

Table 1 Suppl. Characteristics of the putative *PCs* identified in the genome of *P. equestris*. SP - signal peptide, PD - number of plastocyanin-like domains, CBS - copper-binding sites, GB - GPI-anchor signal predicted by *Big-PI Plant Predictor*, GP - GPI-anchor signal predicted by *PSORT*, NG - N-glycosylation sites, AG - putative AG glycomodule, EG - putative extensin glycomodule; +, -, NC mean present, not present, and not checked, respectively.

Name	Gene ID	SP	PD	CBS	GB	GP	NG	AG	EG
PeENODL1	PEQU_00681	+	1	-	+	+	+	+	+
PeENODL2	PEQU_01525	+	1	-	-	-	-	-	-
PeENODL3	PEQU_07653	-	1	-	-	-	-	NC	NC
PeENODL4	PEQU_08393	+	1	-	+	-	+	+	-
PeENODL5	PEQU_08610	+	1	-	-	+	+	+	-
PeENODL6	PEQU_11121	+	1	-	-	-	+	+	-
PeENODL7	PEQU_12079	+	1	-	+	+	+	+	+
PeENODL8	PEQU_13421	-	1	-	+	-	+	NC	NC
PeENODL9	PEQU_15783	+	1	-	+	+	+	+	-
PeENODL10	PEQU_36125	+	1	-	+	+	+	+	-
PeUCL1	PEQU_00112	+	1	+	+	-	+	+	-
PeUCL2	PEQU_00113	+	1	+	+	-	+	+	-
PeUCL3	PEQU_06004	+	1	+	-	+	+	+	+
PeUCL4	PEQU_06005	-	1	+	-	-	+	NC	NC
PeUCL5	PEQU_07626	-	1	+	+	-	+	NC	NC
PeUCL6	PEQU_10123	-	1	+	-	-	+	NC	NC
PeUCL7	PEQU_14669	+	1	+	-	-	-	+	+
PeUCL8	PEQU_15884	-	1	+	-	-	+	NC	NC
PeUCL9	PEQU_15883	+	1	+	-	-	+	-	-
PeUCL10	PEQU_33670	+	1	+	+	-	+	+	+
PeSCL1	PEQU_04519	+	1	+	+	+	+	+	+
PeSCL2	PEQU_06981	+	1	+	+	+	-	-	-
PeSCL3	PEQU_12112	+	1	+	-	-	+	-	-
PeSCL4	PEQU_19442	+	1	+	+	+	+	+	+
PeSCL5	PEQU_39385	-	1	+	+	-	+	NC	NC
PePLCL1	PEQU_01523	+	1	+	-	-	-	-	-
PePLCL2	PEQU_07235	+	1	+	-	-	-	-	-
PePLCL3	PEQU_15885	+	1	+	-	-	-	-	-
PePLCL4	PEQU_40735	-	1	+	-	-	-	NC	NC
Unknown	PEQU_09781	-	1	-	-	-	+	NC	NC

Table 2 Suppl. Classification of PePCs (- not present).

Group	Number	PeENODLs	PeUCLs	PePLCLs	PeSCLs	Unknown
I	12	PeENODL1, PeENODL4, PeENODL5, PeENODL7, PeENODL9, PeENODL10	PeUCL1, PeUCL2, PeUCL3, PeUCL10	-	PeSCL1, PeSCL4	-
II	2	PeENODL6	PeUCL7	-	-	-
III	1	-	-	-	PeSCL2	-
IV	6	PeENODL2	PeUCL9	PePLCL1, PePLCL2, PePLCL3	PeSCL3	
V	3	PeENODL8	PeUCL5	-	PeSCL5	-
VI	6	PeENODL3	PeUCL4, PeUCL6, PeUCL8	PePLCL4	-	PEQU_09781

Table 3 Suppl. Reads per kilobase per million mapped reads (RPKM) of *PePC* genes in the four tissues.

