

1 **Supplementary Material**

2 **Table S1.** GenBank IDs for ITS, LSU, *MCM7*, *RPB2* and *TEF1 $\alpha$*  markers of all 67 taxa used in this project for phylogenetic analysis.

| Species                                | Strain             | ITS      | LSU      | <i>MCM7</i> | <i>RPB2</i> | <i>TEF1A</i> |
|----------------------------------------|--------------------|----------|----------|-------------|-------------|--------------|
| <i>Pseudogeomyces lindneri</i>         | ZY 22.003 T        | OP796797 | OP796792 | OP781436    | N/A         | OP781431     |
| <i>Pseudogeomyces lindneri</i>         | ZY 22.004          | OP796798 | OP796793 | OP781437    | N/A         | OP781432     |
| <i>Pseudogeomyces lindneri</i>         | ZY 22.005          | OP796799 | OP796794 | OP781438    | N/A         | OP781433     |
| <i>Pseudogymnoascus antarcticus</i>    | CHFC-EA569         | JX845280 | MN417282 | MN432493    | MN418135    | MN418131     |
| <i>Pseudogymnoascus appendiculatus</i> | 02NH11             | JX270356 | KF017819 | KF017650    | KF017704    | KF017759     |
| <i>Pseudogymnoascus appendiculatus</i> | 07MA02             | JX270402 | KF017827 | KF017658    | KF017712    | KF017767     |
| <i>Pseudogymnoascus australis</i>      | CHFC-EA567         | MN417287 | MN417284 | MN432491    | MN418137    | MN418133     |
| <i>Pseudogymnoascus camphorae</i>      | GZUIFR<br>22.021 T | ON365914 | ON366341 | ON568921    | ON568971    | ON568906     |

|                                          |                    |          |          |          |          |          |
|------------------------------------------|--------------------|----------|----------|----------|----------|----------|
| <i>Pseudogymnoascus<br/>camphorae</i>    | GZUIFR<br>22.049   | ON365915 | ON366342 | ON568922 | ON568972 | ON568907 |
| <i>Pseudogymnoascus<br/>catenatus</i>    | GZUIFR<br>21.813   | MZ444078 | MZ444105 | MZ490760 | MZ488543 | MZ488520 |
| <i>Pseudogymnoascus<br/>catenatus</i>    | CGMCC<br>3.20472 T | MZ444080 | MZ444107 | MZ490762 | MZ488545 | MZ488522 |
| <i>Pseudogymnoascus<br/>destructans</i>  | 20631.21           | EU884921 | KF017865 | KF017691 | KF017747 | KF017806 |
| <i>Pseudogymnoascus<br/>fujianensis</i>  | CGMCC<br>3.20474 T | MZ444084 | MZ444111 | MZ490766 | MZ488549 | MZ488526 |
| <i>Pseudogymnoascus<br/>fujianensis</i>  | GZUIFR<br>21.820   | MZ444085 | MZ444112 | MZ490767 | MZ488550 | MZ488527 |
| <i>Pseudogymnoascus<br/>griseus</i>      | CHFC-EA568         | MN417288 | MN417285 | MN432492 | MN418138 | MN418134 |
| <i>Pseudogymnoascus<br/>guizhouensis</i> | GZUIFR 376.1<br>T  | MT509369 | MT509383 | MT534209 | MT534223 | MT534234 |
| <i>Pseudogymnoascus<br/>guizhouensis</i> | GZUIFR 376.2       | MT509370 | MT509384 | MT534210 | MT534224 | MT534235 |
| <i>Pseudogymnoascus<br/>lanuginosus</i>  | CHFC-EA570         | MN417286 | MN417283 | MN418139 | MN418136 | MN418132 |

