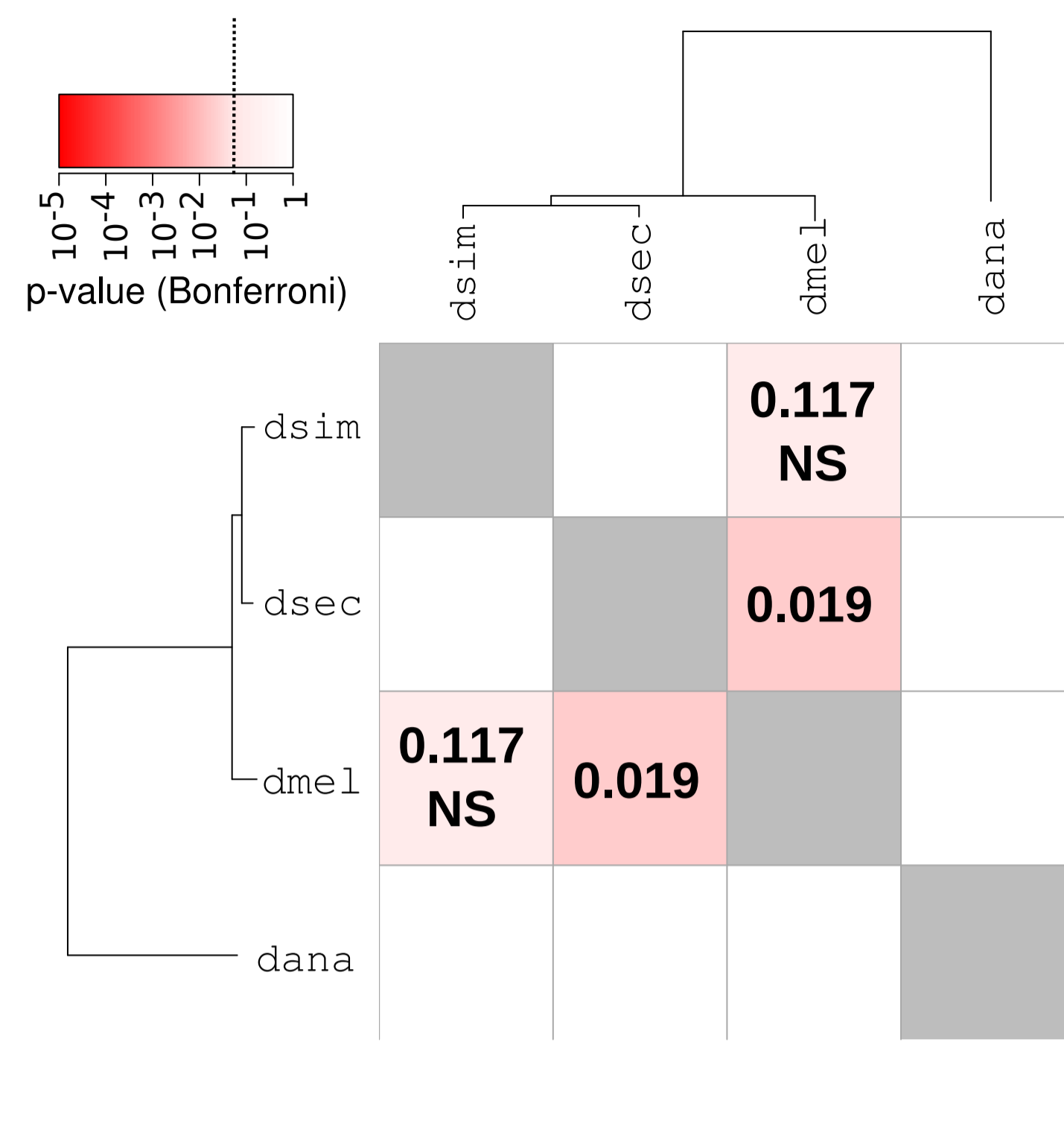
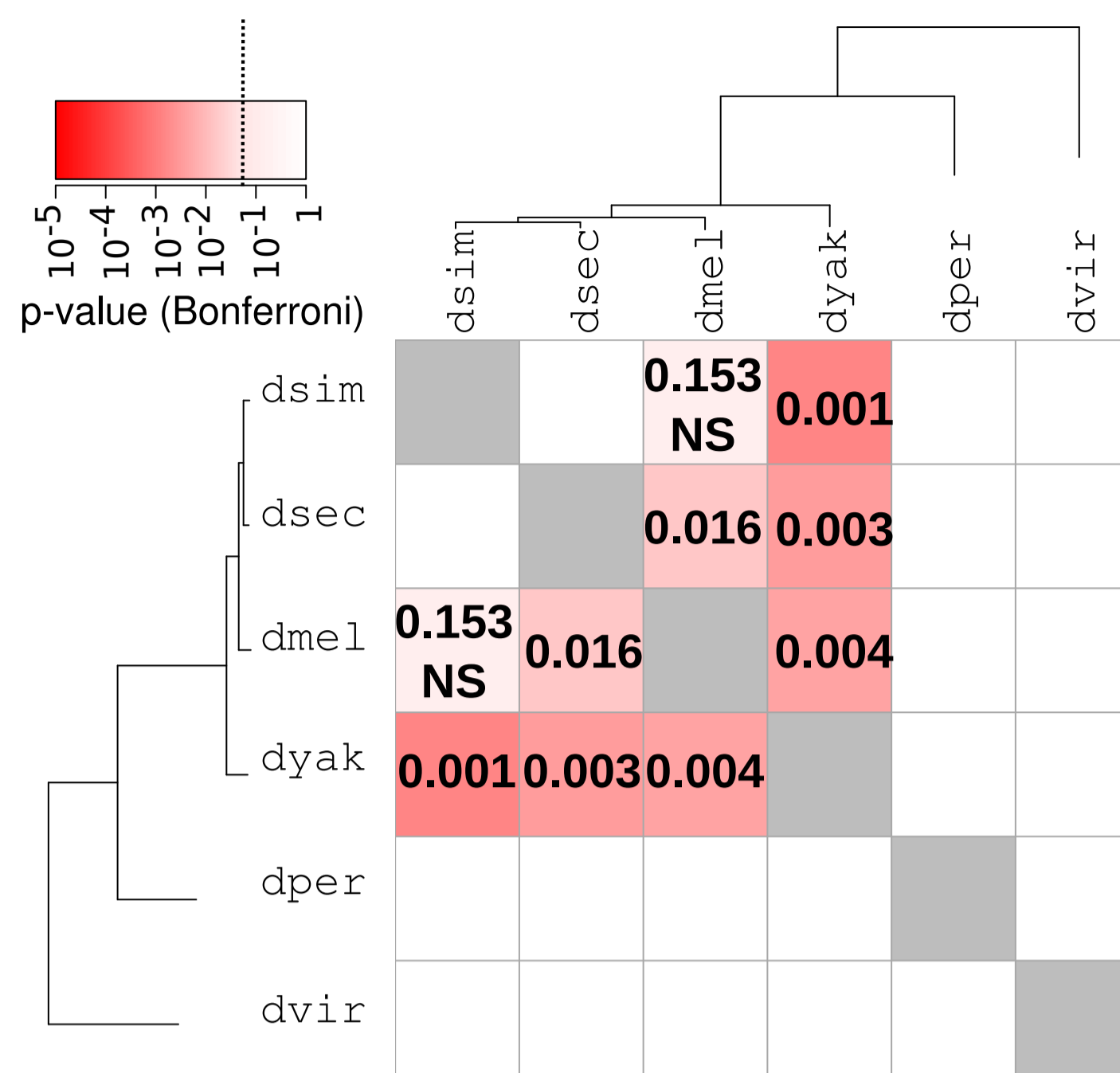


