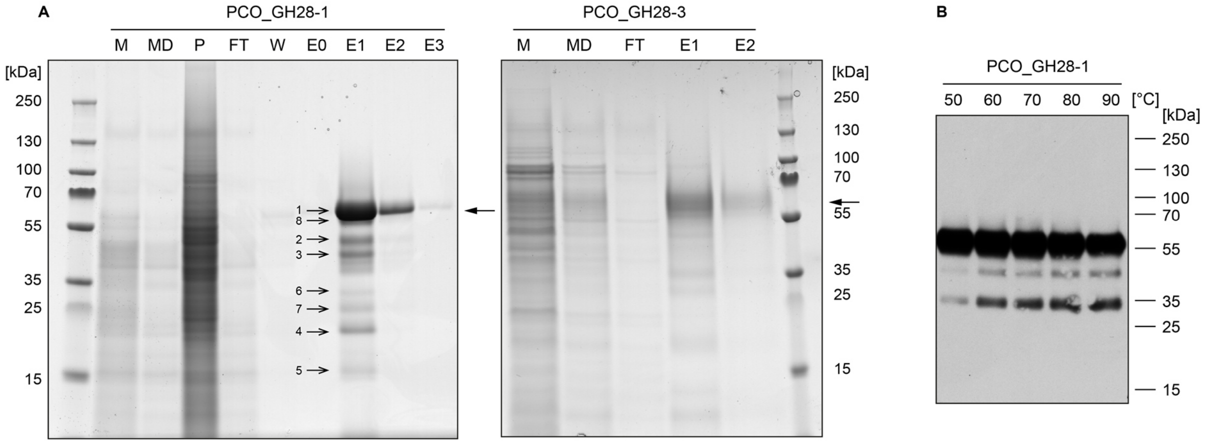
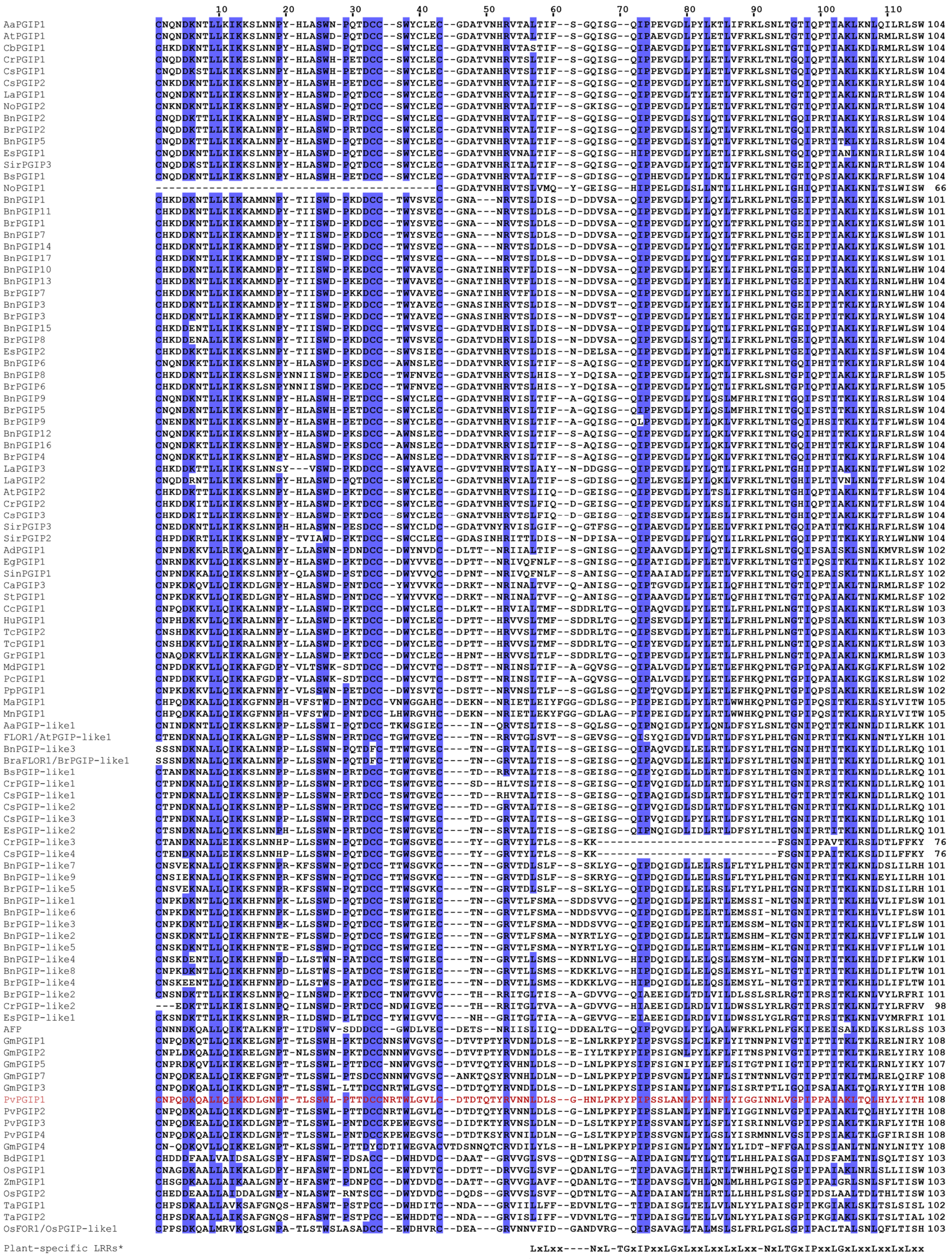


Supplementary Figure 1: Purification of PCO_GH28-1 and -3 and heat-dependent fragmentation of PCO_GH28-1. A) SDS-PAGE and Coomassie staining of exemplary metal ion affinity purification of PCO_GH28-1 and -3 via the His$_6$ tags. Their expected sizes are indicated with an arrow (closed arrowhead). Medium (M), dialyzed medium (MD), precipitated protein (P), flow-though (FT), wash (W) and elution fractions (E0 – E3). Additional bands in the purification of PCO_GH28-1 (arrows with open arrowheads, 1 – 8) were analyzed by MS/MS (see Supplementary Table 2) and identified as fragments of PCO_GH28-1. B) PCO_GH-28-1 was treated with increasing temperatures during sample preparation for SDS-PAGE and detected on the western blot with an anti-V5 antibody.



