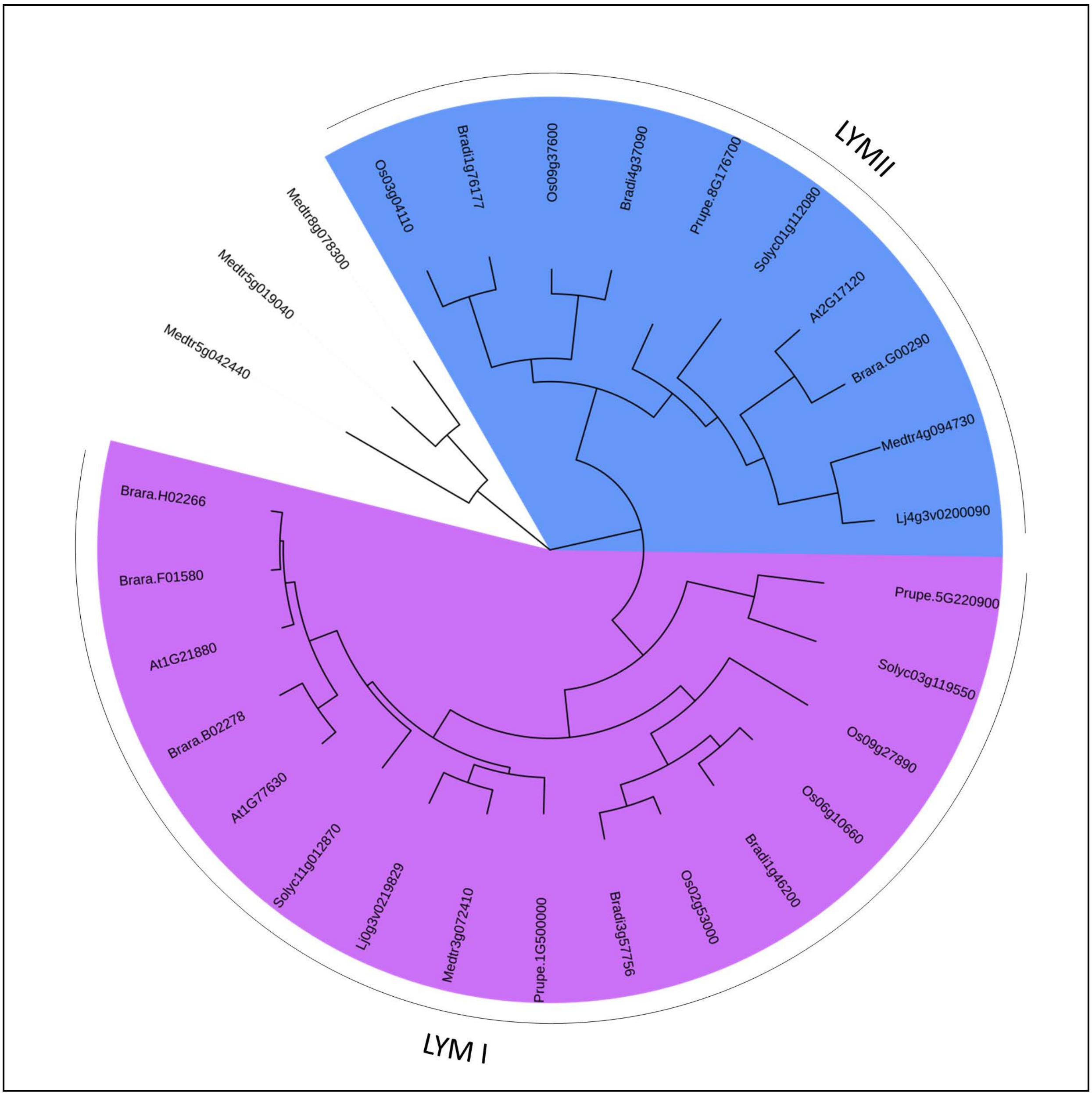

Fig. S1: MrBayes phylogenetic tree of the LYMs. Different phylogenetic groups are shown in different colors. ECR of 3 LYR proteins were used as outgroup sequences. Protein sequence alignment was produced as in Fig. 3. The tree was computed thanks to a bayesian method with MrBayes version 3.2.5 (Huelsenbeck & Ronquist, 2001; Ronquist *et al.*, 2012 ; parameters: ngen= 400000, samplefreq=100, relburnin=yes, burninfrac= 0.25).

