

Figure S1. Genetic distance matrix of CqPYLs CDS sequences. A) Estimates of Evolutionary Divergence between CqPYL Sequences. The number of base substitutions per site from between sequences are shown. Standard error estimates are shown above the diagonal and were obtained by a bootstrap procedure (1000 replicates). Analysis were conducted using the Tamura-Nei model [33]. This analysis involved 20 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. This evolutionary analysis was conducted in MEGA X [32]. B) Genetic distance heatmap. The heatmap plot was constructed with the genetic distance data (showed in A) using CLUSTVIS web tool [34]. Blue square: subgroups with low genetic distance (homoeologous gene pairs).

AtPYR1

AtPYR1 1MPSE LTP.....ERSE LK

AtPYL1 1MANSESSSSPVNEEE.NSQRISTLHQTMPSDLTQ.....DEFTQLS

AtPYL2 1MS SPAVKGLTD.....EQKTE

AtPYL3 1MNLAPIHDP.....SSSS.....TTTTSSSTPYGLTK.....DEFTSLD

CqPYL1a 1MAETSSMEDPPQSSSSHDHPDITTHNLSPPPGLSH.....HEFTSLI

CqPYL1b 1MAETSSIEDPPQSSSSHDQPDITTHNLSPPPGLSH.....QEFTSLI

CqPYL2a 1MNDNS.....LSSWID.TFLI

CqPYL2b 1 MLSEFRLLLLLIIFGGLPFAFGRQIMTPEDSRMTSNSSYSTLGHLGKQVMKAKIDYMMLI

CqPYL2c 1 MLSEFRLLLLLIIFGGLPFAFGRQIMTPEDSRMTSNSSYSTLGHLGKQVMKAKIDYMMLI

CqPYL2d 1MDRNRLTSQS LTA.....EYTKLE

CqPYL2e 1MDRNRLTSQS LTA.....EYTKLE

AtPYR1

AtPYR1 15 NSIAEFHTYQ...LDPGS...CSSLHAQRIHAPPELVMS...IVRRFDKPTQYKHFIK

AtPYL1 42 QSIAEFHTYQ...LGNGR...CSSLLAQRIHAPPETVMS...VVRRFDRPQIYKHFIK

AtPYL2 20 PVIKTYHQFE...PDPIT...CTSLITQRIHAPASVWP...LIRRFDNFERYKHFIK

AtPYL3 35 SIIRTHHTFP...RSPNT...CTSLIAHRVDAPAHAIWR...FVRDFANPNKYKHFIK

CqPYL1a 43 PSITEFHTYR...LNKSRQ...CSSLLAQRIHAPRAVVM...IVRRFDKPTQYKHFIK

CqPYL1b 43 PSITEFHTYR...LNKSRQ...CSSLLAQRIHAPRAVVM...IVRRFDKPTQYKHFIK

CqPYL2a 17 G.....

