



0.3

Fig. S1: Overview phylogeny of the GRAS family.

Midpoint rooted Bayesian inference tree of selected species, including *Lotus japonicus*, *Medicago truncatula*, *Arabidopsis thaliana*, *Physcomitrella patens* and *Marchantia polymorpha*. Line thickness corresponds to posterior probabilities. Colored clades depict RAD1 (red), RAM1 (purple), NSP1 (blue), NSP2 (green) and DELLA (cyan). Note that DELLA proteins were used as outgroup to root each of the trees shown in Fig. 2-4.