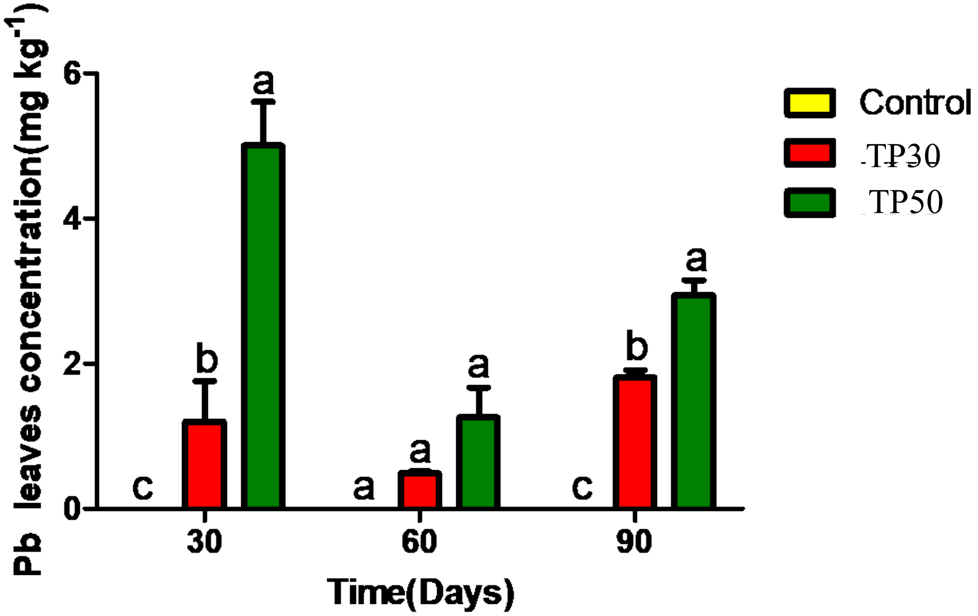

Fig. 1 Suppl. Content of Pb in *Paspalum fasciculatum* leaves under Pb-stress for 90 d. Treatments TP30 and TP50 correspond to 30 and 50 mg(Pb) kg^{-1}(soil), respectively. Means ± SEs, $n = 3$. Different lower-case letters indicate statistical significance ($P < 0.05$) between control and different treatments. X-axis: TIME [d], Y-axis: Pb CONTENT [mg kg^{-1}(f.m.)].

Table 1 Suppl. Functional classifications of identified proteins significantly expressed in *Paspalum fasciculatum* leaves in response to Pb-stress. [a] -Accession: accession number in NCBI database. [b] -MW [kDa]: Molecular weight of the protein. [c] -Coverage: Percentage of the protein sequence covered by the peptides. [d] -Ratio: is the quotient of the normalized peak area of the proteins of each treatment and the control (T/C). [e] -Fold Change: It is a measure that describes the degree of protein change between treatments (Pb50 and Pb30) and control. It is the Log in bases 2 of the ratio (T/C). Only proteins with more/less than 1.5 fold change on abundance level or significant difference ($p < 0.05$) were chosen.

N°	Accession[a]	Protein name	MW [kDa][b]	Coverage[c]	Species	Ratios[d]		Fold Change[e]
						Pb50/TC	Pb30/TC	Pb50/Pb30
Photosynthesis								
1	Q37227	Ribulose bisphosphate carboxylase large chain (Fragment)	49.10	28.89	*Iris germanica*	0.0068	0.0068	-7.20/-7.20
2	Q43843	Ribulose-phosphate 3-epimerase. chloroplastic (Fragment)	29.86	25.35	*Solanum tuberosum*	0.00032	0.00032	-11.60/ -11.60
3	Q32RQ1	Ribulose bisphosphate carboxylase large chain	52.69	16.00	*Zygnema circumcarinatum*	0.00013	0.00013	-12.80/ -12.80
4	Q42961	Phosphoglycerate kinase. chloroplastic	50.14	24.74	*Nicotiana tabacum*	0.00035	0.00036	-11.40/ -11.40
5	P12329	Chlorophyll a-b binding protein 1. chloroplastic	27.79	49.23	*Zea mays*	0.36	0.10	-1.50/-3.30

