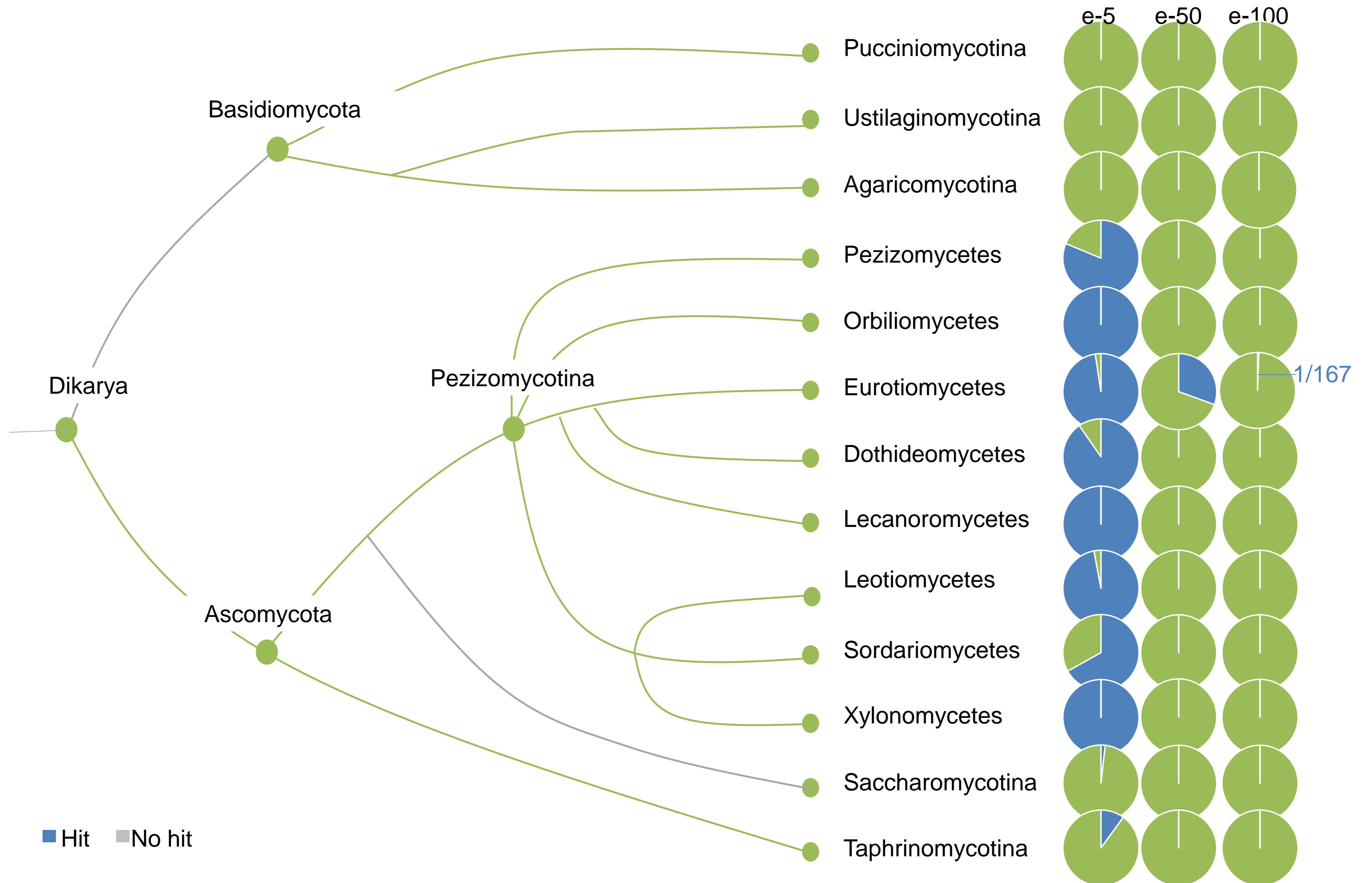
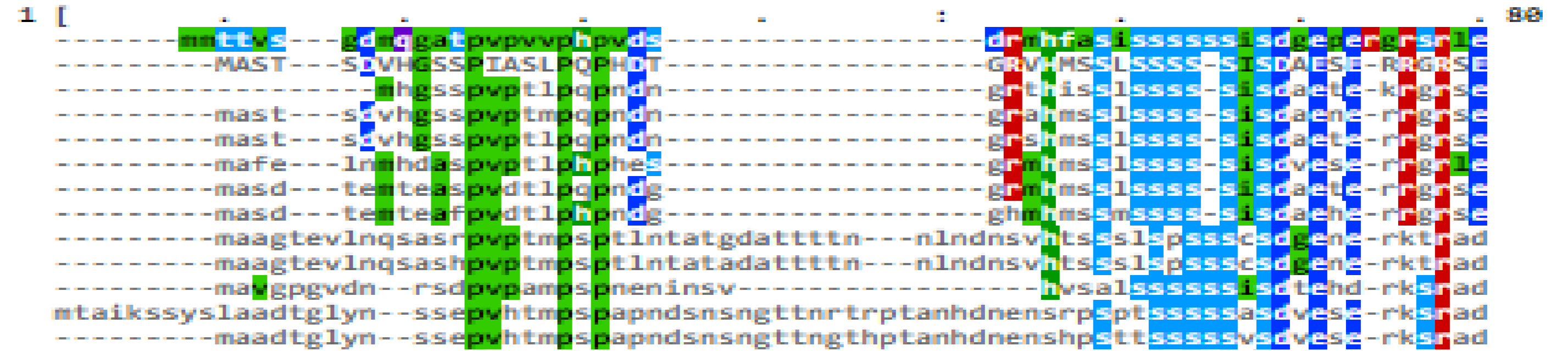


