## Extended Data Fig. 5: The island domain of the *BRI1-BRL* gene family in land plant.

From: The genome of homosporous maidenhair fern sheds light on the euphyllophyte evolution and defences

|                                | 1                   | 10        | 20                              | 30                                       | 40         | 50                            | 60         |
|--------------------------------|---------------------|-----------|---------------------------------|--|------------|-------------------------------|------------|
| Ath AT4G39400_BRI1             | FIAGKR              | YVYIKNDGM | KKECHGA                         | GNLLEFQGIRSEC                            | LNRLSTRNP. | CNITSRVYGGH                   | TSPTFDN    |
| CsalCsa6P486870.1              | FITGKS              | YAYIKNDG. | SKOCH. GA                       | AGNLLEFAGIRQEQ                           | VNRISSKSP. | CNFT.RVYKGM                   | . IOPTFNH  |
| Vvi XP 002278935.2             | LVTGKS              | YVYIRNDG. | SKECH. GA                       | GNLLEYGGIREE                             | MDRISTRNP. | CNFT. RVYKGR                  | . TNPTFNH  |
| Zma NP 001309780.1             | LVLGRP              | YVYLRNDEI | SSECHGH                         | GSLLEFTSIRPEE                            | LSRMPSKKL. | CNFT. RVYMGS                  | . TEYTFNK  |
| Osa NP 001044077.1             | LIVGRP              | YVYLRNDEI | SSECRGR                         | GSLLEFTSIRPDD                            | LSRMPSKKL. | CNFT. RMYVGS                  | . TEYTFNK  |
| ZmalXP_020406078.1             | LVIGRP              | YVYLRNDEI | SSECHGP                         | GSLLEFTSIRPEE                            | LSRMPSKEL. | CNFT. RVYMGS                  | . TEYTFNK  |
| Atr XP_006849476.2             | SGNT                | LAFVRNV   | GNSCKGV                         | <b>GGLLEFAGIRPE</b>                      | LLQVPTLKT. | CDFT.RLYSGA                   | .ALNDWT.   |
| Ath/AT1G55610_BRL1             | SGKQ                | FAFVRNEG. | GTDCRGA                         | <b>GGLVEFEGIRAE</b>                      | LERLPMVHS. | CPAT. RIYSGM                  | . TMYTFS.  |
| Ath AT3G13380_BRL3             | SGKQ                | FAFVRNEG. | GTDCRGA                         | AGGLVEFEGIRAER                           | LEHFPMVHS. | CPKT.RIYSGM                   | . TMYMFS.  |
| Osa NP_001175526.1             |                     |           |                                 | GVLFEFLDIRPDF                            |            |                               |            |
| Zma XP_020408140.1             | SGKQ                | FAFLRNEA. | GNICPGA                         | GVLFEFFDIRPER                            | LAQFPAVHS. | CAST. RIYTGM                  | . TVYTFN.  |
| Zma XP_008659178.1             | SGNT                | LAFVRNV   | GNSCKSV                         | <sup>7</sup> GLLEFAGIRPER                | LLQVPTLKS. | CDFT.RLYSGA                   | .AVSGWT.   |
| Osa NP_001062792.2             | S <mark>G</mark> KQ | FAFLRNEA. | . GNICPGF                       | A <mark>G</mark> V L F E F F G I R P E R | LAEFPAVHL. | CPST.RIYTGT                   | . TVYTFT.  |
| Vvi XP_002265525.3             |                     |           |                                 | A <mark>G</mark> GLVEFEGIRSER            |            |                               |            |
| Gbi cds.evm.model.ctg646.12-1  |                     |           |                                 | AGGLVEFAGIRPEQ                           |            |                               |            |
| Pab MA_170g0010                | SVSGKM              | YAFVRNEG. | GTACRGA                         | A <mark>G</mark> GLVEFAGIRPEQ            | ISRVPALHS. | <b>C</b> QF <b>T . RVYMGT</b> | . TMYQFKE  |
| Gbi cds.evm.model.ctg1495.6-1  | S <mark>G</mark> KL | FAFVRNEG. | GTACRGA                         | A <mark>G</mark> GLLEFAGIRPEQ            | LSRSPMLHS. | CEFT.RVYLGT                   | . TMYRFT.  |
