**Supplementary Table 5.** Number of GO terms and SM categories annotated from gene models with evidence for HGT in *B. meristosporus* CBS 931.73

|  |  |
| --- | --- |
| **Gene Ontology term** | **Number of gene models** |
| No GO | 655 |
| No InterPro | 140 |
| GO:oxidation-reduction process | 59 |
| GO:protein binding | 34 |
| GO:phosphorelay sensor kinase activity | 32 |
| GO:N-acetyltransferase activity | 28 |
| GO:catalytic activity | 26 |
| GO:extracellular space | 25 |
| GO:hydrolase activity | 24 |
| GO:oxidoreductase activity | 23 |
| GO:hydrolase activity, hydrolyzing O-glycosyl compounds | 19 |
| **NRPS** | 18 |
| GO:amino acid transport | 13 |
| GO:transport | 13 |
| GO:methyltransferase activity | 11 |
| GO:proteolysis | 10 |
| GO:ATP binding | 7 |
| GO:FMN binding | 6 |
| GO:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds | 6 |
| GO:DNA binding | 5 |
| **NRPS-Like** | 4 |
| GO:carbon-nitrogen ligase activity, with glutamine as amido-N-donor | 4 |
| GO:chitinase activity | 4 |
| GO:catalase activity | 3 |
| GO:cellular amino acid metabolic process | 3 |
| GO:FAD binding | 3 |
| GO:nucleic acid binding | 3 |
| GO:oxidoreductase activity, acting on other nitrogenous compounds as donors | 3 |
| GO :transferase activity, transferring acyl groups other than amino-acyl groups | 3 |
| GO:aminoacyl-tRNA editing activity | 2 |
| GO:coproporphyrinogen oxidase activity | 2 |
| GO:nucleotide binding | 2 |
| GO:nutrient reservoir activity | 2 |
| GO:phosphogluconate dehydrogenase (decarboxylating) activity | 2 |
| GO:response to oxidative stress | 2 |
| GO:serine-type endopeptidase activity | 2 |
| GO:transmembrane transport | 2 |
| GO:tryptophan synthase activity | 2 |
| GO:zinc ion binding | 2 |
| **PKS** | 2 |
| **Terpene** | 2 |
| GO:cation transmembrane transporter activity | 1 |
| GO:copper ion binding | 1 |
| GO:dihydroorotate dehydrogenase activity | 1 |
| GO:hydrolase activity, acting on glycosyl bonds | 1 |
| GO:integral component of membrane | 1 |
| GO:iron ion binding | 1 |
| GO:lipid metabolic process | 1 |
| GO:lyase activity | 1 |
| GO:MAP kinase activity | 1 |
| GO:nucleobase-containing compound metabolic process | 1 |
| GO:orotate phosphoribosyltransferase activity | 1 |
| GO:oxidoreductase activity, acting on CH-OH group of donors | 1 |
| GO:polysaccharide catabolic process | 1 |
| GO:protein tyrosine phosphatase activity | 1 |
| GO:protein-chromophore linkage | 1 |
| GO:pyridoxal phosphate binding | 1 |
| GO:regulation of transcription, DNA-templated | 1 |
| GO:RNA binding | 1 |
| GO:structural molecule activity | 1 |
| GO:ubiquitin-dependent protein catabolic process | 1 |