CqPYL2b 61 NGKEDIHSANNVGSTPSSPPAAVASSQETTASTRVFLKHLQLSGFRRRFQLPLPLHLSVA

CqPYL2c 61 NGKEDIHSANNVGSTPSSPPAAVASSQETTASTRVFLKHLQLSGFRRRFQLPLPLHLSVA

CqPYL2d 21 DVISTCHSAN...LPPNK...CTSLIIQRIHAPANVVM...YVRAFDNFQAYKYLIK

CqPYL2e 21 DVISTCHSAN...LPPNK...CTSLIIQRIHAPANVVM...YVRAFDNFQAYKYLIK

AtPYR1

AtPYR1 64 SCSEVQN...FEMR VGC TRDVIV SGLPASTSTERLDILDDERRVTGFSITIGG HRLN

AtPYL1 91 SCNVSED...FEMR VGC TRDVNV SGLPASTSTERLDILDDERRVTGFSITIGG HRLN

AtPYL2 69 RCRLISG...DGD VGS VREVTV SGLPASTSTERLEFVDDHRRVLSFRVVG HRLN

AtPYL3 84 SCTIRVNGNGKEIK VGTIREVSV SGLPASTSVELEVLDEEKRLLSFRVVG HRLN

CqPYL1a 93 SCSEVRDN...FTLS VGS TRDVNV SGLPASTSTERLDILDDHRRVTGFTIIGG HRLN

CqPYL1b 93 SCSEVRDN...FTLS VGS TRDVNV SGLPASTSTERLDILDDHRRVTGFTIIGG HRLN

CqPYL2a 18DGSS VGS VREVN SGLPASTSTERLELLDDHRRVLSFRVVG HRLN

CqPYL2b 121 AVIYLLNR...DGSS VGS VREVS SGLPASTSTERLELLDDHRRVLSFRVVG HRLN

CqPYL2c 121 AVIYLLNR...DGSS VGS VREVS SGLPASTSTERLELLDDHRRVLSFRVVG HRLN

CqPYL2d 70 SCTMRG...DGG VGS VRDITV SGLPASTSTERLEMLNDORRILSKFKVIGG HRLN

CqPYL2e 70 SCTMRG...DGG VGS VRDITV SGLPASTSTERLEMLNDORRILSKFKVIGG HRLN

Gate loop

Latch loop

AtPYR1

AtPYR1 120 YKSVTVHRRFEKEN...RIWTVVLESYVVDMPGENSEEDTRMFADTVVKINLQKLATV

AtPYL1 147 YKSVTVHRRFEKEEEEE...RIWTVVLESYVVDMPGENSEEDTRMFADTVIRINLQKLASI

AtPYL2 124 YKSVTVSVNEFLNQDSG...KVYTVVLESYTVDIPGNTAEDTKMFVDTVVKINLQKLGA

AtPYL3 144 YKSVTVSVNEFVVLKDKKKKVYYSVLESYTVDIPGNTAEDTRMFVDTVVKINLQKLAVI

CqPYL1a 149 YKSVTSLHAVNNPDSGE...DDVTIVLESYLVDPGNTAEDTRMFADTVVKINLQKLASV

CqPYL1b 149 YKSVTSLHPVNNPDSGE...DDVTIVLESYLVDPGNTAEDTRMFADTVVKINLQKLASV

CqPYL2a 67 YKSVTVSVNEFFEDDNN...KVYTVVLESYTVDIPGNTAEDTKMFVDTVVKINLQKLGI

CqPYL2b 178 YKSVTVSVNEFFEDDNN...KVYTVVLESYTVDIPGNTAEDTKMFVDTVVKINLQKLGI

CqPYL2c 178 YKSVTVSVNEFFEDDNN...KVYTVVLESYTVDIPGNTAEDTKMFVDTVVKINLQKLGE

CqPYL2d 124 YKSVTVSINEINHGTG...RVYTVVLESYTVDIPGNTAEDTKMFADTVVKINLQKLAEV

CqPYL2e 124 YKSVTVSINEINHGTG...RVYTVVLESYTVDIPGNTAEDTKMFADTVVKINLQKLAEV

AtPYR1

AtPYR1 175 AEAMARNSGDSGSGSQVT.....

AtPYL1 205 TEAMNRNNNNNNSSQVR.....

AtPYL2 181 ATSAPMHDDE.....

AtPYL3 204 STASPT.....

CqPYL1a 207 AAAYVSGDATAVENR.....

CqPYL1b 207 AAAYVSGDAAAVENRAKRSYLGWLWVVSGLSLVFLGLWAVFSGVLVVLGAVDGVYFGAVS

CqPYL2a 124 AMSDLQGNNH.....

CqPYL2b 236 AMSDLQGNNNDE.....

CqPYL2c 236 LVTGYSDDSYAADVDTRRSVTGYVFTLGGSVIYDRA.....

CqPYL2d 179 SEMTAS.....

CqPYL2e 179 SEMTAS.....

AtPYR1

AtPYR1

AtPYL1

AtPYL2

AtPYL3

CqPYL1a

CqPYL1b 267 GVFGVVGVGAVDGVFGAVGGVFGAVGGVFGGF

CqPYL2a

CqPYL2b

CqPYL2c

CqPYL2d

CqPYL2e

Figure S3. Amino acid sequence alignment of At and Nb sub-family III members of ABA receptors. Sequence and secondary structure alignment of ABA receptors are indicated. The secondary structure of the NbPYLs is predicted according to the crystallographic structure of AtPYR1 (Protein DataBank Code 3k3k), and was generated using the ESPRIT program (<http://espruit.ibcp.fr/ESPrut/ESPrut/>). Blue boxes indicate the position of the gate and latch loops. Blue asterisks mark residues involved in interactions with ABA.

