SUPPLEMENTARY DATA

Figs S1–S12: Ancestral character-state reconstruction of DEF- and GLO-like protein interactions. S1–S4, S7 and S8: phylogenetic trees are based on the gene phylogenies. Figs S5, S6, S9–S12: phylogenetic trees were manually drawn based on the species phylogeny. For details of the labelling, see Figure 5.

Fig. S1. Heterodimerization of DEF- with GLO-like proteins.

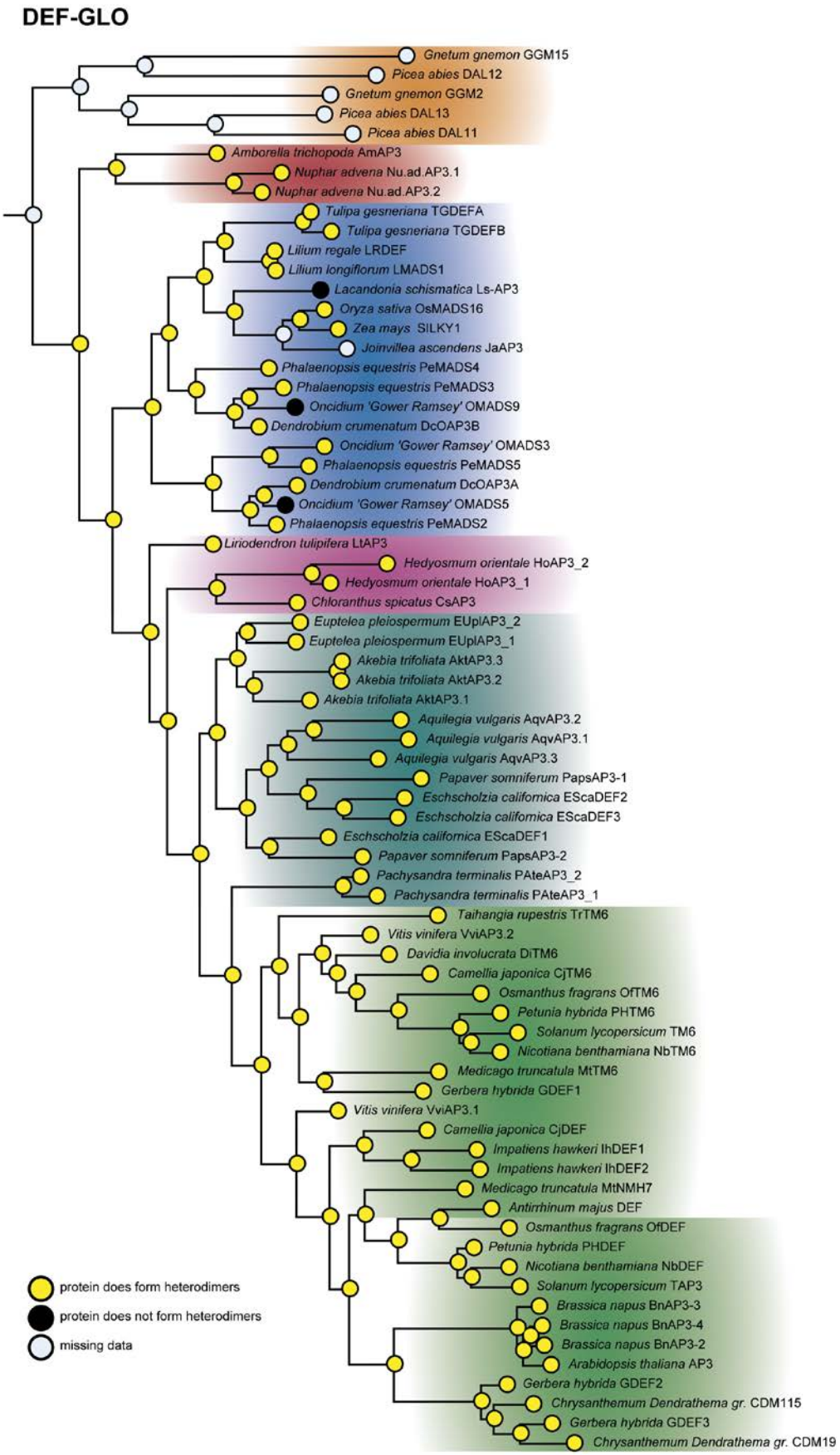


Fig. S2: Homodimerization of DEF-like proteins.

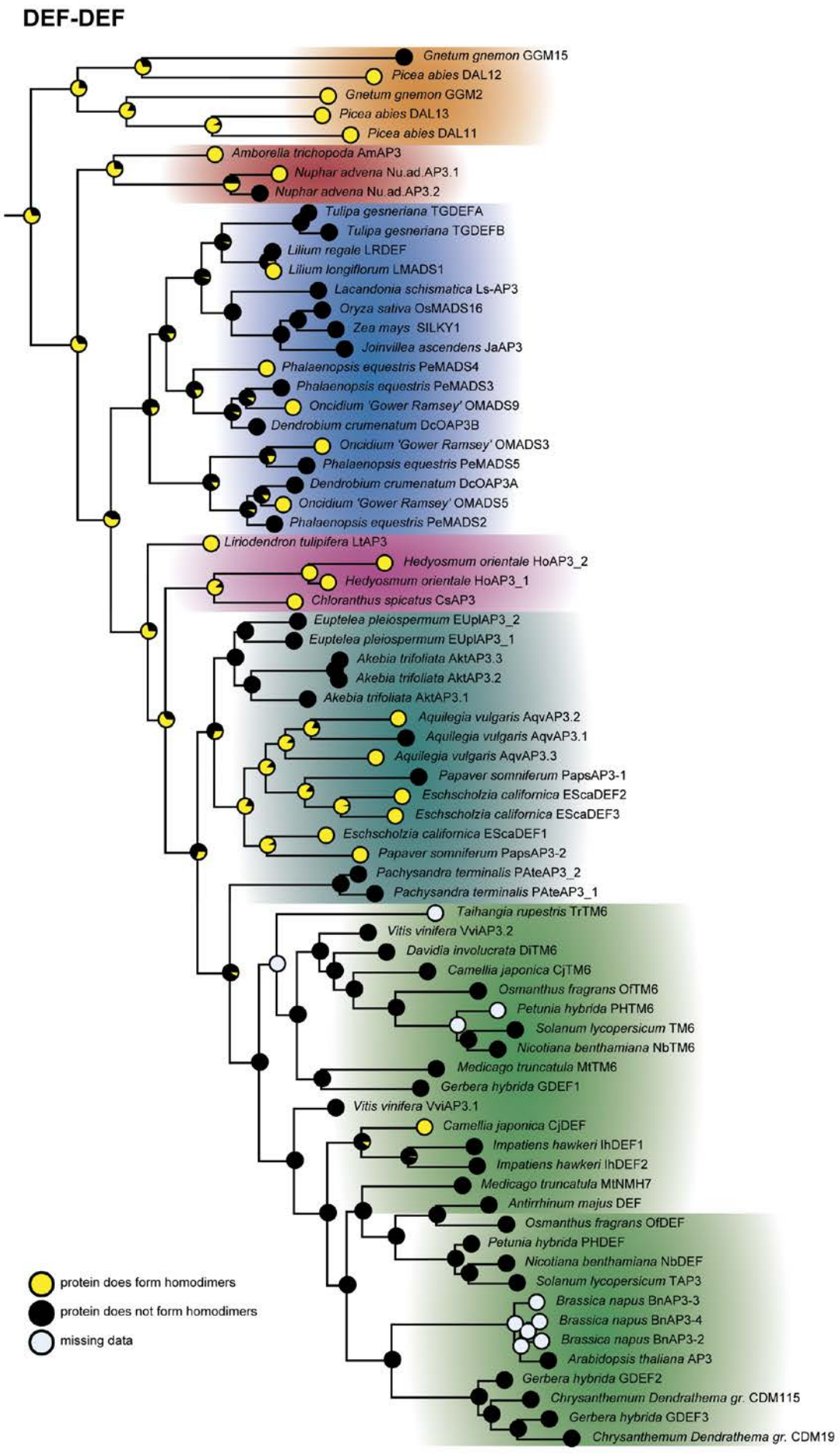


Fig. S3. Heterodimerization of GLO- with DEF-like proteins.