A.



B.

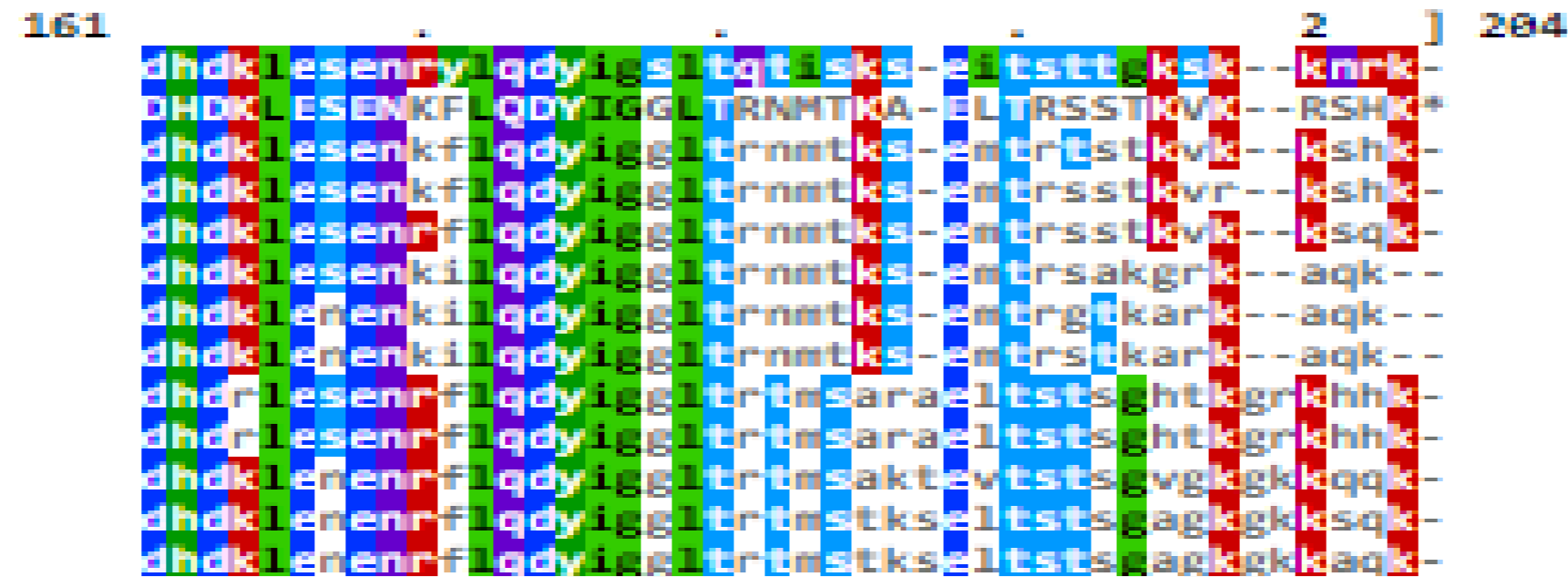
	cov	pid
<i>Talaromyces stipitatus</i>	100.0%	100.0%
<i>Aspergillus fumigatus</i>	97.7%	69.8%
<i>Aspergillus terreus</i>	94.2%	74.4%
<i>Aspergillus flavus</i>	97.7%	71.2%
<i>Aspergillus niger</i>	97.7%	72.4%
<i>Penicillium oxalicum</i>	97.1%	72.2%
<i>Penicillium chrysogenum</i>	97.1%	69.8%
<i>Penicillium roquefortii</i>	97.1%	69.8%
<i>Coccidioides immitis</i>	97.7%	58.6%
<i>Coccidioides posadasii</i>	97.7%	58.6%
<i>Ajellomyces capsulatus</i>	95.3%	62.2%
<i>Trichophyton equinum</i>	98.3%	54.2%
<i>Trichophyton rubrum</i>	97.1%	56.7%