|                                      |                    |          |          |          |          |          |
|--------------------------------------|--------------------|----------|----------|----------|----------|----------|
| <i>Pseudogymnoascus lindneri</i>     | 02NH05             | JX270350 | KF017818 | KF017649 | KF017703 | KF017758 |
| <i>Pseudogymnoascus palmeri</i>      | WSF3629            | KF039897 | KF017870 | KF017696 | KF017751 | KF017811 |
| <i>Pseudogymnoascus papyriferae</i>  | GZUIFR<br>22.020 T | ON365916 | ON366343 | ON568923 | ON568973 | ON568908 |
| <i>Pseudogymnoascus roseus</i>       | 05NY06             | JX270385 | KF017824 | KF017655 | KF017709 | KF017764 |
| <i>Pseudogymnoascus roseus</i>       | 05NY08             | JX270387 | KF017825 | KF017656 | KF017710 | KF017765 |
| <i>Pseudogymnoascus roseus</i>       | 05NY09             | JX270388 | KF017826 | KF017657 | KF017711 | KF017766 |
| <i>Pseudogymnoascus shaanxiensis</i> | GZUIFR<br>HZ5.7 T  | MT509366 | MT509380 | MT534206 | MT534220 | MT534231 |
| <i>Pseudogymnoascus shaanxiensis</i> | GZUIFR<br>21.801   | MZ444066 | MZ444093 | MZ490748 | MZ488531 | MZ488508 |
| <i>Pseudogymnoascus sinensis</i>     | CGMCC<br>3.18493 T | MT509364 | MT509378 | MT534204 | MT534218 | MT534229 |
| <i>Pseudogymnoascus sinensis</i>     | CGMCC<br>3.18494   | MT509365 | MT509379 | MT534205 | MT534219 | MT534230 |

|                                       |         |          |          |          |          |          |
|---------------------------------------|---------|----------|----------|----------|----------|----------|
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 04NY11  | JX270375 | KF017821 | KF017652 | KF017706 | KF017761 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 04NY17A | JX270378 | KF017823 | KF017654 | KF017708 | KF017763 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 10NY08  | JX270432 | KF017829 | KF017659 | KF017714 | KF017769 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 10NY09  | JX270433 | KF017830 | KF017660 | KF017715 | KF017770 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 11MA03  | JX270438 | KF017832 | KF017661 | KF017717 | KF017772 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 11MA05  | JX270440 | KF017833 | KF017662 | KF017718 | KF017773 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 11MA07  | JX270442 | KF017834 | KF017663 | KF017719 | KF017774 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 11MA08  | JX270443 | KF017835 | KF017664 | KF017720 | KF017775 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 12NJ13  | JX270459 | KF017838 | KF017667 | KF017722 | KF017778 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 15PA11  | JX270486 | KF017843 | KF017671 | KF017727 | KF017783 |

|                                       |        |          |          |          |          |          |
|---------------------------------------|--------|----------|----------|----------|----------|----------|
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 17WV03 | JX270510 | KF017844 | KF017672 | KF017728 | KF017784 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 18VA08 | JX270528 | KF017848 | KF017676 | KF017731 | KF017789 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 20KY08 | JX270562 | KF017851 | KF017677 | KF017734 | KF017792 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 20KY10 | JX270563 | KF017852 | KF017678 | KF017735 | KF017793 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 20KY12 | JX270565 | KF017853 | KF017679 | KF017736 | KF017794 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 21IN01 | JX270568 | KF017854 | KF017680 | KF017737 | KF017795 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 21IN05 | JX270572 | KF017855 | KF017681 | KF017738 | KF017796 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 21IN10 | JX270577 | KF017856 | KF017682 | KF017739 | KF017797 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 24MN04 | JX270612 | KF017859 | KF017685 | KF017741 | KF017800 |
| <i>Pseudogymnoascus</i><br><i>sp.</i> | 24MN06 | JX270614 | KF017860 | KF017686 | KF017742 | KF017801 |

|                                               |                           |          |          |          |          |          |
|-----------------------------------------------|---------------------------|----------|----------|----------|----------|----------|
| <i>Pseudogymnoascus</i><br><i>sp.</i>         | 24MN14                    | JX270622 | KF017862 | KF017688 | KF017744 | KF017803 |
| <i>Pseudogymnoascus</i><br><i>sp.</i>         | 24MN18                    | JX270626 | KF017863 | KF017689 | KF017745 | KF017804 |
| <i>Pseudogymnoascus</i><br><i>sp.</i>         | 23014-1-I6                | JX512256 | KF017867 | KF017693 | KF017748 | KF017808 |
| <i>Pseudogymnoascus</i><br><i>sp.</i>         | 15PA10B                   | KF039894 | KF017842 | KF017670 | KF017726 | KF017782 |
| <i>Pseudogymnoascus</i><br><i>sp.</i>         | MN-Mycosel-<br>7          | KF039899 | KF017872 | KF017698 | KF017753 | KF017813 |
| <i>Pseudogymnoascus</i><br><i>sp.</i>         | AK07KGI120<br>2 R1-1 sp.4 | MK448239 | MK443475 | MK448243 | *        | *        |
| <i>Pseudogymnoascus</i><br><i>sp.</i>         | HNDR16 R4-1<br>sp.1       | MK448240 | MK443476 | MK448244 | *        | *        |
| <i>Pseudogymnoascus</i><br><i>verrucosus</i>  | 04NY16                    | JX270377 | KF017822 | KF017653 | KF017707 | KF017762 |
| <i>Pseudogymnoascus</i><br><i>verrucosus</i>  | 24MN13                    | JX270621 | KF017861 | KF017687 | KF017743 | KF017802 |
| <i>Pseudogymnoascus</i><br><i>yunnanensis</i> | CGMCC<br>3.20879          | ON365917 | ON366344 | ON568924 | ON568974 | ON568909 |