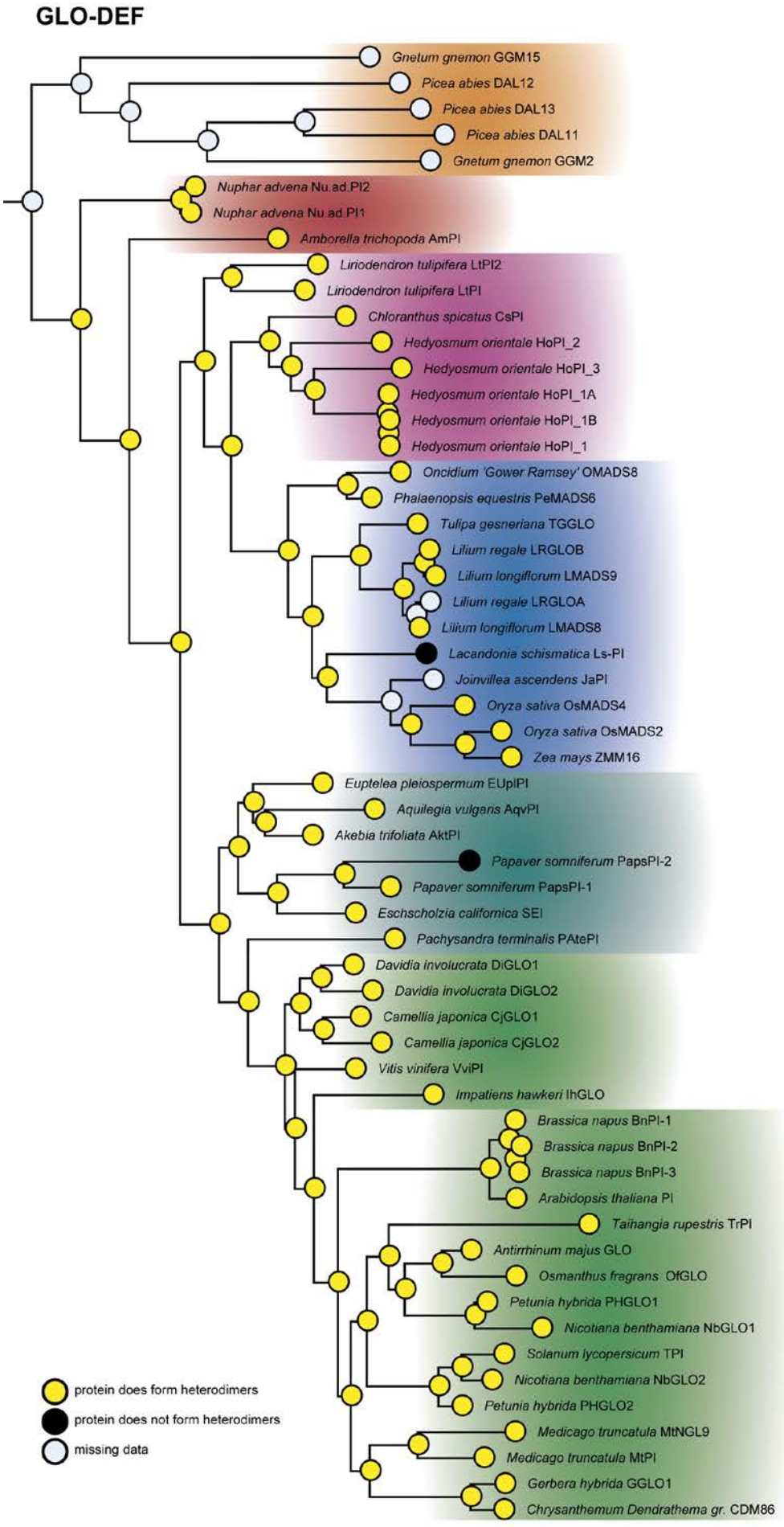


Fig. S4: Homodimerization of GLO-like proteins.

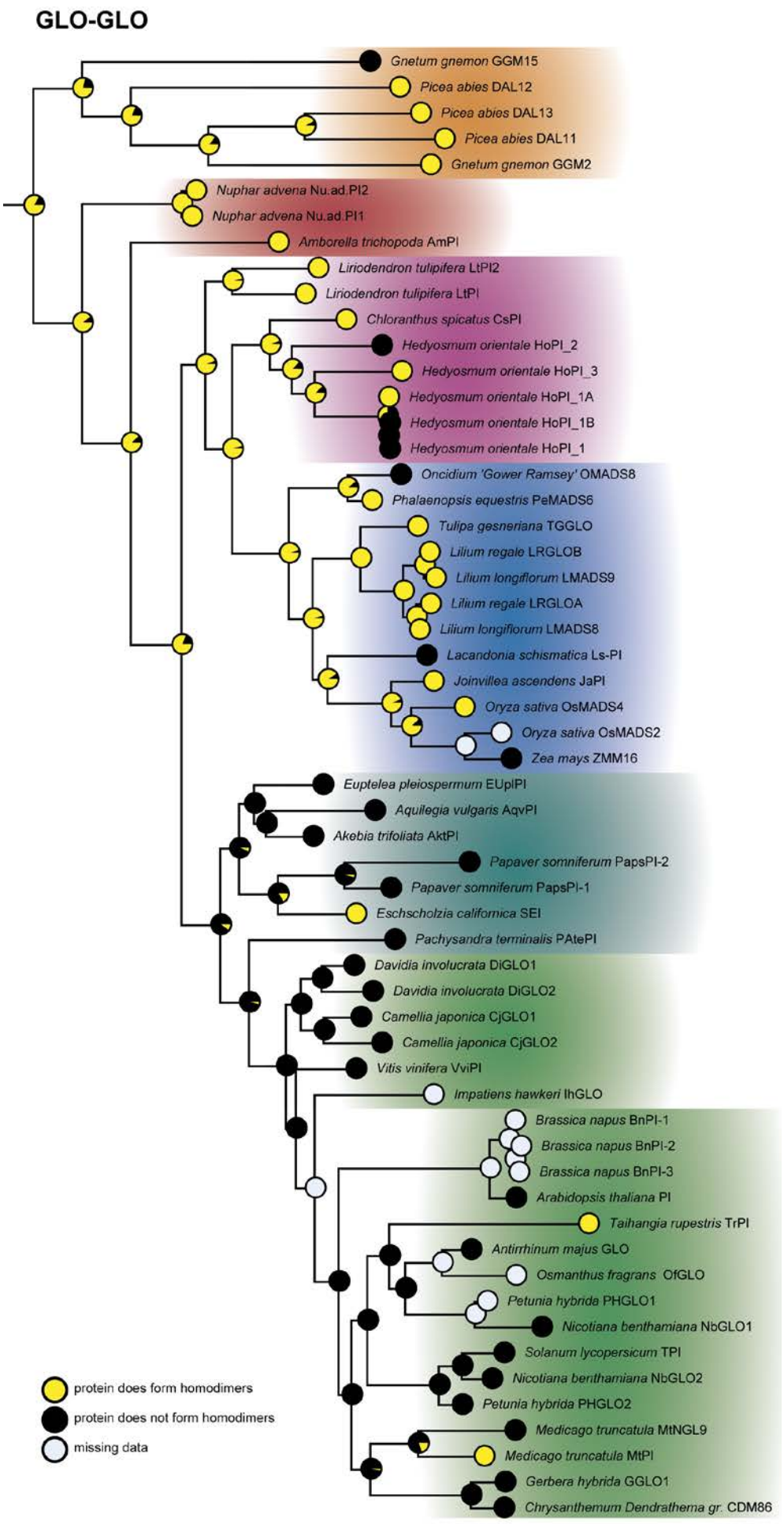


Fig. S5 and S7. Heterodimerization of DEF-like with AGL6/LOFSEP/SEP3-like proteins.
Fig. S5:

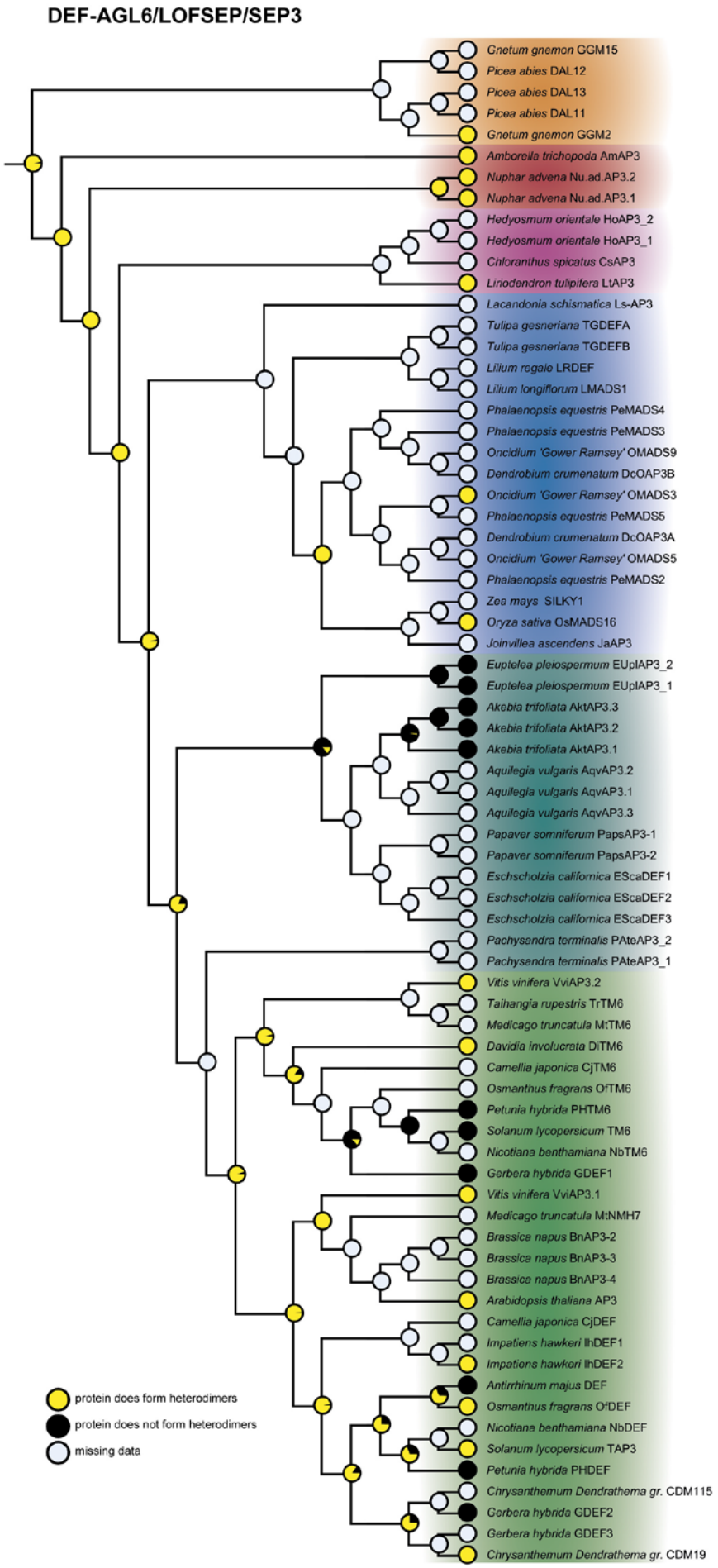


Fig. S5 and S7. Heterodimerization of DEF-like with AGL6/LOFSEP/SEP3-like proteins.
Fig. S7:

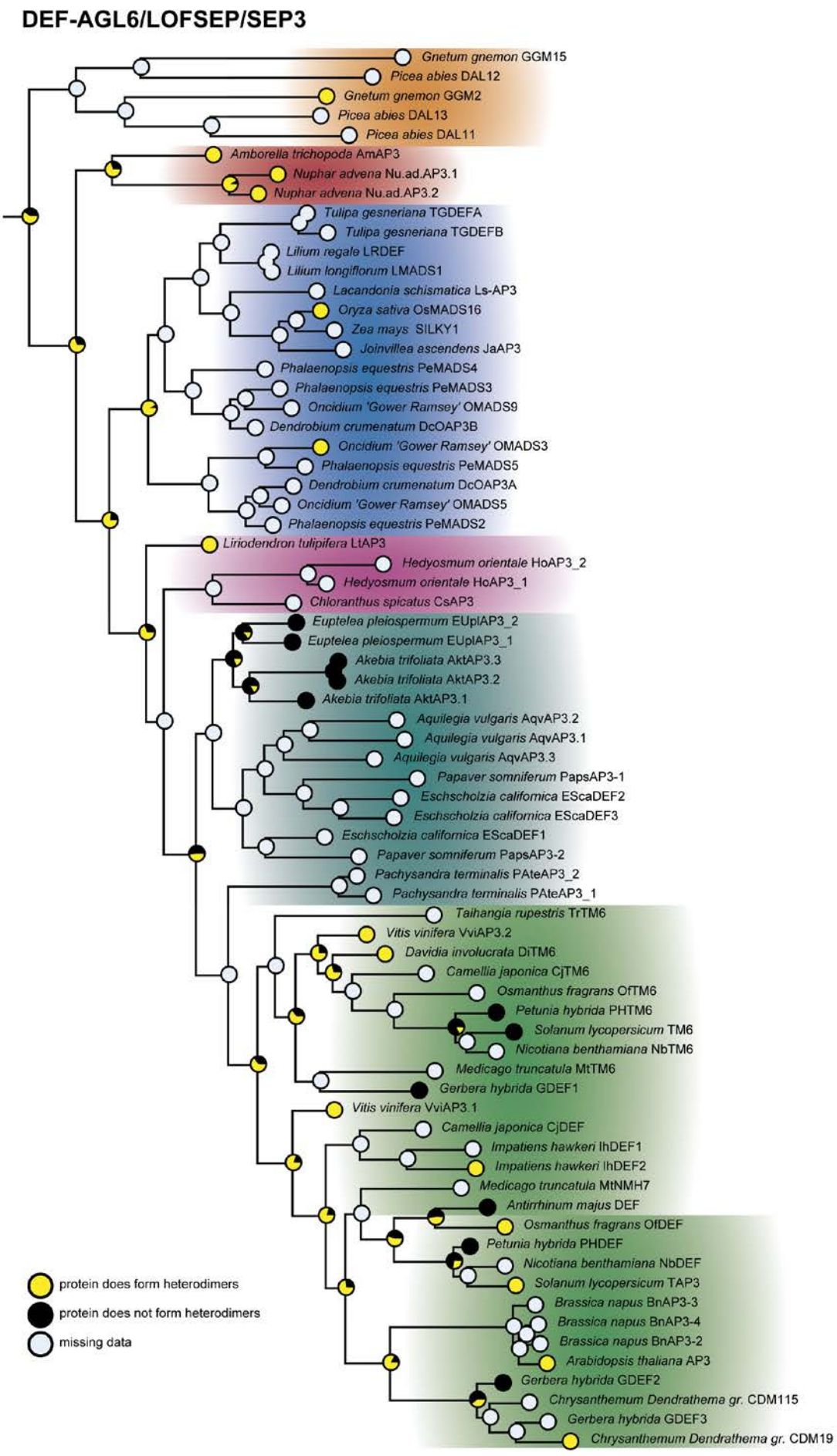


Fig. S6 and S8. Heterodimerization of GLO-like with AGL6/LOFSEP/SEP3-like proteins.
Fig. S6:

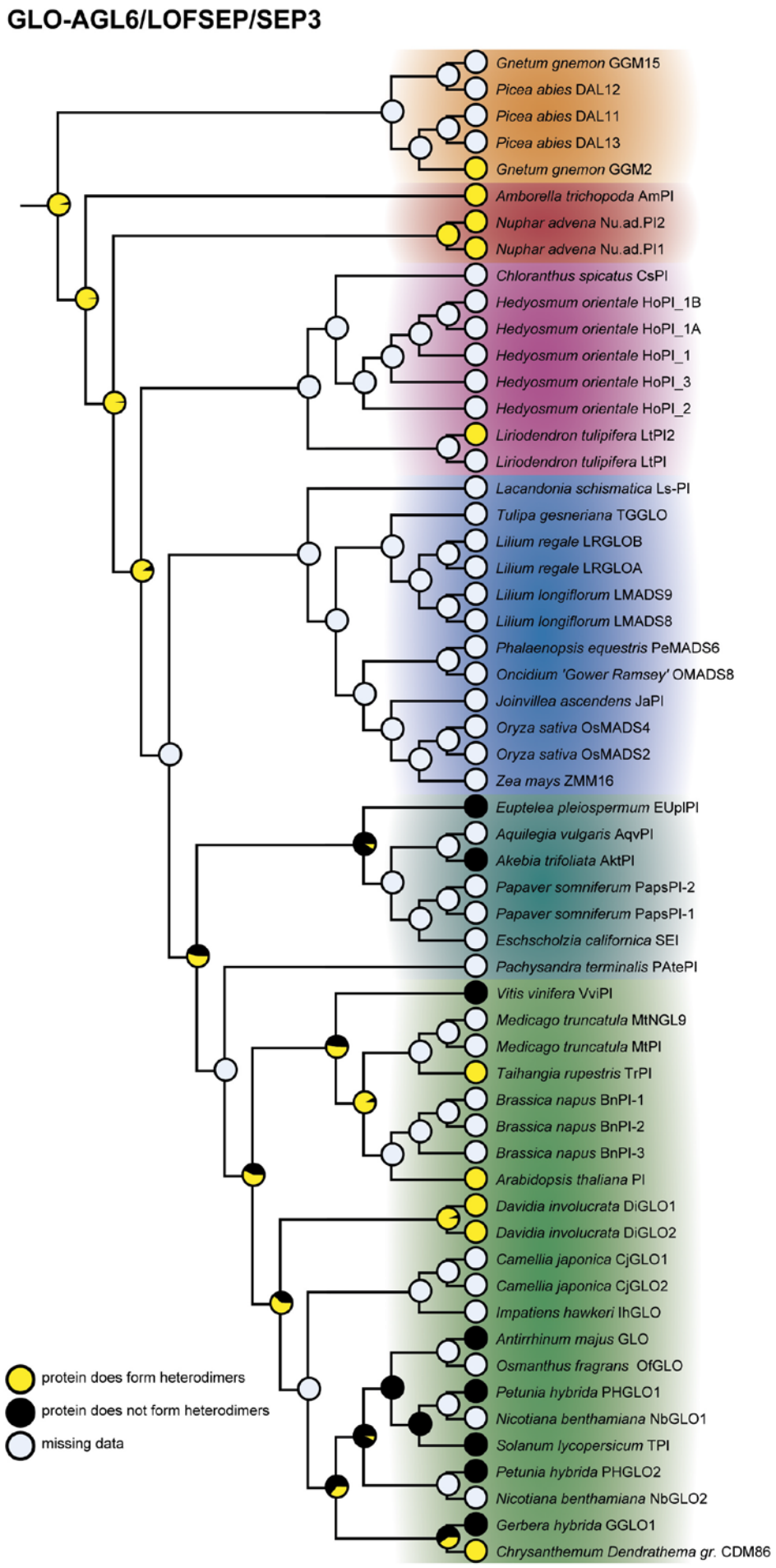


Fig. S6 and S8. Heterodimerization of GLO-like with AGL6/LOFSEP/SEP3-like proteins.
Fig. S8:

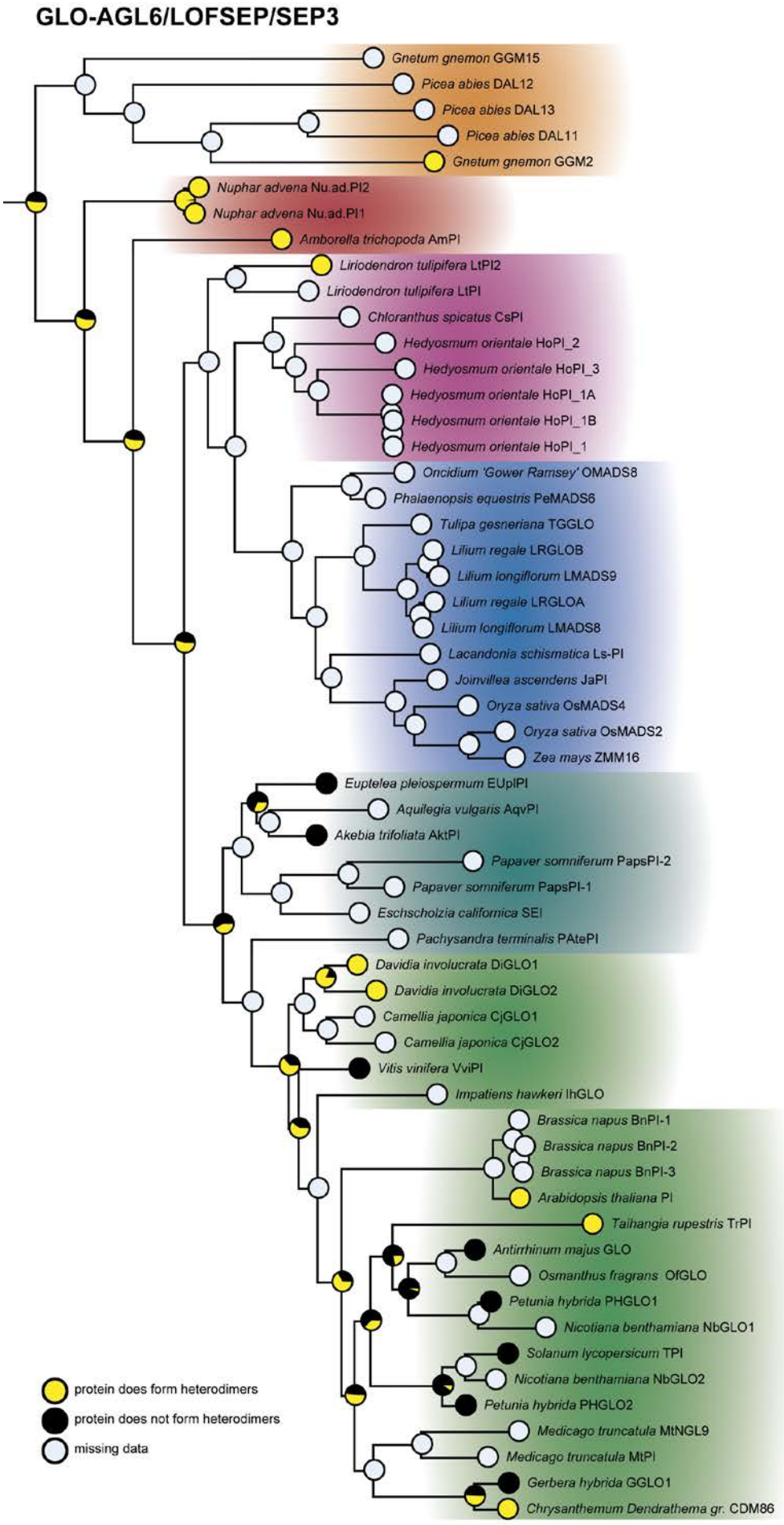


Fig. S9. Homodimerization of DEF-like proteins, comparing yeast two-hybrid (Y2H) and EMSA data.

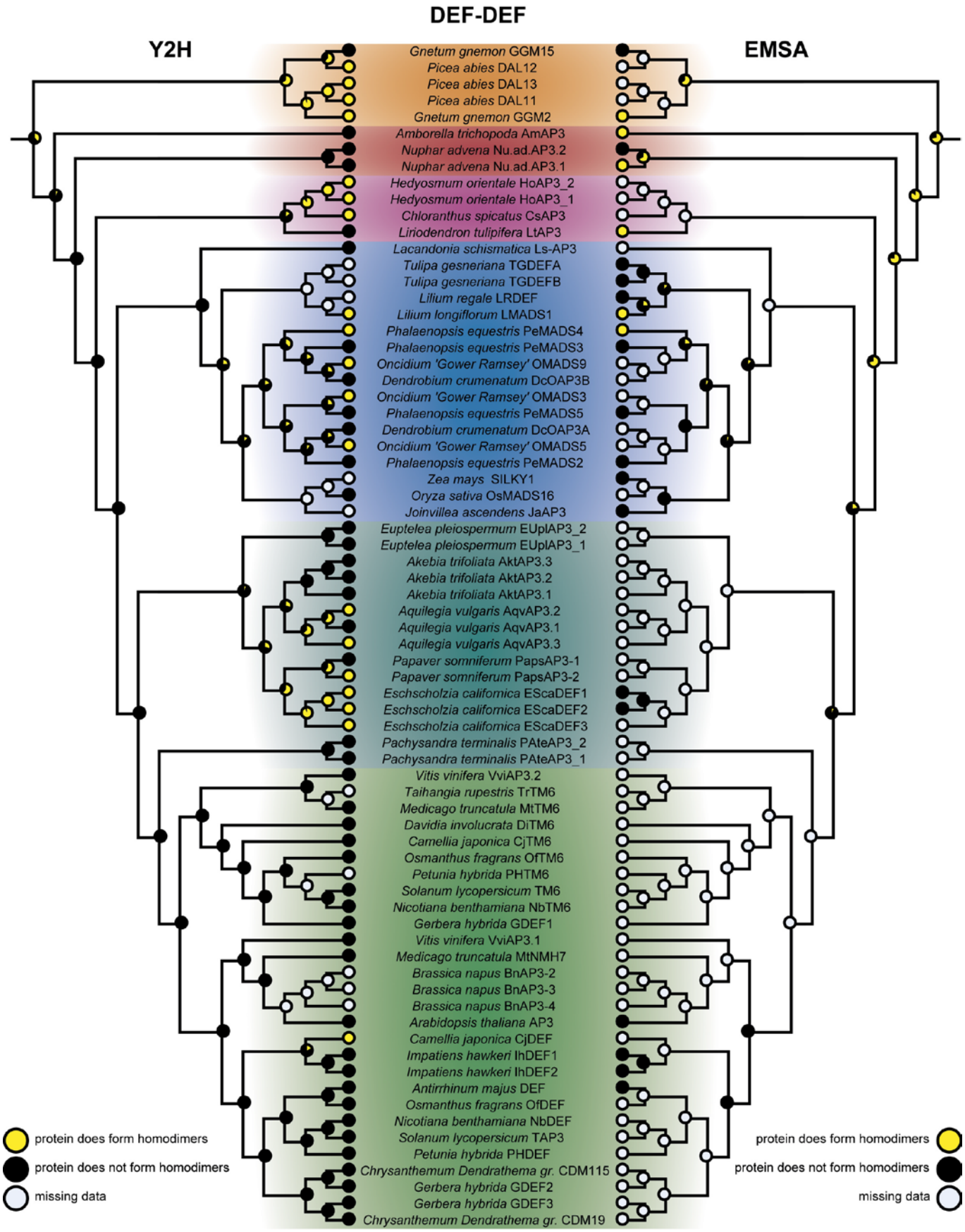


Fig. S10. Heterodimerization of DEF- with GLO-like proteins, comparing Y2H with EMSA data.

