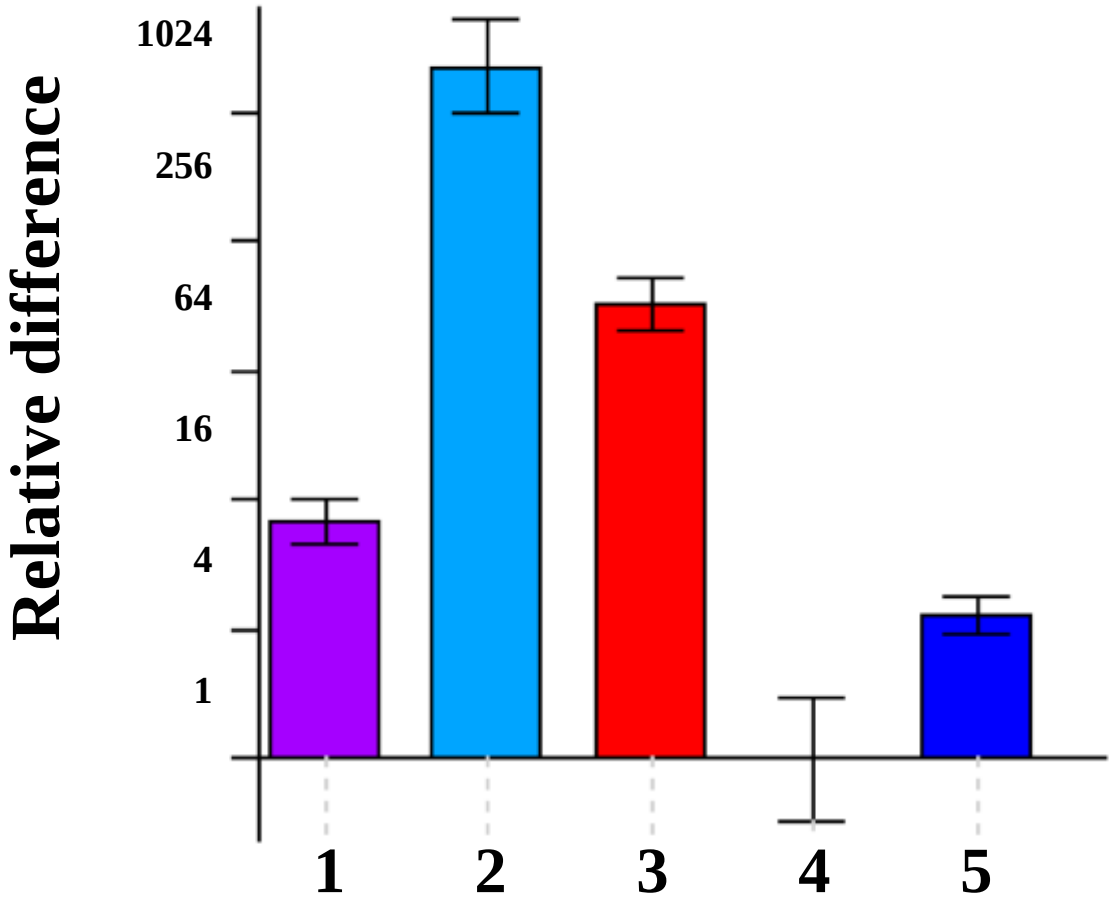

An extensive analysis of *R2R3-MYB* regulatory genes from *Fagus crenata*

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Supplementary Fig. S5
Expression profile of *FcMYB1901* as determined by quantitative RT-PCR using the total RNA from male flower sampled on the day of anthesis (0DPA) and two (2DPA) and four days (4DPA) after the anthesis, and from the petioles of young leaves emerging from twigs supplied with de-ionized water (DW) or 0.1 mM gibberellic acid soluiton (0.1mM GA) as described in Materials and Methods. The quantitative RT-PCR was carried out as described in Materials and Methods.