|                                       |                    |          |          |          |          |          |
|---------------------------------------|--------------------|----------|----------|----------|----------|----------|
| <i>Pseudogymnoascus yunnanensis</i>   | GZUIFR<br>22.047   | ON365918 | ON366345 | ON568925 | ON568975 | ON568910 |
| <i>Pseudogymnoascus yunnanensis</i>   | CGMCC<br>3.20880   | ON365922 | ON366349 | ON568929 | ON568979 | ON568914 |
| <i>Pseudogymnoascus yunnanensis</i>   | CGMCC<br>3.20475 T | MZ444072 | MZ444099 | MZ490754 | MZ488537 | MZ488514 |
| <i>Pseudogymnoascus yunnanensis</i>   | GZUIFR<br>21.808   | MZ444073 | MZ444100 | MZ490755 | MZ488538 | MZ488515 |
| <i>Pseudogymnoascus zhejiangensis</i> | CGMCC<br>3.20476 T | MZ444075 | MZ444102 | MZ490757 | MZ488540 | MZ488517 |
| <i>Pseudogymnoascus zhejiangensis</i> | GZUIFR<br>21.811   | MZ444076 | MZ444103 | MZ490758 | MZ488541 | MZ488518 |
| <i>Pseudogymnoascus zongqii</i>       | CGMCC<br>3.20878 T | ON365919 | ON366346 | ON568926 | ON568976 | ON568911 |
| <i>Pseudogymnoascus zongqii</i>       | GZUIFR<br>22.042   | ON365920 | ON366347 | ON568927 | ON568977 | ON568912 |
| <i>Pseudogymnoascus zongqii</i>       | GZUIFR<br>22.043   | ON365921 | ON366348 | ON568928 | ON568978 | ON568913 |

3 \* Sequences were obtained from this study

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5 **Table S2.** A summary of BLAST hits for AKSP4 and HNDR4 against ITS, LSU and *MCM7* sequences from Wong et al. 2022.

| Gene Marker                   | Location in assembly        | E-value    | Similarity     | Gaps         | Strand           |
|-------------------------------|-----------------------------|------------|----------------|--------------|------------------|
| <b>AKSP4</b>                  |                             |            |                |              |                  |
| <b>ITS (MK448239)</b>         | AKSP4_383: 19594-19745      | 9e-67      | 148/155        | 4/155        | Plus/Minus       |
|                               | AKSP4_640: 2638-2698        | 1e-23      | 59/61          | 1/61         | Plus/Plus        |
|                               | <b>AKSP4_768: 2926-3496</b> | <b>0.0</b> | <b>570/571</b> | <b>0/571</b> | <b>Plus/Plus</b> |
| <b>LSU (MK443475)</b>         | AKSP4_768: 3539-4511        | 0.0        | 973/973        | 0/973        | Plus/Plus        |
| <b><i>MCM7</i> (MK448243)</b> | AKSP4_20: 110460-111073     | 0.0        | 614/614        | 0/614        | Plus/Plus        |
| <b>HNDR4</b>                  |                             |            |                |              |                  |
| <b>ITS (MK448240)</b>         | HNDR4_20: 260379-260531     | 3e-62      | 147/156        | 5/156        | Plus/Plus        |
|                               | <b>HNDR4_329: 2621-3196</b> | <b>0.0</b> | <b>575/575</b> | <b>1/575</b> | <b>Plus/Plus</b> |
| <b>LSU (MK443476)</b>         | HNDR4_329 :3251-4212        | 0.0        | 962/962        | 0/962        | Plus/Plus        |
| <b><i>MCM7</i> (MK448244)</b> | HNDR4_8: 376945-377575      | 0.0        | 630/631        | 0/631        | Plus/Plus        |

