Impacts of exposure to glyphosate and diquat on microbial diversity and community structure shifts in a lateritic paddy soil

Xiaoyu He1, 2, Chunyuan Wu2, 3, 4, 5, Huadong Tan 2, 3, 4, 5\*, Xiao Deng2, 3, 4, 5\*, Yi Li 2, 3, 4, 5

1 National Key Laboratory of Green Pesticide, Key Laboratory of Green Pesticide and Agricultural Bioengineering, Ministry of Education, Center for R&D of Fine Chemicals of Guizhou University, Guiyang 550025, PR China.

2 Environment and Plant Protection Institute, Chinese Academy of Tropical Agricultural Sciences, Haikou 571101, PR China.

3 Danzhou Scientific Observing and Experimental Station of Agro-Environment, Ministry of Agriculture and Rural Affairs, Danzhou 571737, PR China.

4 National Agricultural Experimental Station for Agricultural Environment, Danzhou 571737, PR China.

5 Hainan Engineering Research Center for Non-point Source and Heavy Metal Pollution Control, Danzhou 571737, PR China.

**\*** Correspondence: Huadong Tan, Environment and Plant Protection Institute, Chinese Academy of Tropical Agricultural Sciences, Haikou, China; E-mail: [tanhuadong1991@163.com;](mailto:tanhuadong1991@163.com;) Xiao Deng, Environment and Plant Protection Institute, Chinese Academy of Tropical Agricultural Sciences, Haikou, China; E-mail: dx0928@qq.com.

**Table S1** Primer information

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Type | Region | Primer name | Primer sequence | Product length | Reference |
| 16S | V1-V9 | 27F | AGRGTTTGATYNTGGCTCAG | ~1465 | [1] |
| 1492R | TASGGHTACCTTGTTASGACTT |
| V4 | 515F | GTGYCAGCMGCCGCGGTAA | ~292 | [1-2] |
| 806R | GGACTACNVGGGTWTCTAAT |
| V3-V4 | 341F | CCTACGGGNGGCWGCAG | ~466 | [3] |
| 806R | GGACTACHVGGGTATCTAAT |
| V4-V5 | 515F | GTGCCAGCMGCCGCGGTAA | ~412 | [4] |
| 907R | CCGTCAATTCCTTTGAGTTT |
| V5-V7 | 799F | AACMGGATTAGATACCCKG | ~414 | [5] |
| 1193R | ACGTCATCCCCACCTTCC |
| V4-V5 | Arch519F | CAGCMGCCGCGGTAA | ~416 | [6] |
| Arch915R | GTGCTCCCCCGCCAATTCCT |
| 18S | V4 | 528F | GCGGTAATTCCAGCTCCAA | ~260 | [7] |
| 706R | AATCCRAGAATTTCACCTCT |
| ITS | ITS1 | ITS1\_F\_KYO2 | TAGAGGAAGTAAAAGTCGTAA | ~366 | [8] |
| ITS86R | TTCAAAGATTCGATGATTCAC |
| ITS1-F | CTTGGTCATTTAGAGGAAGTAA | ~321 | [9] |
| ITS2 | GCTGCGTTCTTCATCGATGC |
| ITS2 | ITS3\_KYO2 | GATGAAGAACGYAGYRAA | ~381 | [10] |
| ITS4 | TCCTCCGCTTATTGATATGC |