A

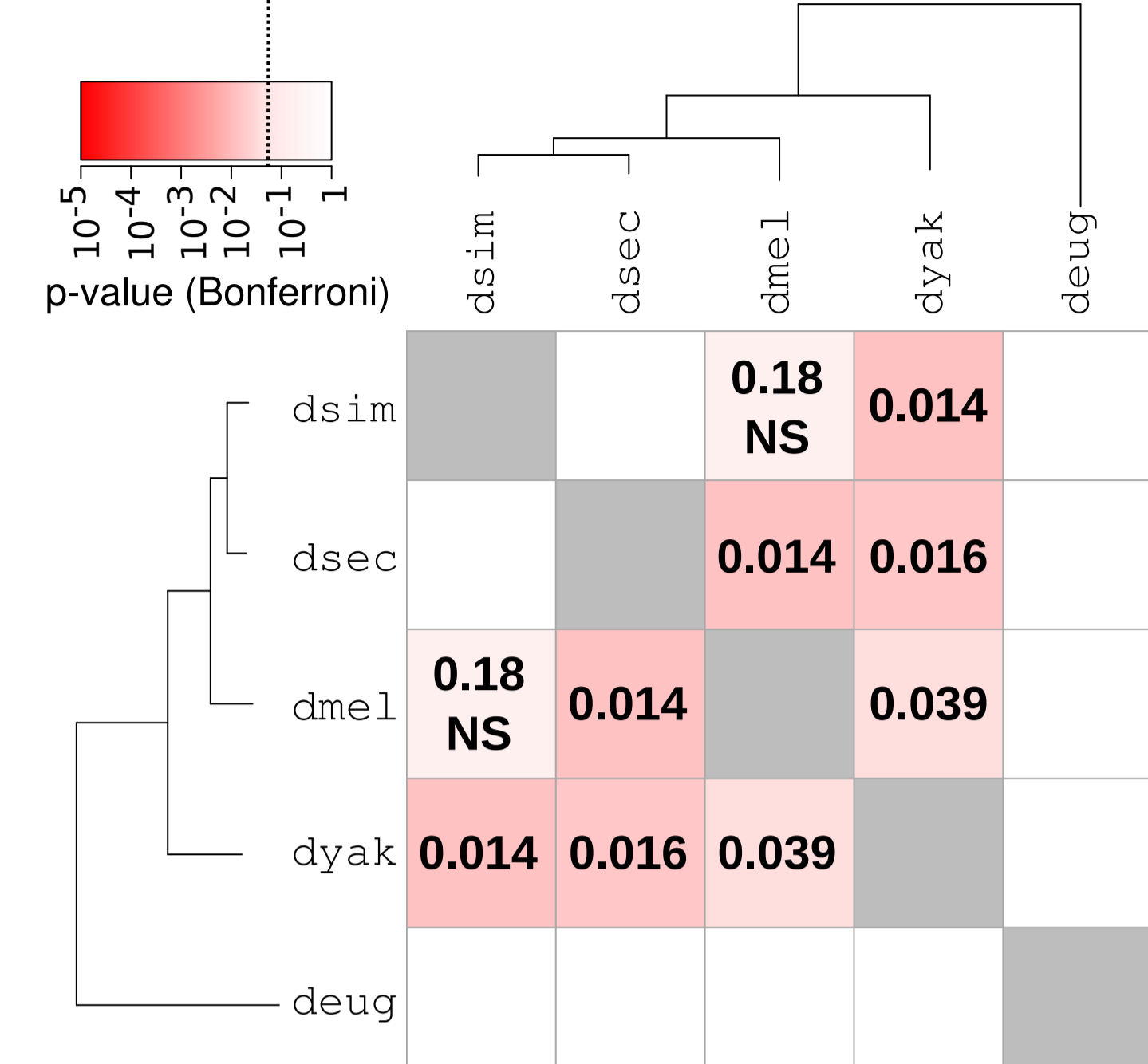
COPIA



Xanthias



new_Xanthias



DM1731

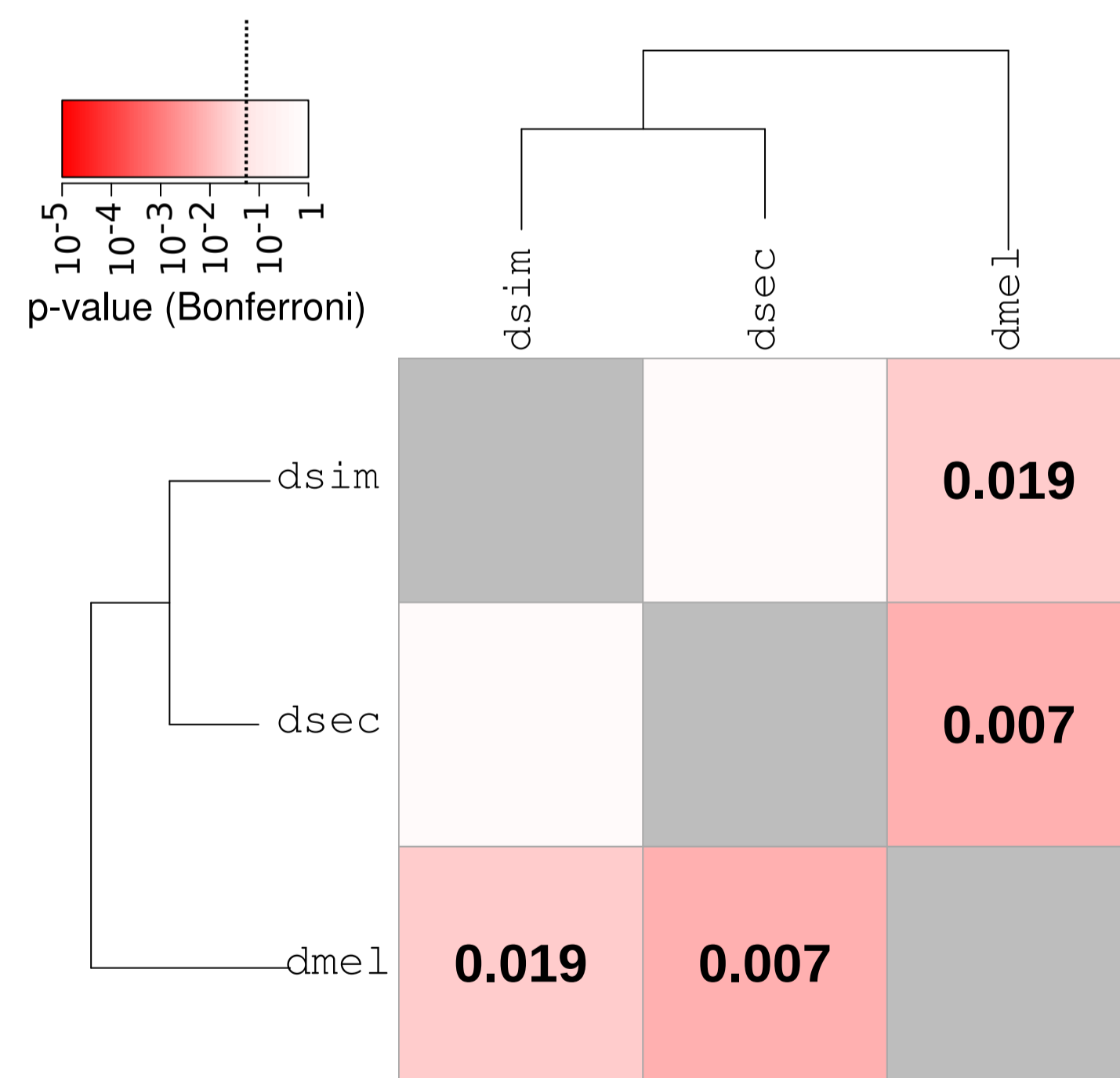