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14 **Table S3.** A summary of BLAST hits for AKSP4 and HNDR4 strains against *RPB2* and *TEF1 $\alpha$*  sequences listed in Table S1.

| Strain                         | Hit(s)      | Location in assembly  | E-value | Similarity | Gaps  | Strand     |
|--------------------------------|-------------|-----------------------|---------|------------|-------|------------|
| <i>RPB2</i>                    |             |                       |         |            |       |            |
| <b>AKSP4</b>                   | ON568973.1  | AKSP4_2:221315-222278 | 0.0     | 959/965    | 1/965 | Plus/Minus |
| <b>HNDR4</b>                   | ON568973.1  | HNDR4_1:547496-548459 | 0.0     | 959/965    | 1/965 | Plus/Plus  |
| <i>TEF1<math>\alpha</math></i> |             |                       |         |            |       |            |
| <b>AKSP4</b>                   | ON5688908.1 | AKSP4_1:323128-324061 | 0.0     | 930/934    | 0/934 | Plus/Minus |
| <b>HNDR4</b>                   | ON5688908.1 | HNDR4_6:263032-263967 | 0.0     | 931/936    | 2/936 | Plus/Plus  |

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28 **Table S4.** The complete list of antiSMASH predictions for *P. griseus* (strain AKSP4) genome assembly using v7.1.0 web version.

| Contig   | Region | Type             | MIBiG database hit                                                              | Similarity (%) |
|----------|--------|------------------|---------------------------------------------------------------------------------|----------------|
| AKSP4_3  | 3.1    | Terpene          | N/A                                                                             | N/A            |
|          | 3.2    | NRPS-like        | choline biosynthetic gene cluster from <i>Aspergillus nidulans</i> FGSC A4      | 100            |
| AKSP4_6  | 6.1    | T1PKS            | N/A                                                                             | N/A            |
| AKSP4_11 | 11.1   | Fungal-RiPP like | N/A                                                                             | N/A            |
| AKSP4_18 | 18.1   | NRPS-like        | N/A                                                                             | N/A            |
| AKSP4_23 | 23.1   | T1PKS            | N/A                                                                             | N/A            |
| AKSP4_29 | 29.1   | T1PKS            | azanigerone A biosynthetic gene cluster from <i>Aspergillus niger</i> ATCC 1015 | 33             |
| AKSP4_31 | 31.1   | NRPS             | N/A                                                                             | N/A            |
| AKSP4_39 | 39.1   | NRPS             | N/A                                                                             | N/A            |
|          | 39.2   | Fungal-RiPP-like | N/A                                                                             | N/A            |

|           |       |                     |                                                                                  |     |
|-----------|-------|---------------------|----------------------------------------------------------------------------------|-----|
| AKSP4_43  | 43.1  | Terpene             | fumonisin B1 biosynthetic gene cluster from <i>Fusarium verticillioides</i>      | 12  |
| AKSP4_49  | 49.1  | T1PKS               | N/A                                                                              | N/A |
| AKSP4_53  | 53.1  | NRPS-like,<br>T1PKS | swainsonine biosynthetic gene cluster from <i>Alternaria oxytropis</i>           | 83  |
| AKSP4_61  | 61.1  | T1PKS               | YWA1 biosynthetic gene cluster from <i>Aspergillus oryzae</i> RIB40              | 100 |
| AKSP4_64  | 64.1  | Fungal-RiPP-like    | N/A                                                                              | N/A |
| AKSP4_77  | 77.1  | Indole              | N/A                                                                              | N/A |
| AKSP4_96  | 96.1  | Terpene             | trichobrasilenol biosynthetic gene cluster from <i>Annulohypoxylon truncatum</i> | 60  |
| AKSP4_101 | 101.1 | T3PKS               | N/A                                                                              | N/A |
| AKSP4_108 | 108.1 | NRPS-like,<br>T1PKS | cichorine biosynthetic gene cluster from <i>Aspergillus nidulans</i> FGSC A4     | 100 |
| AKSP4_110 | 110.1 | T1PKS               | geodin biosynthetic gene cluster from <i>Aspergillus terreus</i> NIH2624         | 75  |
| AKSP4_116 | 116.1 | Fungal-RiPP-like    | N/A                                                                              | N/A |