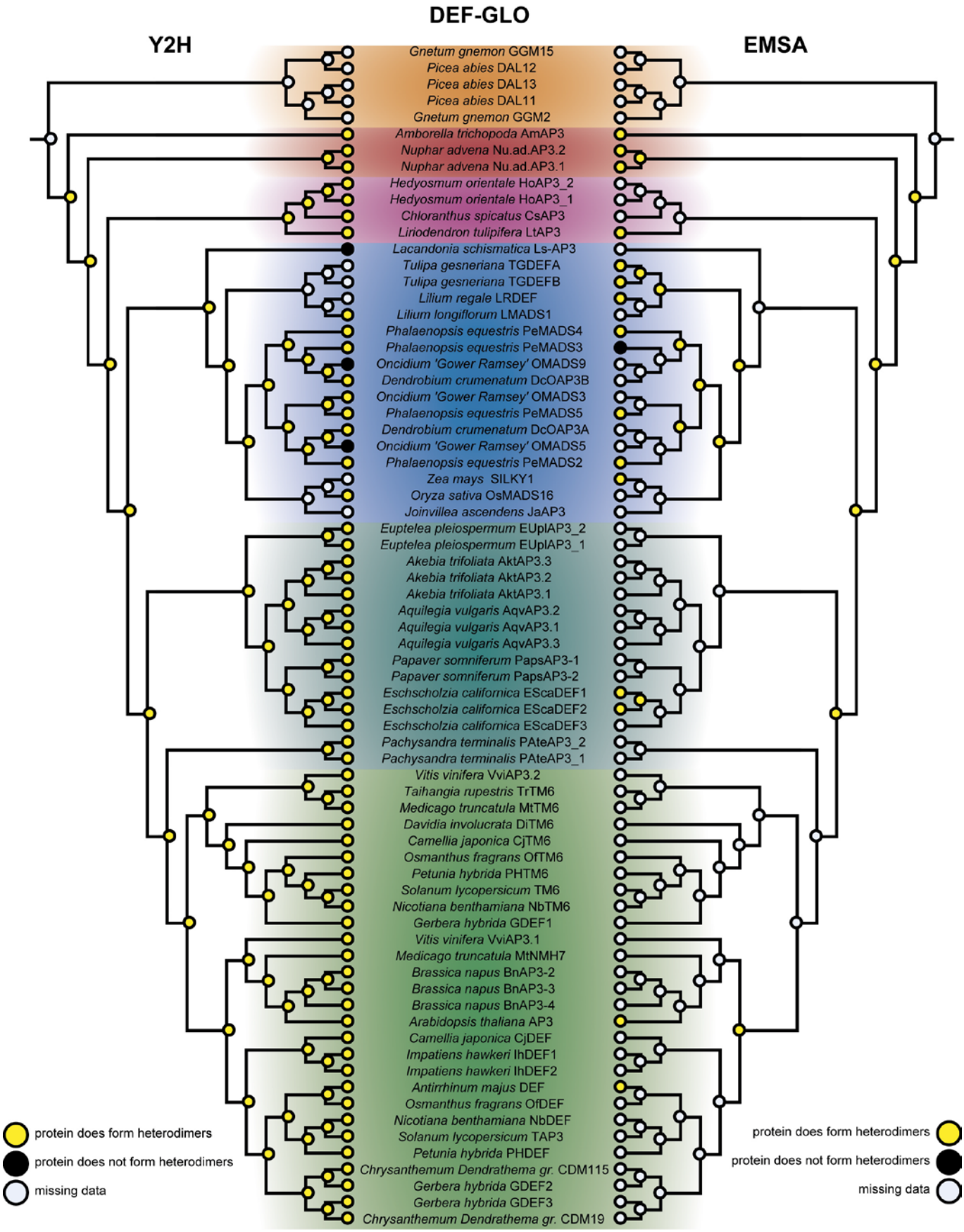


Fig. S11: Homodimerization of GLO-like proteins, comparing Y2H and EMSA data.

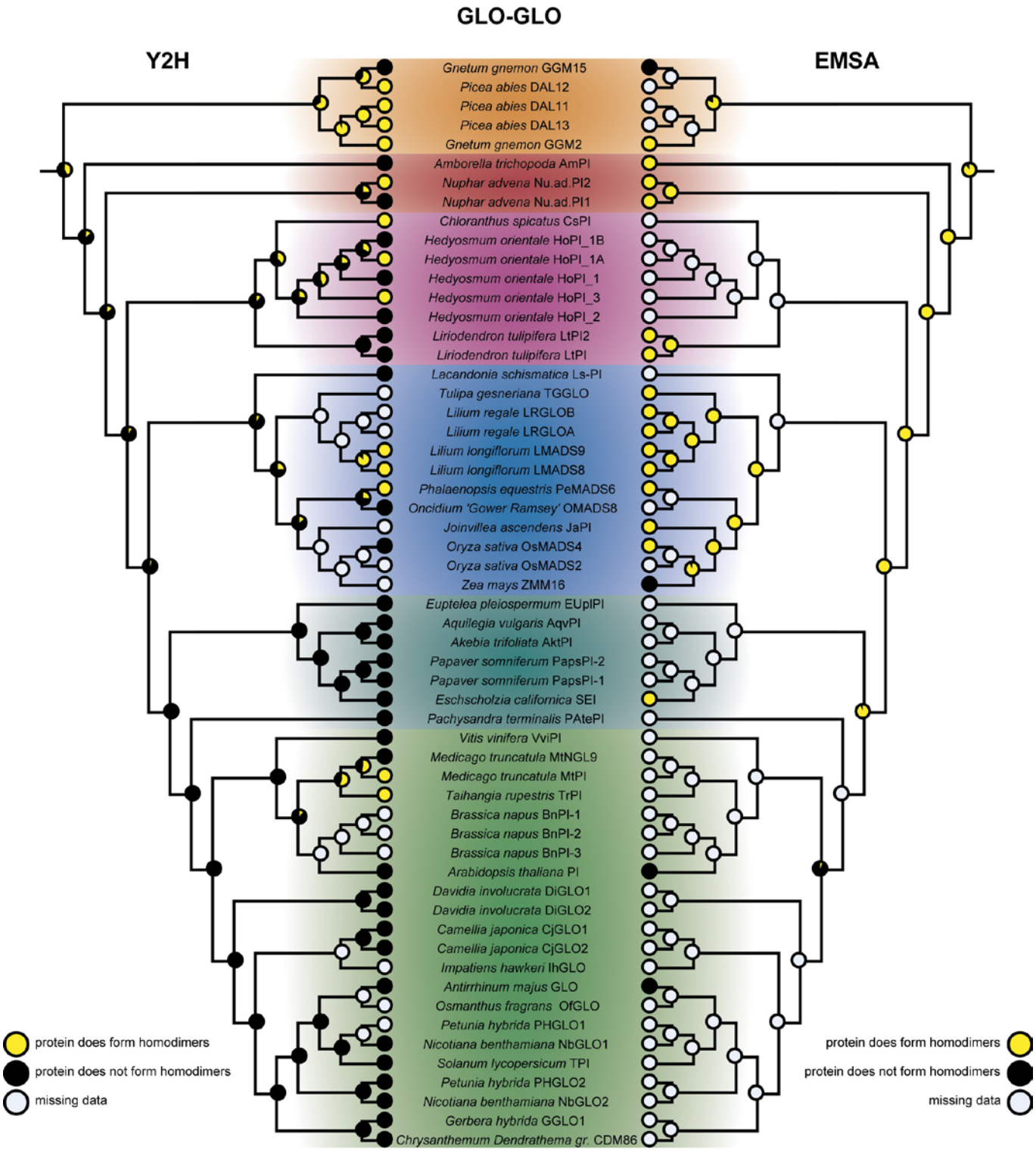


Fig. S12. Heterodimerization of GLO- with DEF-like proteins, comparing Y2H with EMSA data.