| Pab MA_57173g0030              | AGKS                | FAFVRNEG. | .GTACRGA                        | A <mark>G</mark> GLLEFAGIRPEQ            | LSRSPMLHS. | CEFT.RVYLGT                   | . TMYKFT.  |
| Pta PITA_000083922-RA          | AGKS                | FAFVRNEG. | .GTS <mark>C</mark> RG <i>I</i> | A <mark>G</mark> GLLESAGIRSEQ            | LTLSPVLHS. | CEFT.RVYLGT                   | . TVYKFT.  |
| Ath AT2G01950_BRL2             |                     |           |                                 | 7 <mark>G</mark> GLVEFSGIRPER            |            |                               |            |
| Vvi XP_002281730.1             | ILSGNT              | LAFVRNL   | GNSCKGV                         | <mark>/G</mark> GLLEFAGIRPER             | LLQIPTLKT. | CDFT.RMYSGA                   | .VLSLFTK   |
| Csa Csa5P092940.1              | SGNT                | LVFVRNV   | GNSCKGV                         | 7 <mark>G</mark> GLLEFAGIRPER            | LQQEPTLKT. | CDFT.RLYSGP                   | .VLSLFT.   |
| Zma XP_008652521.1             | SGKQ                | FAFLRNEA. | GNICPGF                         | A <mark>G</mark> V L F E F F G I R P E R | LAAFPTVHL. | CPST.RIYTGT                   | .TVYSFD.   |
| Osa NP_001064047.2             |                     |           |                                 | 7 <mark>G</mark> GLLEFAGIRPER            |            |                               |            |
| Atr XP_020527911.1             |                     |           |                                 | 7 <mark>G</mark> GLLEFAGIRPEF            |            |                               |            |
| Atr XP_006842213.2             |                     |           |                                 | AGNLLEMAGIRTEN                           |            |                               |            |
| Pta PITA_000048308-RA          |                     |           |                                 | <b>IGGLLEFAGIRAE</b>                     |            |                               |            |
| Gbi cds.evm.model.ctg1237.8-1  |                     |           |                                 | / <mark>G</mark> GLLEFAGIRPER            |            |                               |            |
| Adc Adc25927_AdcBRL3           |                     |           |                                 | <b>GILLEFGGINEA</b>                      |            |                               |            |
| Adc Adc25928_AdcBRL4           | · · · · · E         | FAFVRNL.  | GYKCR.GI                        | <b>GILLEFGGINEAA</b>                     | LASTPLRSA. | CNLT. RLYVED                  | , SLNGDS . |
| Adc Adc07598_AdcBRL1           |                     |           |                                 | 1 <mark>G</mark> FMVDYTGITTEA            |            |                               |            |
| Adc Adc30882_AdcBRL2           |                     |           |                                 | GTLLEFAGITPEA                            |            |                               |            |
| Afi Azfi_s0656.g081109         |                     |           |                                 | <b>IGTLLEFAGITEEA</b>                    |            |                               |            |
| Scu Sacu_v1.1_s0165.g024112    |                     |           |                                 | 4 GMLLEFSGLAEEA                          |            |                               |            |
| Itaiw_v1_contig_191_t45581     |                     |           |                                 | GALMEFQGIKHDD                            |            |                               |            |
| Itaiw_v1_contig_191_t45584     |                     |           |                                 | GALMEFQGIKHDD                            |            |                               |            |
| Apu evm.model.utg000043I.986.1 | EKFR                | FAFVKNI.  | GPN <mark>O</mark> Q.GI         | GGLMEFSGIRLEE                            | LLS.PRLIS. | NFT.LFSGPI                    | NNFYNWR.   |

The island domains were extracted from peptide of *BRI1-BRL* homologues and aligned by MUSCLE. The conserved sites were indicated with red boxes.