

Supplementary Information

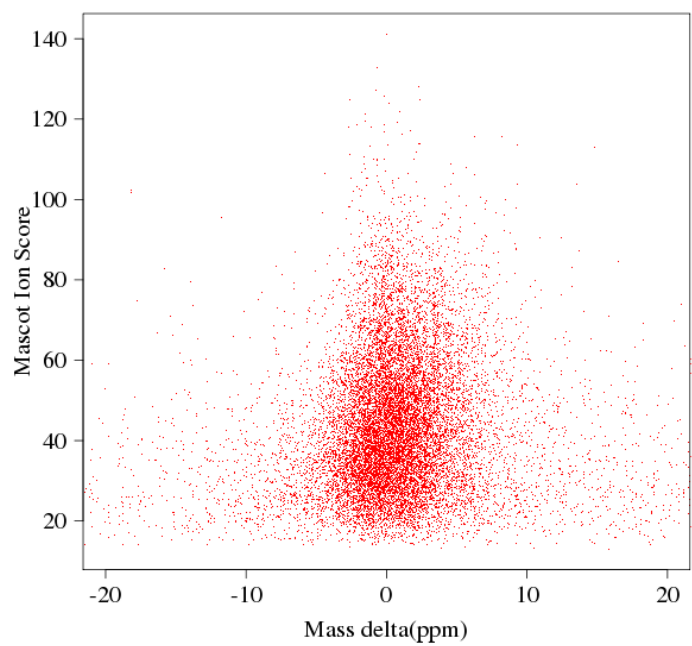


Figure S1. The error distribution of the peptide spectra match quality in *P. lactiflora* lateral branches.