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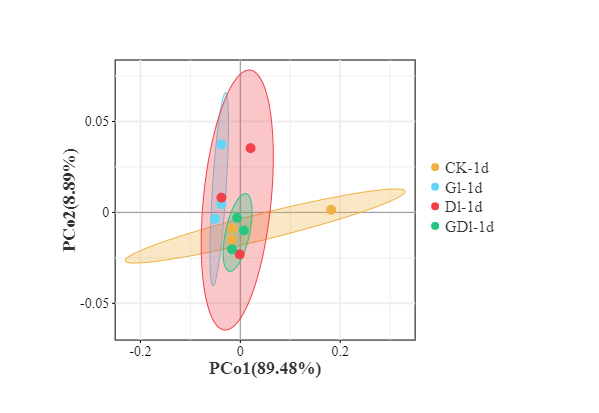
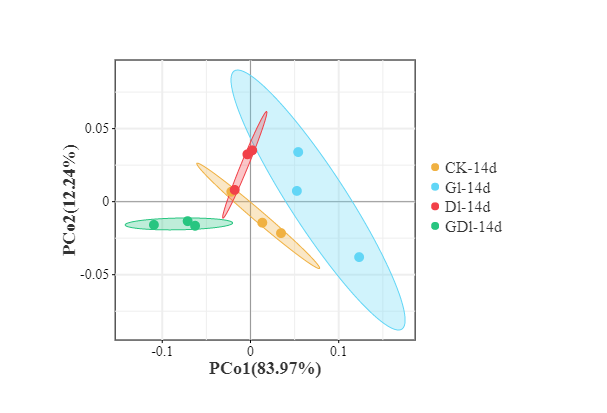
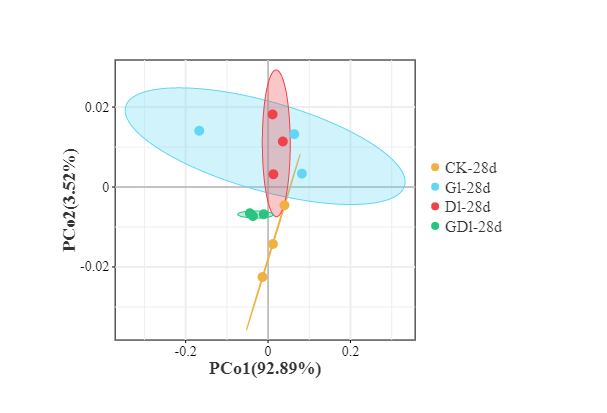
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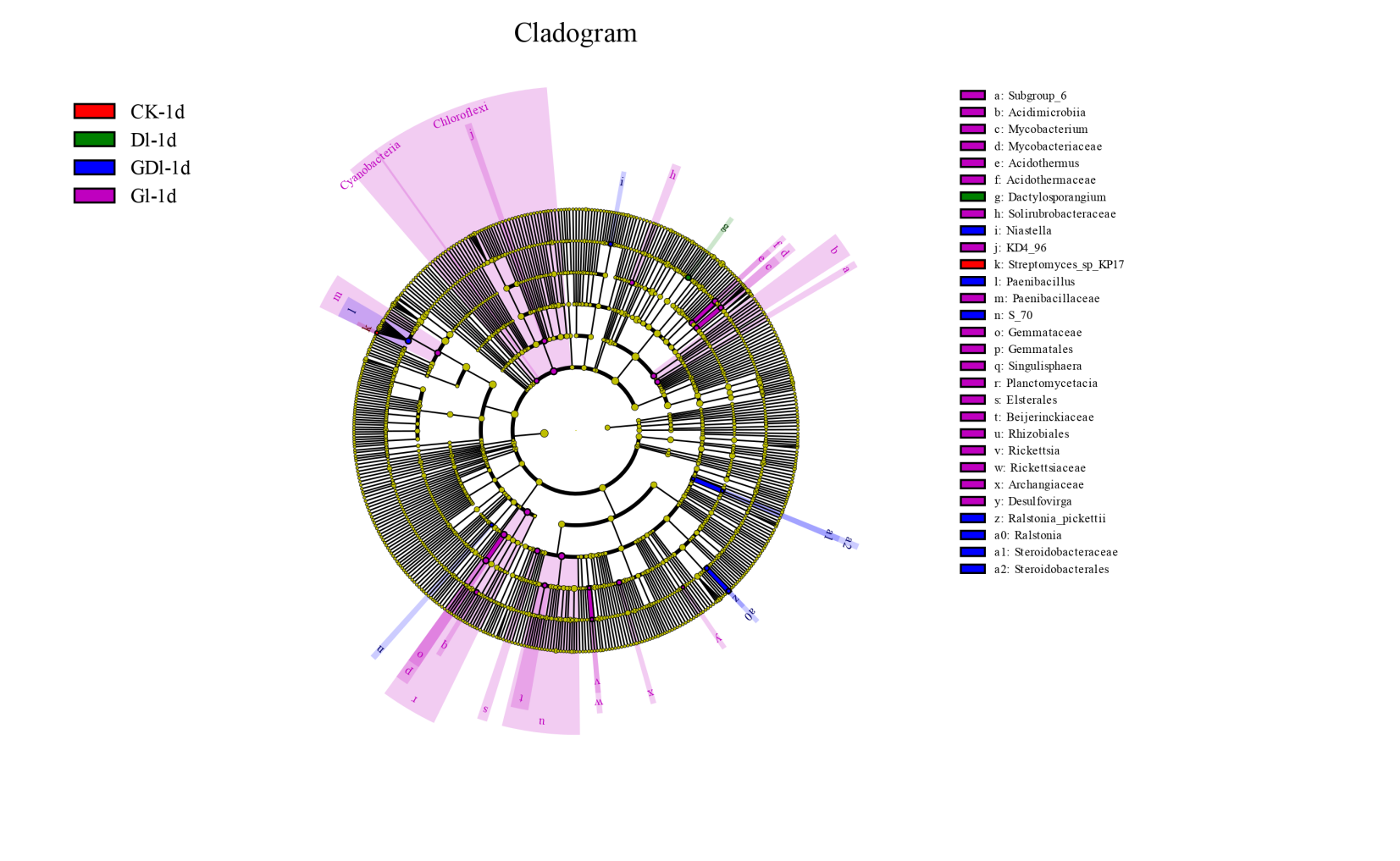


(a)

(b)