6	P04782	Chlorophyll a-b binding protein 25. chloroplastic	28.14	28.195	*Petunia sp.*	0.0031	0.0031	-8.30/-8.30
7	P12332	Chlorophyll a-b binding protein. chloroplastic (Fragment)	22.02	19.02	*Silene latifolia subsp. alba*	0.0018	0.0018	-9.10/-9.10
8	Q9SQL2	Chlorophyll a-b binding protein P4. chloroplastic	27.21	18.25	*Pisum sativum*	0.00058	0.00058	-11.00/-11.00
9	P15194	Chlorophyll a-b binding protein type 2 member 1B. chloroplastic	29.01	31.38	*Pinus sylvestris*	0.00021	0.00021	-12.20/-12.20
10	P12328	Chlorophyll a-b binding protein of LHCII type I. chloroplastic	28.35	15.1515152	*Lemna gibba*	0.00016	0.00016	-12.50/-12.50
11	B1NWD5	ATP synthase subunit alpha. chloroplastic	55.56	29.78	*Manihot esculenta*	1.41	0.0042	0.50/-8.00
12	Q332X1	ATP synthase subunit beta. chloroplastic	53.53	42.16	*Lactuca sativa*	0.00098	0.00098	-10.90/ -10.90

13	Q8SLY2	ATP synthase subunit beta. chloroplastic	52.91	32.45	*Chaetosphaeridium globosum*	0.00048	0.00048	-10.90/ -10.90
14	A4GYR7	ATP synthase subunit beta. chloroplastic	53.67	37.95	*Populus trichocarpa*	8.48E-05	8.48E-05	-13.50/ -13.50
15	P46722	NAD(P)H-quinone oxidoreductase subunit I. chloroplastic	21.14	51.11	*Zea mays*	0.0010	0.0010	-10.00/ -10.00
16	O64981	Ribulose bisphosphate carboxylase/oxygenase activase. chloroplastic	48.17	18.36	*Phaseolus vulgaris*	3.34	1.63	1.80/ 0.70
17	P50318	Phosphoglycerate kinase 2. chloroplastic	49.90	22.38	*Arabidopsis thaliana*	1.00	783.22	0.00/9.60
18	P09672	Glyceraldehyde-3-phosphate dehydrogenase A. chloroplastic (Fragment)	25.08	47.63	*Sinapis alba*	2.78	1.39	1.50/ 0.50
19	P11155	Pyruvate phosphate dikinase 1. chloroplastic	102.60	19.95	*Zea mays*	8.71	2.28	3.10/ 1.20

20	Q41048	Oxygen-evolving enhancer protein 3-1. chloroplastic	23.11	37.78	*Zea mays*	3.60	2.52	1.90/1.30
21	A6YGB8	Photosystem II protein D1	38.12	18.31	*Pleurastrum terricola*	1.00	15130.51	0.00/13.90
22	P36886	Photosystem I reaction center subunit psaK	13.71	15.26	*Hordeum vulgare*	2.05	1.34	1.00/ 0.40
23	Q8S8W4	Cytochrome f	19.37	35.20	*Atropa belladonna*	1798.10	1.00	10.80/0.00
Protein metabolism								
24	O81154	Cysteine synthase	34.32	19.38	*Solanum tuberosum*	0.0067	0.0067	-7.20/ -7.20
25	P17093	40S ribosomal protein S11	17.82	16.98	*Glycine max*	0.0092	0.0092	-6.80/ -6.80
26	Q949H0	40S ribosomal protein S7	22.06	16.75	*Hordeum vulgare*	0.0032	0.0032	-8.30/-8.30
27	P51427	40S ribosomal protein S5-2	22.90	25.60	*Arabidopsis thaliana*	0.00076	0.00076	-10.40/-10.40
28	Q05761	40S ribosomal protein S13	17.04	50.33	*Zea mays*	7.95	1.35	2.90/ 0.40