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                                10        20        30        40        50        60        70        80        90       100       110
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Plant-specific LRRs*                                                     LxLxx----NxL-TGxIPxxLGxLxxLxxLxLxx-NxLTGxIPxxLGxLxxLxxLxLxx
                                                                                  LRR1                        LRR2            LRR3

*(as published for PvPGIP1 (marked in red) by Leckie et al 1999)
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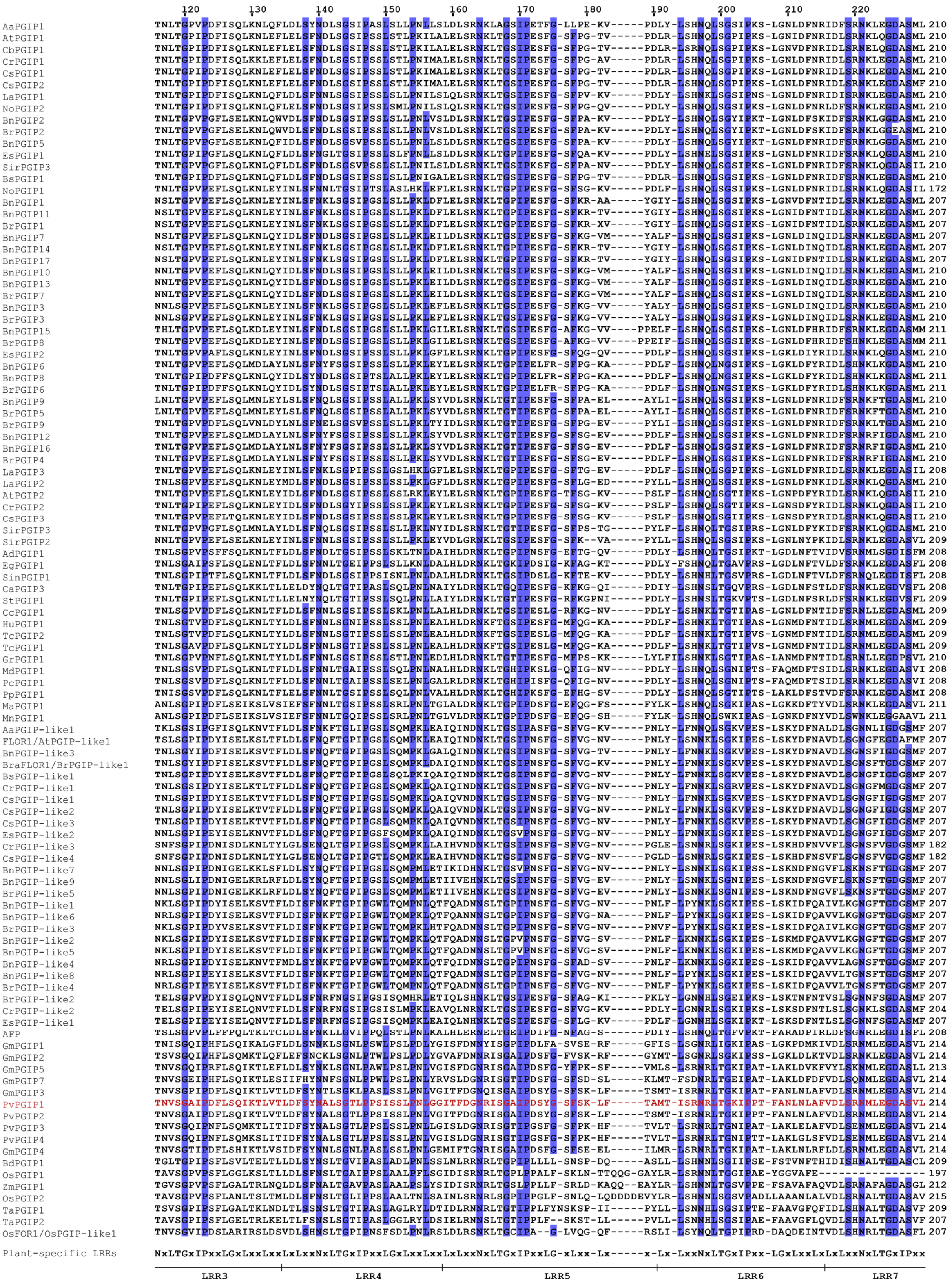

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OsFOR1/OsPGIP-like1      TNVSGVIPDSLARIRSLDSVDLSHNSLTGPIPNSFSDLPNLRSLDLRSNKLTGCIPA--G-LVQG-QF-----RSLI-LSYNQLTGPIPRD-DAQDEINTVDLSHNRLTGDASFL 207

Plant-specific LRRs      NxLTGxIPxxLGxLxxLxxLxLxxNxLTGxIPxxLGxLxxLxxLxLxxNxLTGxIPxxLG-xLxx-Lx-----x-Lx-LxxNxLTGxIPxx-LGxLxxLxLxLxxNxLTGxIPxx