|           |       |                  |                                                                               |     |
|-----------|-------|------------------|-------------------------------------------------------------------------------|-----|
| AKSP4_136 | 136.1 | T1PKS            | tricholignan A biosynthetic gene cluster from <i>Trichoderma harzianum</i>    | 22  |
| AKSP4_142 | 142.1 | Fungal-RiPP-like | N/A                                                                           | N/A |
| AKSP4_145 | 145.1 | NRPS, T1PKS      | phyllostictine A biosynthetic gene cluster from <i>Phyllosticta cirsii</i>    | 20  |
| AKSP4_147 | 147.1 | T1PKS            | F9775A biosynthetic gene cluster from <i>Aspergillus nidulans</i> FGSC A4     | 50  |
| AKSP4_159 | 159.1 | Fungal-RiPP-like | N/A                                                                           | N/A |
| AKSP4_161 | 161.1 | NRPS-like        | N/A                                                                           | N/A |
| AKSP4_162 | 162.1 | Terpene          | clavaric acid biosynthetic gene cluster from <i>Hypholoma sublateritium</i>   | 100 |
| AKSP4_163 | 163.1 | Terpene          | clavaric acid biosynthetic gene cluster from <i>Hypholoma sublateritium</i>   | 100 |
| AKSP4_167 | 167.1 | T1PKS            | secalonic acids biosynthetic gene cluster from <i>Claviceps purpurea</i> 20.1 | 12  |
| AKSP4_172 | 172.1 | Terpene          | squalestatin S1 biosynthetic gene cluster from <i>Aspergillus</i> sp. Z5      | 40  |

|           |       |                  |                                                                        |     |
|-----------|-------|------------------|------------------------------------------------------------------------|-----|
| AKSP4_175 | 175.1 | Fungal-RiPP-like | N/A                                                                    | N/A |
| AKSP4_183 | 183.1 | T1PKS            | ochratoxin A biosynthetic gene cluster from <i>Aspergillus steynii</i> | 100 |
| AKSP4_189 | 189.1 | Fungal-RiPP-like | N/A                                                                    | N/A |
| AKSP4_200 | 200.1 | NRPS             | N/A                                                                    | N/A |
| AKSP4_221 | 221.1 | T1PKS            | oxyjavanicin biosynthetic gene cluster from <i>Fusarium fujikuroi</i>  | 37  |
| AKSP4_231 | 231.1 | T1PKS            | N/A                                                                    | N/A |
| AKSP4_233 | 233.1 | NRPS             | N/A                                                                    | N/A |
| AKSP4_235 | 235.1 | NRPS             | N/A                                                                    | N/A |
| AKSP4_236 | 236.1 | T1PKS            | N/A                                                                    | N/A |
| AKSP4_252 | 252.1 | T1PKS            | N/A                                                                    | N/A |
| AKSP4_264 | 264.1 | T1PKS            | N/A                                                                    | N/A |
| AKSP4_272 | 272.1 | NRPS-like        | N/A                                                                    | N/A |

|           |       |             |                                                                                                            |     |
|-----------|-------|-------------|------------------------------------------------------------------------------------------------------------|-----|
| AKSP4_297 | 297.1 | NRPS-like   | cyclo-(D-Phe-L-Phe-D-Val-L-Val) biosynthetic gene cluster from <i>Penicillium rubens</i> Wisconsin 54-1255 | 100 |
| AKSP4_315 | 315.1 | T1PKS       | N/A                                                                                                        | N/A |
| AKSP4_319 | 319.1 | T1PKS       | N/A                                                                                                        | N/A |
| AKSP4_327 | 327.1 | T1PKS       | N/A                                                                                                        | N/A |
| AKSP4_335 | 335.1 | NRPS        | N/A                                                                                                        | N/A |
| AKSP4_337 | 337.1 | T1PKS       | scytalone biosynthetic gene cluster from <i>Pestalotiopsis fici</i> W106-1                                 | 40  |
| AKSP4_394 | 394.1 | T1PKS       | scytalone biosynthetic gene cluster from <i>Pestalotiopsis fici</i> W106-1                                 | 40  |
| AKSP4_420 | 420.1 | NRPS        | N/A                                                                                                        | N/A |
| AKSP4_448 | 448.1 | Terpene     | N/A                                                                                                        | N/A |
| AKSP4_462 | 462.1 | T1PKS, NRPS | N/A                                                                                                        | N/A |
| AKSP4_464 | 464.1 | NRPS        | N/A                                                                                                        | N/A |
| AKSP4_531 | 531.1 | T1PKS       | ustilaginoidin N biosynthetic gene cluster from <i>Ustilaginoidea virens</i>                               | 30  |

|           |       |         |                                                                             |     |
|-----------|-------|---------|-----------------------------------------------------------------------------|-----|
| AKSP4_568 | 568.1 | NRPS    | N/A                                                                         | N/A |
| AKSP4_617 | 617.1 | T1PKS   | N/A                                                                         | N/A |
| AKSP4_708 | 708.1 | Terpene | clavaric acid biosynthetic gene cluster from <i>Hypholoma sublateritium</i> | 100 |