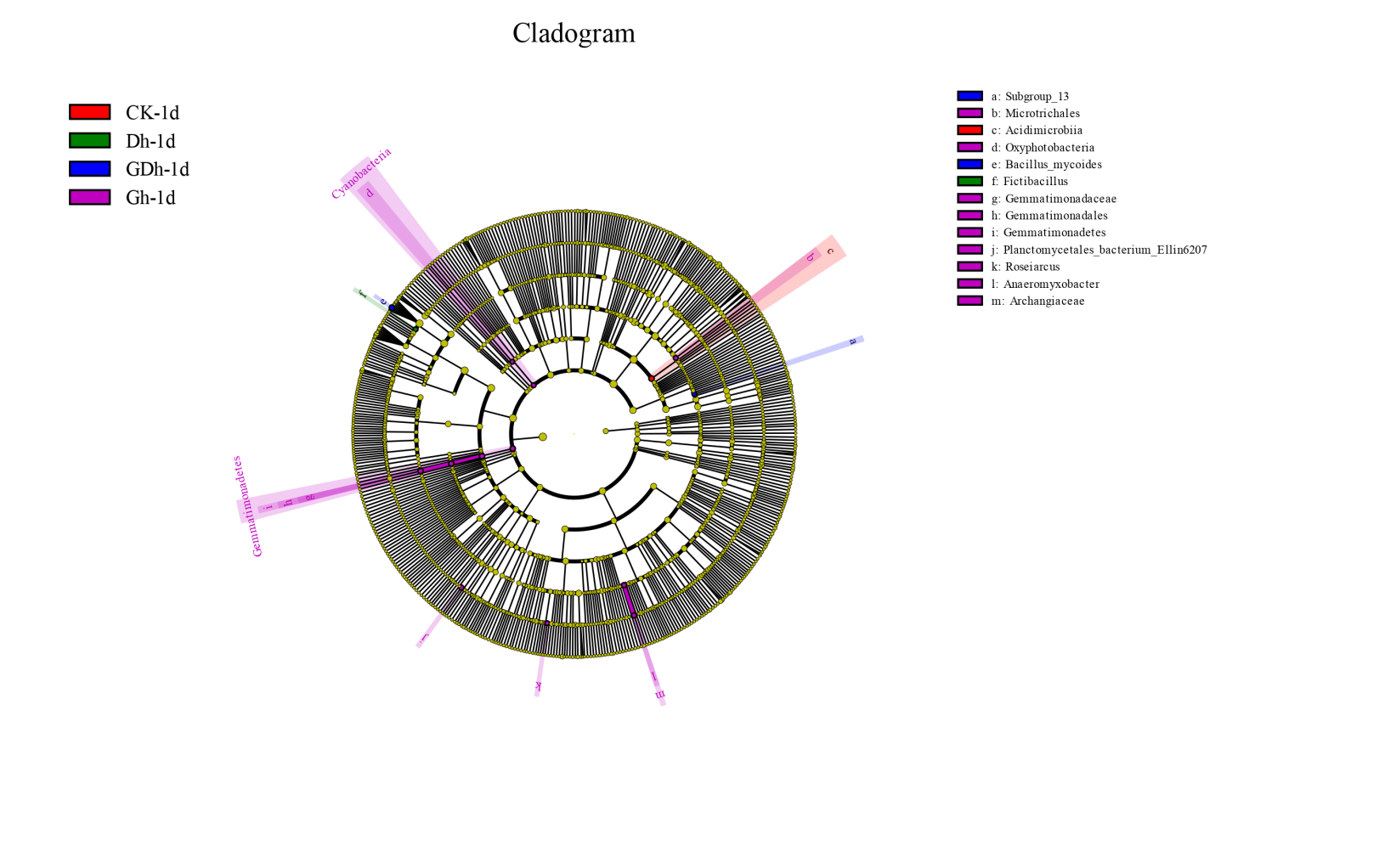
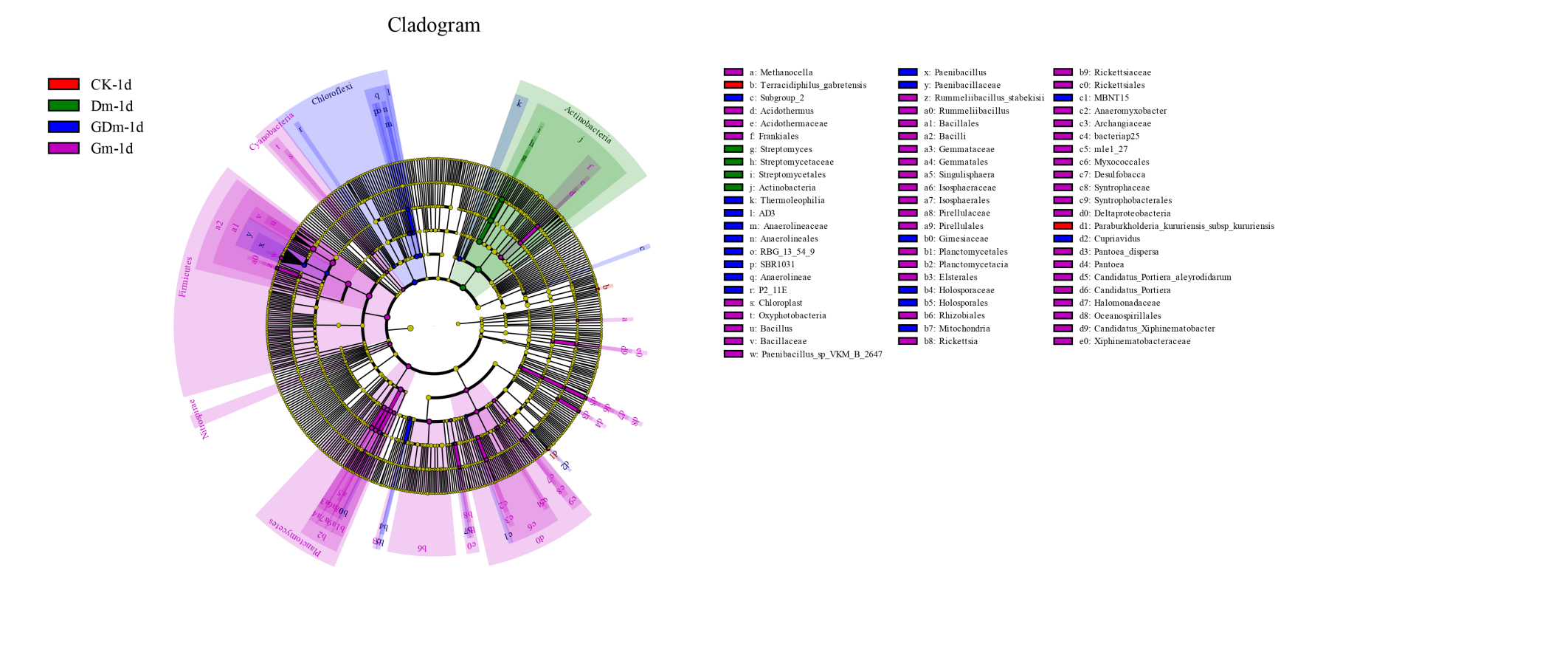
(c)