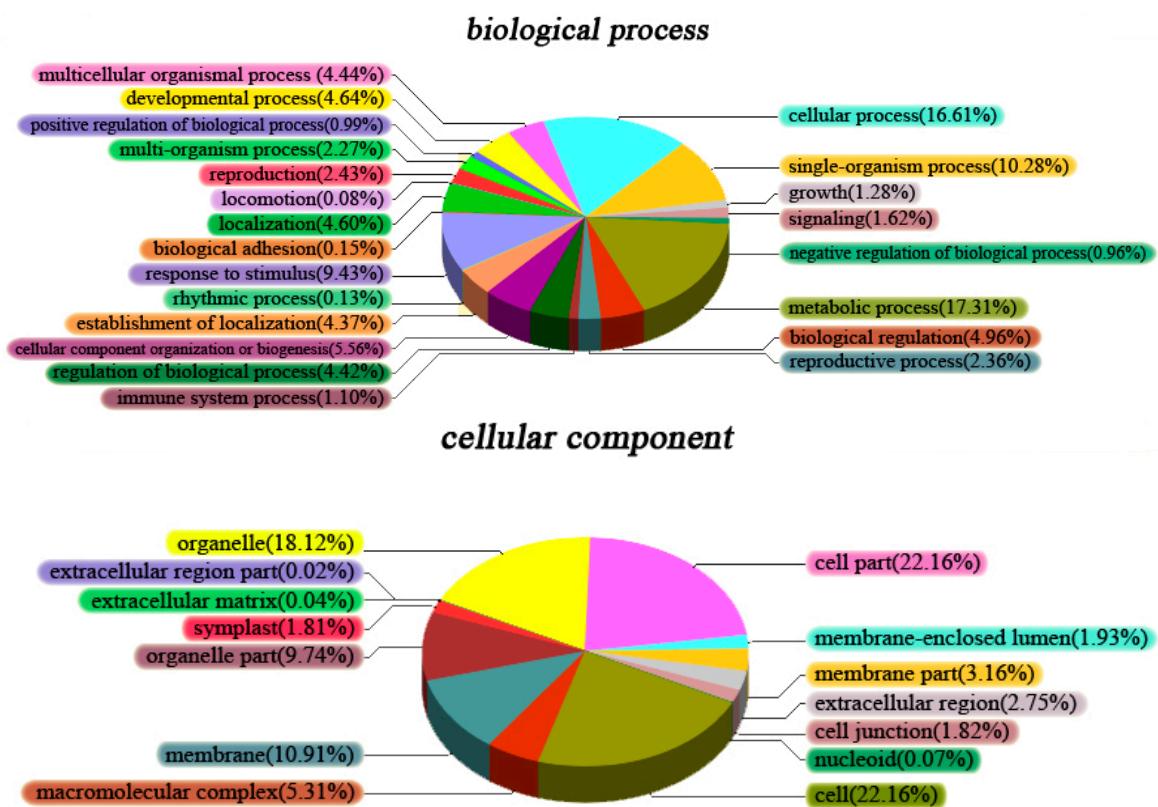


Figure S2. *Cont.*

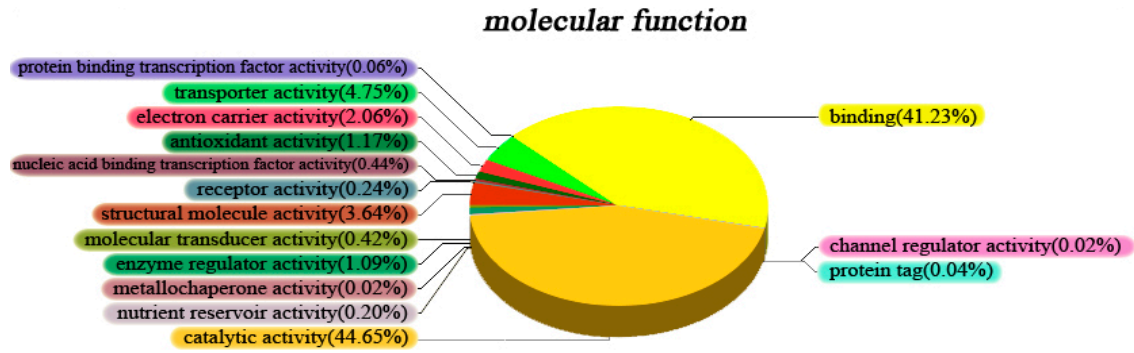


Figure S2. The GO analysis of total identified proteins in *P. lactiflora* lateral branches. GO: gene ontology.