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39 **Table S5.** The complete list of antiSMASH predictions for *P. australis* (strain HNDR4) genome assembly using v7.1.0 web version.

| Contig   | Region | Type             | MiBiG database hit                                                          | Similarity (%) |
|----------|--------|------------------|-----------------------------------------------------------------------------|----------------|
| HNDR4_1  | 1.1    | NRPS-like        | choline biosynthetic gene cluster from <i>Aspergillus nidulans</i> FGSC A4  | 100            |
|          | 1.2    | Terpene          | N/A                                                                         | N/A            |
|          | 1.3    | T1PKS            | N/A                                                                         | N/A            |
| HNDR4_3  | 3.1    | T1PKS            | N/A                                                                         | N/A            |
| HNDR4_4  | 4.1    | Terpene          | clavaric acid biosynthetic gene cluster from <i>Hypholoma sublateritium</i> | 100            |
| HNDR4_9  | 9.1    | Fungal-RiPP-like | N/A                                                                         | N/A            |
| HNDR4_10 | 10.1   | NRPS             | N/A                                                                         | N/A            |
|          | 10.2   | NRPS             | N/A                                                                         | N/A            |
| HNDR4_11 | 11.1   | Terpene, T1PKS   | geodin biosynthetic gene cluster from <i>Aspergillus terreus</i> NIH2624    | 74             |
|          | 11.2   | Terpene          | N/A                                                                         | N/A            |



|          |      |                      |                                                                              |     |
|----------|------|----------------------|------------------------------------------------------------------------------|-----|
| HNDR4_13 | 13.1 | T1PKS                | N/A                                                                          | N/A |
| HNDR4_15 | 15.1 | T1PKS                | ustilaginoidin N biosynthetic gene cluster from <i>Ustilaginoidea virens</i> | 46  |
| HNDR4_16 | 16.1 | T3PKS                | N/A                                                                          | N/A |
| HNDR4_22 | 22.1 | T1PKS,<br>NRPS       | phyllostictine A biosynthetic gene cluster from <i>Phyllosticta cirsii</i>   | 20  |
| HNDR4_23 | 23.1 | T1PKS                | ochratoxin A biosynthetic gene cluster from <i>Aspergillus steynii</i>       | 100 |
|          | 23.2 | T1PKS                | YWA1 biosynthetic gene cluster from <i>Aspergillus oryzae</i> RIB40          | 100 |
| HNDR4_26 | 26.1 | T1PKS                | tricholignan A biosynthetic gene cluster from <i>Trichoderma harzianum</i>   | 33  |
| HNDR4_27 | 27.1 | Fungal-<br>RiPP-like | N/A                                                                          | N/A |
| HNDR4_35 | 35.1 | NRPS,<br>T1PKS       | N/A                                                                          | N/A |
| HNDR4_38 | 38.1 | Fungal-<br>RiPP-like | N/A                                                                          | N/A |
|          | 38.2 | NRPS                 | shearinine D biosynthetic gene cluster from <i>Penicillium janthinellum</i>  | 9   |

|          |      |                      |                                                                                  |     |
|----------|------|----------------------|----------------------------------------------------------------------------------|-----|
|          | 38.3 | NRPS-like            | N/A                                                                              | N/A |
| HNDR4_39 | 39.1 | T1PKS                | N/A                                                                              | N/A |
| HNDR4_40 | 40.1 | Terpene              | trichobrasilenol biosynthetic gene cluster from <i>Annulohypoxylon truncatum</i> | 60  |
| HNDR4_42 | 42.1 | NRPS-like,<br>T1PKS  | cichorine biosynthetic gene cluster from <i>Aspergillus nidulans</i> FGSC A4     | 100 |
| HNDR4_46 | 46.1 | Fungal-<br>RiPP-like | N/A                                                                              | N/A |
| HNDR4_48 | 48.1 | T1PKS                | N/A                                                                              | N/A |
| HNDR4_49 | 49.1 | Fungal_RiPP<br>-like | N/A                                                                              | N/A |
| HNDR4_50 | 50.1 | T1PKS                | N/A                                                                              | N/A |
| HNDR4_57 | 57.1 | Fungal-<br>RiPP-like | N/A                                                                              | N/A |
| HNDR4_62 | 62.1 | NRPS-like            | N/A                                                                              | N/A |