**Figure S1.** Principal coordinate analysis for the bacterial communities at the phylum level. .

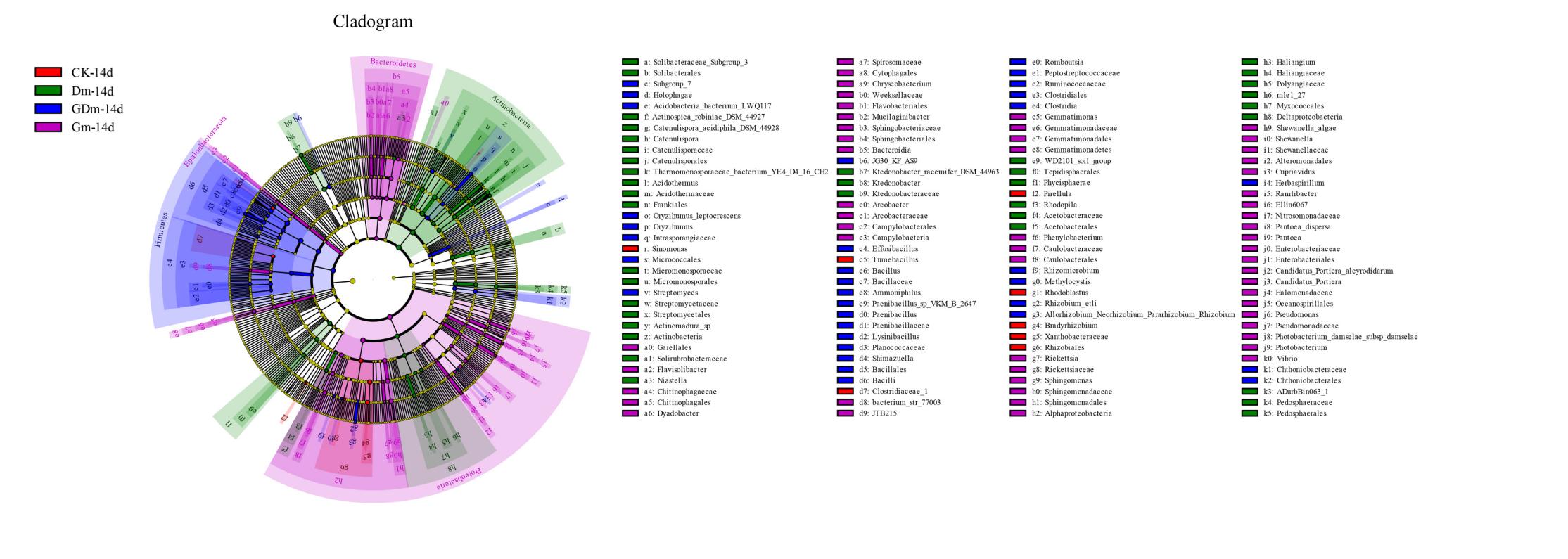