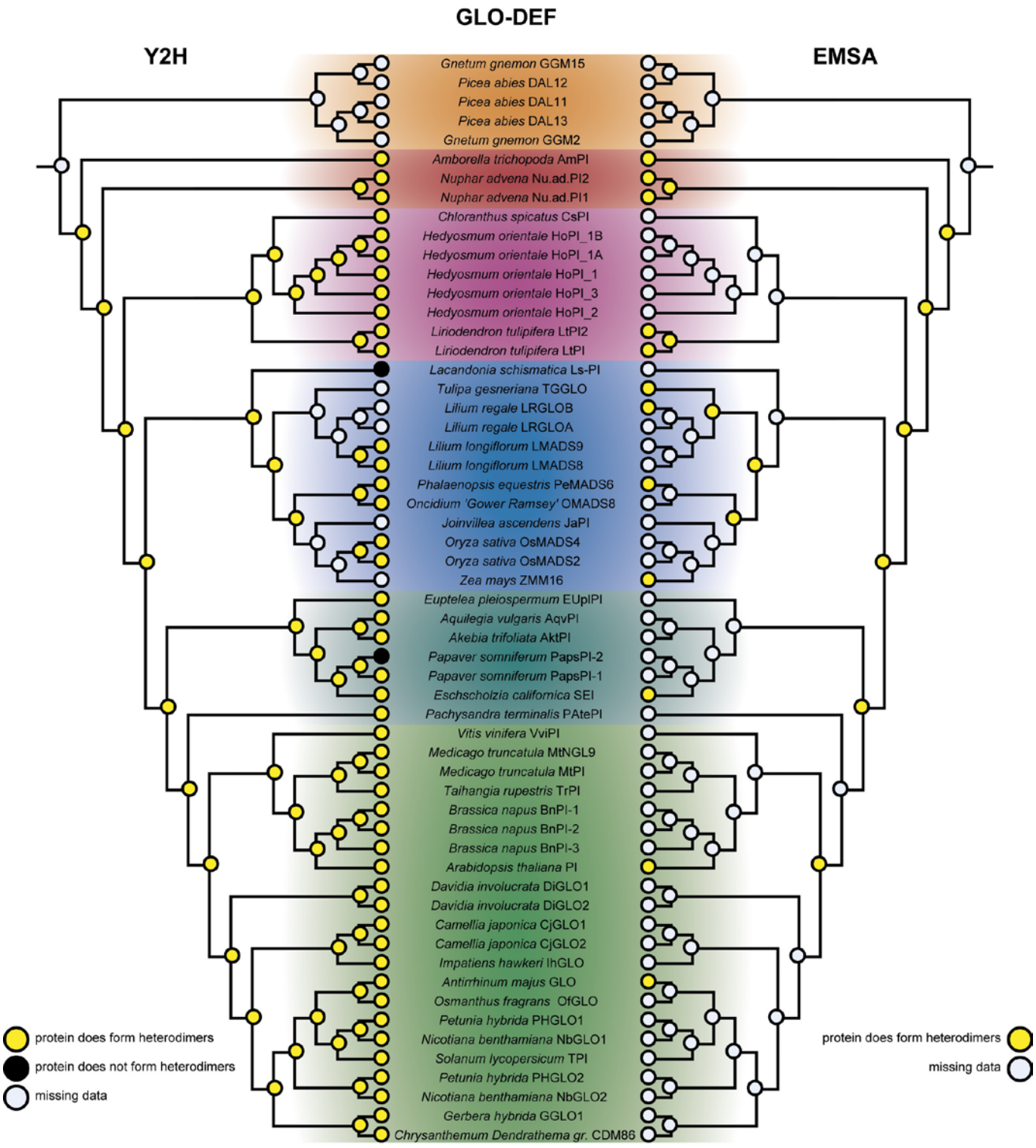


Fig. S13. Representative yeast two-hybrid results for MADS-domain proteins from *L. tulipifera*. For details of the labelling, see Figure 2.

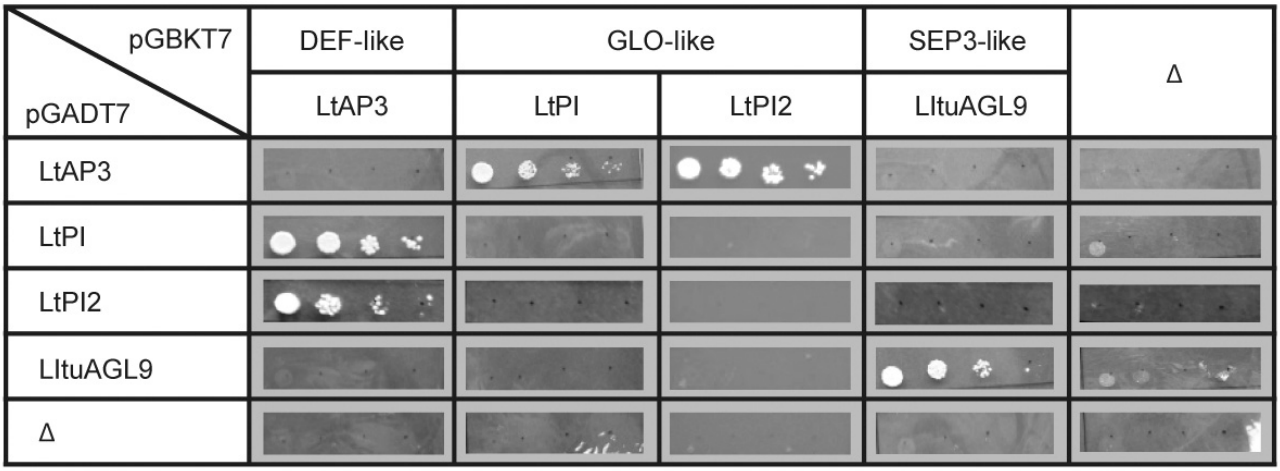
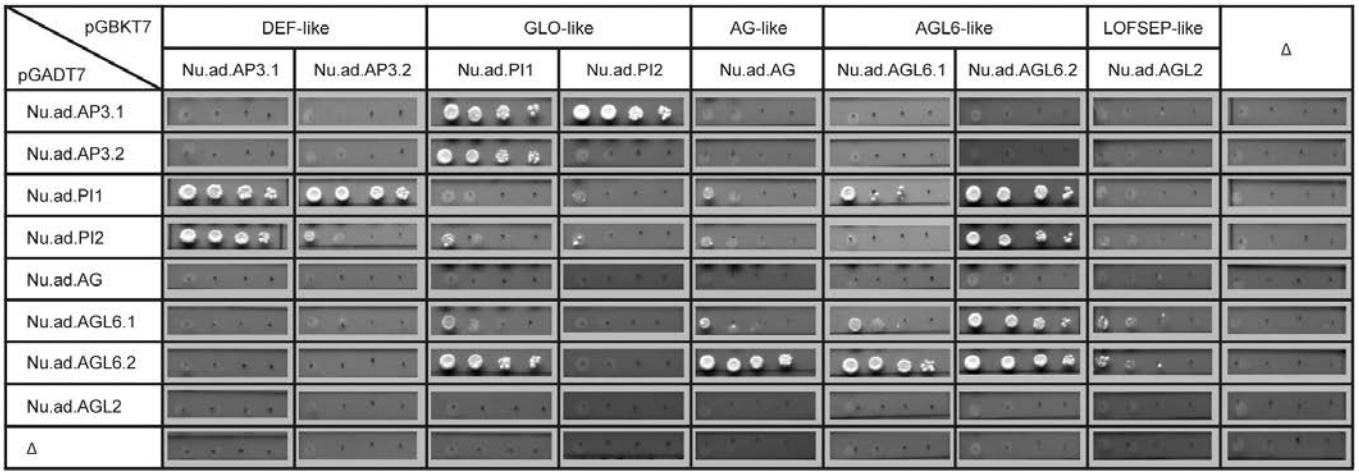
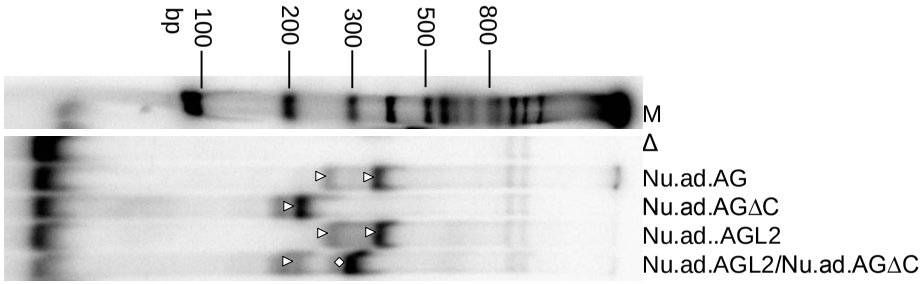


Fig. S14. Representative yeast two-hybrid results for MADS-domain proteins from *N. advena*. For details of the labelling, see Figure 2.