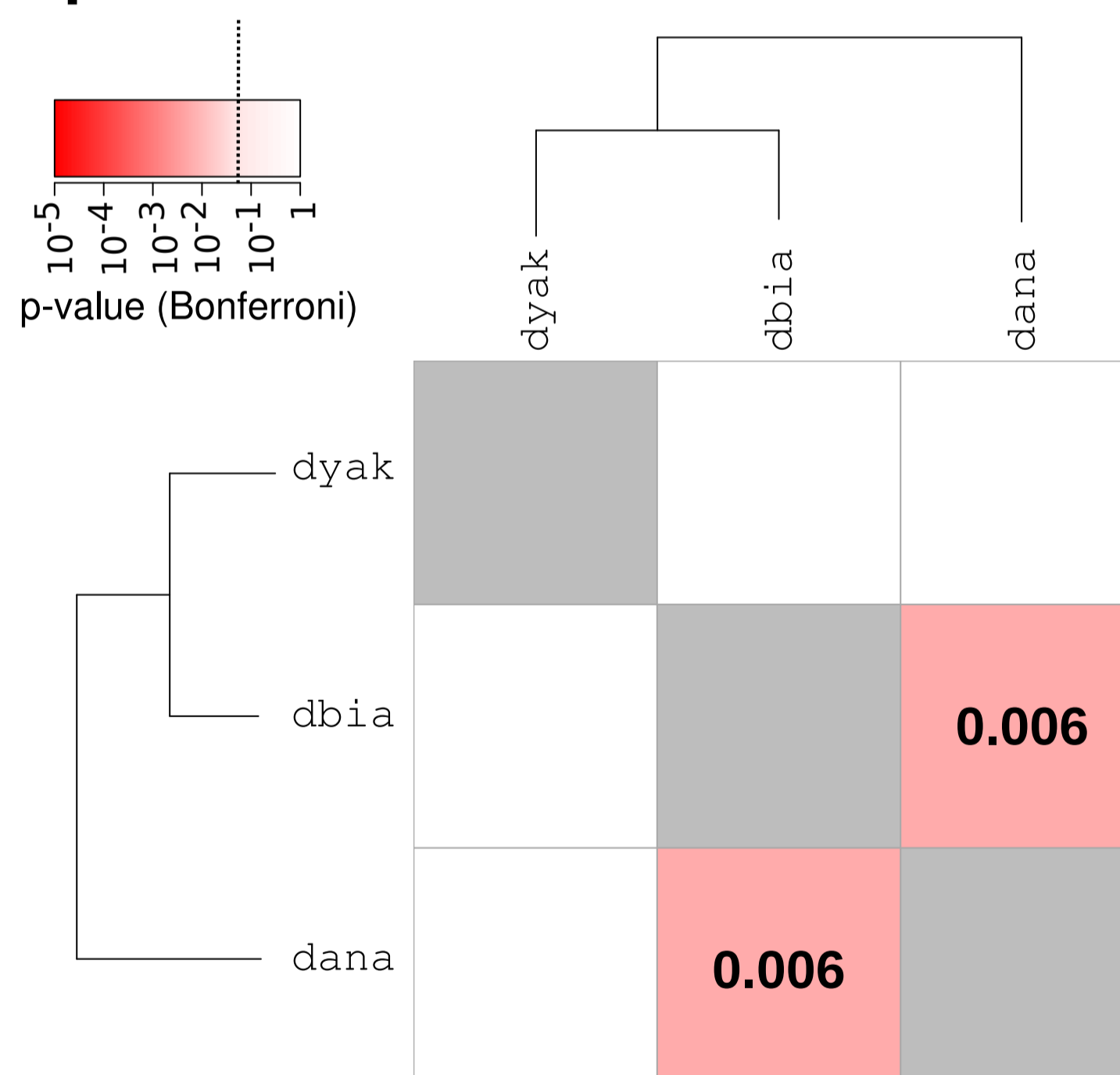
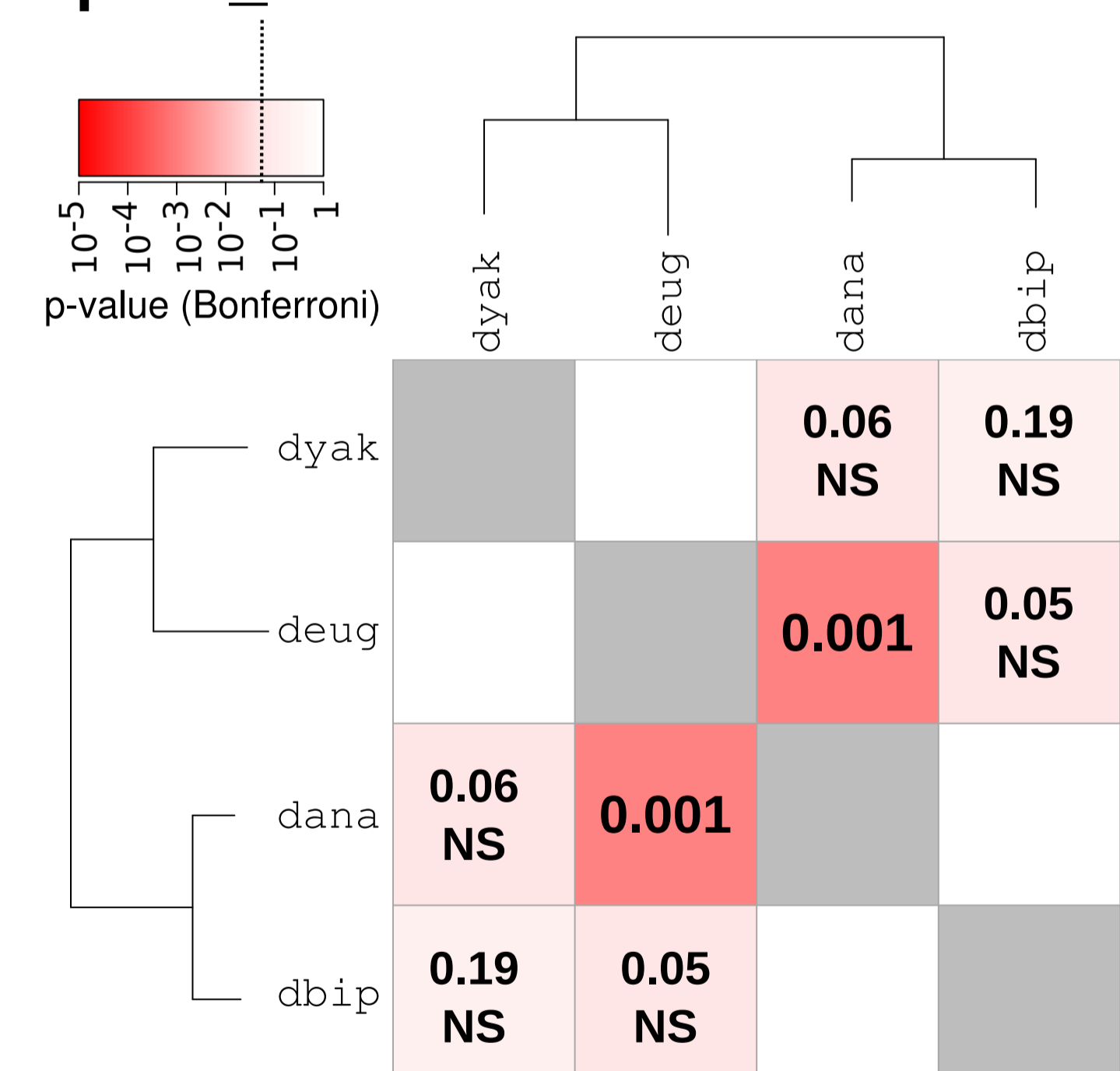
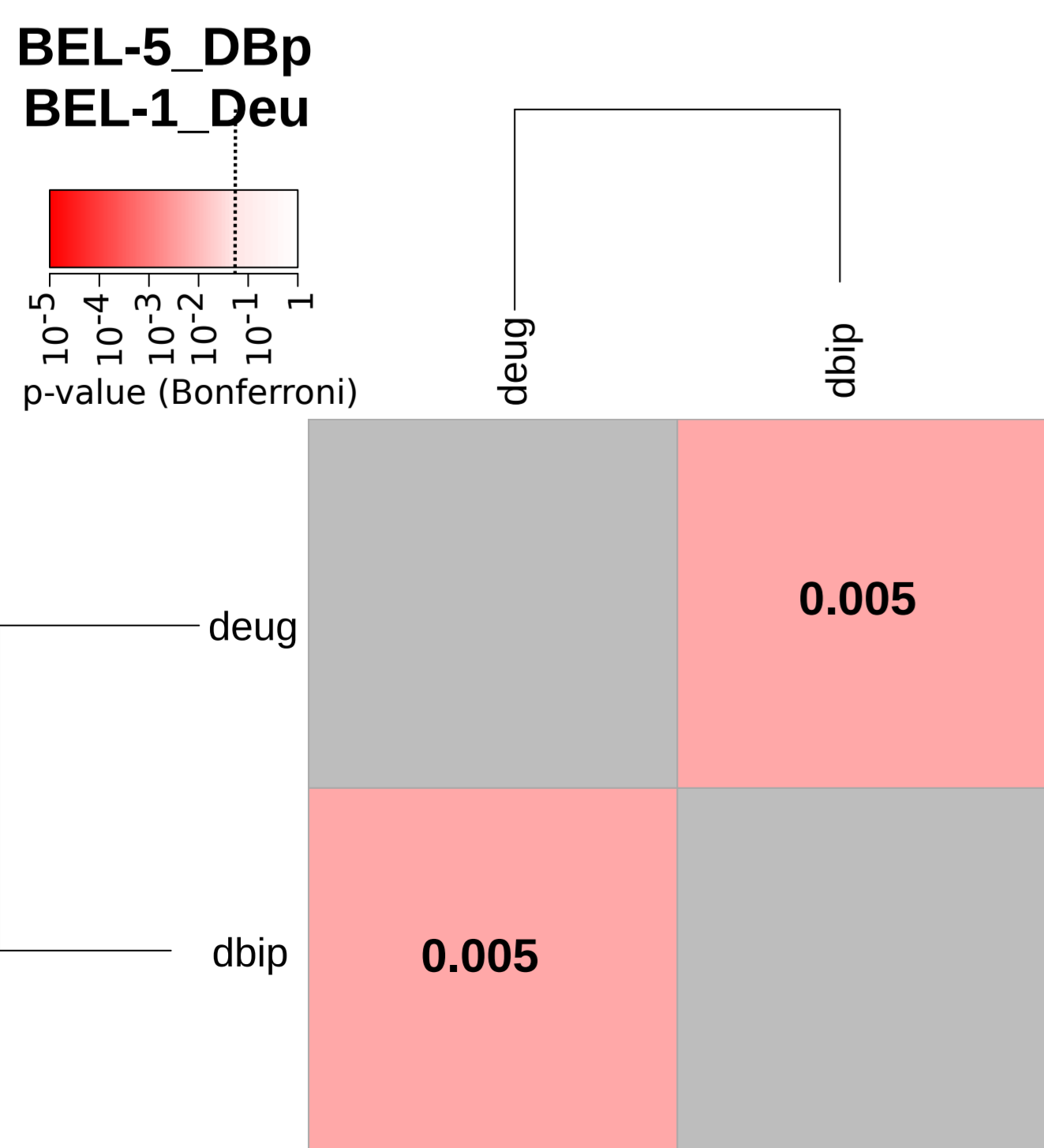
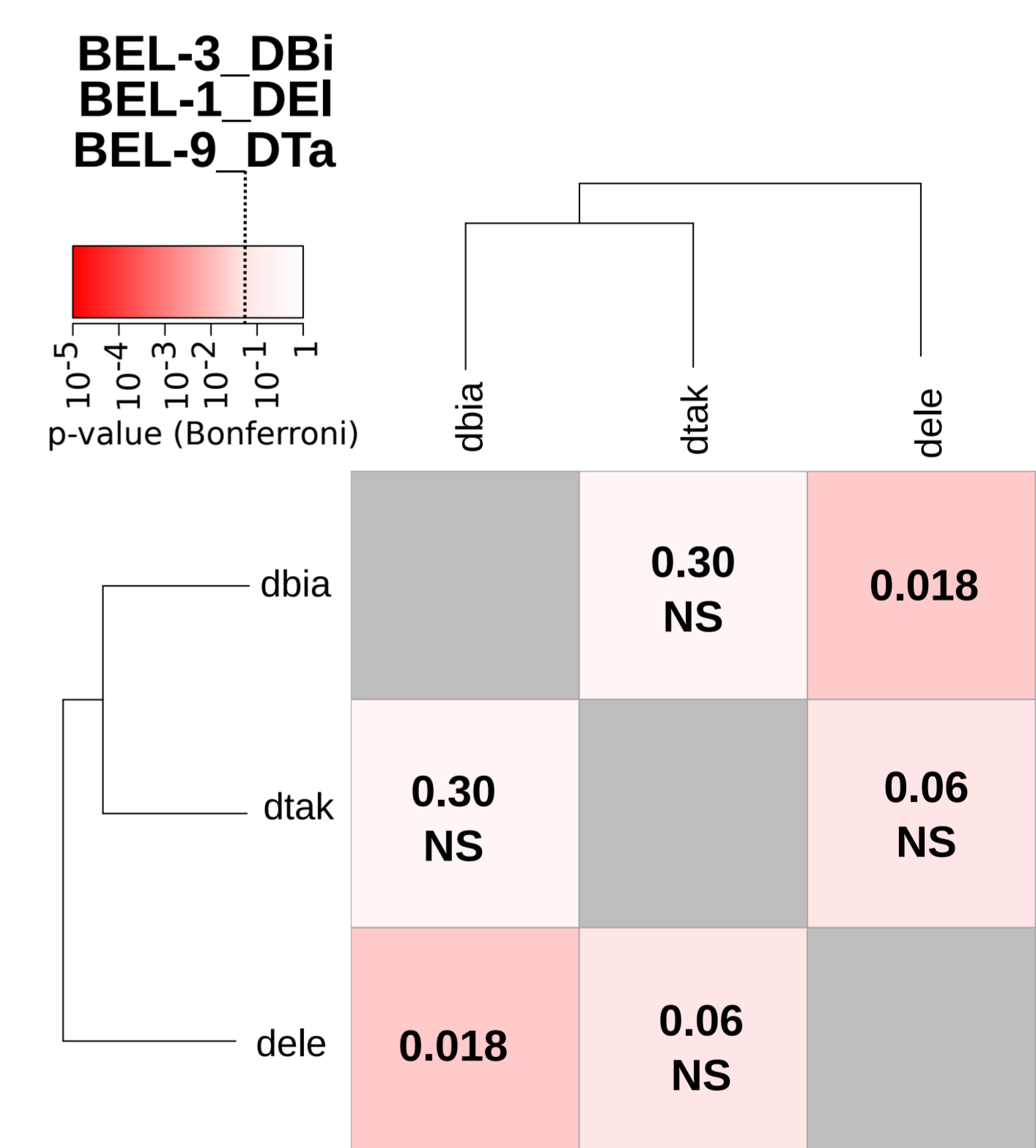