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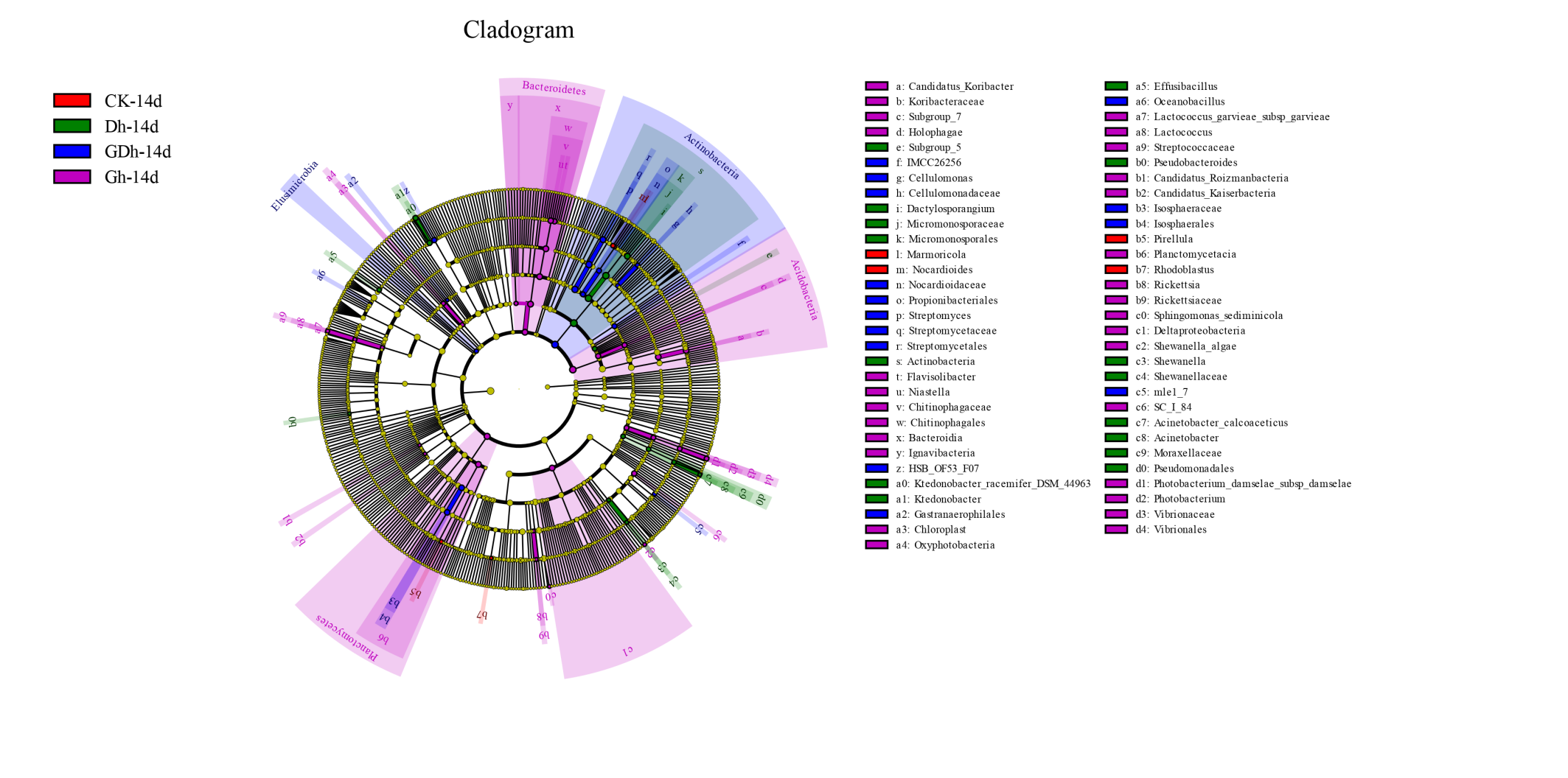
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