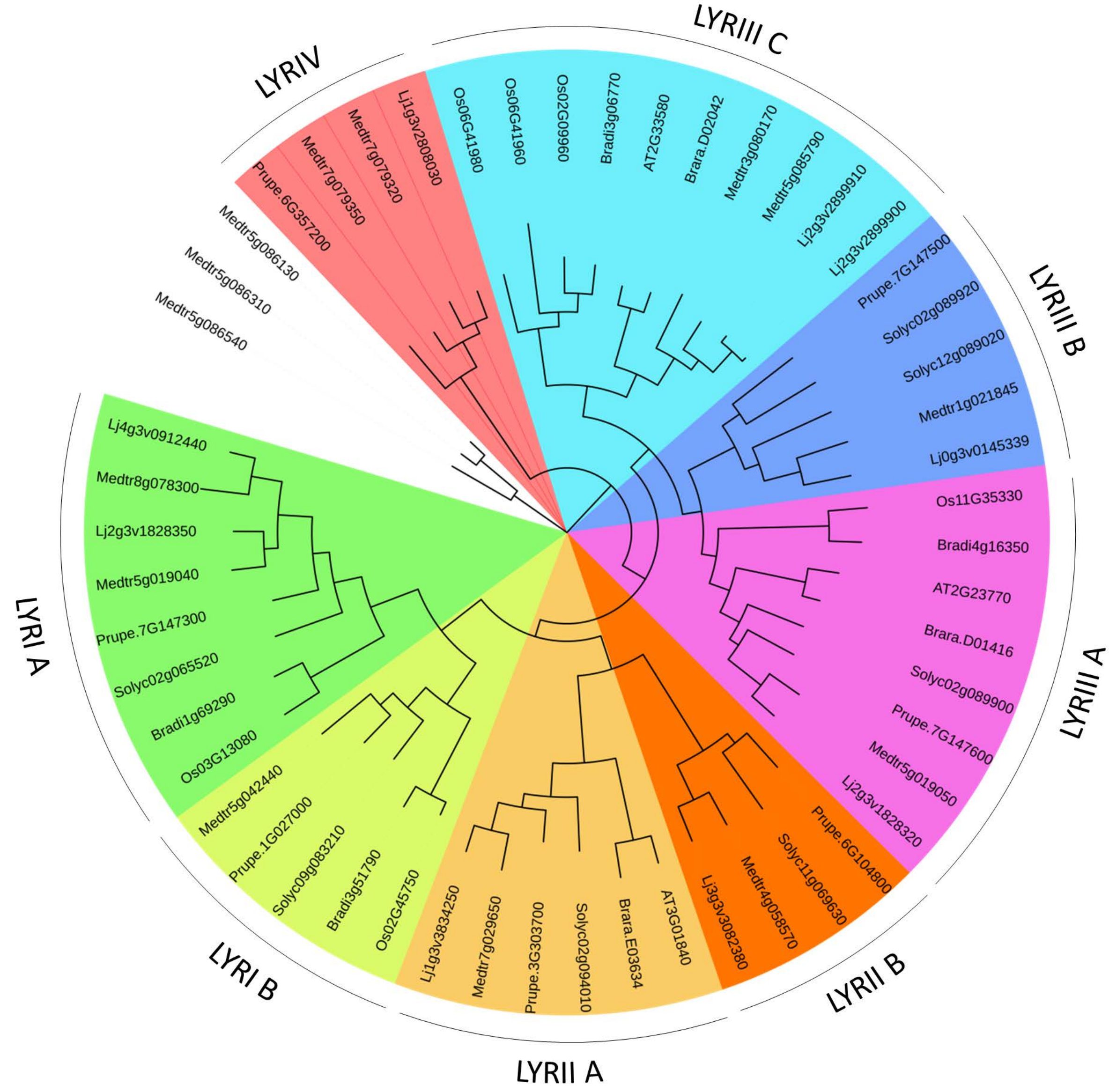

Fig. S2: MrBayes phylogenetic tree of the LYRs. Different phylogenetic groups are shown in different colors. ECR of 3 LYK proteins were used as outgroup sequences. Tree was built as in Fig. S1.