                         |   LRR3   |      LRR4      |         LRR5          |       LRR6       |  LRR7   |
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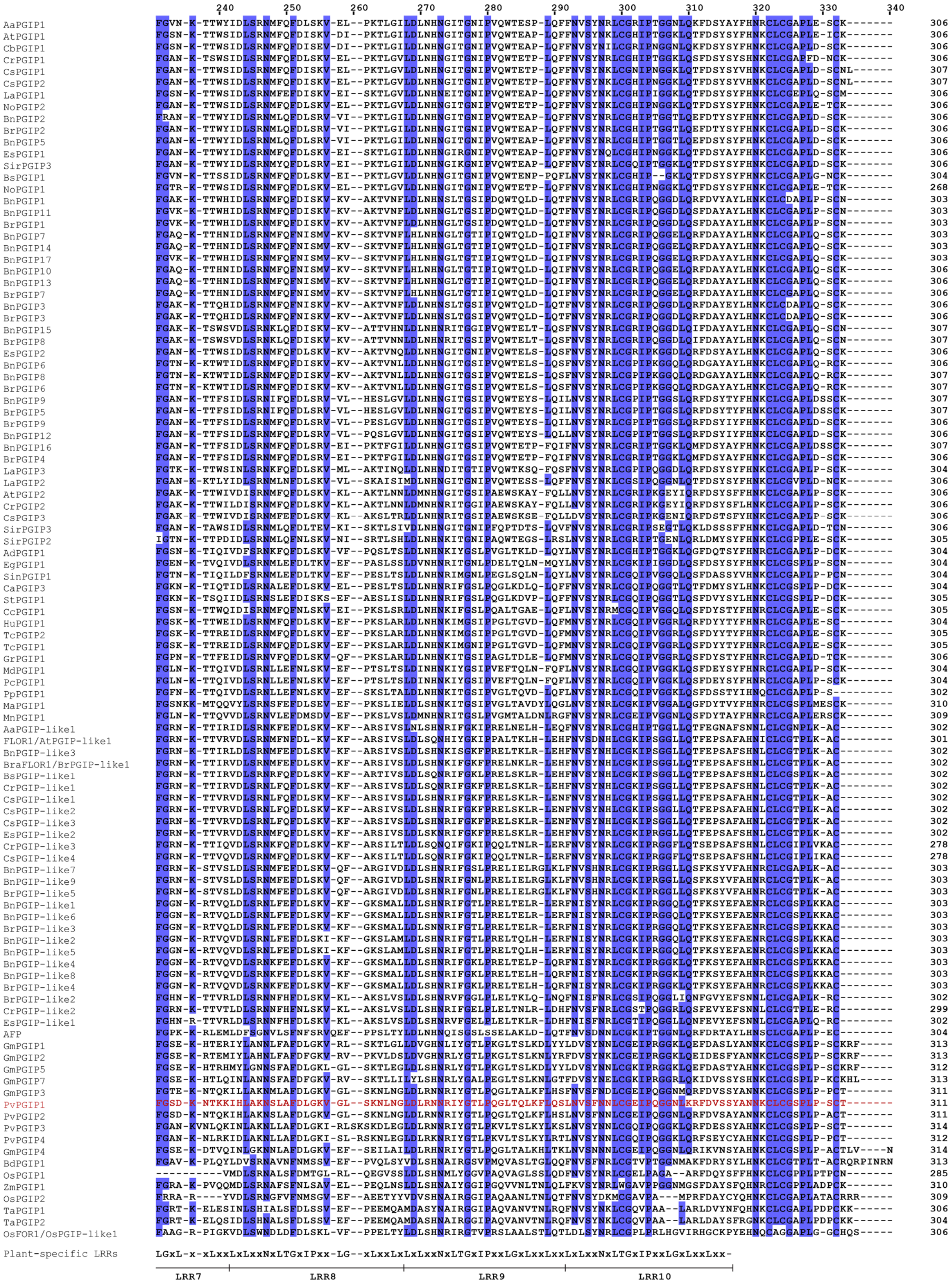
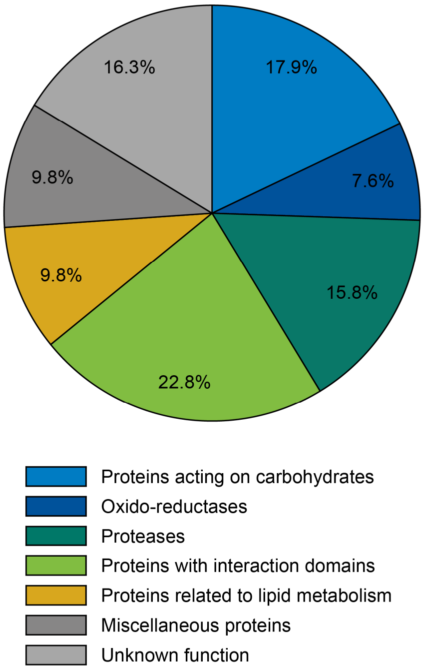
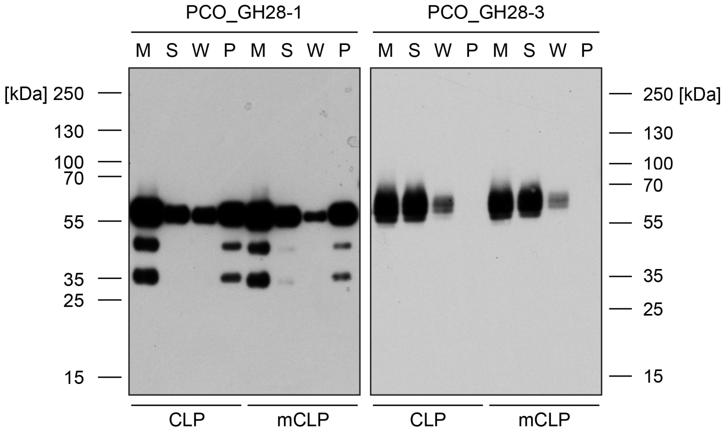


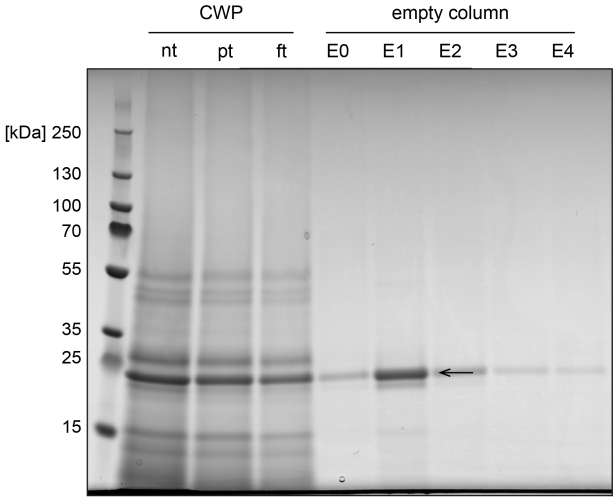
Supplementary Figure 2: Alignment of PGIPs and PGIP-like proteins. Conserved amino acid residues above 80% identity are highlighted in blue. Leucine-rich repeats (LRRs) were displayed below as reported by Leckie *et al.* (1999) for PvPGIP2 from *Phaseolus vulgaris* (highlighted in red). For full sequences, see Supplementary Table 3.