Name	Gene ID	RPKM flower	leaf	stem	root
PeENODL1	PEQU_00681	37.28	35.46	11.95	0.00
PeENODL2	PEQU_01525	0.07	0.00	0.41	0.24
PeENODL3	PEQU_07653	34.06	47.29	78.35	27.88
PeENODL4	PEQU_08393	6.45	0.00	0.11	0.00
PeENODL5	PEQU_08610	436.17	0.00	0.00	0.00
PeENODL6	PEQU_11121	0.56	0.00	0.00	0.09
PeENODL7	PEQU_12079	261.66	70.21	102.30	13.87
PeENODL8	PEQU_13421	146.48	36.94	42.37	6.18
PeENODL9	PEQU_15783	94.04	0.00	108.63	0.08
PeENODL10	PEQU_36125	3.20	26.32	4.75	15.19
PeUCL1	PEQU_00112	3.15	0.00	1.24	0.81
PeUCL2	PEQU_00113	3.96	19.82	4.28	0.09
PeUCL3	PEQU_06004	0.63	0.91	3.45	41.28
PeUCL4	PEQU_06005	0.84	0.00	2.21	0.39
PeUCL5	PEQU_07626	12.34	2.82	10.12	10.06
PeUCL6	PEQU_10123	18.33	29.52	144.11	3.50
PeUCL7	PEQU_14669	33.63	32.31	47.92	7.97
PeUCL8	PEQU_15884	0.06	0.00	0.64	0.00
PeUCL9	PEQU_15883	0.14	0.00	0.00	0.00
PeUCL10	PEQU_33670	0.17	0.00	25.42	8.28
PeSCL1	PEQU_04519	63.09	39.63	202.31	436.02
PeSCL2	PEQU_06981	0.00	0.00	0.32	0.18
PeSCL3	PEQU_12112	142.16	32.94	214.80	88.41
PeSCL4	PEQU_19442	6.34	56.22	126.84	107.89
PeSCL5	PEQU_39385	233.07	8.23	76.66	0.23
PePLCL1	PEQU_01523	6.21	0.00	45.70	0.00
PePLCL2	PEQU_07235	32.98	12.13	92.40	4.29
PePLCL3	PEQU_15885	0.00	0.00	0.00	0.00
PePLCL4	PEQU_40735	0.00	0.00	0.00	0.00
PEQU_09781	PEQU_09781	0.00	0.00	0.00	0.00