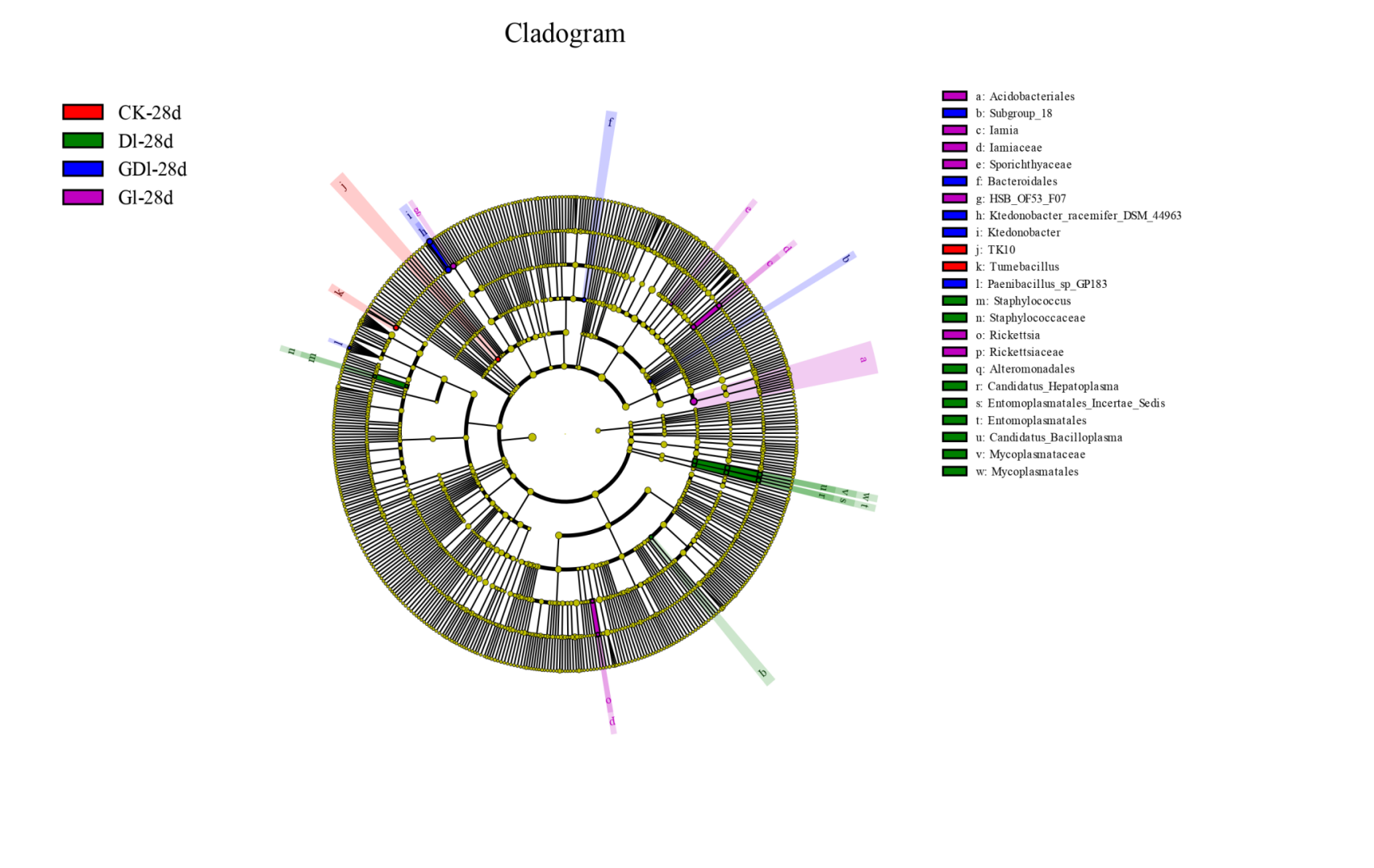
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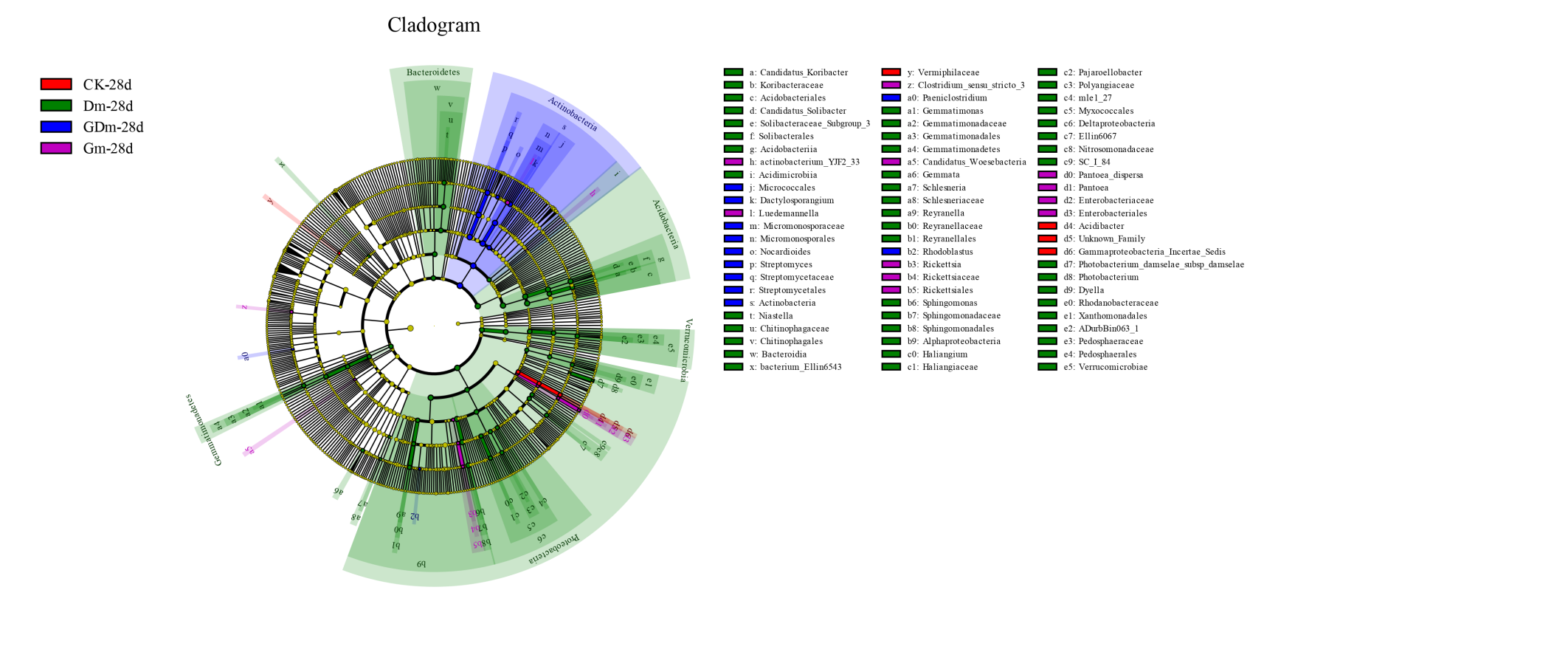