	cov	pid
<i>Talaromyces stipitatus</i>	100.0%	100.0%
<i>Aspergillus fumigatus</i>	97.7%	69.8%
<i>Aspergillus terreus</i>	94.2%	74.4%
<i>Aspergillus flavus</i>	97.7%	71.2%
<i>Aspergillus niger</i>	97.7%	72.4%
<i>Penicillium oxalicum</i>	97.1%	72.2%
<i>Penicillium chrysogenum</i>	97.1%	69.8%
<i>Penicillium roquefortii</i>	97.1%	69.8%
<i>Coccidioides immitis</i>	97.1%	69.8%
<i>Coccidioides posadasii</i>	97.7%	58.6%
<i>Ajellomyces capsulatus</i>	97.7%	58.6%
<i>Trichophyton equinum</i>	95.3%	62.2%
<i>Trichophyton rubrum</i>	98.3%	54.2%
	97.1%	56.7%



	cov	pid
<i>Talaromyces stipitatus</i>	100.0%	100.0%
<i>Aspergillus fumigatus</i>	97.7%	69.8%
<i>Aspergillus terreus</i>	94.2%	74.4%
<i>Aspergillus flavus</i>	97.7%	71.2%
<i>Aspergillus niger</i>	97.7%	72.4%
<i>Penicillium oxalicum</i>	97.1%	72.2%
<i>Penicillium chrysogenum</i>	97.1%	69.8%
<i>Penicillium roquefortii</i>	97.1%	69.8%
<i>Coccidioides immitis</i>	97.7%	58.6%
<i>Coccidioides posadasii</i>	97.7%	58.6%
<i>Ajellomyces capsulatus</i>	95.3%	62.2%
<i>Trichophyton equinum</i>	98.3%	54.2%
<i>Trichophyton rubrum</i>	97.1%	56.7%



Supplementary Figure S1 - The distribution ZipD related proteins throughout the fungal tree of life. (A) BlastP analyses using the mature ZipD protein sequence were performed, at the expected (e-value) cut-off thresholds of $1.0e-5$, $1.0e-50$ and $1.0e-100$, on the predicted proteomes of 791 fungi, representing the 13 different taxonomic classes or subphyla within Dikarya, as presented on the JGI MycoCosm portal. Diagrammatic representation of the fungal tree of life (not indicative of evolutionary time) adapted from the JGI MycoCosm. Pie charts show the number of species genomes within each taxonomic class with at least one protein similar to ZipD at the indicated BlastP thresholds. (B) Multiple sequence alignment by using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>) and Mview (<https://www.ebi.ac.uk/Tools/msa/mview/>) of selected species of Eurotiomycetes. Sequences and Blastp alignments were obtained from

https://www.yeastgenome.org/blastfungal?uploadFile=&program=blastp#XP_002150417.1.

When compared with *A. fumigatus*: *A. oryzae* [e-value= $2e-67$, identity=92 %, score=207 bits (527)], *A. flavus* [e-value= $2e-67$, identity=92%, score=207 bits (527)], *A. niger* [e-value= $2e-64$, identity=92 %, score=199 bits (507)], *A. terreus* [e-value= $2e-61$, identity=90%, score=191 bits (486)], *P. chrysogenum* [e-value= $7e-55$, identity=84%, score=175 bits (444)], *P. oxalicum* [e-value= $1e-54$, identity=87%, score=174 bits (442)], *P. roquefortii* [e-value= $2e-49$, identity=82%, score= 161 bits (407)], *T. stipitatus* [e-value= $1e-39$, identity=78%, score=207 bits (344)], *C. immitis* [e-value= $1e-38$, identity= 80%, score=134 bits (338)], *C. posadasii* (e-value= $2e-38$, identity= 80%, score=138 (338)), *T. equinum* [e-value= $2e-36$, identity= 78 %, score=129 bits (325)], *T. rubrum* [e-value= $5e-36$, identity=82%, score=128 bits (321)], and *A. capsulatus* [e-value= $5e-36$, identity=80%, score= 127 bits (320)].