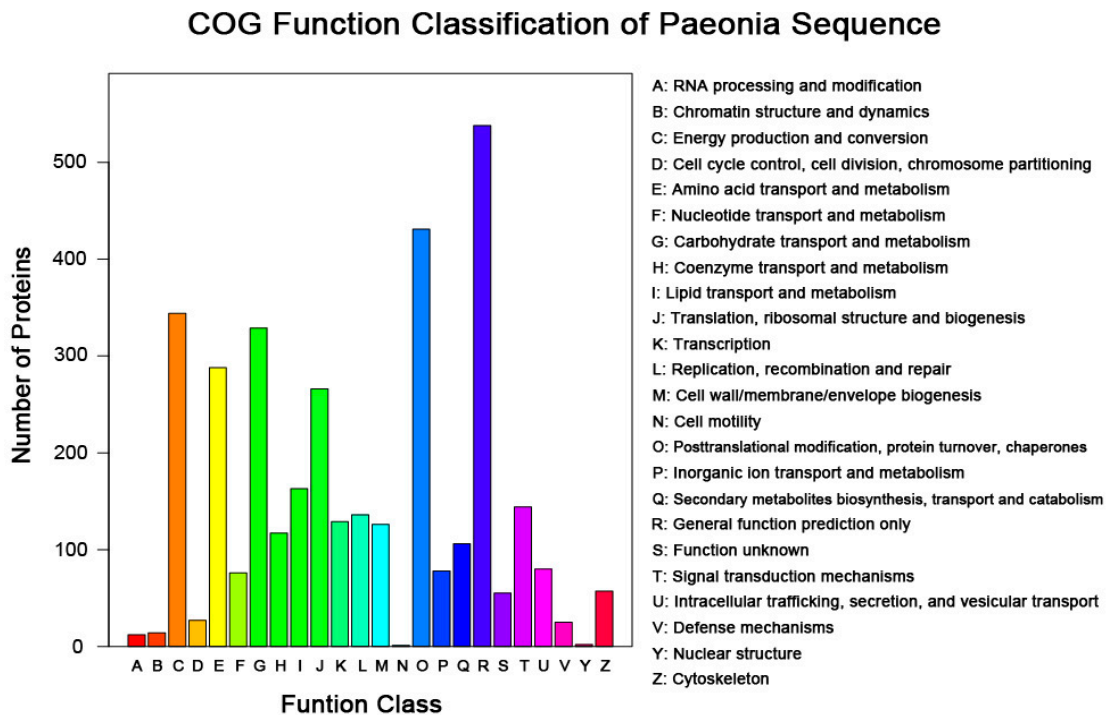


Figure S3. The COG analysis of total identified proteins in *P. lactiflora* lateral branches. COG: cluster of orthologous groups of proteins.

Table S6. 74 KEGG pathways with pathway ID information.

No.	Pathway	DEPs with Pathway Annotation (165)	Pathway ID
1	Metabolic pathways	90 (54.55%)	ko01100
2	Biosynthesis of secondary metabolites	55 (33.33%)	ko01110
3	Phenylpropanoid biosynthesis	14 (8.48%)	ko00940
4	Glyoxylate and dicarboxylate metabolism	12 (7.27%)	ko00630
5	Carbon fixation in photosynthetic organisms	13 (7.88%)	ko00710
6	Ribosome	14 (8.48%)	ko03010
7	Cysteine and methionine metabolism	7 (4.24%)	ko00270
8	Tryptophan metabolism	3 (1.82%)	ko00380
9	One carbon pool by folate	4 (2.42%)	ko00670

Table S6. *Cont.*

No.	Pathway	DEPs with Pathway Annotation (165)	Pathway ID
10	Flavonoid biosynthesis	5 (3.03%)	ko00941
11	Alanine, aspartate and glutamate metabolism	7 (4.24%)	ko00250
12	Photosynthesis—antenna proteins	3 (1.82%)	ko00196
13	Propanoate metabolism	5 (3.03%)	ko00640
14	Isoflavonoid biosynthesis	2 (1.21%)	ko00943
15	Pentose and glucuronate interconversions	5 (3.03%)	ko00040
16	Vitamin B6 metabolism	3 (1.82%)	ko00750
17	Glycolysis/Gluconeogenesis	10 (6.06%)	ko00010
18	Histidine metabolism	2 (1.21%)	ko00340
19	Arginine and proline metabolism	6 (3.64%)	ko00330
20	Phenylalanine metabolism	6 (3.64%)	ko00360
21	Nitrogen metabolism	4 (2.42%)	ko00910
22	Linoleic acid metabolism	2 (1.21%)	ko00591
23	Purine metabolism	7 (4.24%)	ko00230
24	Glycine, serine and threonine metabolism	6 (3.64%)	ko00260
25	Peroxisome	5 (3.03%)	ko04146
26	Amino sugar and nucleotide sugar metabolism	7 (4.24%)	ko00520
27	Ascorbate and aldarate metabolism	5 (3.03%)	ko00053
28	Cyanoamino acid metabolism	3 (1.82%)	ko00460
29	Lysine degradation	2 (1.21%)	ko00310
30	Galactose metabolism	4 (2.42%)	ko00052
31	Selenocompound metabolism	2 (1.21%)	ko00450
32	Stilbenoid, diarylheptanoid and gingerol biosynthesis	2 (1.21%)	ko00945
33	Glycerolipid metabolism	2 (1.21%)	ko00561
34	Phenylalanine, tyrosine and tryptophan biosynthesis	3 (1.82%)	ko00400
35	Flavone and flavonol biosynthesis	1 (0.61%)	ko00944
36	Pyruvate metabolism	5 (3.03%)	ko00620
37	Terpenoid backbone biosynthesis	2 (1.21%)	ko00900
38	Riboflavin metabolism	1 (0.61%)	ko00740
39	Tyrosine metabolism	3 (1.82%)	ko00350
40	beta-Alanine metabolism	2 (1.21%)	ko00410
41	Glycosphingolipid biosynthesis—ganglio series	1 (0.61%)	ko00604
42	Glycosaminoglycan degradation	1 (0.61%)	ko00531
43	Proteasome	3 (1.82%)	ko03050
44	Fatty acid metabolism	3 (1.82%)	ko00071
45	Ether lipid metabolism	1 (0.61%)	ko00565
46	Valine, leucine and isoleucine degradation	2 (1.21%)	ko00280
47	Sphingolipid metabolism	1 (0.61%)	ko00600
48	Limonene and pinene degradation	1 (0.61%)	ko00903
49	Lysine biosynthesis	1 (0.61%)	ko00300
50	Plant hormone signal transduction	3 (1.82%)	ko04075
51	RNA degradation	3 (1.82%)	ko03018
52	Photosynthesis	4 (2.42%)	ko00195
53	Isoquinoline alkaloid biosynthesis	1 (0.61%)	ko00950
54	Porphyrin and chlorophyll metabolism	1 (0.61%)	ko00860