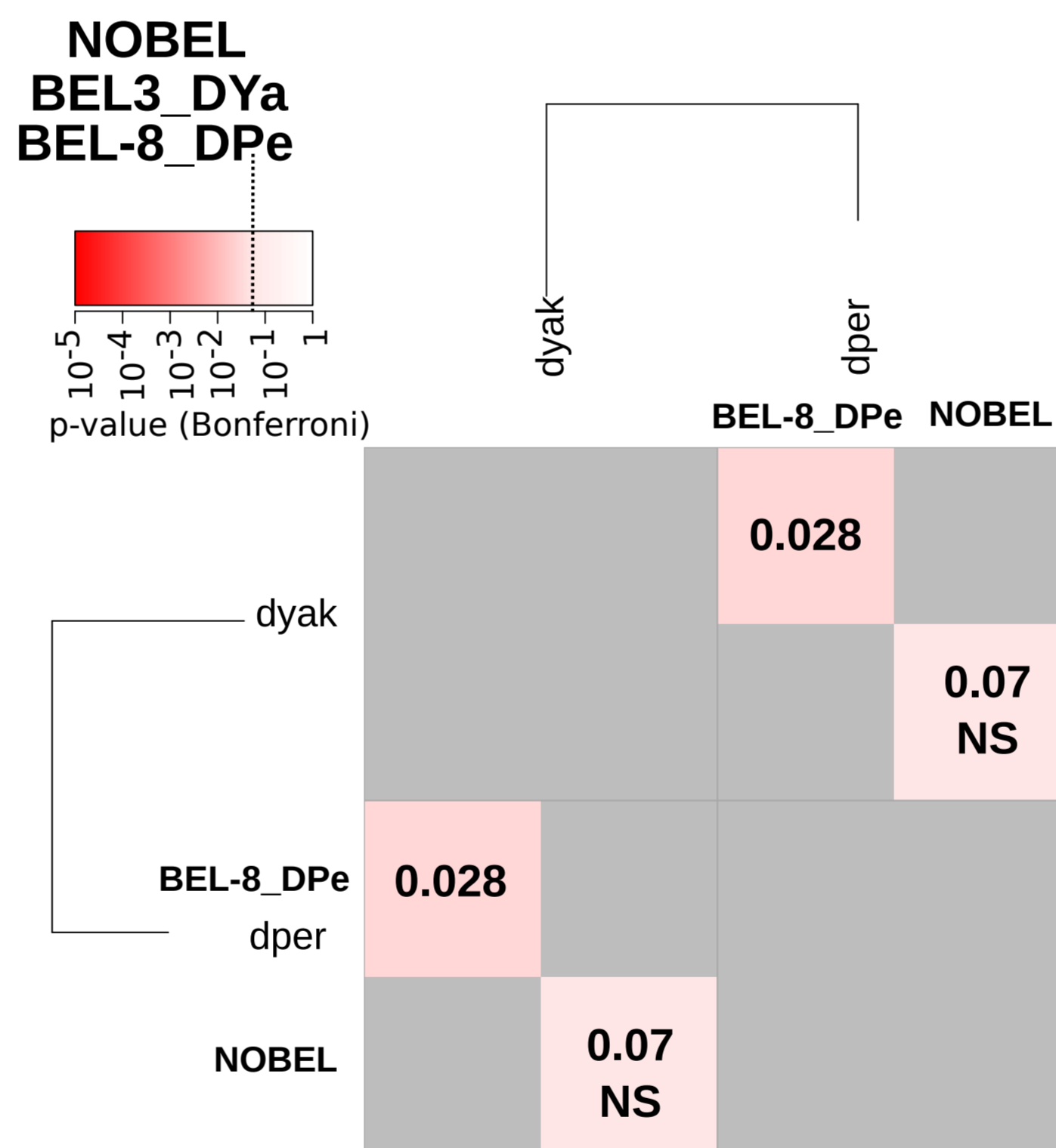
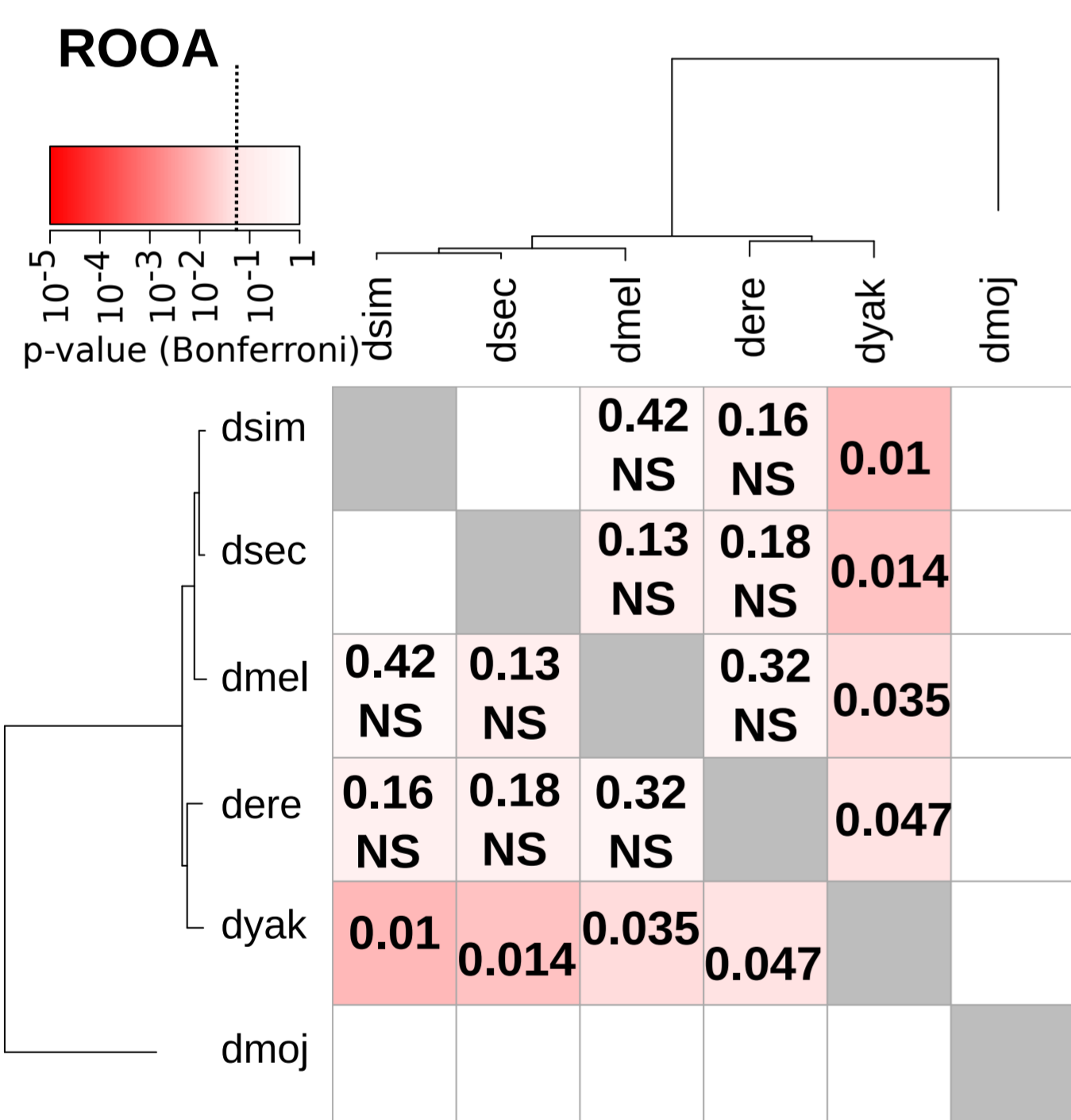
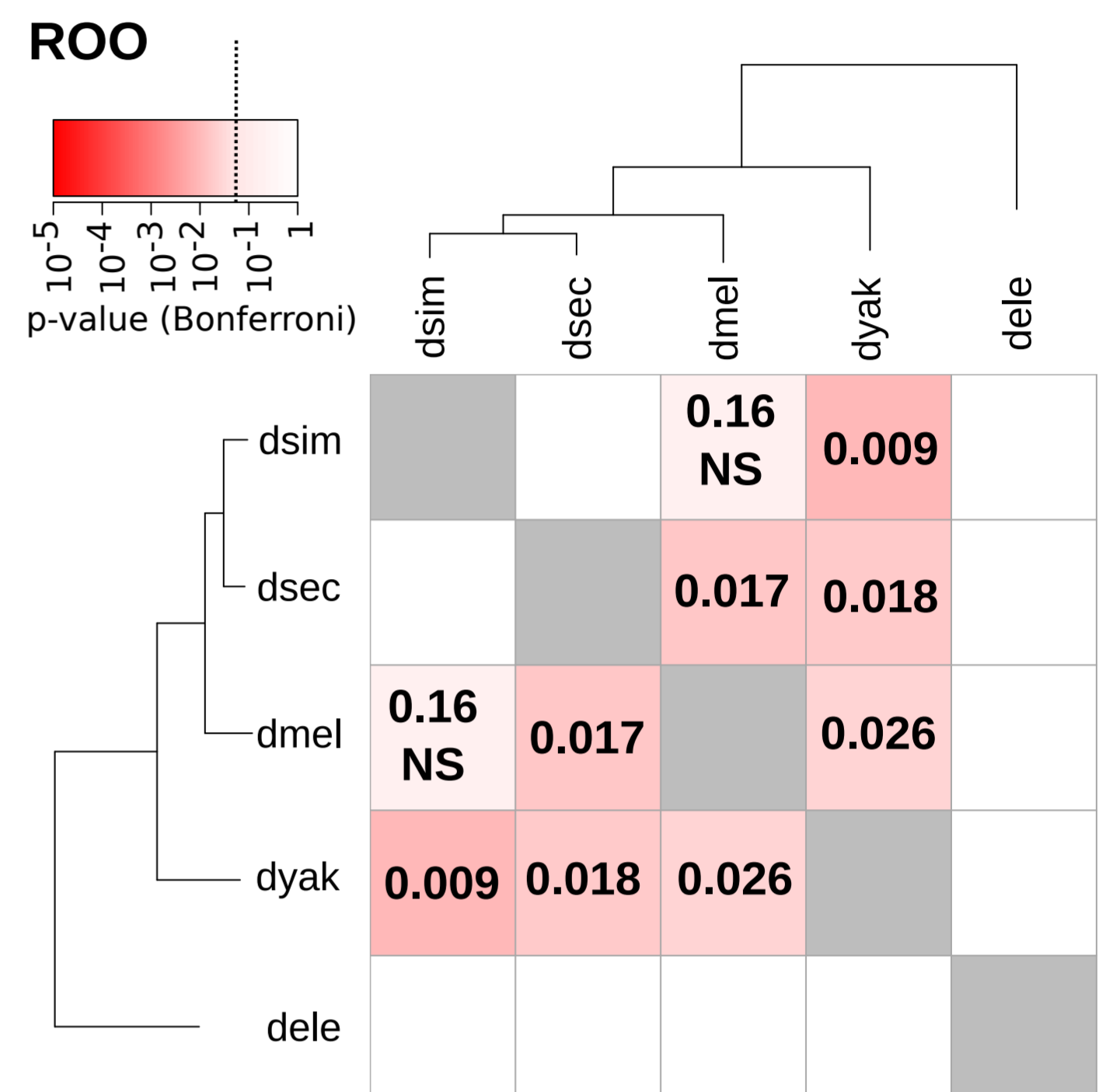