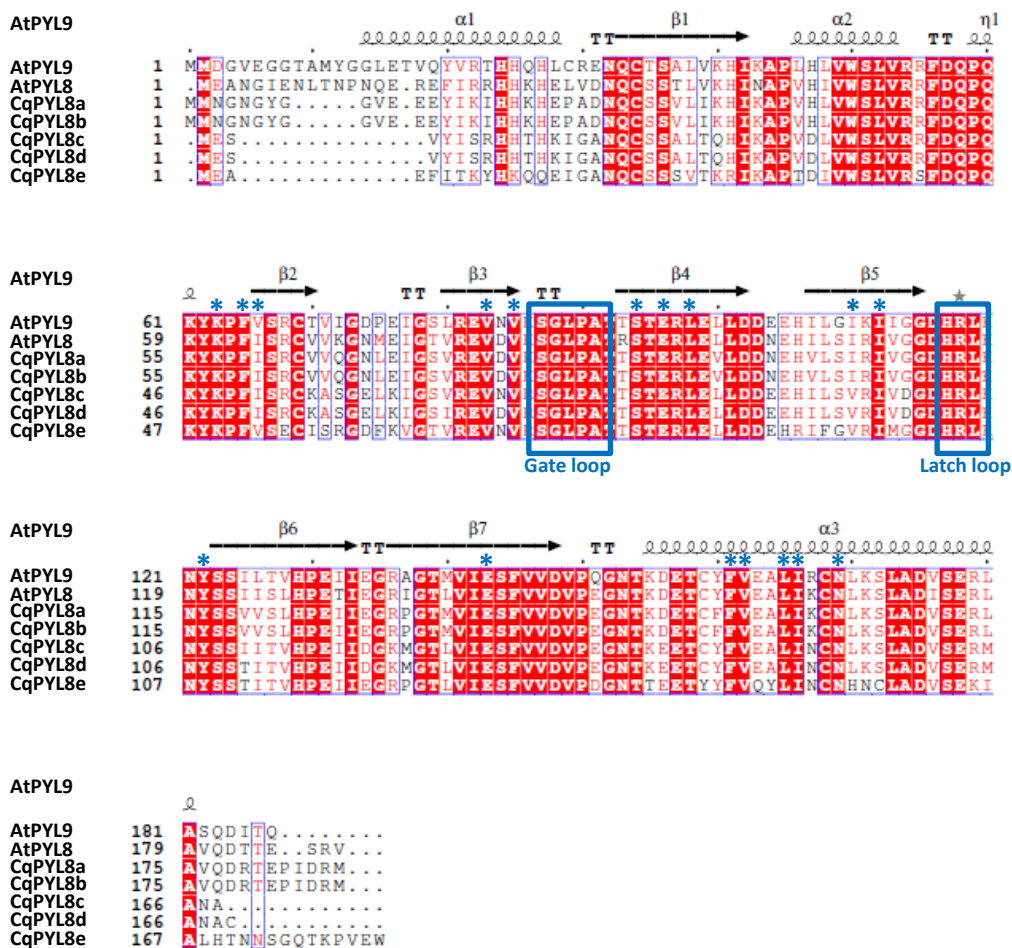


Figure S4. Amino acid sequence alignment of At and Nb sub-family I members of ABA receptors. Sequence and secondary structure alignment of ABA receptors are indicated. The secondary structure of the NbPYLs is predicted according to the crystallographic structure of AtPYL9 (Protein DataBank Code 3w9r), and was generated using the ESPRIPT program (<http://espruit.ibcp.fr/ESPrut/ESPrut/>). Blue boxes indicate the position of the gate and latch loops. Blue asterisks mark residues involved in interactions with ABA.