PePLCL1	WTFNTAAW	PNAKGSRF	FRAGD	VLVFKYN	RMLNVVAVNA	AGYNGCAAK	GGK	IYKT	GNDRIALAR	GPNYFI	SIPG	ICEGG	80		
PeENODL2	WNTNVGNW	HFQKS	FNEND	VLIFNYD	KTQGNVTVDD	VGYSDCTVTPGAQ	FWDG	GNDRIALQS	GDTFFI	SVSN	LCDQG	79			
PeUCL8	WDLNVITN	WAKGKTF	NAGD	ILEFKYN	TAEINNVVLKRRQDF	FENCNVASGS	KIYDTRDPIKLKR	GYNYFI	SKYN	ICGGGLK	63				
PePLCL4				LIEFNYN	TAEINNVVLKRRQDF	FENCNVASGS	KIYDTRDPIKLKR	GYNYFI	SKYN	ICGGGLK	63				
PeUCL9	WALKVIPY	WGTGKKFY	AGD	TLVFKYN	PEEINVMVESALDF	NNCNVSDNA	MIYDFGND	SIILKQ	RYNYFF	GKWN	ICGAG	80			
PePLCL3	WYKMTSN	WSNGKKFY	AGD	TLVFKYN	PGEINVIKVN	AEDYTF	FCRVPANV	KVYESGNDHIKLKR	GDNYFI	CGIFG	ICGIG	79			
PeUCL1	WTLGVNYT	KWAEGRKF	VVD	NLVFNYA	PGRINVLAVGG	AAFSSCNKTAETP	PLTT	GKDPVALNKAGRKYWI	SIGD	HCREG	81				
PeUCL2	WTLGVNYT	KWAEGRKF	VVD	QITFNYY	RGKINVLKVRGEAF	NSCNKLGQVP	PLTS	GNSFIFITGGRKWIYI	AFED	HCQRG	82				
PePLCL2	WNTG	VD	YSSWTSKTF	FAVGD	SLAFAYG	AGTITVNEVSA	NDYQSCSTSNYL	STDSSGSTTILRTSGTHYFV	CGVPG	HCIGG	82				
PeUCL7	WTTG	VD	YTTWVSDKTF	FKVGD	KLVIYYKC	VSIAKAYHFSHG	WGARSSHTTILG	LQLFKYGGLSADEVSK	SDYDSC	TSGNAI	QSHSDGSTTILKLEAGTRYFI	CGTPG	ICDGG	111	
PeUCL3	WDTG	AD	LYSWPENKHF	HVG		SLLFQYS	QYISVNQVDE	NGYRNC	NASNAI	LRSSNGNTSVRLTTPGEKYFI	CGVLS	ICLGG	80		
PeUCL4	WDIS	AD	LYSWPATKLF	YIGD		VLLFQYS	PYHDVNQVDR	NGFSNC	NASNAM	LKSTDGNTYVPLNATGDKYFI	CGVLS	ICLGG	80		
PeUCL10	WDTG	AD	LATWPEARVFS	VGD		ILSFQYS	SYHTVNQVDK	NGYNTC	NASNAI	LTSSGGNTTVPVLSVGD	KYFI	ICFVG	80		
PeENODL6	WVVKPDE	SYNIWAAMKRF	QVND	KLGN	DNSVLNPLNHKDYF	IILCFCSFW	YKKGDSV	LVQVK	KDYDSC	NSSNPI	KKFDNGD	TVFMDRSGPFYFI	CGEGD	ICDGG	106
PeENODL3	WVRKPAE	KYNSWAERMRF	QVKD	KLNNLTPSFDSSM	QILVINDCLTEILNFYALFG	FAVFNKKGDSV	LVQVK	EDYDSC	NTKNPI	KRFEDEG	KTVFVDRSGPFYFI	CGADG	ICDGG	118	
PeENODL1	WTVPTDPSMSYNQWAEKNRF	QIGD	TLCE	IFNLKHFFS	NSSCTLQWHIVFV	YQPDQSV	LVQVK	IAYKHC	NTSSYI	ARFDDG	NTVFTLNMSGPFYFI	CGVEG	NCIRN	106	
PeENODL9	WKIPSSSSADSLNQWAEKNRF	QVGD		YLWVN	YDAEKDSV	LVQVK	TDYLT	CNITSPI	AEHKDGD	TKLRLRRSGAHYFI	CGVEGA	CVKG	86		
PeENODL4	WRVPEDNNPDFYTTWATNLRF	HVG		SLVF	EYKND	SVIRVEK	IGYYHC	NESGNG	TLLKDG	SAVFLLDKPGFFFF	SGNVE	ICCKG	84		
PeENODL10	WRVPDNSNPDPFYTAWSKLRF	QVGD		TIVF	EYKND	SVIRVEK	RGYYHC	NESGNG	ALYKDG	STVFFLDKPGLLYFV	SNIE	ICCKM	84		
PeENODL5	WAIPSSKNPDFYNKWASNNRF	QVND		TIHF	KYDKDSY	MMVTE	SEYKCR	SMHPI	FFSNNG	RTKFKFDRVGLFYFI	CGVSG	ICERG	84		
PeSCL4	WTIPPNAS	FYPKWADSQQ	FVVG	TLVFN	FPTSA	ITVAEVPK	SSYNVCS	NRNQVG	PILSTG	PATVPLTSAGEHYFI	CTITG	ICSLN	85		
PEQU_09781	WSIPVNSD	FYFAWSSNQSF	FIGD	NLVFRFD	TGLYDV	KQVSR	REFESCAENAF	RSFEI	GATVSLVEEGMHYFI	CSFGN	YCFLG	84			
PeUCL5	WDLG	TD	LGSSSSQTF	FAPGD	TLTFSF	GSF	SVVEVPK	ADYAACTMNNPI	KAYTGG	SAVVKLSSSGKRYFI	CGTPG	ICSQG	80		
PeSCL5				FIYN	KSP	INLVETK	TDYHSC	NSASPI	ATHATG	NDSSIPINRYGHRFFI	CGFPG	ICAAQ	58		
PeSCL1	WTIINSPN	YTLWASNKA	AFHQGD	TLLFKYN	KQFINV	LEVKE	ADFTACKNTSAI	KEYD	TGDDSI	IKSVGHSYFI	CGFPG	ICQGG	82		
PeSCL3	WTILNSPN	YTAWASKTF	HFHVG	IVTFNYN	KQFINV	LEVSK	ADYNACTNHSTL	AMFYSG	KDSITIKTAGHHYI	CGVPG	ICQLG	83			
PeSCL2	WTVNDKSY	YTGWAKSK	KFHVGD	VLLFRYD	KQFINV	VQVDK	KGYHK	NAAKPI	AGFNTGHDS	VTIRSDHLFYFI	CGTPG	ICEAG	83		
PeENODL7	WNPGVNYT	LWVNKHP	PFHVG	WLVFYYQ	SGMADV	VQVDE	TAYNKDASHPI	NYSKGR	SYAFELNETKRYFI	CSYG	YCYQG	82			
PeENODL8	WGIPPPSLPNLYAHVVLNHHFHMGD			SLLFLYP	PSQDNV	VQVTE	RAFNA	CVTDPI	LKMEDG	NSIFNLSTPGTFYFI	CGVSG	ICDKR	86		
PeUCL3	WTFGFNYT	DWALKTAPFHLNDTLG		KLIMA	AVFKYDP		PNATTHA	SVYLKDLQRFNG	CDLKRAQVVG	NMQGGG	GEGLEFVLKRKNYYFV	ICEKQGF	ICSTGL	103	
ruler	1	10	20	30	40	50	60	70	80	90	100	110	120	130	

Fig. 1 Suppl. Multiple sequence alignment of the plastocyanin-like domains (PCLDs) of the PePCs. The conserved amino acid residues (His, Cys, His, Met/Gln) involved in copper binding are indicated with a *red* background. Cys residues involved in disulfide linkages are indicated with a *yellow* background. Amino acid residues conserved in the ENODLs are indicated with a *purple* background.