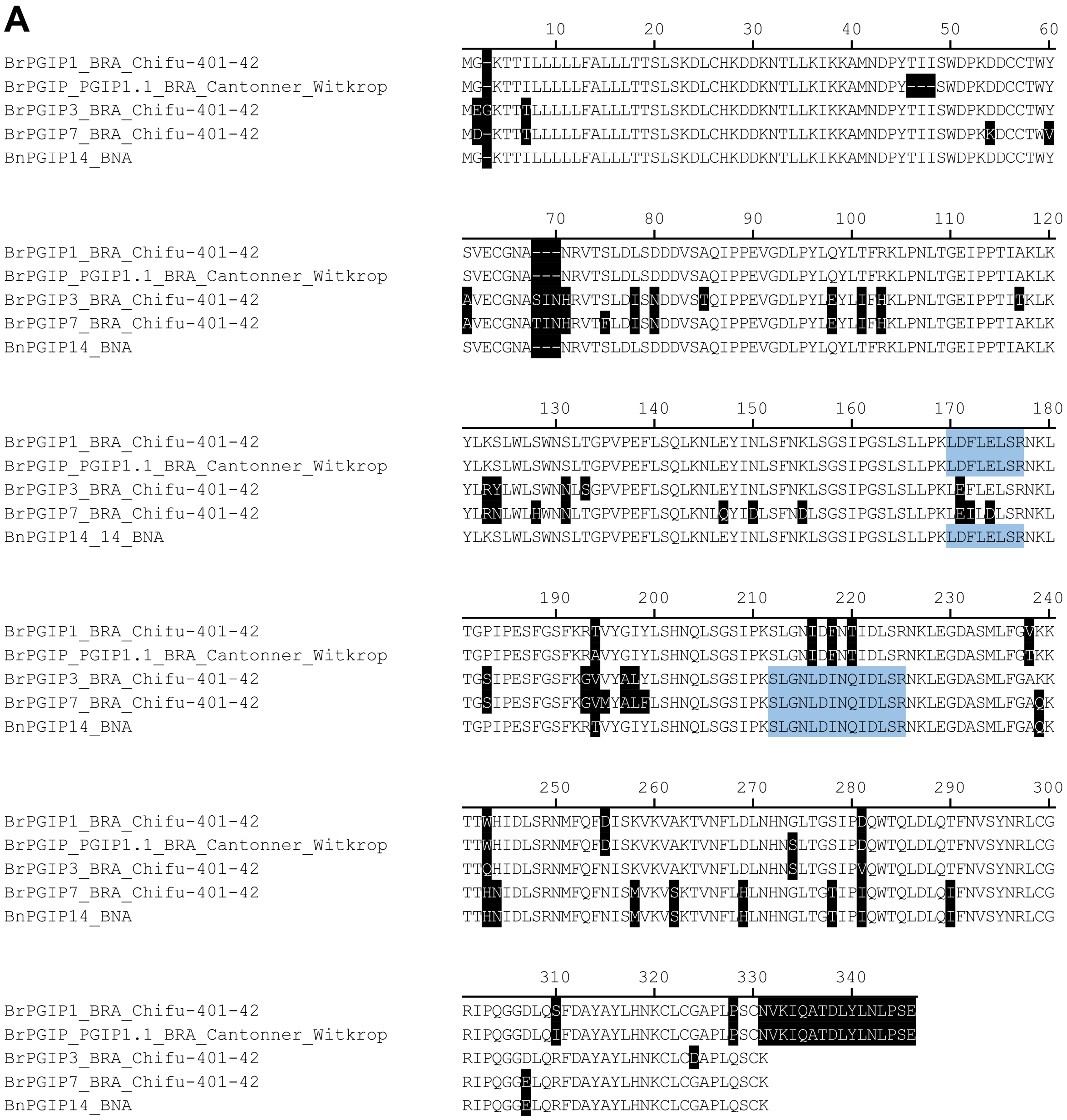
Supplementary Figure 3: Predicted functional classes from *B. rapa* ssp. *pekinensis* cell wall proteins (CWPs). The annotation of proteins is based on the presence of functional domains predicted by InterPro, GO Term and BLAST bioinformatics analysis. Analysis includes only proteins that possess a signal peptide for the secretory pathway according to SignalP and were predicted to be localized extracellularly by DeepLoc analysis. For a full list of identified proteins, see Supplementary Table 4.



Supplementary Figure 4: Binding of *P. cochleariae* PG family members PCO_GH28-1 and -3 to pectic substrates. Culture medium containing PCO_GH28-1 and -3 (M) was incubated with cross-linked pectin (CLP) and methylated CLP (mCLP), respectively. Centrifugation separated the pectin pellet and associated proteins (P) from the supernatant (S). Unbound proteins were removed from the pellet by washing (W). The volumes applied to the western blot were chosen in such a way that the cumulative signals of S, W and P correspond to the initially used amount of M. The PG family members were detected in a western blot with an anti-V5 antibody. The additional bands below the PCO_GH28-1 signal in the western blot were analyzed by LC-MS/MS and assigned to fragments of the PG, which occur as an artefact of the sample boiling for SDS-PAGE (Supplementary Figure 1, Supplementary Table 2).



Supplementary Figure 5: SDS-PAGE of pull-down assay of *B. rapa* ssp. *pekinensis* CWPs with an empty column (negative control). Non-treated (nt) CWP extracts were pre-treated (pt) with column resin to reduce unspecific binding to the column and then passed over columns without immobilized protein. Proteins not interacting with the column material were in the flow-through (ft), while interacting proteins were eluted from the column analogous to the PG family member columns. Elution fraction E1 was analyzed by LC-MS/MS. For detailed information on interacting LRR and total proteins, see Supplementary Table 6. E0 – 4: elution fractions 1 – 4.



