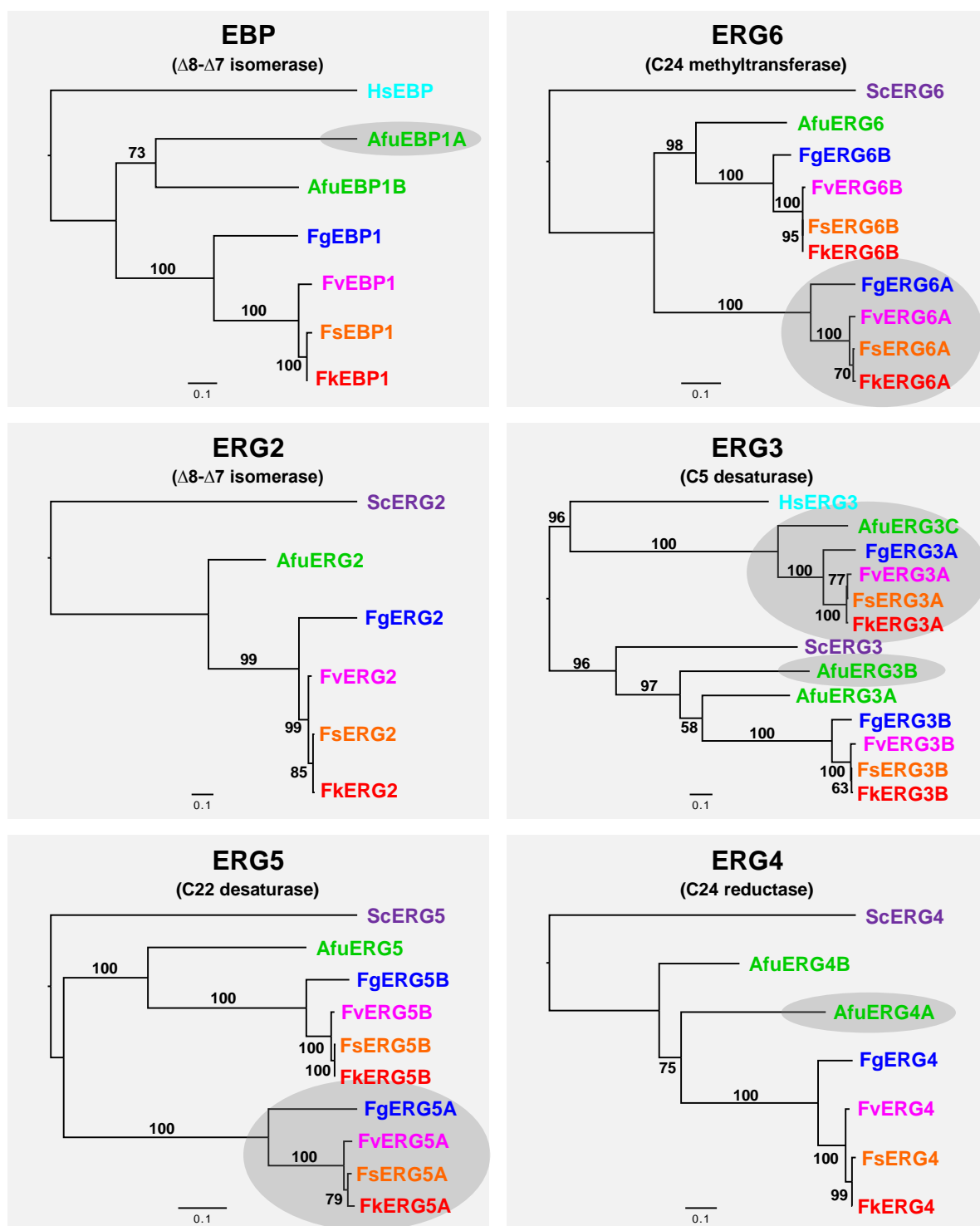
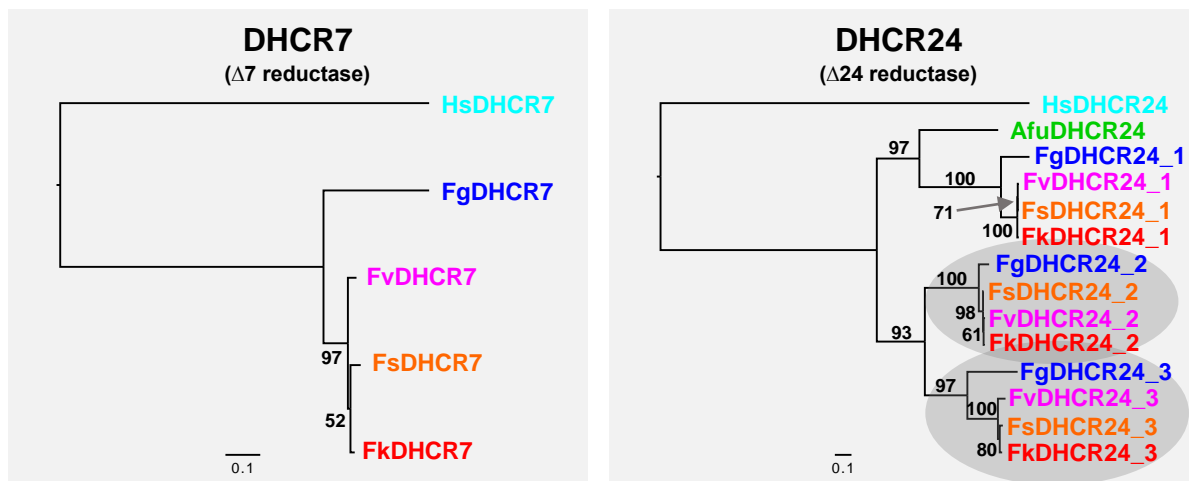


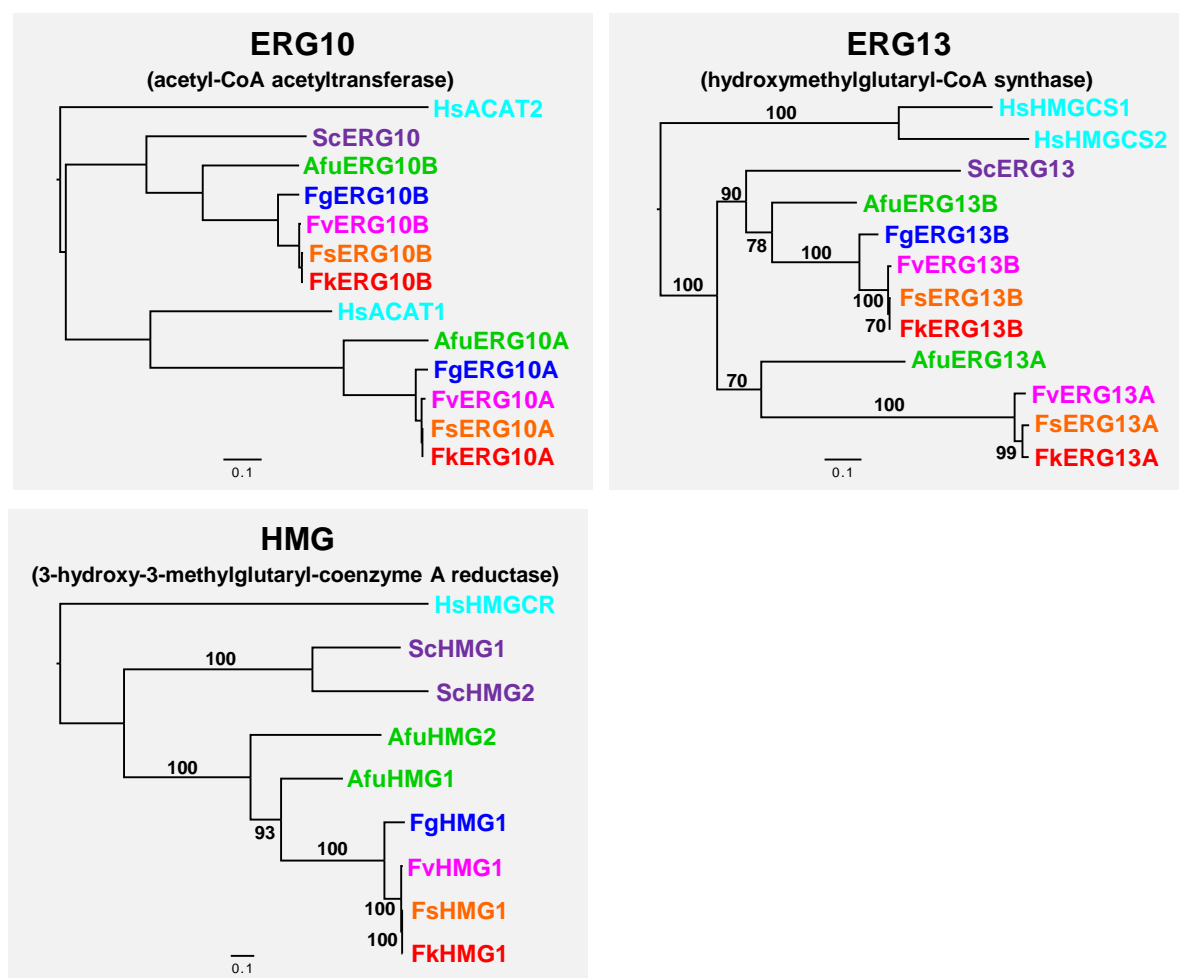
**Figure S1a.** Phylogeny of all *erg7*, *cyp51* (*ERG11*), *erg24* and *erg25/26/27* complex homologs (midpoint rooted). The grey-shaded areas highlight *erg* orthologs that have possibly evolved novel substrate specificities. Species name abbreviations and their designated colours are as follows: *Homo sapiens* (Hs; cyan), *Saccharomyces cerevisiae* (Sc; purple), *Aspergillus fumigatus* (Afu; green), *Fusarium graminearum* (Fg; blue), *F. vanettenii* (Fv; pink), *F. solani sensu stricto* FSSC5 (Fs; orange), *F. keratoplasticum* (Fk; red). \* = partial sequence only. The percentage bootstrap support of 100 replicates is shown for all branches. The scale bars indicate the number of amino acid substitutions per position.



**Figure S1b.