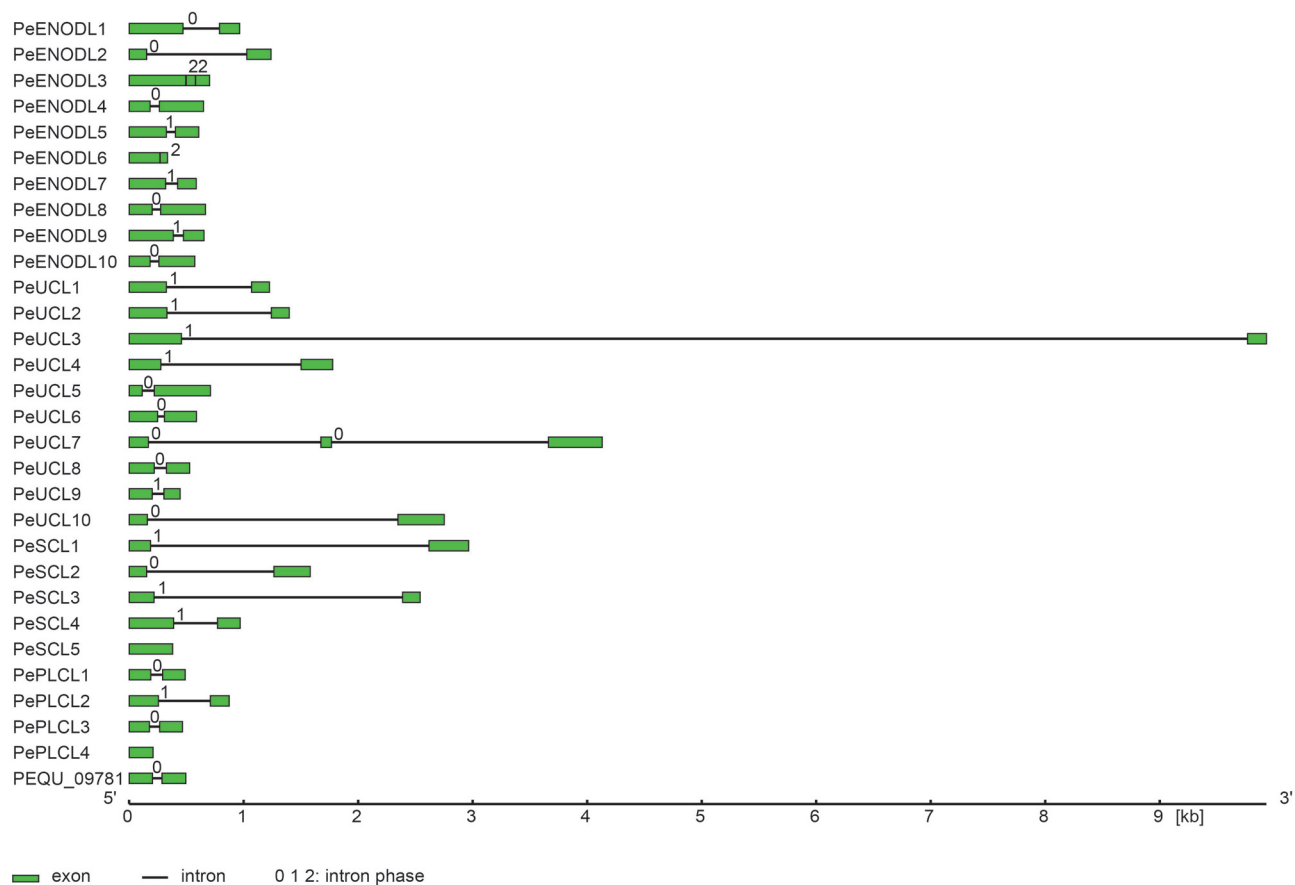


Fig. 2 Suppl. Exon-intron structures of PC genes in *P. equestris*. Green blocks indicate exons, and black lines indicate introns. Numbers 0, 1, and 2 on black lines indicate intron phases.