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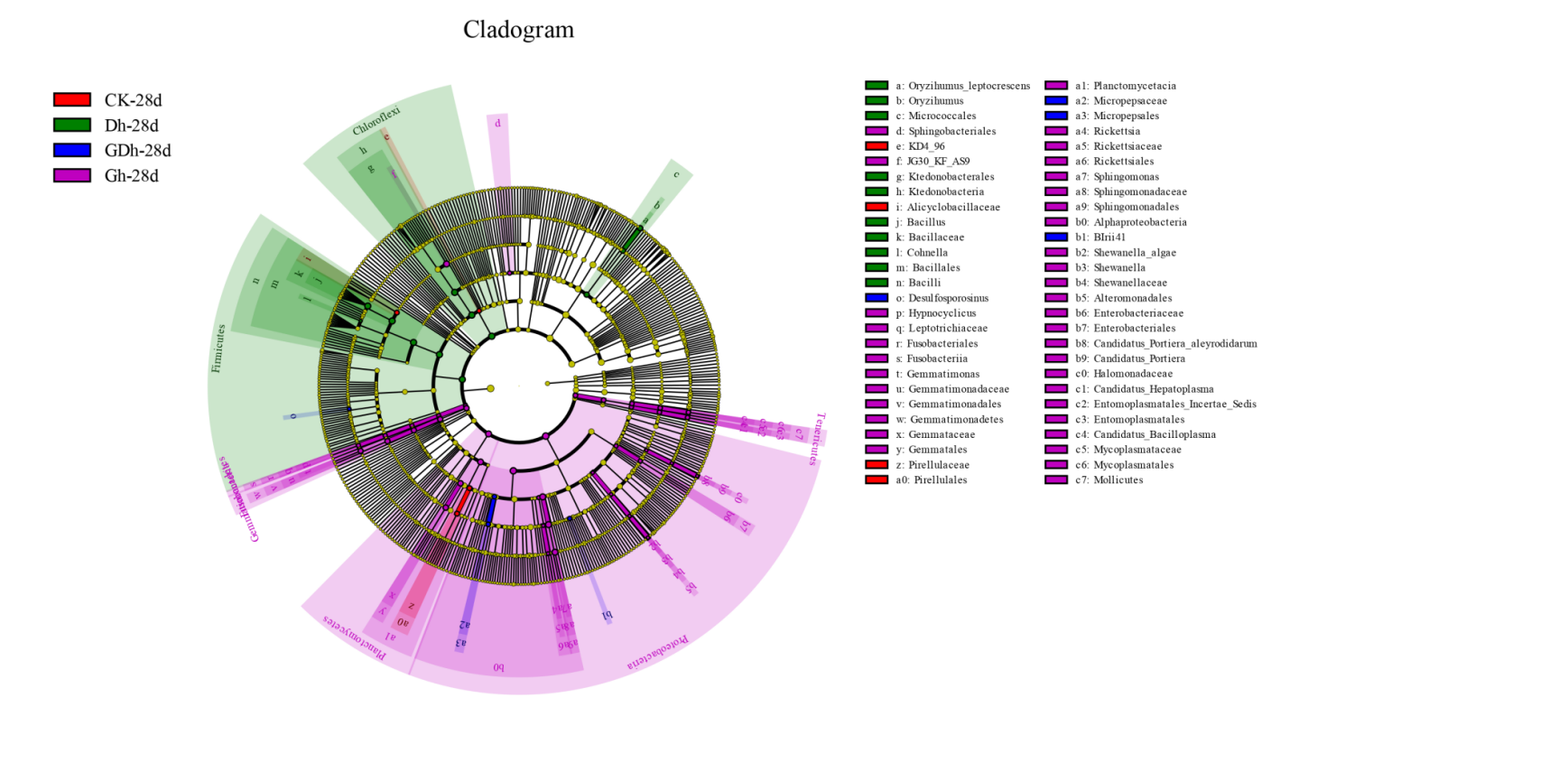
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(f)