** Phylogeny of *ebp*, *erg6*, *erg2*, *erg3*, *erg5* and *erg4* homologs (midpoint rooted). The grey-shaded areas highlight *erg* orthologs that have possibly evolved novel substrate specificities. Species name abbreviations and their designated colours are as follows: *Homo sapiens* (Hs; cyan), *Saccharomyces cerevisiae* (Sc; purple), *Aspergillus fumigatus* (Afu; green), *Fusarium graminearum* (Fg; blue), *F. vanettenii* (Fv; pink), *F. solani sensu stricto* FSSC5 (Fs; orange), *F. keratoplasticum* (Fk; red). The percentage bootstrap support of 100 replicates is shown for all branches. The scale bars indicate the number of amino acid substitutions per position.



**Figure S1c.** Phylogeny of all human *dhcr7* and *dhcr24* homologs (midpoint rooted). The grey-shaded areas highlight *erg* orthologs that have possibly evolved novel substrate specificities. Species name abbreviations and their designated colours are as follows: *Homo sapiens* (Hs; cyan), *Saccharomyces cerevisiae* (Sc; purple), *Aspergillus fumigatus* (Afu; green), *Fusarium graminearum* (Fg; blue), *F. vanettenii* (Fv; pink), *F. solani sensu stricto* FSSC5 (Fs; orange), *F. keratoplasticum* (Fk; red). The percentage bootstrap support of 100 replicates is shown for all branches. The scale bars indicate the number of amino acid substitutions per position.



**Figure S1d.** Phylogeny of all *erg10*, *erg13*, and *hmg* homologs (midpoint rooted). All other mevalonate pathway genes are not duplicated and therefore excluded from the phylogenetic comparisons. Species name abbreviations and their designated colours are as follows: *Homo sapiens* (Hs; cyan), *Saccharomyces cerevisiae* (Sc; purple), *Aspergillus fumigatus* (Afu; green), *Fusarium graminearum* (Fg; blue), *F. vanettenii* (Fv; pink), *F. solani sensu stricto* FSSC5 (Fs; orange), *F. keratoplasticum* (Fk; red). The percentage bootstrap support of 100 replicates is shown for all branches. The scale bars indicate the number of amino acid substitutions per position.