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BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop          MG-KTTILLLLLFALLLTTSLSKDLCHKDDKNTLLKIKKAMNDPY---SWDPKDDCCTWY
BrPGIP3_BRA_Chifu-401-42                      MEGKTTTLLLLLFALLLTTSLSKDLCHKDDKNTLLKIKKAMNDPYTIISWDPKDDCCTWY
BrPGIP7_BRA_Chifu-401-42                      MD-KTTTLLLLLFALLLTTSLSKDLCHKDDKNTLLKIKKAMNDPYTIISWDPKKDCCTWV
BnPGIP14_BNA                                  MG-KTTILLLLLFALLLTTSLSKDLCHKDDKNTLLKIKKAMNDPYTIISWDPKDDCCTWY

BrPGIP1_BRA_Chifu-401-42                      SVECGNA---NRVTSLDLSDDDVSAQIPPEVGDLPYLQYLTFRKLPNLTGEIPPTIAKLK
BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop          SVECGNA---NRVTSLDLSDDDVSAQIPPEVGDLPYLQYLTFRKLPNLTGEIPPTIAKLK
BrPGIP3_BRA_Chifu-401-42                      AVECGNASINHRVTSLDISNDDVSTQIPPEVGDLPYLEYLIFHKLPNLTGEIPPTITKLK
BrPGIP7_BRA_Chifu-401-42                      AVECGNATINHRVTFLDISNDDVSAQIPPEVGDLPYLEYLIFHKLPNLTGEIPPTIAKLK
BnPGIP14_BNA                                  SVECGNA---NRVTSLDLSDDDVSAQIPPEVGDLPYLQYLTFRKLPNLTGEIPPTIAKLK

BrPGIP1_BRA_Chifu-401-42                      YLKSLWLSWNSLTGPVPEFLSQLKNLEYINLSFNKLSGSIPGSLSLLPKLDFLELSRNKL
BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop          YLKSLWLSWNSLTGPVPEFLSQLKNLEYINLSFNKLSGSIPGSLSLLPKLDFLELSRNKL
BrPGIP3_BRA_Chifu-401-42                      YLRYLWLSWNNLSGPVPEFLSQLKNLEYINLSFNKLSGSIPGSLSLLPKLEFLELSRNKL
BrPGIP7_BRA_Chifu-401-42                      YLRNLWLHWNNLTGPVPEFLSQLKNLQYIDLSFNDLSGSIPGSLSLLPKLEILDLSRNKL
BnPGIP14_14_BNA                               YLKSLWLSWNSLTGPVPEFLSQLKNLEYINLSFNKLSGSIPGSLSLLPKLDFLELSRNKL

BrPGIP1_BRA_Chifu-401-42                      TGPIPESFGSFKRTVYGIYLSHNQLSGSIPKSLGNIDFNTIDLSRNKLEGDASMLFGVKK
BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop          TGPIPESFGSFKRAVYGIYLSHNQLSGSIPKSLGNIDFNTIDLSRNKLEGDASMLFGTKK
BrPGIP3_BRA_Chifu-401-42                      TGSIPESFGSFKGVVYALYLSHNQLSGSIPKSLGNLDINQIDLSRNKLEGDASMLFGAKK
BrPGIP7_BRA_Chifu-401-42                      TGSIPESFGSFKGVMYALFLSHNQLSGSIPKSLGNLDINQIDLSRNKLEGDASMLFGAQK
BnPGIP14_BNA                                  TGPIPESFGSFKRTVYGIYLSHNQLSGSIPKSLGNLDINQIDLSRNKLEGDASMLFGAQK

BrPGIP1_BRA_Chifu-401-42                      TTWHIDLSRNMFQFDISKVKVAKTVNFLDLNHNGLTGSIPDQWTQLDLQTFNVSYNRLCG
BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop          TTWHIDLSRNMFQFDISKVKVAKTVNFLDLNHNSLTGSIPDQWTQLDLQTFNVSYNRLCG
BrPGIP3_BRA_Chifu-401-42                      TTQHIDLSRNMFQFNISKVKVAKTVNFLDLNHNSLTGSIPVQWTQLDLQTFNVSYNRLCG
BrPGIP7_BRA_Chifu-401-42                      TTHNIDLSRNMFQFNISMVKVSKTVNFLHLNHNGLTGTIPIQWTQLDLQIFNVSYNRLCG
BnPGIP14_BNA                                  TTHNIDLSRNMFQFNISMVKVSKTVNFLHLNHNGLTGTIPIQWTQLDLQIFNVSYNRLCG

BrPGIP1_BRA_Chifu-401-42                      RIPQGGDLQSFDAYAYLHNKCLCGAPLPSCNVKIQATDLYLNLPSE
BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop          RIPQGGDLQIFDAYAYLHNKCLCGAPLPSCNVKIQATDLYLNLPSE
BrPGIP3_BRA_Chifu-401-42                      RIPQGGDLQRFDAYAYLHNKCLCDAPLQSCK
BrPGIP7_BRA_Chifu-401-42                      RIPQGGELQRFDAYAYLHNKCLCGAPLQSCK
BnPGIP14_BNA                                  RIPQGGELQRFDAYAYLHNKCLCGAPLQSCK
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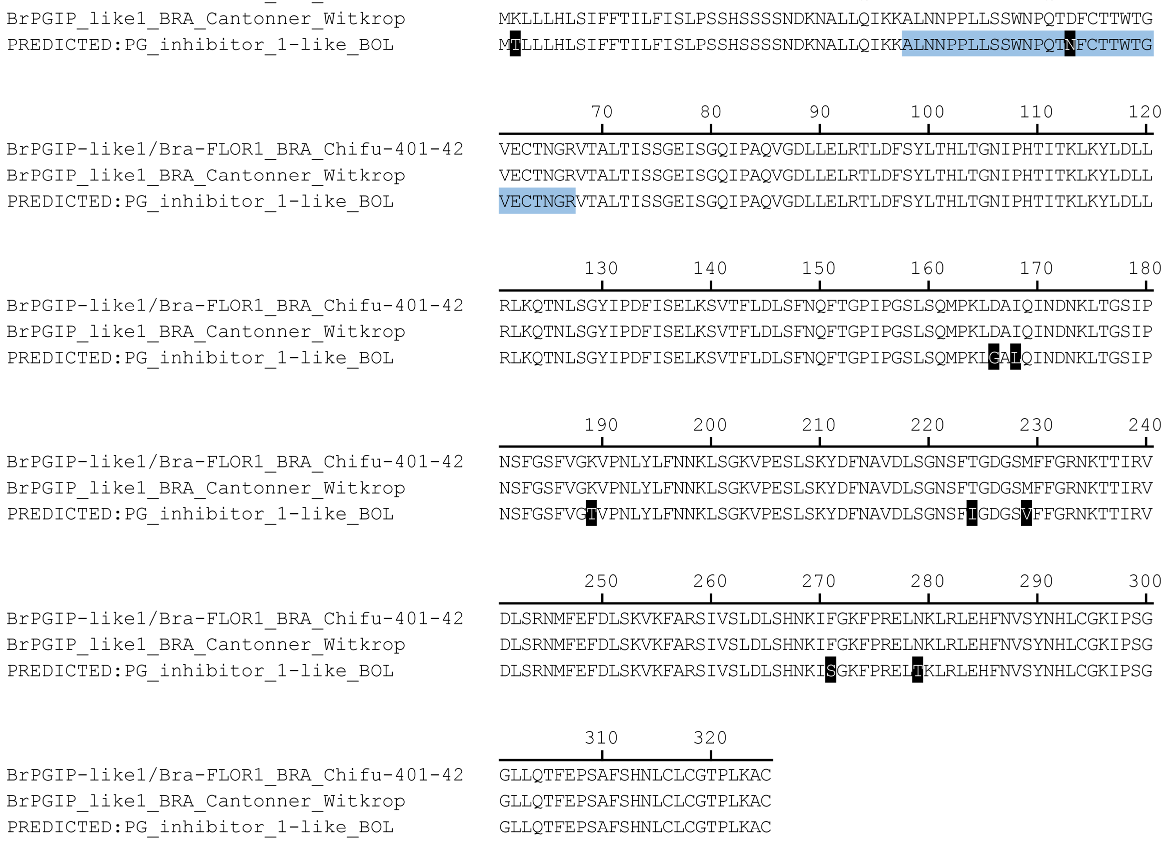