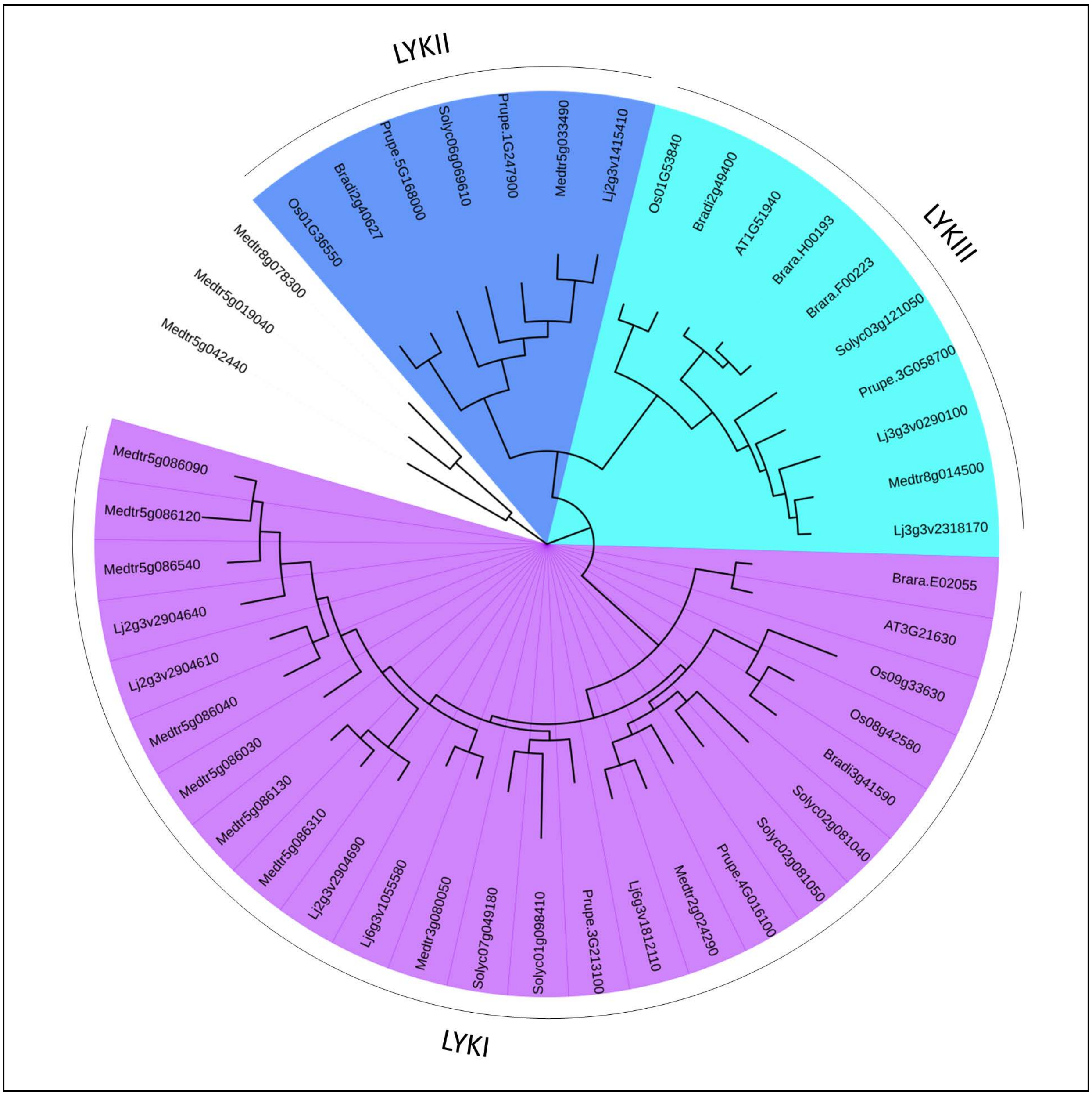

Fig. S3: MrBayes phylogenetic tree of the LYKs. Different phylogenetic groups are shown in different colors. ECR of 3 LYR proteins were used as outgroup sequences. Tree was built as in Fig. S1.