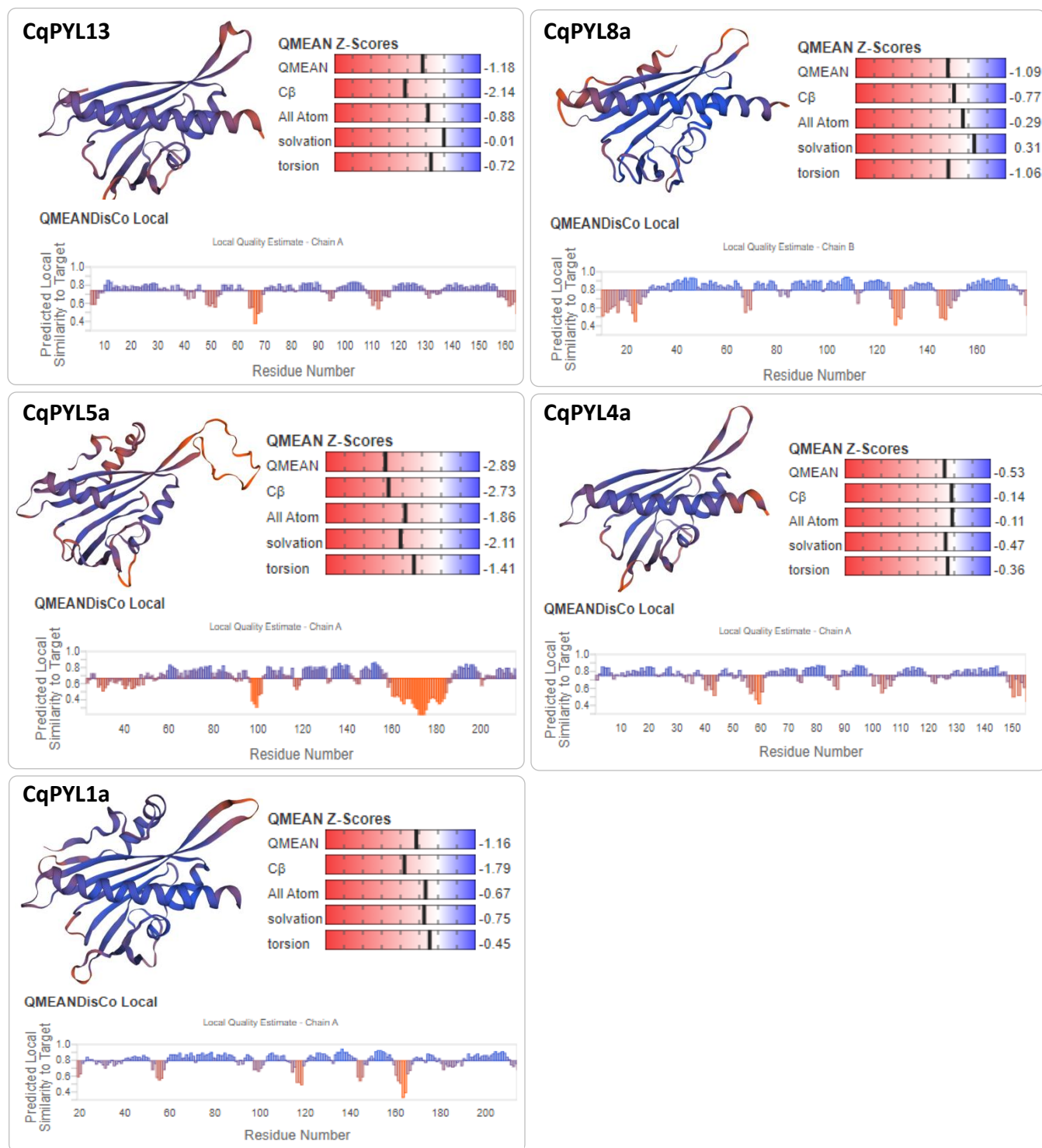


Figure S5. Swiss-Model CqPYL protein homology modeling. CqPYLs topology were predicted by homology modeling using Swiss-Model and showed as cartoons. A quality estimation by QMEANDisCo local score and some QMEAN Z-scores were provided for each model.