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BrPGIP_like1_BRA_Cantonner_Witkrop         MKLLLHLSIFFTILFISLPSSHSSSSNDKNALLQIKKALNNPPLLSSWNPQTDFCTTWTG
PREDICTED:PG_inhibitor_1-like_BOL          MTLLLHLSIFFTILFISLPSSHSSSSNDKNALLQIKKALNNPPLLSSWNPQTNFCTTWTG

                                                  70        80        90       100       110       120
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42    VECTNGRVTALTISSGEISGQIPAQVGDLLELRTLDFSYLTHLTGNIPHTITKLKYLDLL
BrPGIP_like1_BRA_Cantonner_Witkrop         VECTNGRVTALTISSGEISGQIPAQVGDLLELRTLDFSYLTHLTGNIPHTITKLKYLDLL
PREDICTED:PG_inhibitor_1-like_BOL          VECTNGRVTALTISSGEISGQIPAQVGDLLELRTLDFSYLTHLTGNIPHTITKLKYLDLL

                                                 130       140       150       160       170       180
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42    RLKQTNLSGYIPDFISELKSVTFLDLSFNQFTGPIPGSLSQMPKLDAIQINDNKLTGSIP
BrPGIP_like1_BRA_Cantonner_Witkrop         RLKQTNLSGYIPDFISELKSVTFLDLSFNQFTGPIPGSLSQMPKLDAIQINDNKLTGSIP
PREDICTED:PG_inhibitor_1-like_BOL          RLKQTNLSGYIPDFISELKSVTFLDLSFNQFTGPIPGSLSQMPKLGALQINDNKLTGSIP

                                                 190       200       210       220       230       240
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42    NSFGSFVGKVPNLYLFNNKLSGKVPESLSKYDFNAVDLSGNSFTGDGSMFFGRNKTTIRV
BrPGIP_like1_BRA_Cantonner_Witkrop         NSFGSFVGKVPNLYLFNNKLSGKVPESLSKYDFNAVDLSGNSFTGDGSMFFGRNKTTIRV
PREDICTED:PG_inhibitor_1-like_BOL          NSFGSFVGTVPNLYLFNNKLSGKVPESLSKYDFNAVDLSGNSFIGDGSVFFGRNKTTIRV

                                                 250       260       270       280       290       300
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42    DLSRNMFEFDLSKVKFARSIVSLDLSHNKIFGKFPRELNKLRLEHFNVSYNHLCGKIPSG
BrPGIP_like1_BRA_Cantonner_Witkrop         DLSRNMFEFDLSKVKFARSIVSLDLSHNKIFGKFPRELNKLRLEHFNVSYNHLCGKIPSG
PREDICTED:PG_inhibitor_1-like_BOL          DLSRNMFEFDLSKVKFARSIVSLDLSHNKISGKFPRELTKLRLEHFNVSYNHLCGKIPSG

                                                 310       320
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42    GLLQTFEPSAFSHNLCLCGTPLKAC
BrPGIP_like1_BRA_Cantonner_Witkrop         GLLQTFEPSAFSHNLCLCGTPLKAC
PREDICTED:PG_inhibitor_1-like_BOL          GLLQTFEPSAFSHNLCLCGTPLKAC
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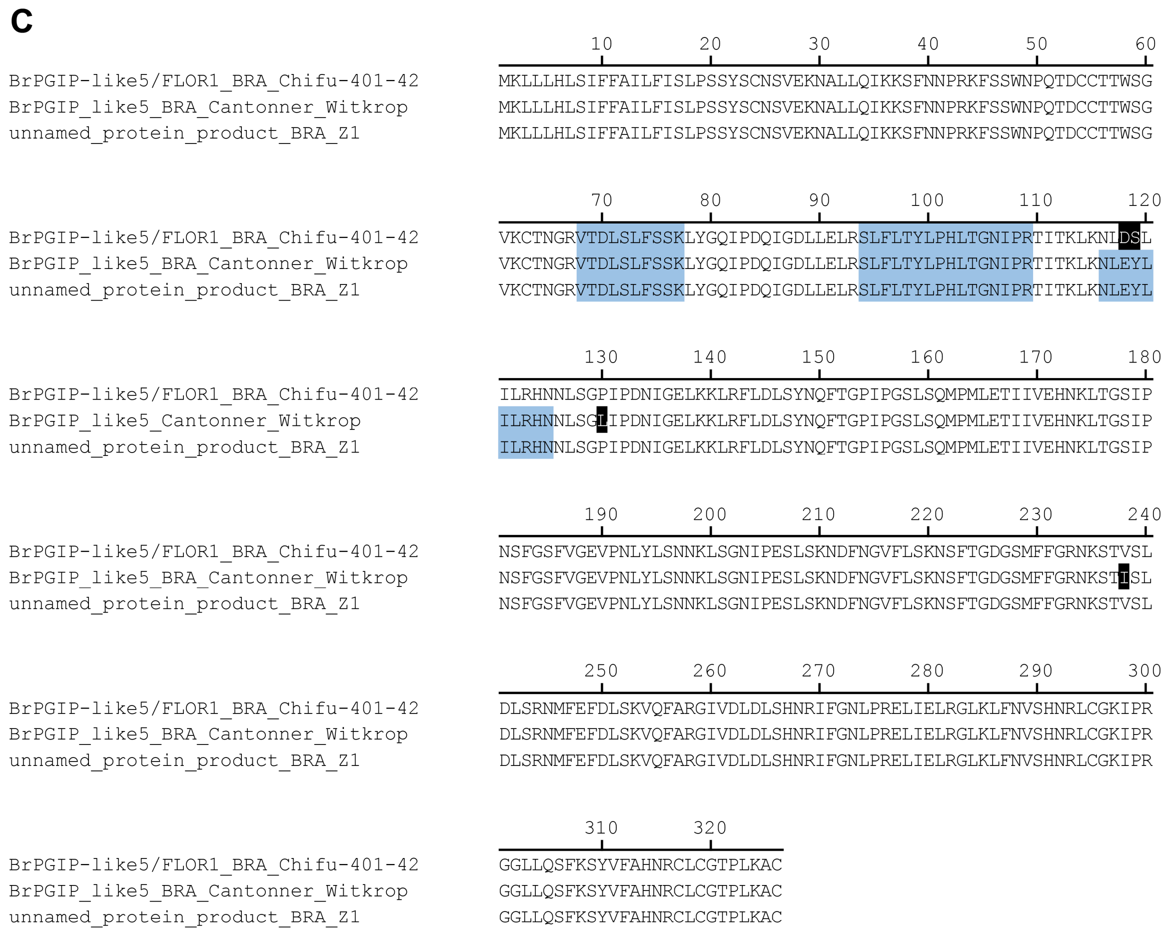

