Number of spectra
0.4%	7.6%	1+	1+	2761	70309
0.4%	7.6%	1+	2+	672	70309
0.3%	0.2%	2+	2+	359	57543

* Additionally, minimum peptide identity probability of 95% and minimum protein identity probability of 90%.

Table S4 Analysis of potential trans-membrane proteins

Protein access number	Functional annotation in *Zea mays*	Protein molecular weight (Da)	Presence in fertile stages (mm)
GRMZM2G032564	60 S ribosome protein	26208.7	1.5 and 2.0
GRMZM2G065355	heat shock factor-binding protein 1 isoform	33596.6	1.5
GRMZM2G104025	heat shock factor-binding protein 1 isoform	37596.6	2.0

Figure S1

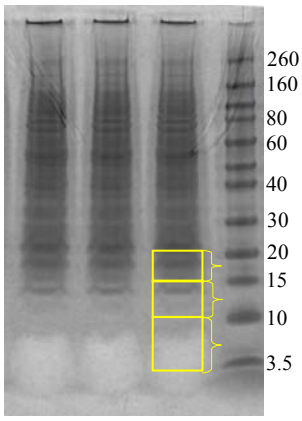


Figure S2

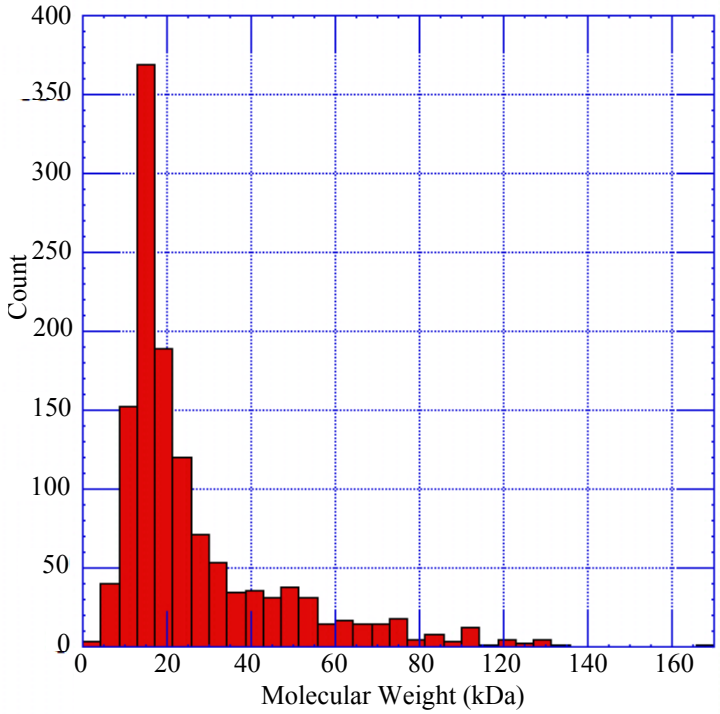

Count
Molecular Weight (kDa)
0
50
100
150
200
250
300
350
400
0
20
40
60
80
120
140
160