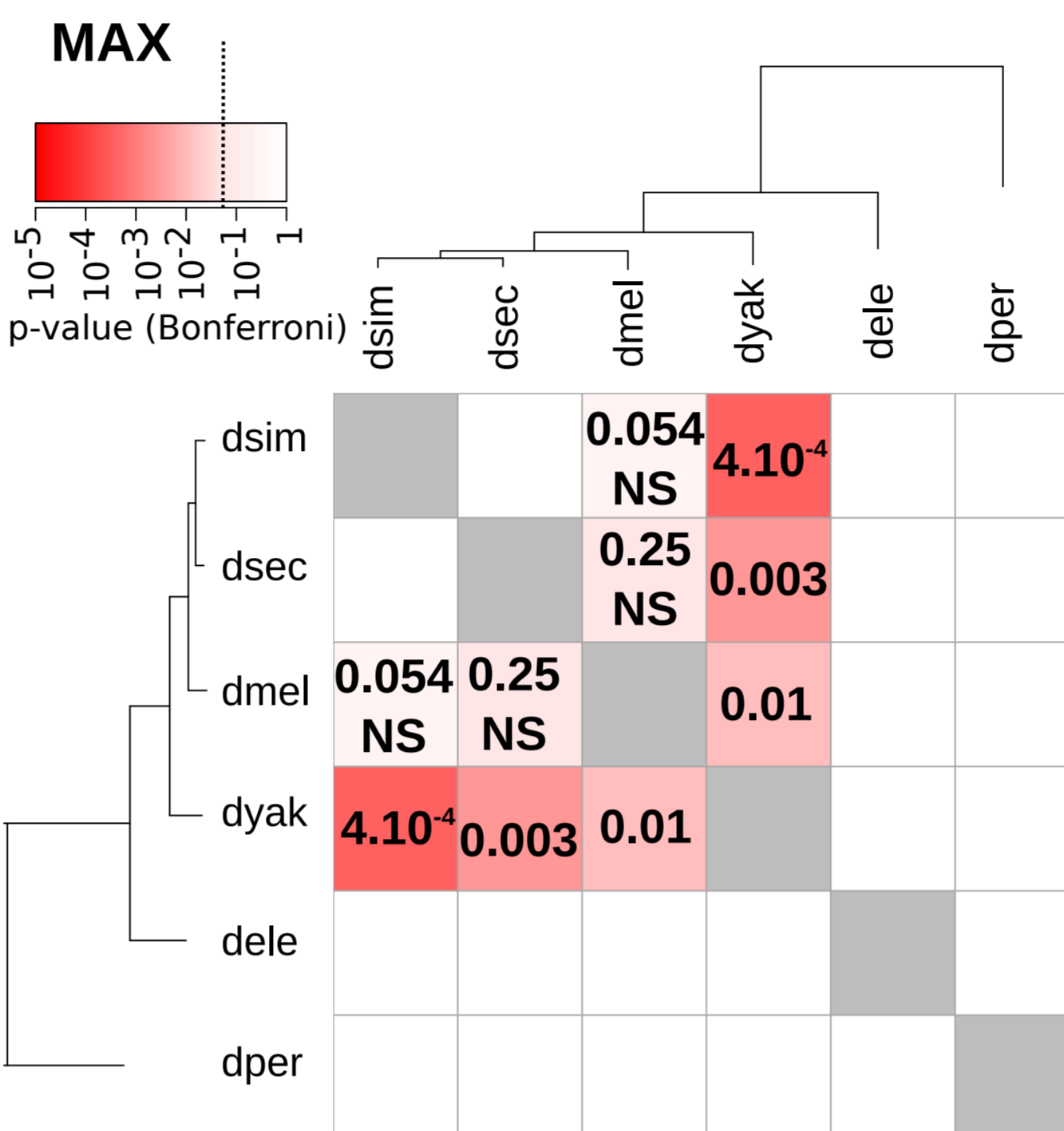
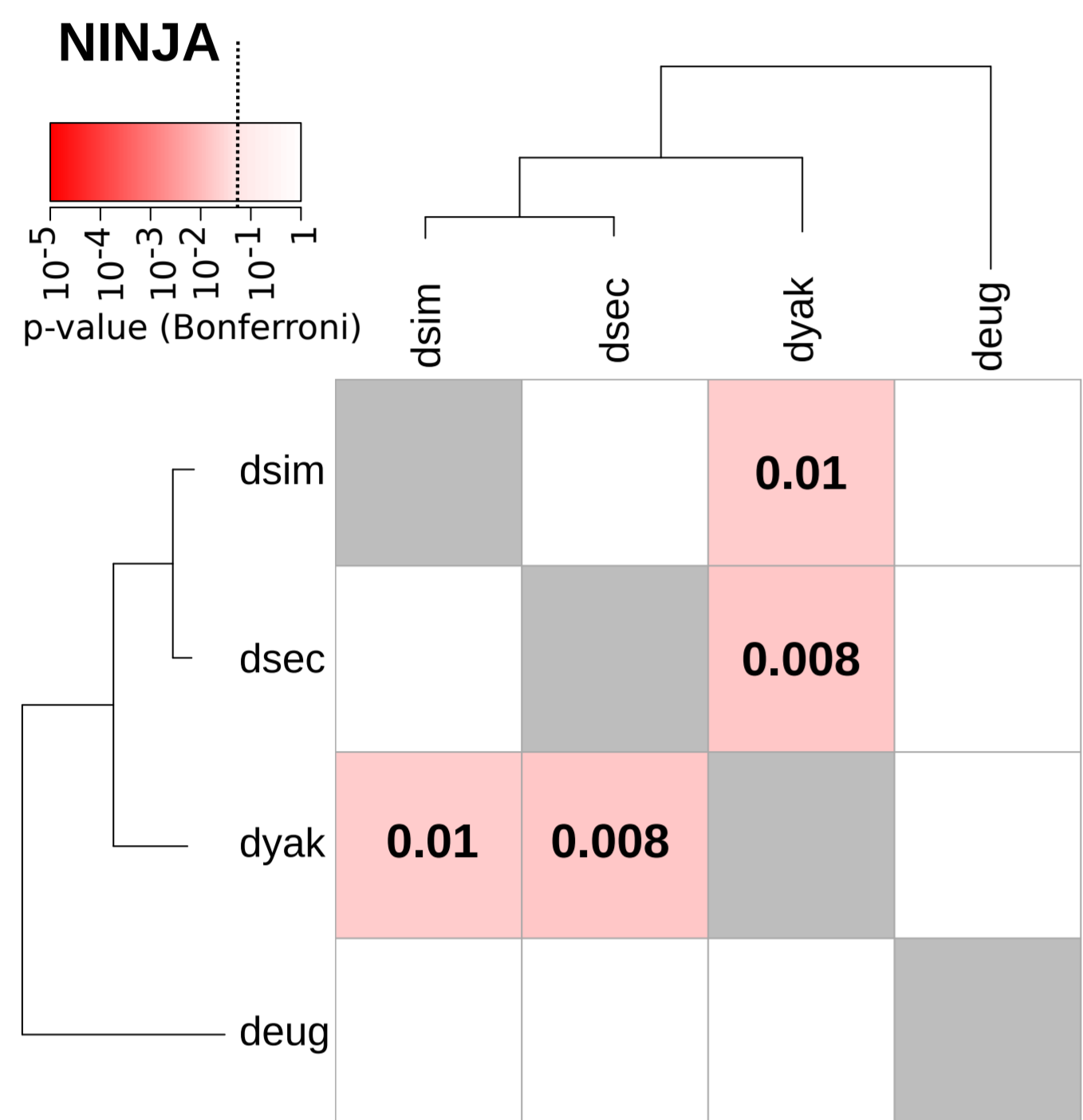
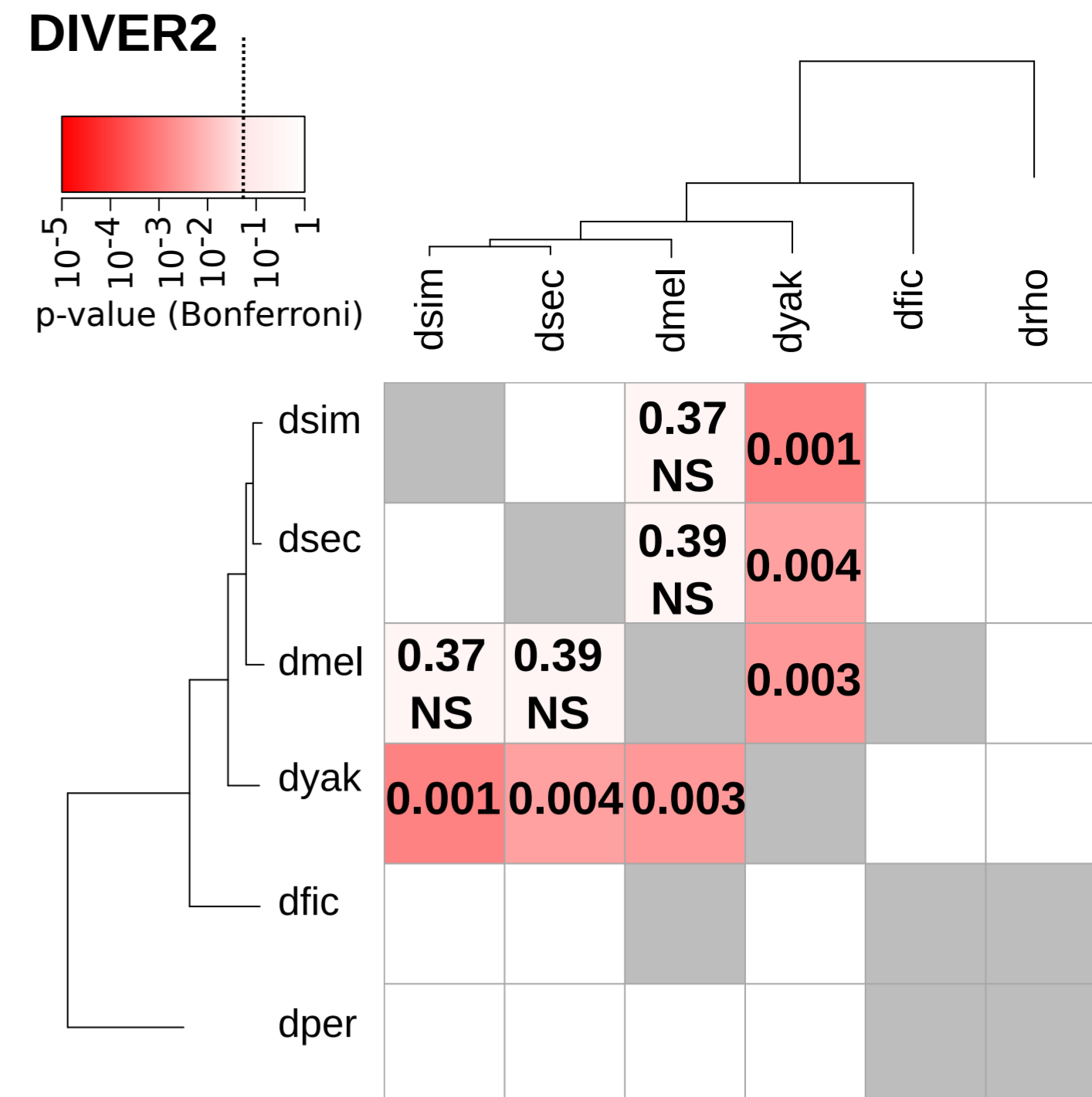
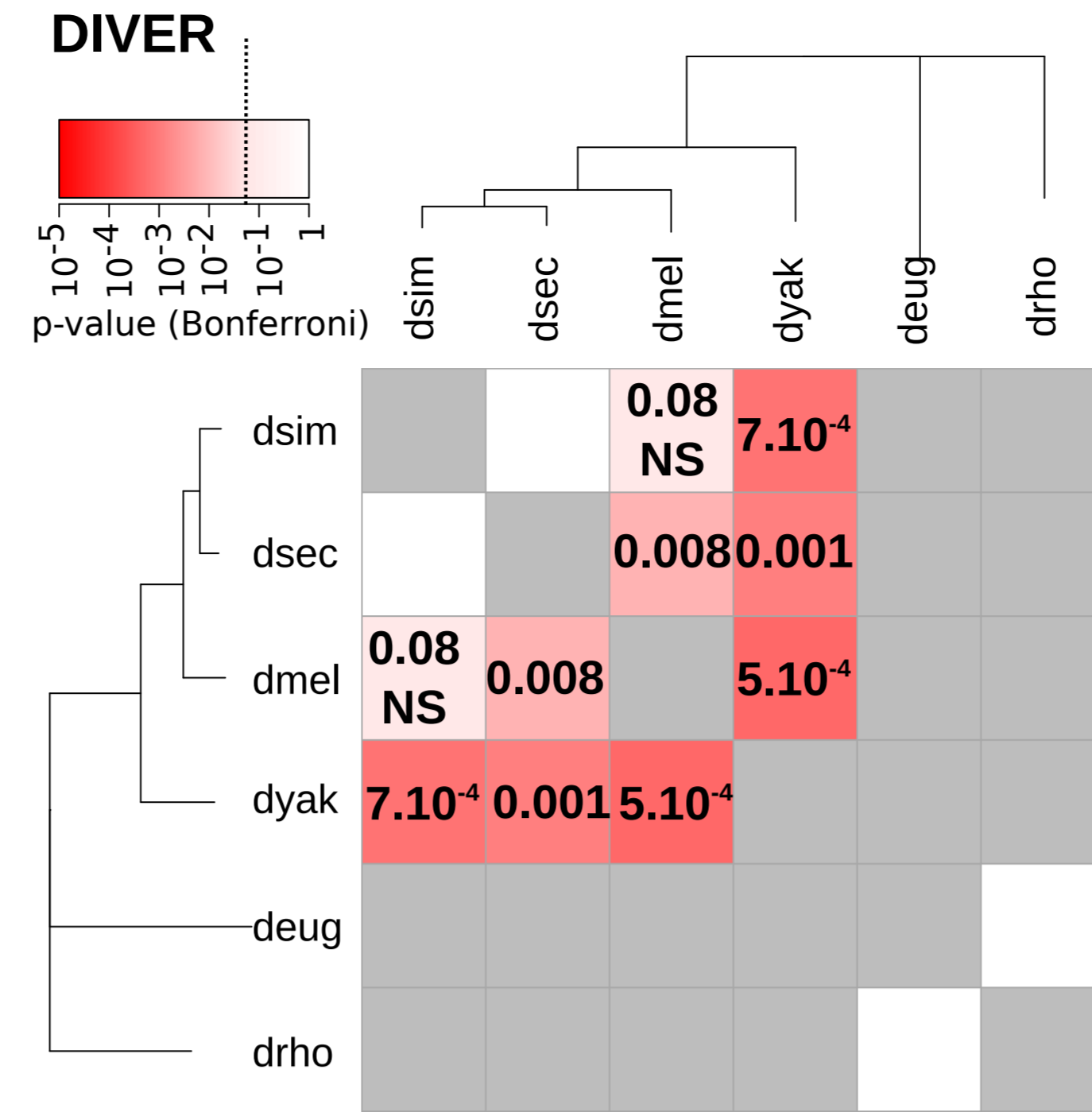