|           |       |                  |                                                                               |     |
|-----------|-------|------------------|-------------------------------------------------------------------------------|-----|
| HNDR4_68  | 68.1  | T1PKS            | secalonic acids biosynthetic gene cluster from <i>Claviceps purpurea</i> 20.1 | 12  |
| HNDR4_73  | 73.1  | Fungal-RiPP-like | N/A                                                                           | N/A |
| HNDR4_77  | 77.1  | T1PKS            | N/A                                                                           | N/A |
| HNDR4_91  | 91.1  | NRPS             | UNII-YC2Q1O94PT biosynthetic gene cluster from <i>Alternaria alternata</i>    | 100 |
| HNDR4_105 | 105.1 | Terpene          | clavaric acid biosynthetic gene cluster from <i>Hypholoma sublateritium</i>   | 100 |
| HNDR4_119 | 119.1 | Fungal-RiPP-like | N/A                                                                           | N/A |
| HNDR4_120 | 120.1 | Fungal-RiPP-like | N/A                                                                           | N/A |
| HNDR4_122 | 122.1 | NRPS-like        | N/A                                                                           | N/A |
| HNDR4_123 | 123.1 | T1PKS            | N/A                                                                           | N/A |
| HNDR4_129 | 129.1 | T1PKS            | F9775A biosynthetic gene cluster from <i>Aspergillus nidulans</i> FGSC A4     | 50  |
| HNDR4_131 | 131.1 | T1PKS            | secalonic acids biosynthetic gene cluster from <i>Claviceps purpurea</i> 20.1 | 18  |

|           |       |                      |                                                                              |     |
|-----------|-------|----------------------|------------------------------------------------------------------------------|-----|
| HNDR4_136 | 136.1 | NRPS                 | N/A                                                                          | N/A |
| HNDR4_146 | 146.1 | NRPS                 | curvupallide-B biosynthetic gene cluster from <i>Cochliobolus pallescens</i> | 11  |
| HNDR4_165 | 165.1 | NRPS                 | N/A                                                                          | N/A |
| HNDR4_166 | 166.1 | NRPS                 | N/A                                                                          | N/A |
| HNDR4_170 | 170.1 | T1PKS                | N/A                                                                          | N/A |
| HNDR4_188 | 188.1 | T1PKS                | N/A                                                                          | N/A |
| HNDR4_223 | 223.1 | Terpene              | squalestatin S1 biosynthetic gene cluster from <i>Aspergillus sp. Z5</i>     | 40  |
| HNDR4_265 | 265.1 | Fungal-<br>RiPP-like | N/A                                                                          | N/A |
| HNDR4_343 | 343.1 | Fungal-<br>RiPP-like | N/A                                                                          | N/A |

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44 **Table S6.** Details of antiSMASH results of the matching genes for compounds potentially produced by predicted BGCs in *P. griseus* (strain  
45 AKSP4).

