Table S1. Enriched GO terms of tissue-specific proteins of nonmodified and phosphorylated protein datasets using single enrichment analysis (SEA). Different colors in the right columns reflect different significance levels of overrepresentation; yellow: FDR ≤0.05, orange: FDR ≤0.01, red: FDR ≤0.001.

				Nonmodified proteins				Phosphorylated proteins			
No	**GO Term**	**Ontology**	**Description**	**MZ**	**EZ**	**C**	**S**	**MZ**	**EZ**	**C**	**S**
1	GO:0006139	Biological process (p)	Nucleobase, nucleoside, nucleotide and nucleic acid metabolic process								
2	GO:0006350		Transcription								
3	GO:0006807		Nitrogen compound metabolic process								
4	GO:0016070		RNA metabolic process								
5	GO:0006351		Transcription, DNA-dependent								
6	GO:0032774		RNA biosynthetic process								
7	GO:0045449		Regulation of transcription								
8	GO:0010468		Regulation of gene expression								
9	GO:0019219		Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process								
10	GO:0051171		Regulation of nitrogen compound metabolic process								
11	GO:0009889		Regulation of biosynthetic process								
12	GO:0010556		Regulation of macromolecule biosynthetic process								
13	GO:0031326		Regulation of cellular biosynthetic process								
14	GO:0060255		Regulation of macromolecule metabolic process								
15	GO:0019222		Regulation of metabolic process								
16	GO:0031323		Regulation of cellular metabolic process								
17	GO:0006259		DNA metabolic process								
18	GO:0080090		Regulation of primary metabolic process								
19	GO:0006355		Regulation of transcription, DNA-dependent								
20	GO:0051252		Regulation of RNA metabolic process								
21	GO:0010467		Gene expression								
22	GO:0050789		Regulation of biological process								
23	GO:0050794		Regulation of cellular process								
24	GO:0044260		Cellular macromolecule metabolic process								
25	GO:0034645		Cellular macromolecule biosynthetic process								
26	GO:0009059		Macromolecule biosynthetic process								
27	GO:0065007		Biological regulation								
28	GO:0055114		Oxidation reduction								
29	GO:0009698		Phenylpropanoid metabolic process								
30	GO:0009808		Lignin metabolic process								
31	GO:0046271		Phenylpropanoid catabolic process								
32	GO:0046274		Lignin catabolic process								
33	GO:0042219		Cellular amino acid derivative catabolic process								
34	GO:0019439		Aromatic compound catabolic process								
35	GO:0019748		Secondary metabolic process								
36	GO:0006575		Cellular amino acid derivative metabolic process								
37	GO:0016310		Phosphorylation								
38	GO:0043687		Post-translational protein modification								
39	GO:0006468		Protein amino acid phosphorylation								

Table S1 continued.