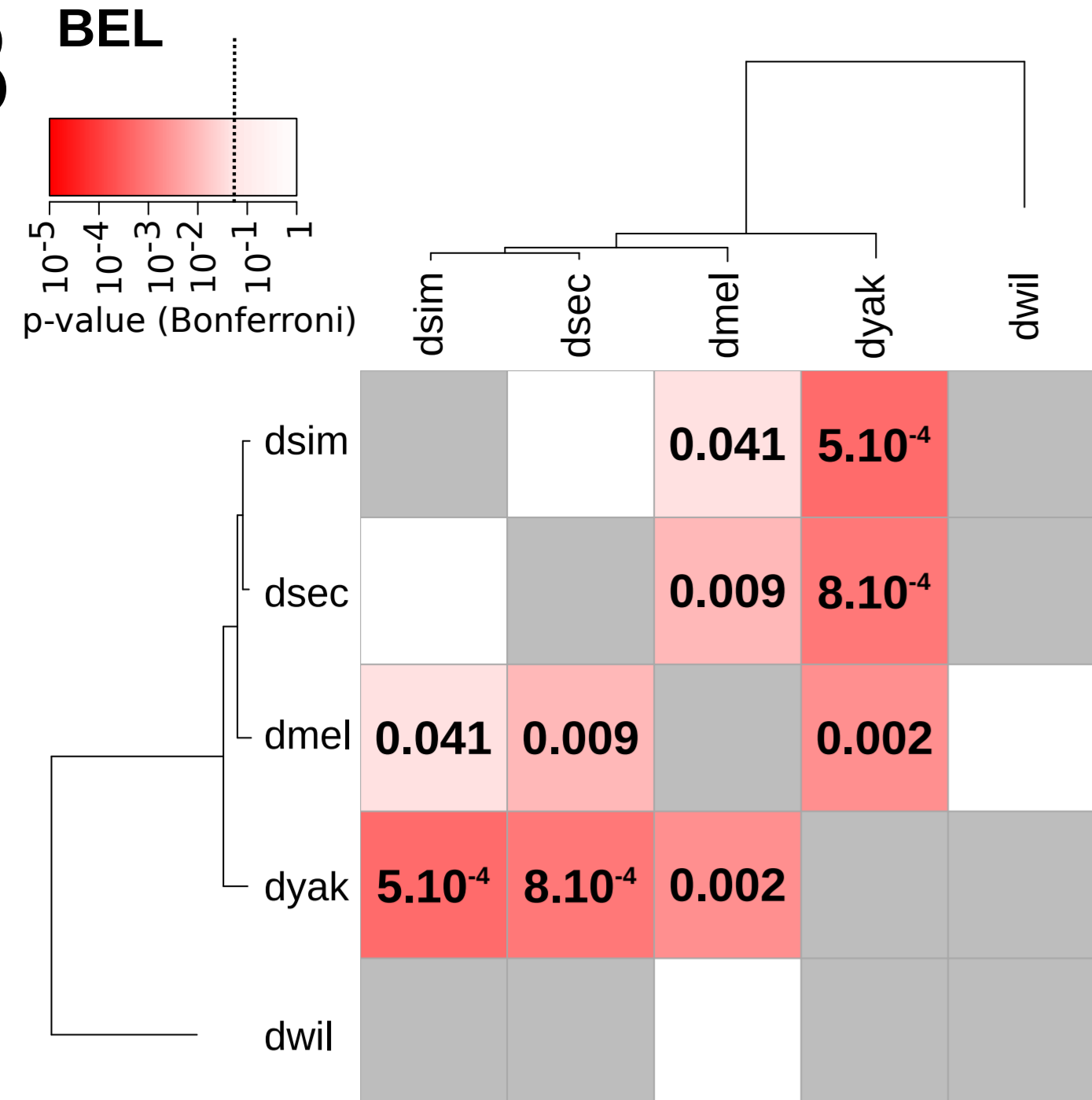
copia-2_DYa
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Figure S1: graphical matrix view generated by the VHICA method for HT cases in the A) *Ty1/Copia* superfamily, B) *BEL/Pao* and C,D,E) *Ty3/Gypsy* superfamilies.