bp
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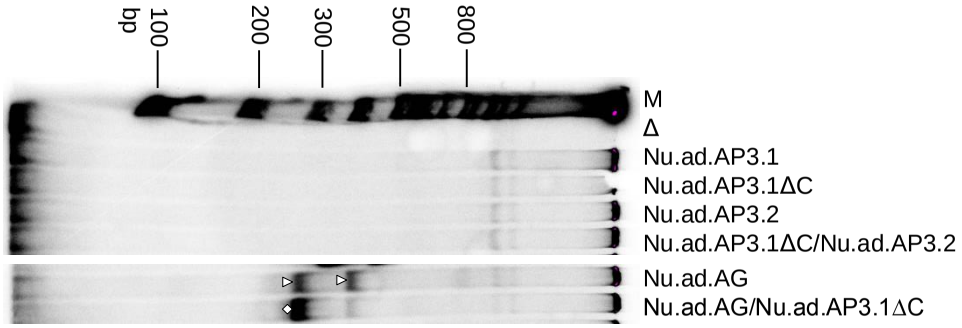
200
300
500
800
M
Δ
Nu.ad.AG
Nu.ad.AGΔC
Nu.ad..AGL2
Nu.ad.AGL2/Nu.ad.AGΔC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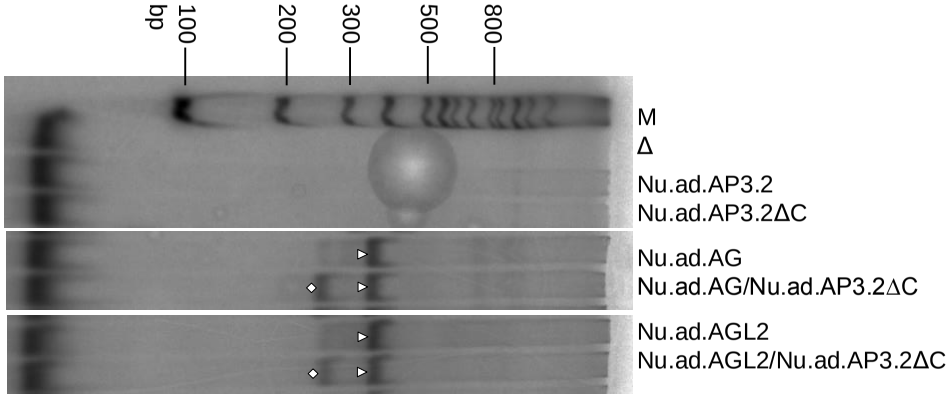
100
200
300
500
800
M
Δ
Nu.ad.AP3.1
Nu.ad.AP3.1ΔC
Nu.ad.AP3.2
Nu.ad.AP3.1ΔC/Nu.ad.AP3.2
Nu.ad.AG
Nu.ad.AG/Nu.ad.AP3.1ΔC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500
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Nu.ad.AP3.2ΔC
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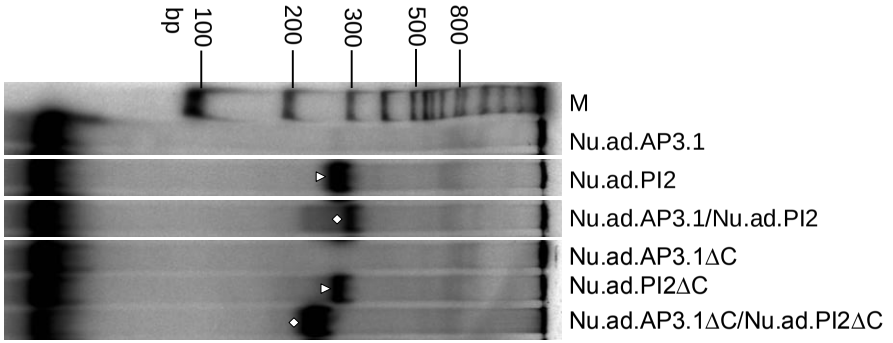
Nu.ad.AG/Nu.ad.AP3.2ΔC
Nu.ad.AGL2
Nu.ad.AGL2/Nu.ad.AP3.2ΔC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200
300
500
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Nu.ad.PI2
Nu.ad.AP3.1/Nu.ad.PI2
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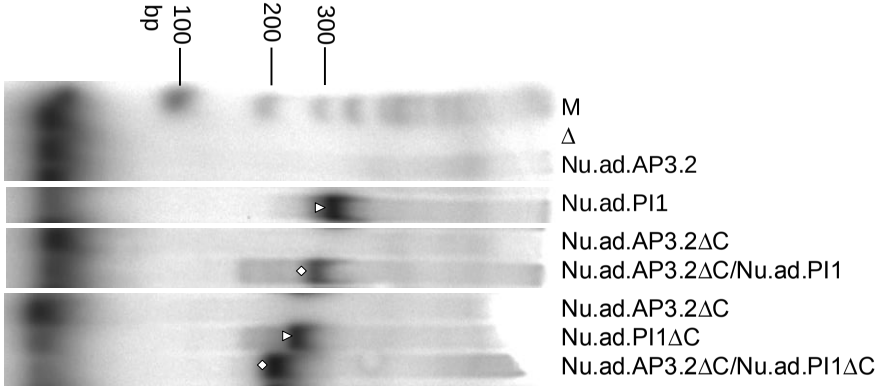
Nu.ad.PI2ΔC
Nu.ad.AP3.1ΔC/Nu.ad.PI2ΔC


bp
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200
300
M
Δ
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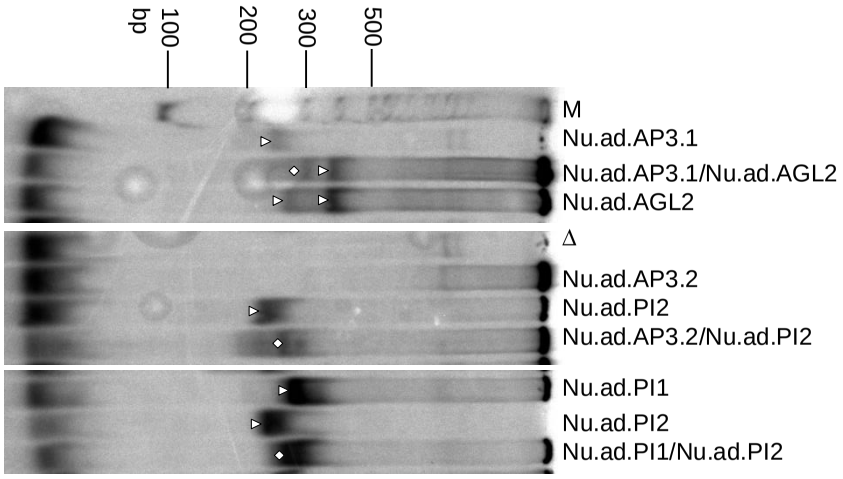
Nu.ad.PI1
Nu.ad.AP3.2ΔC
Nu.ad.AP3.2ΔC/Nu.ad.PI1
Nu.ad.AP3.2ΔC
Nu.ad.PI1ΔC
Nu.ad.AP3.2ΔC/Nu.ad.PI1ΔC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100
200
300
500
M
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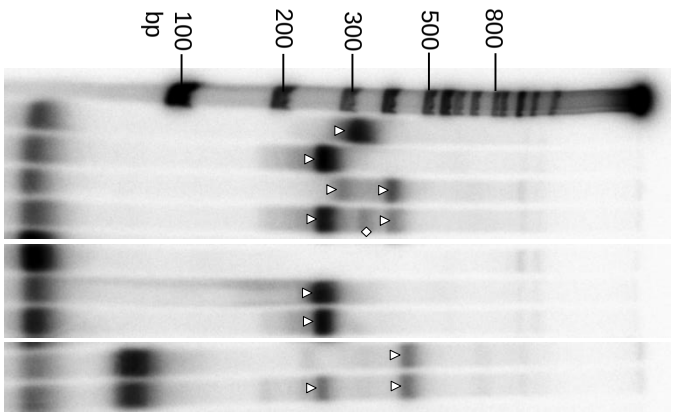
Nu.ad.AP3.1/Nu.ad.AGL2
Nu.ad.AGL2
Δ
Nu.ad.AP3.2
Nu.ad.PI2
Nu.ad.AP3.2/Nu.ad.PI2
Nu.ad.PI1
Nu.ad.PI2
Nu.ad.PI1/Nu.ad.PI2