| Gene Location                                                         | MIBiG Protein | Description                     | MIBiG Cluster | Percentage Identity (%) | Percentage Coverage (%) |
|-----------------------------------------------------------------------|---------------|---------------------------------|---------------|-------------------------|-------------------------|
| Choline (from <i>Aspergillus nidulans</i> FGSC A4, CH236925.1)        |               |                                 |               |                         |                         |
| *AKSP4_000402                                                         | EAA62478.1    | hypothetical_protein            | BGC0002276    | 66                      | 95                      |
| Swainsonine (from <i>Alternaria oxytropis</i> , KY365741.1)           |               |                                 |               |                         |                         |
| *AKSP4_003828                                                         | AQV04230.1    | SwnK                            | BGC0001794    | 67                      | 99.8                    |
| AKSP4_003829                                                          | AQV04229.1    | SwnH2                           |               | 79                      | 100.3                   |
| AKSP4_003831                                                          | AQV04226.1    | SwnR                            |               | 67                      | 100                     |
| AKSP4_003832                                                          | AQV04227.1    | SwnN                            |               | 69                      | 100                     |
| AKSP4_003833                                                          | AQV04228.1    | SwnH1                           |               | 76                      | 100                     |
| Trichobrasilenol (from <i>Annulohypoxylon truncatum</i> , MT383109.1) |               |                                 |               |                         |                         |
| *AKSP4_005505                                                         | QOE88885.1    | cytochrome_P450_monooxygenase   | BGC0002260    | 63                      | 72                      |
| AKSP4_005506                                                          | QOE88883.1    | brasilane_synthase              |               | 70                      | 101                     |
| AKSP4_005507                                                          | QOE88884.1    | N-acetylglucosamine_transferase |               | 67                      | 92                      |
| Geodin (from <i>Aspergillus terreus</i> NIH2624, CH476605.1)          |               |                                 |               |                         |                         |
| AKSP4_005941                                                          | EAU31632.1    | predicted_protein               | BGC0002592    | 57                      | 100                     |
| AKSP4_005942                                                          | EAU31631.1    | predicted_protein               |               | 57                      | 99.7                    |
| AKSP4_005943                                                          | EAU31630.1    | conserved_hypothetical_protein  |               | 78                      | 75                      |
| AKSP4_005944                                                          | EAU31629.1    | predicted_protein               |               | 57                      | 65.7                    |

|               |            |                                |  |    |      |
|---------------|------------|--------------------------------|--|----|------|
| AKSP4_005945  | EAU31628.1 | conserved_hypothetical_protein |  | 72 | 55.1 |
| AKSP4_005946  | EAU31627.1 | hypothetical_protein           |  | 62 | 99.1 |
| *AKSP4_005949 | EAU31624.1 | hypothetical_protein           |  | 64 | 99.8 |
| AKSP4_005950  | EAU31623.1 | conserved_hypothetical_protein |  | 70 | 99.1 |
| AKSP4_005951  | EAU31622.1 | conserved_hypothetical_protein |  | 71 | 99.4 |

\*Core gene

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62 **Table S7.** Details of antiSMASH results of the matching genes for compounds potentially produced by predicted BGCs in *P. australis* (strain  
63 HNDR4).

| Gene Location                                                         | MIBiG Protein | Description                     | MIBiG Cluster | Percentage Identity (%) | Percentage Coverage (%) |
|-----------------------------------------------------------------------|---------------|---------------------------------|---------------|-------------------------|-------------------------|
| Choline (from <i>Aspergillus nidulans</i> FGSC A4, CH236925.1)        |               |                                 |               |                         |                         |
| *HNDR4_000034                                                         | EAA62478.1    | hypothetical_protein            | BGC0002276    | 67                      | 95                      |
| geodin (from <i>Aspergillus terreus</i> NIH2624, CH476605.1)          |               |                                 |               |                         |                         |
| HNDR4_002033                                                          | EAU31622.1    | conserved_hypothetical_protein  | BGC0002592    | 71                      | 99.4                    |
| HNDR4_002034                                                          | EAU31623.1    | conserved_hypothetical_protein  |               | 70                      | 99.1                    |
| *HNDR4_002035                                                         | EAU31624.1    | hypothetical_protein            |               | 64                      | 99.8                    |
| HNDR4_002038                                                          | EAU31627.1    | hypothetical_protein            |               | 62                      | 99.1                    |
| HNDR4_002039                                                          | EAU31628.1    | conserved_hypothetical_protein  |               | 72                      | 55.1                    |
| HNDR4_002040                                                          | EAU31629.1    | predicted_protein               |               | 57                      | 63.7                    |
| HNDR4_002041                                                          | EAU31630.1    | conserved_hypothetical_protein  |               | 75                      | 73.7                    |
| HNDR4_002042                                                          | EAU31631.1    | predicted_protein               |               | 57                      | 99.7                    |
| HNDR4_002043                                                          | EAU31632.1    | predicted_protein               |               | 57                      | 100.0                   |
| trichobrasilenol (from <i>Annulohypoxylon truncatum</i> , MT383109.1) |               |                                 |               |                         |                         |
| HNDR4_005084                                                          | QOE88884.1    | N-acetylglucosamine_transferase | BGC0002260    | 66                      | 100.0                   |
| *HNDR4_005085                                                         | QOE88883.1    | brasilane_synthase              |               | 70                      | 96.9                    |
| HNDR4_005086                                                          | QOE88885.1    | cytochrome_P450_monooxygenase   |               | 66                      | 104.8                   |

64 \*Core gene