The matrix square represent all pairwise comparisons. Each square is colored according to the P-value calculated for the null hypothesis of vertical transmission. Red color indicates cases of potential horizontal transfers. When the square is divided into rectangles, each one represents one sublineage (meaning sequence variant of a given family present in the given species). The dot line indicates threshold ($P_{value} = 0.05$) to discriminate between vertical transmission and HT. We have indicated in the red squares the computed P-values, indicating those that are non significant (NS). For more details see Wallau et al. 2016

B**Figure S1 continued**

C

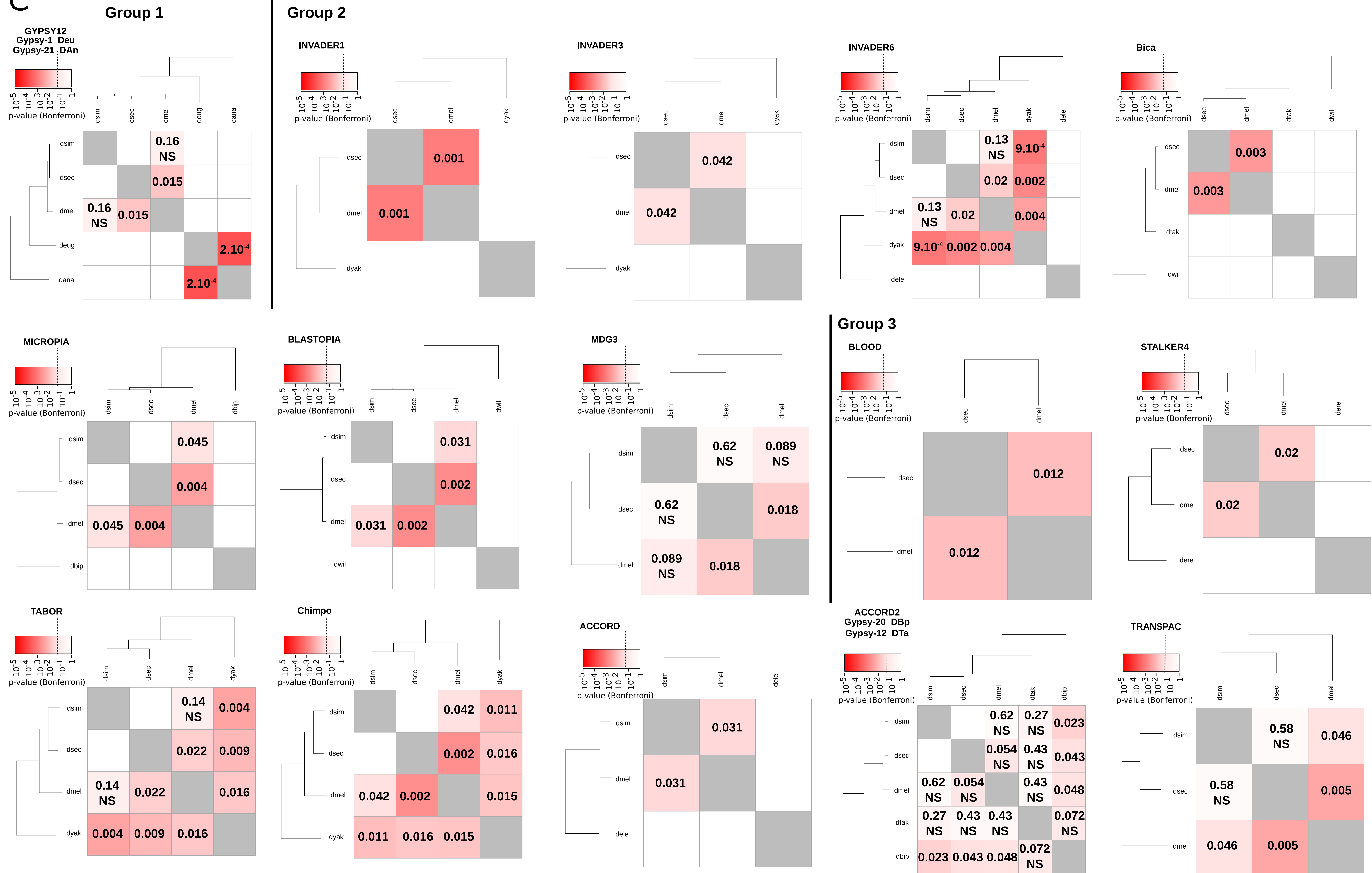
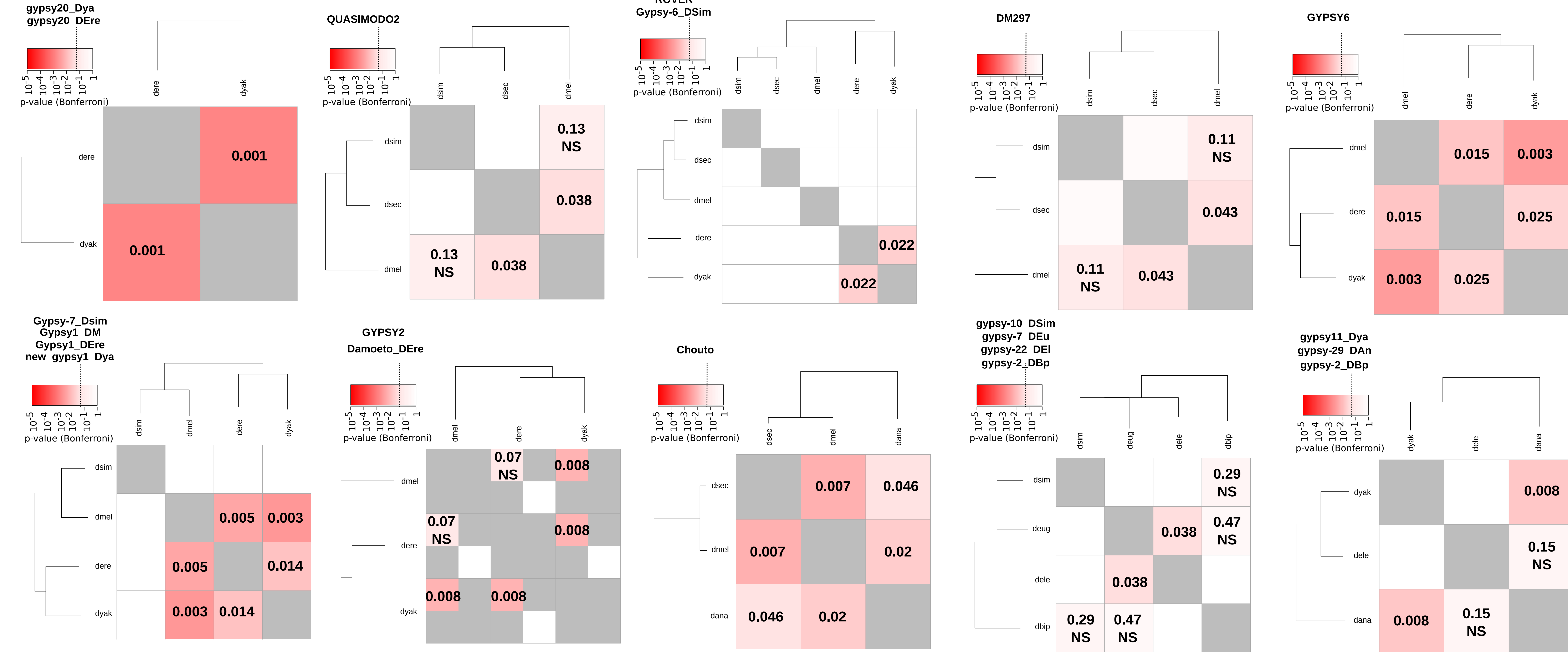


Figure S1 continued

D**Group 3 (continued)****Figure S1 continued**

E

Group 3 (continued)

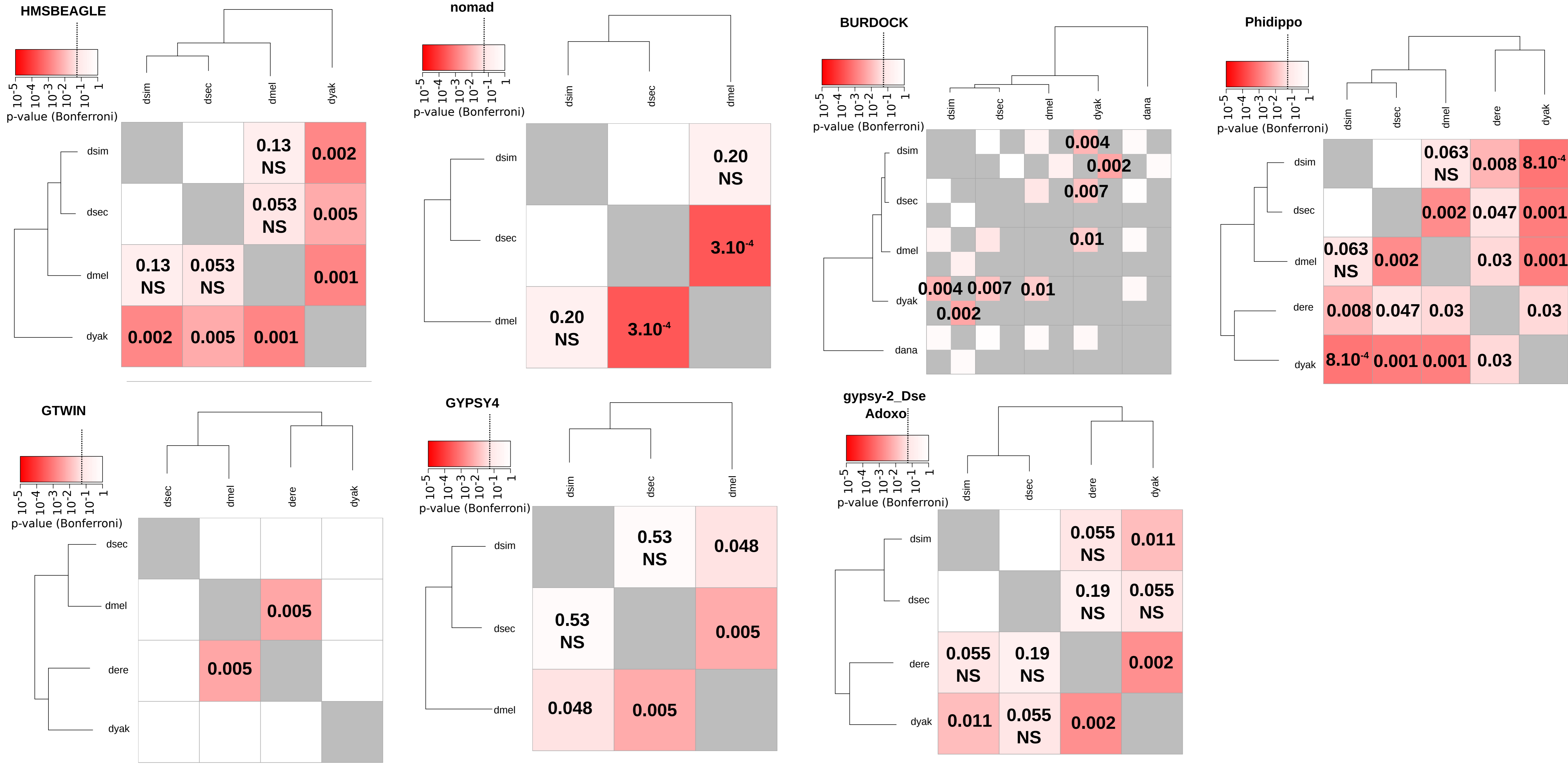


Figure S1 continued