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                                                         10        20        30        40        50        60
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BrPGIP_like5_BRA_Cantonner_Witkrop         MKLLLHLSIFFAILFISLPSSYSCNSVEKNALLQIKKSFNNPRKFSSWNPQTDCCTTWSG
unnamed_protein_product_BRA_Z1             MKLLLHLSIFFAILFISLPSSYSCNSVEKNALLQIKKSFNNPRKFSSWNPQTDCCTTWSG

                                                         70        80        90       100       110       120
BrPGIP-like5/FLOR1_BRA_Chifu-401-42        VKCTNGRVTDLSLFSSKLYGQIPDQIGDLLELRSLFLTYLPHLTGNIPRTITKLKNLDSL
BrPGIP_like5_BRA_Cantonner_Witkrop         VKCTNGRVTDLSLFSSKLYGQIPDQIGDLLELRSLFLTYLPHLTGNIPRTITKLKNLEYL
unnamed_protein_product_BRA_Z1             VKCTNGRVTDLSLFSSKLYGQIPDQIGDLLELRSLFLTYLPHLTGNIPRTITKLKNLEYL

                                                        130       140       150       160       170       180
BrPGIP-like5/FLOR1_BRA_Chifu-401-42        ILRHNNLSGPIPDNIGELKKLRFLDLSYNQFTGPIPGSLSQMPMLETIIVEHNKLTGSIP
BrPGIP_like5_Cantonner_Witkrop             ILRHNNLSGLIPDNIGELKKLRFLDLSYNQFTGPIPGSLSQMPMLETIIVEHNKLTGSIP
unnamed_protein_product_BRA_Z1             ILRHNNLSGPIPDNIGELKKLRFLDLSYNQFTGPIPGSLSQMPMLETIIVEHNKLTGSIP

                                                        190       200       210       220       230       240
BrPGIP-like5/FLOR1_BRA_Chifu-401-42        NSFGSFVGEVPNLYLSNNKLSGNIPESLSKNDFNGVFLSKNSFTGDGSMFFGRNKSTVSL
BrPGIP_like5_BRA_Cantonner_Witkrop         NSFGSFVGEVPNLYLSNNKLSGNIPESLSKNDFNGVFLSKNSFTGDGSMFFGRNKSTISL
unnamed_protein_product_BRA_Z1             NSFGSFVGEVPNLYLSNNKLSGNIPESLSKNDFNGVFLSKNSFTGDGSMFFGRNKSTVSL

                                                        250       260       270       280       290       300
BrPGIP-like5/FLOR1_BRA_Chifu-401-42        DLSRNMFEFDLSKVQFARGIVDLDLSHNRIFGNLPRELIELRGLKLFNVSHNRLCGKIPR
BrPGIP_like5_BRA_Cantonner_Witkrop         DLSRNMFEFDLSKVQFARGIVDLDLSHNRIFGNLPRELIELRGLKLFNVSHNRLCGKIPR
unnamed_protein_product_BRA_Z1             DLSRNMFEFDLSKVQFARGIVDLDLSHNRIFGNLPRELIELRGLKLFNVSHNRLCGKIPR