				Nonmodified proteins				Phosphorylated proteins			
No	**GO Term**	**Ontology**	**Description**	**MZ**	**EZ**	**C**	**S**	**MZ**	**EZ**	**C**	**S**
40	GO:0006796	Biological process (p)	Phosphate metabolic process								
41	GO:0006793		Phosphorus metabolic process								
42	GO:0006464		Protein modification process								
43	GO:0043412		Macromolecule modification								
44	GO:0009152		Purine ribonucleotide biosynthetic process								
45	GO:0009150		Purine ribonucleotide metabolic process								
46	GO:0009260		Ribonucleotide biosynthetic process								
47	GO:0009259		Ribonucleotide metabolic process								
48	GO:0009165		Nucleotide biosynthetic process								
49	GO:0006163		Purine nucleotide metabolic process								
50	GO:0006164		Purine nucleotide biosynthetic process								
51	GO:0046034		ATP metabolic process								
52	GO:0046483		Heterocycle metabolic process								
53	GO:0006754		ATP biosynthetic process								
54	GO:0009199		Ribonucleoside triphosphate metabolic process								
55	GO:0009206		Purine ribonucleoside triphosphate biosynthetic process								
56	GO:0009205		Purine ribonucleoside triphosphate metabolic process								
57	GO:0009201		Ribonucleoside triphosphate biosynthetic process								
58	GO:0009141		Nucleoside triphosphate metabolic process								
59	GO:0009142		Nucleoside triphosphate biosynthetic process								
60	GO:0009144		Purine nucleoside triphosphate metabolic process								
61	GO:0009145		Purine nucleoside triphosphate biosynthetic process								
62	GO:0006753		Nucleoside phosphate metabolic process								
63	GO:0009117		Nucleotide metabolic process								
64	GO:0055086		Nucleobase, nucleoside and nucleotide metabolic process								
65	GO:0007154		Cell communication								
66	GO:0003677	Molecular function (f)	DNA binding								
67	GO:0003700		Transcription factor activity								
68	GO:0043565		Sequence-specific DNA binding								
69	GO:0003676		Nucleic acid binding								
70	GO:0043566		Structure-specific DNA binding								
71	GO:0030528		Transcription regulator activity								
72	GO:0003774		Motor activity								
73	GO:0003777		Microtubule motor activity								
74	GO:0020037		Heme binding								
75	GO:0046906		Tetrapyrrole binding								
76	GO:0004497		Monooxygenase activity								
77	GO:0005506		Iron ion binding								
78	GO:0009055		Electron carrier activity								
79	GO:0016747		Transferase activity, transferring acyl groups other than amino-acyl groups								
80	GO:0016491		Oxidoreductase activity								
81	GO:0016746		Transferase activity, transferring acyl groups								

Table S1 continued.

				Nonmodified proteins				Phosphorylated proteins			
No	**GO Term**	**Ontology**	**Description**	**MZ**	**EZ**	**C**	**S**	**MZ**	**EZ**	**C**	**S**
82	GO:0005507	Molecular function (f)	Copper ion binding								
83	GO:0008471		Laccase activity								
84	GO:0016682		Oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor								
85	GO:0016679		Oxidoreductase activity, acting on diphenols and related substances as donors								
86	GO:0016798		Hydrolase activity, acting on glycosyl bonds								
87	GO:0004553		Hydrolase activity, hydrolyzing O-glycosyl compounds								
88	GO:0015291		Secondary active transmembrane transporter activity								
89	GO:0016773		Phosphotransferase activity, alcohol group as acceptor								
90	GO:0004674		Protein serine/threonine kinase activity								
91	GO:0004672		Protein kinase activity								
92	GO:0016301		Kinase activity								
93	GO:0016772		Transferase activity, transferring phosphorus-containing groups								
94	GO:0022804		Active transmembrane transporter activity								
95	GO:0015405		P-P-bond-hydrolysis-driven transmembrane transporter activity								
96	GO:0042626		ATPase activity, coupled to transmembrane movement of substances								
97	GO:0015399		Primary active transmembrane transporter activity								
98	GO:0016820		Hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances								
99	GO:0015662		ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism								
100	GO:0043492		ATPase activity, coupled to movement of substances								
101	GO:0022857		Transmembrane transporter activity								
102	GO:0005215		Transporter activity								
103	GO:0005524		ATP binding								
104	GO:0032559		Adenyl ribonucleotide binding								
105	GO:0042625		ATPase activity, coupled to transmembrane movement of ions								
106	GO:0030554		Adenyl nucleotide binding								
107	GO:0001883		Purine nucleoside binding								
108	GO:0001882		Nucleoside binding								
109	GO:0022891		Substrate-specific transmembrane transporter activity								
110	GO:0022892		Substrate-specific transporter activity								
111	GO:0016740		Transferase activity								
112	GO:0008047		Enzyme activator activity								
113	GO:0032555		Purine ribonucleotide binding								
114	GO:0032553		Ribonucleotide binding								
115	GO:0015075		Ion transmembrane transporter activity								
116	GO:0005096		GTPase activator activity								
117	GO:0017076		Purine nucleotide binding								
118	GO:0003824		Catalytic activity								

Table S1 continued.

				Nonmodified proteins				Phosphorylated proteins			
No	**GO Term**	**Ontology**	**Description**	**MZ**	**EZ**	**C**	**S**	**MZ**	**EZ**	**C**	**S**
119	GO:0048046	Cellular component (c)	Apoplast								
120	GO:0005576		Extracellular region								