Table S6. Cont.

No.	Pathway	DEPs with Pathway Annotation (165)	Pathway ID
55	alpha-Linolenic acid metabolism	2 (1.21%)	ko00592
56	Starch and sucrose metabolism	5 (3.03%)	ko00500
57	Phagosome	3 (1.82%)	ko04145
58	Butanoate metabolism	1 (0.61%)	ko00650
59	Tropane, piperidine and pyridine alkaloid biosynthesis	1 (0.61%)	ko00960
60	mRNA surveillance pathway	2 (1.21%)	ko03015
61	Glycerophospholipid metabolism	1 (0.61%)	ko00564
62	Citrate cycle (TCA cycle)	2 (1.21%)	ko00020
63	Aminoacyl-tRNA biosynthesis	2 (1.21%)	ko00970
64	Other glycan degradation	1 (0.61%)	ko00511
65	Ribosome biogenesis in eukaryotes	1 (0.61%)	ko03008
66	Glutathione metabolism	2 (1.21%)	ko00480
67	Fructose and mannose metabolism	2 (1.21%)	ko00051
68	Ubiquitin mediated proteolysis	1 (0.61%)	ko04120
69	Pyrimidine metabolism	1 (0.61%)	ko00240
70	Plant-pathogen interaction	2 (1.21%)	ko04626
71	Endocytosis	1 (0.61%)	ko04144
72	Protein processing in endoplasmic reticulum	2 (1.21%)	ko04141
73	RNA transport	1 (0.61%)	ko03013
74	Oxidative phosphorylation	1 (0.61%)	ko00190

Table S7. Candidate DEPs involved in the growth inhibition of *P. lactiflora* lateral branches under PBZ application.

Accession	Species	Description	Abbreviation	Coverage (%)	Mass (Da)	Ratio (PBZ/Control)
Defense and stress response						
gi 223547351	<i>Ricinus communis</i>	lipoxygenase	LOX	1.2	121,118	1.641
gi 557104863	<i>Arabidopsis thaliana</i>	peroxiredoxin-2E	PRX2E	12.3	29,350	1.622
gi 67008247	<i>Andrographis paniculata</i>	catalase	CAT	22.8	36,540	1.256
gi 223540303	<i>Ricinus communis</i>	heat-shock protein	HSP	9.3	22,372	1.593
Hormone related proteins						
gi 375314636	<i>Paeonia lactiflora</i>	1-aminocyclopropane-1-carboxylate oxidase	ACO	11.9	44,259	1.321
gi 158564566	<i>Paeonia suffruticosa</i>	auxin-repressed protein	ARP	19.8	16,150	1.262
gi 350538405	<i>Solanum lycopersicum</i>	isopentenyl diphosphate isomerase	IPI	14.5	32,568	0.392
gi 75250205	<i>Hevea brasiliensis</i>	geranylgeranyl pyrophosphate synthase	GGPS	3.8	48,208	0.666
Carbohydrate transport and metabolism						
gi 17017255	<i>Nicotiana tabacum</i>	aquaporin	AQP	8.4	34,867	1.499
gi 150416573	<i>Gossypium hirsutum</i>	aquaporin PIP1-2	PIP1-2	8.4	35,692	1.638
Lipid transport and metabolism						
gi 1698844	<i>Ricinus communis</i>	phospholipase D	PLD	12.5	105,167	1.339
Protein transport and metabolism						
gi 343172102	<i>Silene latifolia</i>	20S proteasome subunit alpha type 7	PSA7	16.5	33,107	1.217
gi 222842473	<i>Populus trichocarpa</i>	ATP-dependent 26S proteasome regulatory subunit	PRS	27.9	53,879	1.269
Energy metabolism						
gi 225432854	<i>Vitis vinifera</i>	pyruvate kinase isozyme A	PKIA	11.1	72,564	0.769
gi 356525744	<i>Glycine max</i>	phosphoglycerate kinase	PGK	18	53,925	0.721
gi 355485086	<i>Medicago truncatula</i>	glyceraldehyde-3-phosphate dehydrogenase	GAPDH	11.7	53,435	0.414
Cell structure related proteins						
gi 82394883	<i>Gerbera jamesonii</i>	xyloglucan endotransglucosylase	XT	8.4	39,213	0.711
gi 3287956	<i>Glycine max</i>	actin-3	ACTIN3	31.9	48,198	0.517
gi 527182282	<i>Genlisea aurea</i>	actin	ACTIN	33.3	36,707	0.504
gi 359475114	<i>Vitis vinifera</i>	isoflavone reductase	IFR	5.2	33,592	0.687
gi 223540897	<i>Ricinus communis</i>	isoflavone reductase	IFR	3.8	42,856	0.503