Figure S3

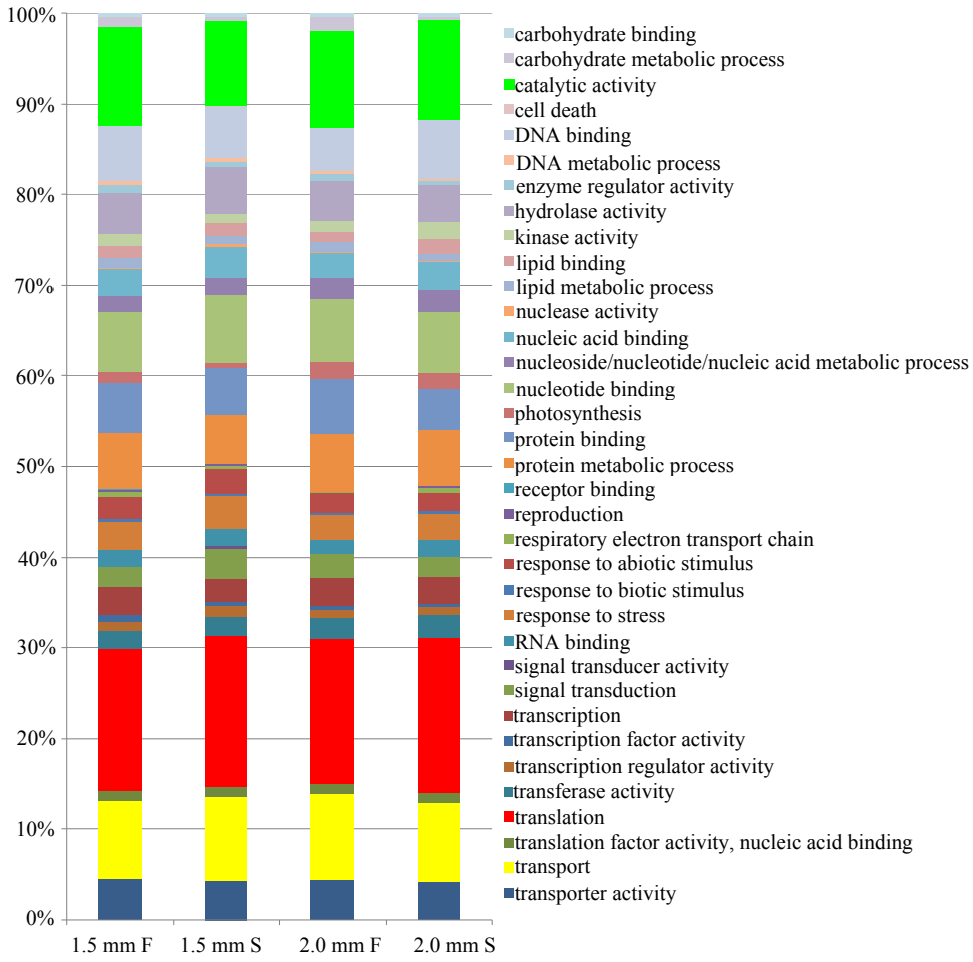

100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
1.5 mm F
1.5 mm S
2.0 mm F
2.0 mm S
carbohydrate binding
carbohydrate metabolic process
catalytic activity
cell death
DNA binding
DNA metabolic process
enzyme regulator activity
hydrolase activity
kinase activity
lipid binding
lipid metabolic process
nuclease activity
nucleic acid binding
nucleoside/nucleotide/nucleic acid metabolic process
nucleotide binding
photosynthesis
protein binding
protein metabolic process
receptor binding
reproduction
respiratory electron transport chain
response to abiotic stimulus
response to biotic stimulus
response to stress
RNA binding
signal transducer activity
signal transduction
transcription
transcription factor activity
transcription regulator activity
transferase activity
translation
translation factor activity, nucleic acid binding
transport
transporter activity

Figure S4

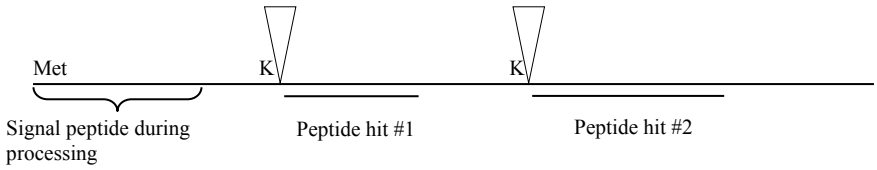
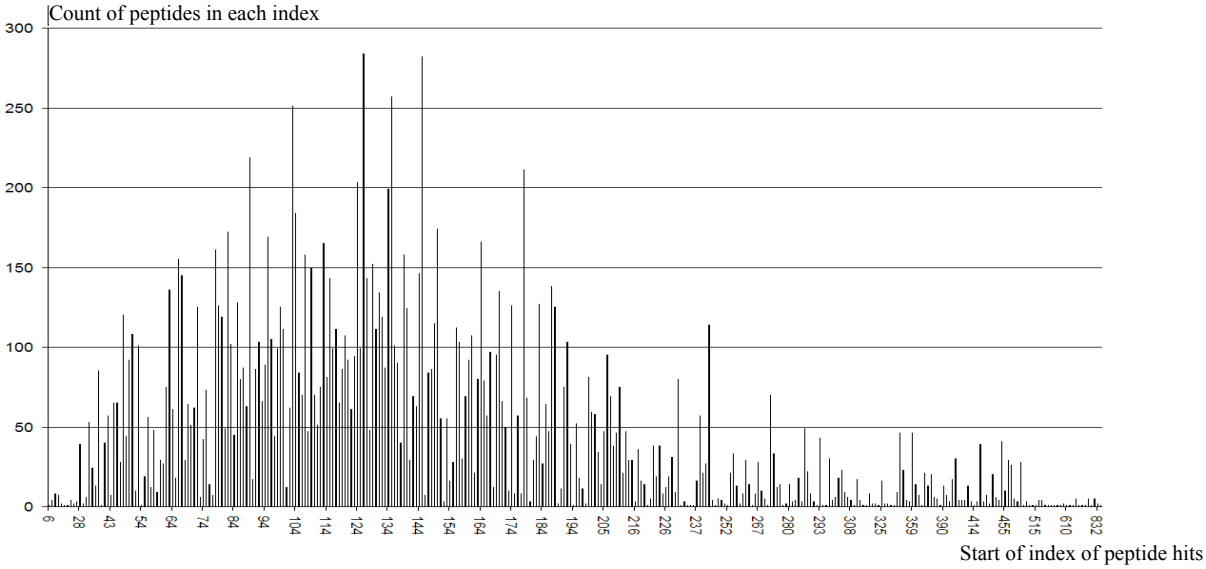

Met
K
K
Signal peptide during processing
Peptide hit #1
Peptide hit #2

Figure S5


Count of peptides in each index
300
250
200
150
100
50
0
6
28
43
54
64
74
84
94
104
114
124
134
144
154
164
174
184
194
205
216
226
237
252
267
280
293
308
325
359
390
414
455
515
610
832
Start of index of peptide hits