Table S4. Singular enrichment analysis (SEA) of proteins being organ-specifically accumulated among nonmodified proteins of maize. As reference 16,680 unique nonmodified proteins were used.

Overrepresented GO terms of root-specific nonmodified proteins

GO Term	Ontology	Description	Number in input list	Number in reference	p-value	FDR
GO:0042221	Biological process (p)	Response to chemical stimulus	57	194	3.5e-15	4.9e-12
GO:0006979		Response to oxidative stress	45	134	1.1e-14	7.5e-12
GO:0009808		Lignin metabolic process	6	7	4,00e-06	0.0011
GO:0046274		Lignin catabolic process	6	7	4,00e-06	0.0011
GO:0046271		Phenylpropanoid catabolic process	6	7	4,00E-06	0.0011
GO:0042219		Cellular amino acid derivative catabolic process	6	8	1.5e-05	0.0034
GO:0012501		Programmed cell death	11	30	4.3e-05	0.0068
GO:0042546		Cell wall biogenesis	6	9	4.1e-05	0.0068
GO:0006915		Apoptosis	11	30	4.3e-05	0.0068
GO:0050896		Response to stimulus	103	752	7.4e-05	0.01
GO:0071554		Cell wall organization or biogenesis	17	68	0.00012	0.015
GO:0009698		Phenylpropanoid metabolic process	6	11	0.00019	0.022
GO:0016265		Death	11	36	0.00028	0.028
GO:0008219		Cell death	11	36	0.00028	0.028
GO:0070882		Cellular cell wall organization or biogenesis	6	12	0.00035	0.033
GO:0006950		Response to stress	90	675	0.00044	0.038
GO:0019439		Aromatic compound catabolic process	7	17	0.00048	0.04
GO:0016684	Molecular function (f)	Oxidoreductase activity, acting on peroxide as acceptor	46	141	1.9e-14	8.5e-12
GO:0004601		Peroxidase activity	46	141	1.9e-14	8.5e-12
GO:0020037		Heme binding	69	283	1.6e-13	3.5e-11
GO:0046906		Tetrapyrrole binding	69	283	1.6e-13	3.5e-11
GO:0016209		Antioxidant activity	46	155	8.6e-13	1.6e-10
GO:0009055		Electron carrier activity	88	471	5.2e-10	7.9e-08
GO:0005506		Iron ion binding	74	383	2.3e-09	3,00E-07
GO:0016757		Transferase activity, transferring glycosyl groups	54	298	1.9e-06	0.00022
GO:0008417		Fucosyltransferase activity	6	7	4,00E-06	0.0003
GO:0008107		Galactoside 2-alpha-L-fucosyltransferase activity	6	7	4,00E-06	0.0003
GO:0031127		Alpha(1,2)-fucosyltransferase activity	6	7	4,00E-06	0.0003
GO:0008471		Laccase activity	6	7	4,00E-06	0.0003
GO:0005507		Copper ion binding	17	58	1.3e-05	0.0009
GO:0016758		Transferase activity, transferring hexosyl groups	42	229	1.7e-05	0.0011
GO:0016491		Oxidoreductase activity	134	999	2.4e-05	0.0014
GO:0046914		Transition metal ion binding	154	1180	2.9e-05	0.0016
GO:0016682		Oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	6	9	4.1e-05	0.0022
GO:0046872		Metal ion binding	181	1472	0.00016	0.0079
GO:0043167		ion binding	181	1475	0.00018	0.0079
GO:0043169		cation binding	181	1475	0.00018	0.0079
GO:0016762		xyloglucan:xyloglucosyl transferase activity	8	20	0.00024	0.01
GO:0016740		transferase activity	192	1623	0.00067	0.028
GO:0005576	Cellular component (c)	extracellular region	40	149	6.6e-10	1.1e-07
GO:0048046		apoplast	15	40	1.3e-06	0.00011

Table S4 continued.