                                                        310       320
BrPGIP-like5/FLOR1_BRA_Chifu-401-42        GGLLQSFKSYVFAHNRCLCGTPLKAC
BrPGIP_like5_BRA_Cantonner_Witkrop         GGLLQSFKSYVFAHNRCLCGTPLKAC
unnamed_protein_product_BRA_Z1             GGLLQSFKSYVFAHNRCLCGTPLKAC
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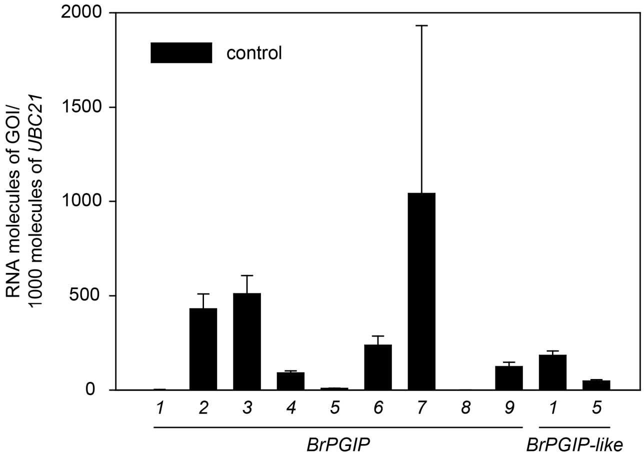
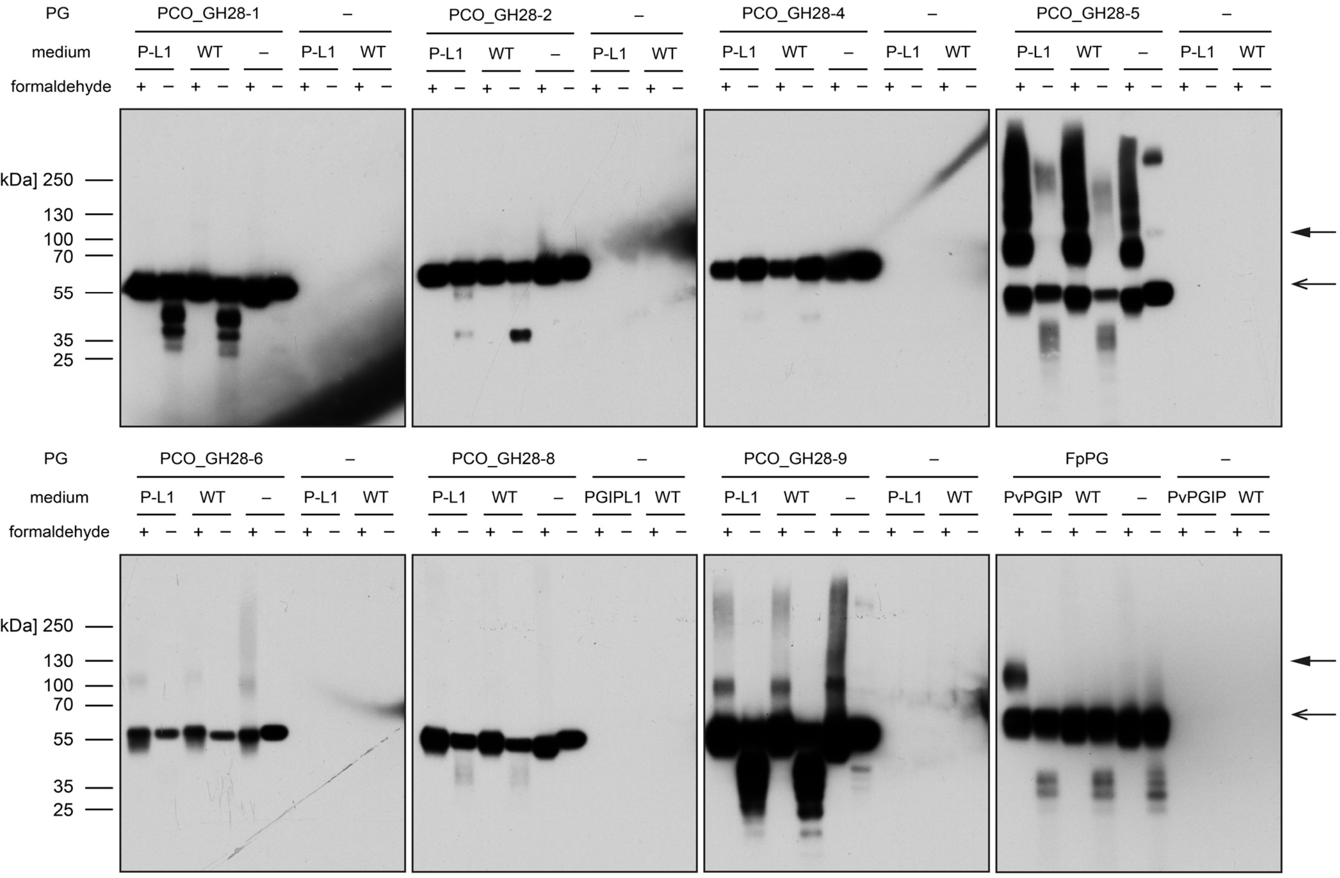
Supplementary Figure 6: Alignment of BrPGIPs and BrPGIP-like proteins with homologs from different *B. rapa* ssp. *pekinensis* cultivars and Brassica species. CWPs for the pull-down assay were obtained from the *B. rapa* ssp. *pekinensis* (BRA) cultivar "Cantonner Witkrop," while sequences for mass spectrometry and bioinformatic analyses were obtained from the NCBI database and originate from the "Chifu-401-42" cultivar. If the Mascot analyses resulted in hits other than from the "Chifu-401-42" sequences, we aligned those together with the sequences from "Cantonner Witkrop." Matching peptides from the Mascot analyses were marked in blue, amino acid differences were highlighted in black. A) For the hit BnPGIP14 (ABX46560.1) from *B. napus* (BNA), one peptide matched to BrPGIP1 and -1.1, while the second matched BrPGIP3 and -7. B) One amino acid difference between the detected peptide and the BrPGIP-like1 sequences resulted in the identification of the homologous "Predicted: polygalacturonase inhibitor-like1" (XP_013617122.1) from *B. oleraceae* var. *oleracea* (BOL). C) All peptides match perfectly with the hit "unnamed protein product" (VDC72802.1) from the *B. rapa* cultivar "Z1" and BrPGIP-like5 from "Cantonner Witkrop," but differ in one amino acid from the BrPGIP-like5/FLOR1 sequence (XP_009146639) from "Chifu-401-42." Altogether, we are confident that discrepancies resulted from cultivar-dependent or even individual-dependent amino acid differences and that the proteins we identified were BrPGIP1.1 and -3 as well as BrPGIP-like1 and -like5.



Supplementary Figure 7: Expression of *BrPGIPs* and *BrPGIP-like proteins* in untreated *B. rapa* ssp. *pekinensis*. The expression levels of the *BrPGIPs* and *BrPGIP-like proteins* were quantified by RT-qPCR, and transcript abundance was expressed as RNA molecules of the gene of interest (GOI) per 1000 RNA molecules of the reference gene *UBIQUITIN-CONJUGATING ENZYME 21 (UBC21)*. Error bars indicate the standard error of the mean (SEM).



Supplementary Figure 8: Interaction assay of PCO_GH28-1, -2, -4, -5, -6, -8, -9 with BrPGIP-like1-containing culture medium. Culture medium from BrPGIP-like1-expressing (P-L1) as well as wild-type (WT) yeast was incubated with various *P. cochleariae* PG family members and cross-linked with formaldehyde. The PG family members were detected in a western blot with an anti-V5 antibody. Arrows indicate the expected size of PG family members (open arrowhead) and PG-PGIP complex (closed arrowhead).