29	P46252	60S acidic ribosomal protein P2A	11.35	35.71	*Zea mays*	3.95	2.76	1.90/ 1.50
30	Q9AT35	60S ribosomal protein L23a	17.51	17.53	*Daucus carota*	0.73	3.43	-0.40/1.80
31	Q6EN80	30S ribosomal protein S19. chloroplastic	10.68	19.35	*Oryza nivara*	3.25	1.78	1.70/ 0.80
32	A2YXU2	Proteasome subunit alpha type-7-A	27.27	35.34	*Oryza sativa subsp. indica*	1.02	3.16	0.04/1.70
Carbohydrate and energy metabolism								
33	P12863	Triosephosphate isomerase. cytosolic	27.00	38.33	*Zea mays*	0.23	0.47	-1.10/-2.10
34	P26517	Glyceraldehyde-3-phosphate dehydrogenase 1. cytosolic	36.49	44.21	*Hordeum vulgare*	0.00061	0.00061	-10.70/ -10.70
35	P26518	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	36.95	20.52	*Magnolia liliiflora*	0.0028	0.0028	-8.50/-8.50
36	Q8LK61	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	53.01	20.36	*Triticum aestivum*	0.0045	0.0045	-7.80/-7.80

37	P42895	Enolase 2	48.13	45.06	*Zea mays*	0.012	0.012	-6.40/-6.40
38	P80269	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8. mitochondrial	26.36	23.14	*Solanum tuberosum*	0.0023	0.0023	-8.80/-8.80
39	Q9XFA2	Phosphoenolpyruvate carboxykinase (ATP) 2	68.59	22.52	*Urochloa panicoides*	0.0015	0.61	-9.40/-0.70
40	O24047	Malate dehydrogenase. cytoplasmic	35.47	25.60	*Mesembryanthemum crystallinum*	0.0046	0.0046	-7.70/ -7.70
41	Q9ZP06	Malate dehydrogenase 1. mitochondrial	35.78	18.47	*Arabidopsis thaliana*	0.0030	0.0030	-8.40/ -8.40
42	P92549	ATP synthase subunit alpha. mitochondrial	55.01	26.03	*Arabidopsis thaliana*	0.0013	0.49	-29.60/-1.00
43	Q6AVT2	Glucose-1-phosphate adenylyltransferase large subunit 1. chloroplastic/amyloplastic	55.39	17.41	*Oryza sativa subsp. japonica*	0.0031	0.0031	-8.30/ -8.30
44	P55238	Glucose-1-phosphate adenylyltransferase small subunit.	56.01	41.32	*Hordeum vulgare*	0.0019	1.00	-8.90/0.010

		chloroplastic/amyloplastic						
45	Q43247	Glyceraldehyde-3-phosphate dehydrogenase 3. cytosolic	36.42	37.38	*Zea mays*	2.97	1.72	1.60/0.80
46	P00056	Cytochrome c	12.00	39.63	*Zea mays*	2.58	3.47	1.40/1.80
Antioxidant defense and stress response								
47	Q6ZFU6	Thioredoxin reductase NTRB	34.65	17.22	*Oryza sativa subsp. japonica*	0.0038	0.0038	-8.00/ -8.00
48	Q69SV0	Probable L-ascorbate peroxidase 8. chloroplastic	51.15	19.24	*Oryza sativa subsp. japonica*	0.0031	0.0031	-8.30/ -8.30
49	O23877	Ferredoxin-NADP reductase. embryo isozyme. chloroplastic	41.78	16.93	*Oryza sativa subsp. japonica*	0.0049	0.0049	-7.70/ -7.70
50	P38559	Glutamine synthetase root isozyme 1	39.22	24.64	*Zea mays*	0.0098	0.0098	-6.70/-6.70
51	P38561	Glutamine synthetase root isozyme 3	39.14	40.44	*Zea mays*	0.0014	0.0014	-6.20/-6.20
52	Q6Z965	12-oxophytodienoate reductase 7	43.65	18.52	*Oryza sativa subsp. japonica*	0.0065	0.0065	-7.20/ -7.20