Table S7. Cont.

Accession	Species	Description	Abbreviation	Coverage (%)	Mass (Da)	Ratio (PBZ/Control)
Cell wall metabolism						
gi 470133240	<i>Fragaria vesca</i>	bifunctional 3-dehydroquinate dehydratase/ shikimate dehydrogenase	DHD/SHD	4.1	68,103	0.78
gi 67867090	<i>Ulmus americana</i>	phenylalanine ammonia-lyase	PAL	2.9	67,303	0.358
gi 385718959	<i>Paeonia lactiflora</i>	phenylalanine ammonia-lyase	PAL	22.7	89,039	0.341
gi 285028552	<i>Fagopyrum esculentum</i>	phenylalanine ammonia-lyase	PAL	11.2	90,728	0.321
gi 363541683	<i>Medicago sativa</i>	phenylalanine ammonia-lyase	PAL	8.7	63,676	0.308
gi 459353590	<i>Paeonia lactiflora</i>	cinnamate 4-hydroxylase	C4H	33.9	68,846	0.448
gi 31414896	<i>Fragaria x ananassa</i>	cinnamoyl CoA reductase	CCR	5.6	46,058	0.504
gi 227286085	<i>Codonopsis lanceolata</i>	cinnamoyl CoA reductase	CCR	8.3	45,020	0.425
gi 347730541	<i>Quercus suber</i>	cinnamyl alcohol dehydrogenase 2	CAD2	8.2	31,545	0.462
gi 62734979	<i>Linum usitatissimum</i>	cinnamyl alcohol dehydrogenase	CAD	5.5	35,894	0.405
gi 470121238	<i>Fragaria vesca</i>	pectinesterase/pectinesterase inhibitor 35-like	PE/PEI35L	2.4	71,889	0.448
gi 541135565	<i>Betula luminifera</i>	sucrose synthase 2	SUS2	9.2	106,948	0.378
gi 213868495	<i>Ipomoea batatas</i>	UDP-glucose pyrophosphorylase	UGPase	8.5	64,370	0.48

Table S8. Gene-specific primers sequence for detection by Q-PCR.

Gene	Forward Primer (5'–3')	Reverse Primer (5'–3')
<i>Actin</i>	GCAGTGTTCCCCAGTATT	TCTTTTCCATGTCATCCC
<i>ACO</i>	GCCTCATCTTACTCTTCCAA	GCAAGCGACATCCTATTACC
<i>PAL</i>	TGCCTCGCTACTTACCCT	GCTCCTCCTCAAATGCTG
<i>C4H</i>	GCACGACAGGAGTAACAA	CACTCAATGGACCACAGC
<i>ARP</i>	GAGGTCGCTTTCTATGCC	AGATTGCTGCCAGGGTTG