Figure S7. Detailed phylogenetic tree of cis-isoprene transferases and nuclear receptors

Primary sequences of the ligand-binding domains of 'early' nuclear receptors were compared to a compendium of sequences for DHDPPS and its evolutionary relative, and obligate partner, NUS1/NOGOBR. Although NUS1 and NOGOBR are generally thought to be orthologous, this remains to be confirmed.

**Methods.** Clustal omega alignment and phylogenetic reconstructions were performed using the function 'build' of ETE3 v3.1.1 (Huerta-Cepas et al., 2016) as implemented on the GenomeNet website at the University of Kyoto (https://www.genome.jp/tools/ete/). The tree was inferred using RAxML v8.1.20 run with model PROTGAMMAJTT and default parameters (Stamatakis, 2014); branch supports were computed from 100 bootstrapped trees (Figure S7, below).

**Conclusions.** The rooted tree, as computed, depicts NRs as being a branch of the DHDPPS/NOGOBR/NUS1 group of cis-isoprene transferases. Some programs give slightly different results, placing NRs most closely to NUS1, whereas this tree splits DHDPPS/NUS1/NOGOBR into subgroups. However, all such trees highlight the close relationship,
based on protein primary structure, between NRs and this specific subgroup of cis-isoprene transferases. It is notable that the inferred evolutionary distance between NRs and the cis-isoprene transferases is comparable to the inferred distance between the different members of the cis-isoprene transferase subgroup.

References