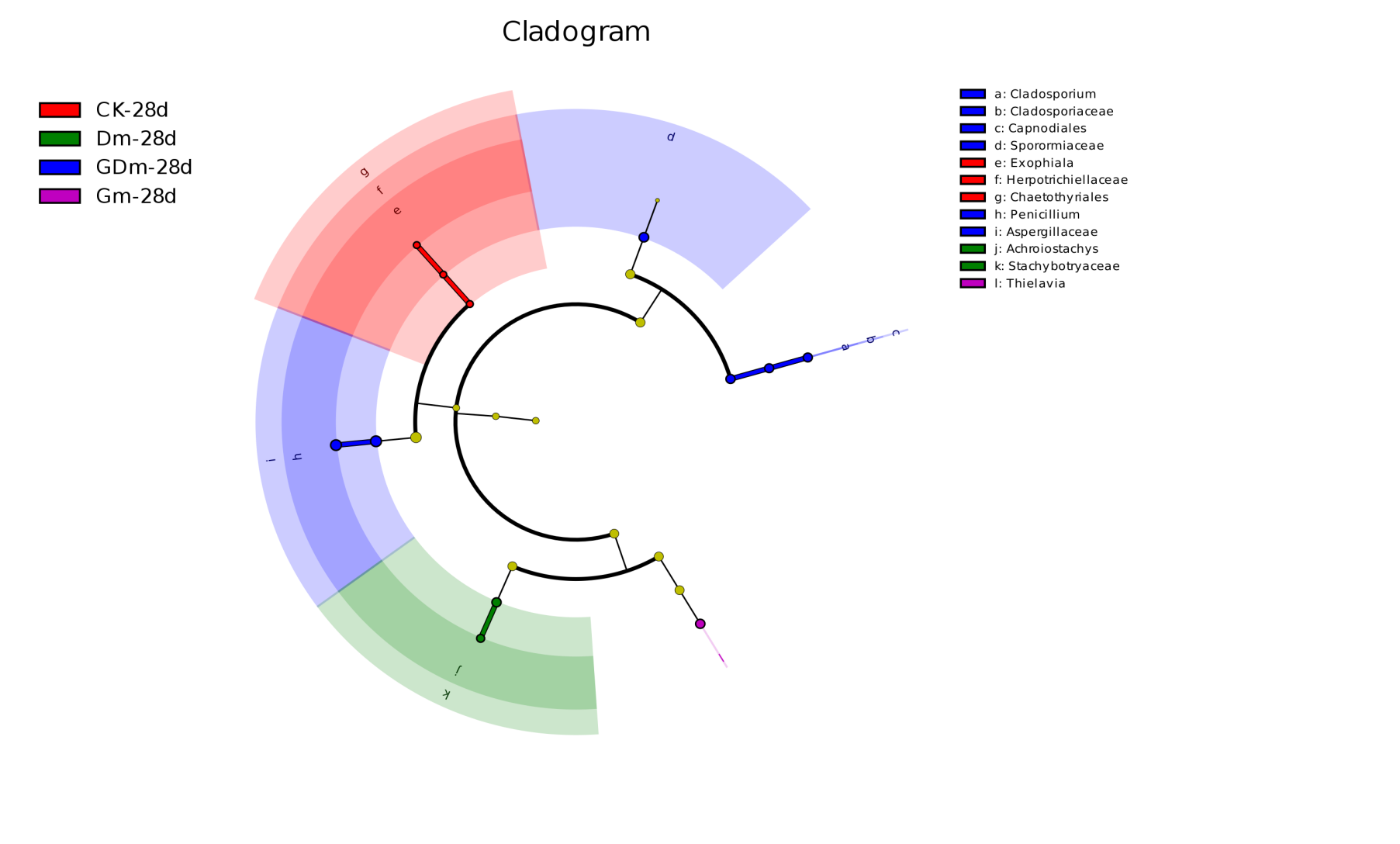


(g)



(h)

**Figure S2.** Cladograms of line discriminant analysis effect size (LEfSe) analyses of bacteria.



CK-28d

Dm-28d

GDm-28d

Gm-28d

a: Cladosporium

b: Cladosporiaceae

c: Capnodiales

d: Sporormiaceae

e: Exophiala

f: Herpotrichiellaceae

g: Chaetothyriales

h: Penicllium

i: Aspergillaceae

j: Achroiostachys

k: Stachybotryaceae

l: Thielavia

Cladogram

**Figure S3.** Cladograms of line discriminant analysis effect size (LEfSe) analyses of fungus.