53	Q6Z7B0	Heat shock 70 kDa protein BIP1	73.34	27.81	*Oryza sativa subsp. japonica*	0.011	0.011	-6.40/ -6.40
54	Q84Q72	18.1 kDa class I heat shock protein	18.07	26.08	*Oryza sativa subsp. japonica*	0.0091	0.0091	-6.80/ -6.80
55	P14655	Glutamine synthetase. chloroplastic	46.61	18.69	*Oryza sativa subsp. japonica*	1.00	168.83	0.00/7.40
56	Q9SMB1	Spermidine synthase 1	35.12	15.78	*Oryza sativa subsp. japonica*	3.33	5.64	2.50/1.70
57	A5H8G4	Peroxidase 1	38.33	17.71	*Zea mays*	4.73	3.82	2.20/1.90
58	Q9ZP21	Thioredoxin M-type. chloroplastic	19.12	15.4285714	*Triticum aestivum*	3.307	1.545	1.70/0.60
59	P27322	Heat shock cognate 70 kDa protein 2	70.66	30.74	*Solanum lycopersicum*	946.69	1.00	9.90/0.00
60	Q9BAE0	ATP-dependent zinc metalloprotease FTSH. chloroplastic	75.63	19.83	*Medicago sativa*	222.38	294.93	7.80/8.20
61	P35480	Chaperonin CPN60. mitochondrial	62.31	16.013	*Brassica napus*	1.00	44.56	0.00/5.50
62	P24629	Heat shock cognate 70 kDa protein 1	71.24	23.23	*Solanum lycopersicum*	3.38	1.05	1.80/ 0.10

63	Q02028	Stromal 70 kDa heat shock-related protein. chloroplastic	75.46	24.50	*Pisum sativum*	2.92	0.48	1.60/ -1.10
proteins involved in RNA processing								
64	O48556	Soluble inorganic pyrophosphatase	24.35	30.37	*Zea mays*	0.0048	0.0048	-7.70/ -7.70
65	Q99070	Glycine-rich RNA-binding protein 2	16.35	23.80	*Sorghum bicolor*	6.41	3.50	2.7/01.70
Proteins involved in Growth and development								
66	P53492	Actin-7	41.70	44.031	*Arabidopsis thaliana*	0.0051	0.0051	-7.60/ -7.60
67	O23979	Soluble inorganic pyrophosphatase	24.03	29.30	*Hordeum vulgare subsp. vulgare*	0.0011	0.0011	-9.80/ -9.80
68	P02582	Actin-1	41.59	20.26	*Zea mays*	1.00	54.94	0.00/5.80
69	P20904	Actin	41.73	28.38	*Volvox carteri*	4.70	2.83	2.20/ 1.50
Signal Transduction								
70	O49513	Ras-related protein RABA1e	24.31	23.04	*Arabidopsis thaliana*	389.43	915.52	8.60/9.80

71	Q43463	Ras-related protein Rab7	23.09	15.53	*Glycine max*	1.00	158.75	0.00/7.30
72	P49104	Ras-related protein Rab-2-B	23.04	35.71	*Zea mays*	1.00	120.52	0.00/ 6.90
73	P92963	Ras-related protein RABB1c	23.15	37.44	*Arabidopsis thaliana*	3.54	2.33	1.80/1.20
74	Q9SP07	14-3-3-like protein	29.23	39.76	*Lilium longiflorum*	7.28	2.41	2.90/ 1.30
75	Q6ZKC0	14-3-3-like protein GF14-C	28.80	44.92	*Oryza sativa subsp. japonica*	3.93	2.45	1.90/ 1.30
Membrane transport and cell wall metabolism								
76	Q05737	GTP-binding protein YPTM2	22.46	46.79	*Zea mays*	260.97	108.67	8.00/ 6.80
77	P27081	ADP.ATP carrier protein. mitochondrial (Fragment)	41.802	17.8756477	*Solanum tuberosum*	1	117.096	0.00/ 6.90
78	Q84VG0	Probable calcium-binding protein CML7	16.67	16.89	*Oryza sativa subsp. japonica*	2.95	1.88	1.60/ 0.90
79	Q7XPY2	Plasma membrane ATPase	104.75	19.03	*Oryza sativa subsp. japonica*	2.84	1.93	1.50/0.90

80	Q43433	V-type proton ATPase subunit B 2 (Fragment)	43.21	31.86	*Gossypium hirsutum*	2.65		1.59	1.40/0.70