Overrepresented GO terms of seed-specific nonmodified proteins

GO term	**Ontology**	**Description**	**Number in input list**	**Number in BG/Ref**	**p-value**	**FDR**
GO:0006952	Biological process (p)	Defense response	16	35	1.7e-06	0.0029
GO:0010556		Regulation of macromolecule biosynthetic process	104	561	7.5e-05	0.021
GO:0009889		Regulation of biosynthetic process	104	561	7.5e-05	0.021
GO:0031326		Regulation of cellular biosynthetic process	104	561	7.5e-05	0.021
GO:0031323		Regulation of cellular metabolic process	105	569	8.4e-05	0.021
GO:0045449		Regulation of transcription	102	545	6,00E-05	0.021
GO:0010468		Regulation of gene expression	106	565	4.1e-05	0.021
GO:0019219		Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	102	554	0.00011	0.021
GO:0051171		Regulation of nitrogen compound metabolic process	102	554	0.00011	0.021
GO:0080090		Regulation of primary metabolic process	108	609	0.00031	0.049
GO:0060255		Regulation of macromolecule metabolic process	110	621	0.00029	0.049
GO:0004497	Molecular function (f)	Monooxygenase activity	38	147	1.4e-05	0.0062
GO:0003700		Transcription factor activity	47	191	6.4e-06	0.0062
GO:0030528		Transcription regulator activity	71	337	1.6e-05	0.0062
GO:0043565		Sequence-specific DNA binding	43	186	7.3e-05	0.014
GO:0004867		Serine-type endopeptidase inhibitor activity	12	28	7.4e-05	0.014
GO:0045735		Nutrient reservoir activity	15	40	6.3e-05	0.014
GO:0004866		Endopeptidase inhibitor activity	14	41	0.00034	0.05
GO:0030414		Peptidase inhibitor activity	14	41	0.00034	0.05

Overrepresented GO terms of leaf-specific nonmodified proteins

GO term	**Ontology**	**Description**	**Number in input list**	**Number in BG/Ref**	**p-value**	**FDR**
GO:0015979	Biological process (p)	Photosynthesis	50	67	9.5e-37	1.2e-33
GO:0019684		Photosynthesis, light reaction	24	30	1,00E-19	6.4e-17
GO:0009765		Photosynthesis, light harvesting	20	23	4.7e-18	2,00E-15
GO:0065007		Biological regulation	183	1322	7.6e-07	0.00024
GO:0006091		Generation of precursor metabolites and energy	46	243	5.3e-06	0.0013
GO:0042592		Homeostatic process	76	496	3,00E-05	0.0064
GO:0050789		Regulation of biological process	123	895	3.9e-05	0.0071
GO:0065008		Regulation of biological quality	77	515	6.1e-05	0.0097
GO:0050794		Regulation of cellular process	113	828	9.6e-05	0.014
GO:0009628		Response to abiotic stimulus	63	422	0.00026	0.033
GO:0048871		Multicellular organismal homeostasis	59	398	0.00046	0.034
GO:0022402		Cell cycle process	6	12	0.00039	0.034
GO:0050826		Response to freezing	59	398	0.00046	0.034
GO:0042309		Homoiothermy	59	398	0.00046	0.034
GO:0009409		Response to cold	59	398	0.00046	0.034
GO:0001659		Temperature homeostasis	59	398	0.00046	0.034
GO:0010468		Regulation of gene expression	79	565	0.00041	0.034
GO:0009266		Response to temperature stimulus	59	399	0.00049	0.035
GO:0019222		Regulation of metabolic process	85	627	0.00068	0.045
GO:0008152		Metabolic process	552	4982	0.00079	0.047
GO:0031323		Regulation of cellular metabolic process	78	569	0.00078	0.047
GO:0045449		Regulation of transcription	75	545	0.00086	0.047
GO:0044237		Cellular metabolic process	404	3583	0.00085	0.047
GO:0034357	Cellular component (c)	Photosynthetic membrane	30	35	4.9e-26	1.3e-23
GO:0009579		Thylakoid	30	36	2.7e-25	3.6e-23
GO:0009521		Photosystem	24	26	8.1e-23	7.3e-21
GO:0044436		Thylakoid part	19	23	2.2e-16	1.5e-14
GO:0009523		Photosystem II	13	14	6.2e-13	3.4e-11
GO:0009522		Photosystem I	11	12	5.9e-11	2.3e-09
GO:0009654		Oxygen evolving complex	11	12	5.9e-11	2.3e-09

Table S4 continued.

Overrepresented GO terms of leaf-specific nonmodified proteins						
GO term	**Ontology**	**Description**	**Number in input list**	**Number in BG/Ref**	**p-value**	**FDR**
GO:0019898	Cellular component (c)	Extrinsic to membrane	9	11	2.8e-08	9.3e-07
GO:0042651		Thylakoid membrane	9	12	1,00E-07	3,00E-06
GO:0009538		Photosystem I reaction center	6	7	4.5e-06	0.00012
GO:0009536		Plastid	8	19	0.00018	0.0045
GO:0043229		Intracellular organelle	195	1648	0.0015	0.031
GO:0043226		Organelle	195	1648	0.0015	0.031