bp
100
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300
500
800
M
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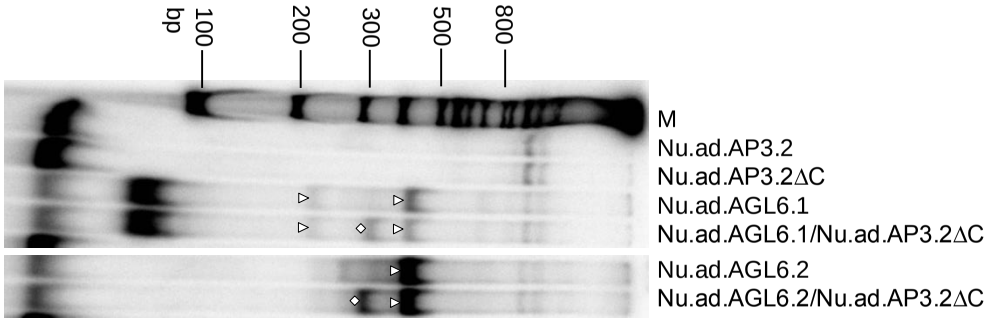
Nu.ad.AGL2
Nu.ad.AGL2/Nu.ad.PI1ΔC
Δ
Nu.ad.PI2
Nu.ad.PI2ΔC
Nu.ad.AGL6.1
Nu.ad.AGL6.1/Nu.ad.PI2ΔC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200
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500
800
M
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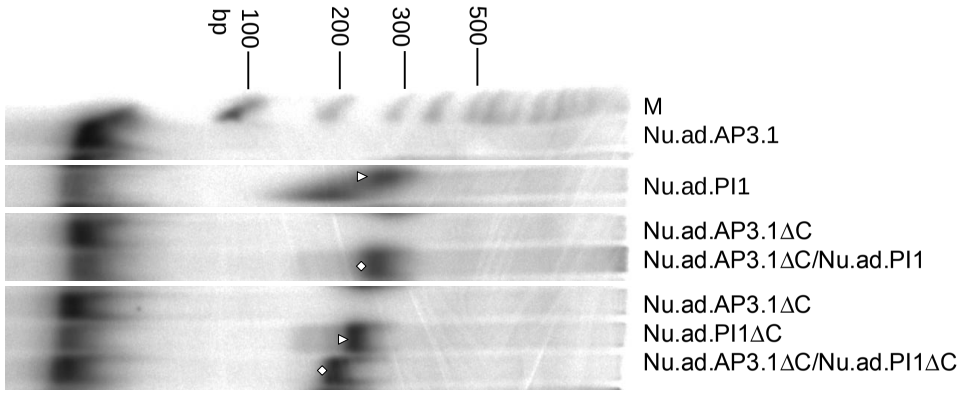
Nu.ad.AP3.2ΔC
Nu.ad.AGL6.1
Nu.ad.AGL6.1/Nu.ad.AP3.2ΔC
Nu.ad.AGL6.2
Nu.ad.AGL6.2/Nu.ad.AP3.2ΔC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200
300
500
M
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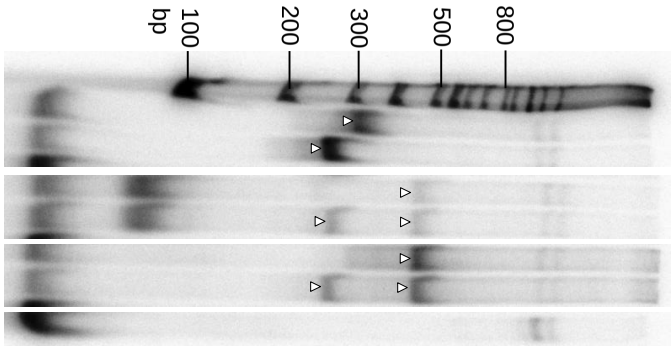
Nu.ad.PI1
Nu.ad.AP3.1ΔC
Nu.ad.AP3.1ΔC/Nu.ad.PI1
Nu.ad.AP3.1ΔC
Nu.ad.PI1ΔC
Nu.ad.AP3.1ΔC/Nu.ad.PI1ΔC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500
800
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Nu.ad.AGL6.1
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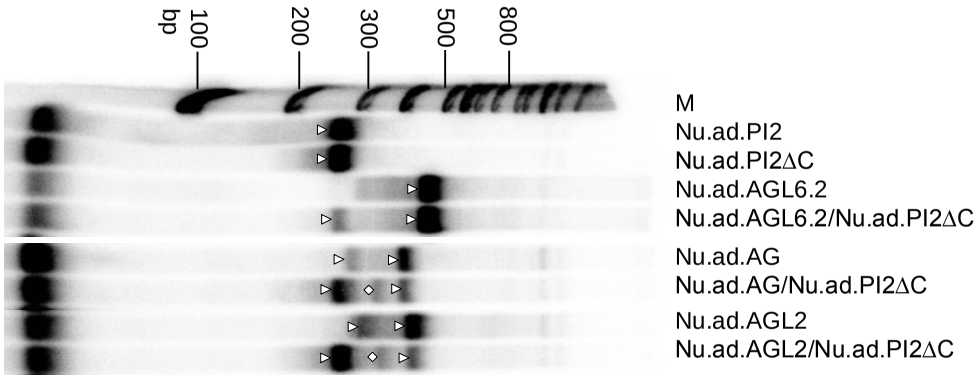
Nu.ad.AGL6.2
Nu.ad.AGL6.2/Nu.ad.PI1ΔC
Δ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300
500
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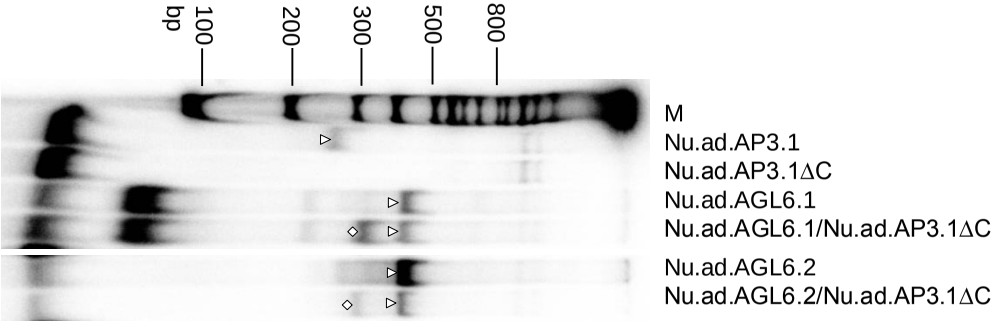
Nu.ad.PI2ΔC
Nu.ad.AGL6.2
Nu.ad.AGL6.2/Nu.ad.PI2ΔC
Nu.ad.AG
Nu.ad.AG/Nu.ad.PI2ΔC
Nu.ad.AGL2
Nu.ad.AGL2/Nu.ad.PI2ΔC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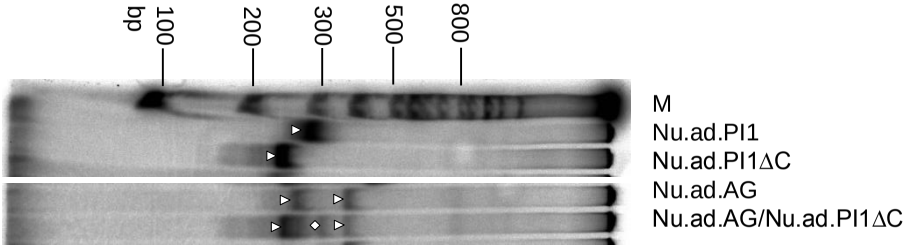
Nu.ad.AP3.1ΔC
Nu.ad.AGL6.1
Nu.ad.AGL6.1/Nu.ad.AP3.1ΔC
Nu.ad.AGL6.2
Nu.ad.AGL6.2/Nu.ad.AP3.1ΔC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800
M
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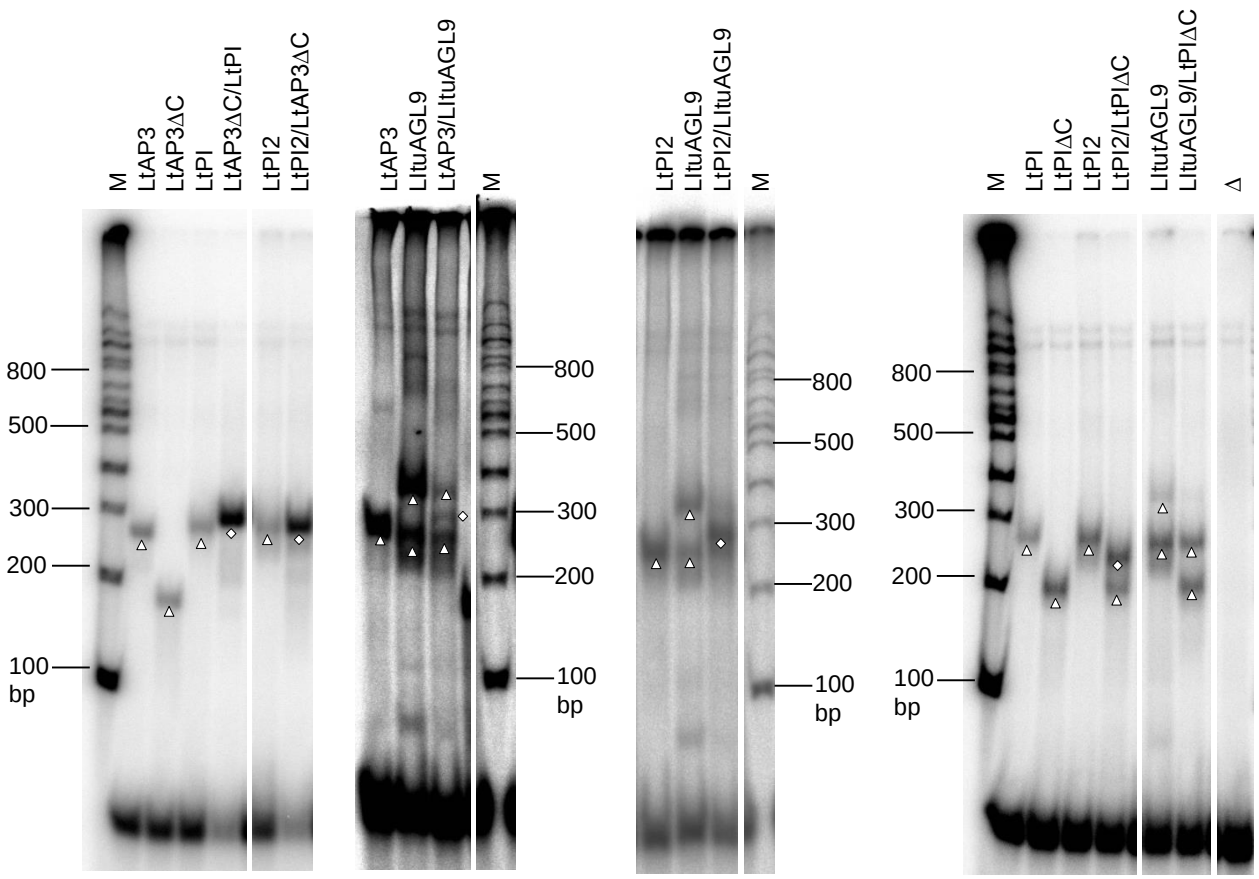
Nu.ad.PI1ΔC
Nu.ad.AG
Nu.ad.AG/Nu.ad.PI1ΔC



Supplementary Figure 15: EMSA results for MADS-domain proteins from *N. advena* and *L. tulipifera.* Band and lane labelling is as in Figure 3. For reasons not entirely clear, some heteromeric complexes have an reduced electrophoretic mobility when compared to each of the corresponding homomeric complexes (compare LtAP3ΔC and LtPI with LtAP3ΔC/LtPI, for example). Also for reasons not clear, Nu.ad.PI2- and Nu.ad.PI2ΔC-DNA complexes have almost identical electrophoretic mobilities. Beyond the expected homomeric protein-DNA complex, an additional band of very high electrophoretic mobility was resolved for Nu.ad.AGL6.1; the nature of this band is unknown.