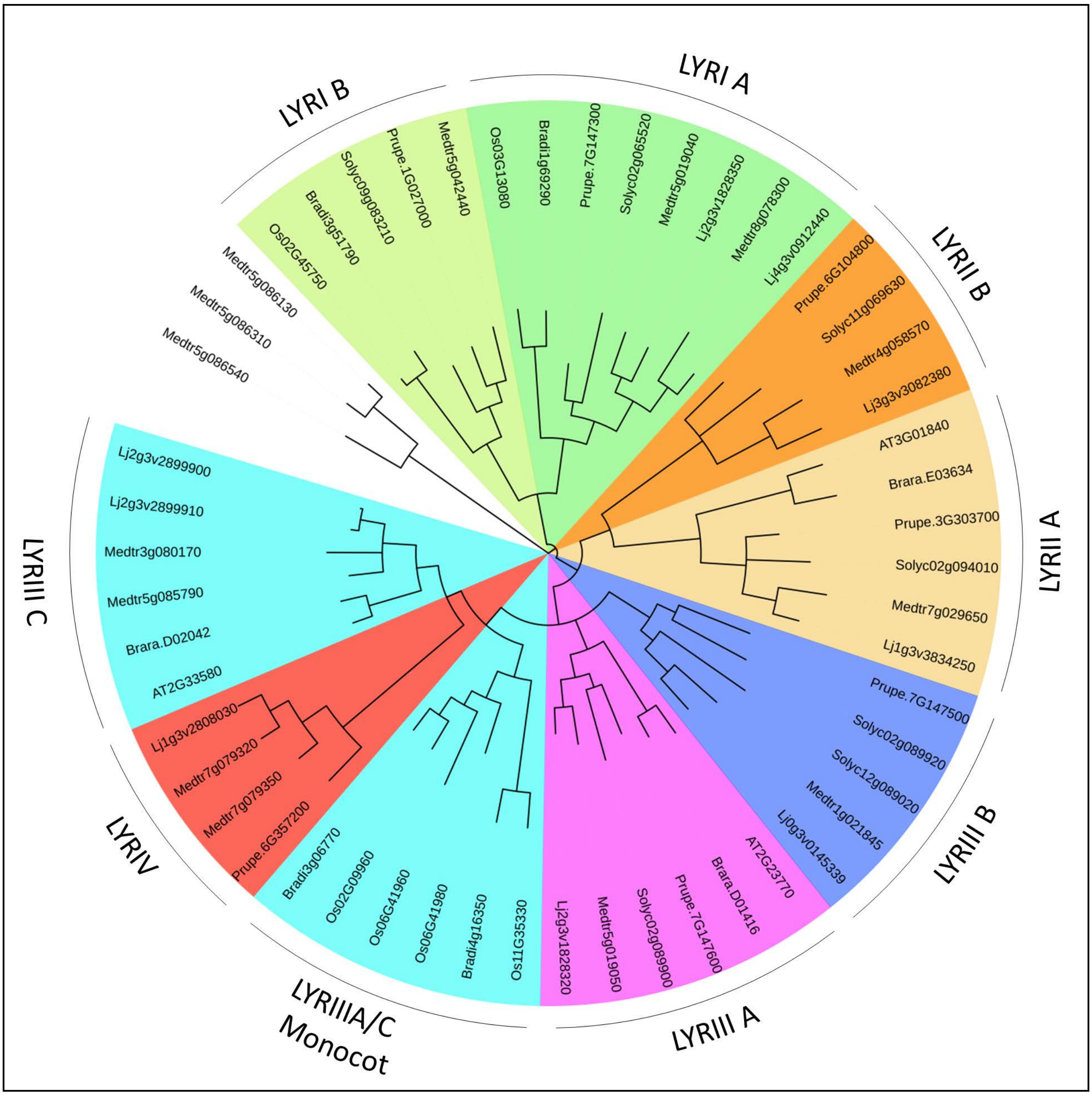

Fig. S4: MrBayes phylogenetic tree of the LYRs using Gblock. Different phylogenetic groups are shown in different colors. ECR of 3 LYK proteins were used as outgroup sequences. Tree was built as in Fig. S1.

References:

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Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol* 61: 539-542.