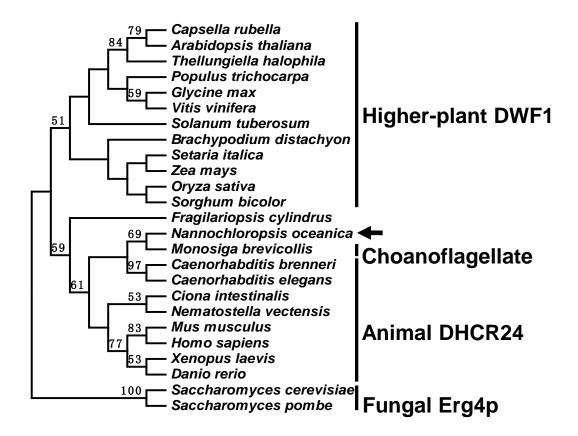
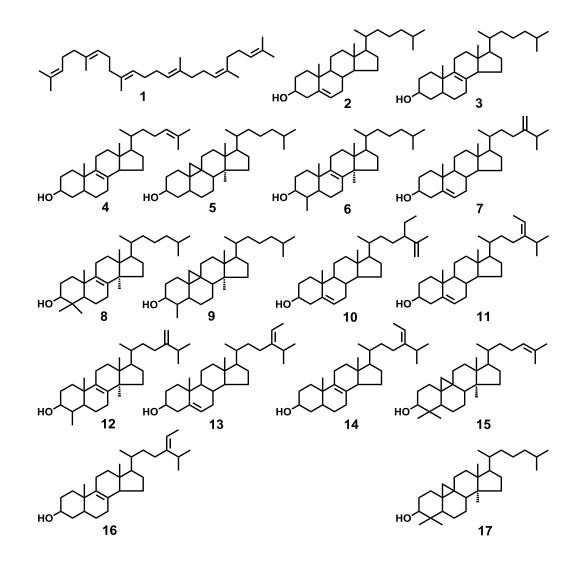


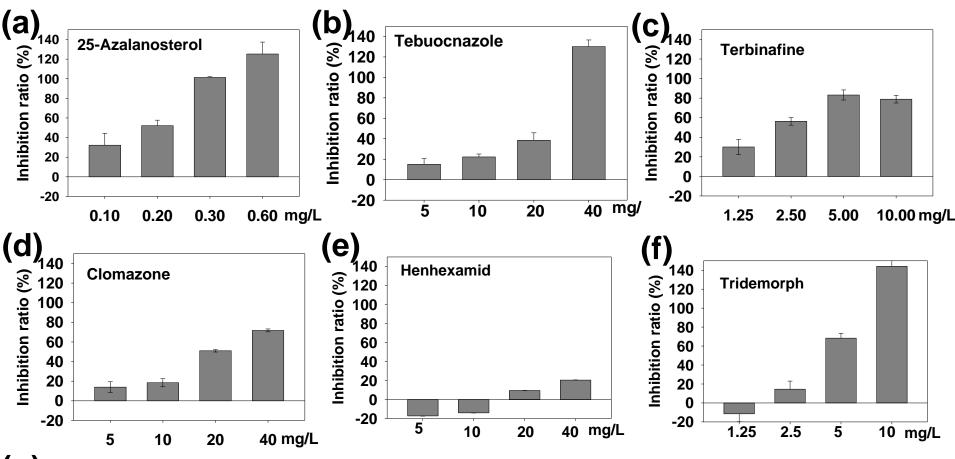
Figure S1. Phylogenetic relationship of organisms studied here.



**Figure S2.** Phylogenetic analysis of the sterol 24(25) isomerase reductase (DWF1) and 24-dehydrocholesterol reductase (DHCR24) using the Phy ML 3.0 program. Protein identity and conserved domains of proteins used to build the tree are listed in Data S1.

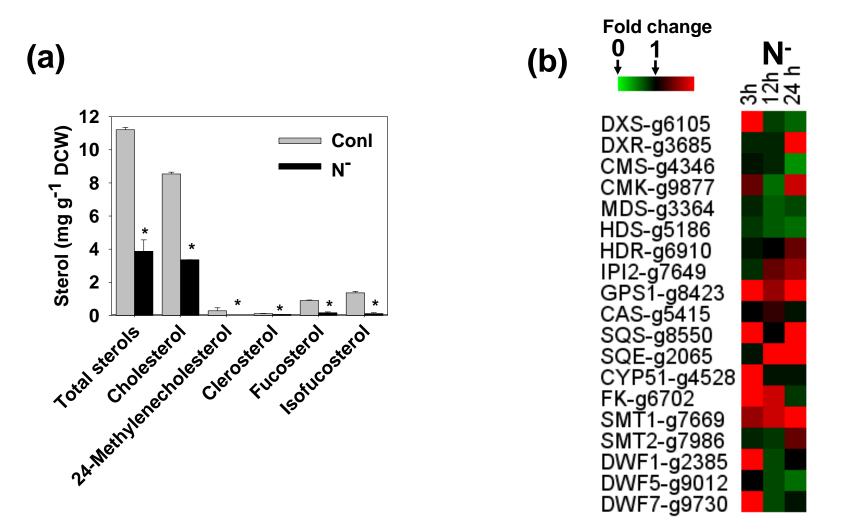


**Figure S3.** Identification of the sterol compounds extracted from *N. oceanica*. 1: squalene, 2: cholesterol, 3: cholest-8enol, 4: desmosterol, 5: pollinastanol, 6: 4,14-dimethylcholest-8-enol, 7: 24-methylenecholesterol, 8: 24(25)dihydrolanosterol, 9: 4-methylpollinasterol, 10: 24-methylcholesta-5, 25(27)-dienol, 11: fucosterol, 12: obtusifoliol, 13: isofucosterol, 14: stigmasta-8, 24(28) *E*-dienol, 15: cycloartenol, 16: stigmasta-8, 24(28) *Z*-dienol, 17: cycloartanol.



(**G**)<sub>250</sub> (**S**) 200 (**S**) 200 **Amphotericin B 150 150 100 100 1.25** 2.5 5 10 mg/L

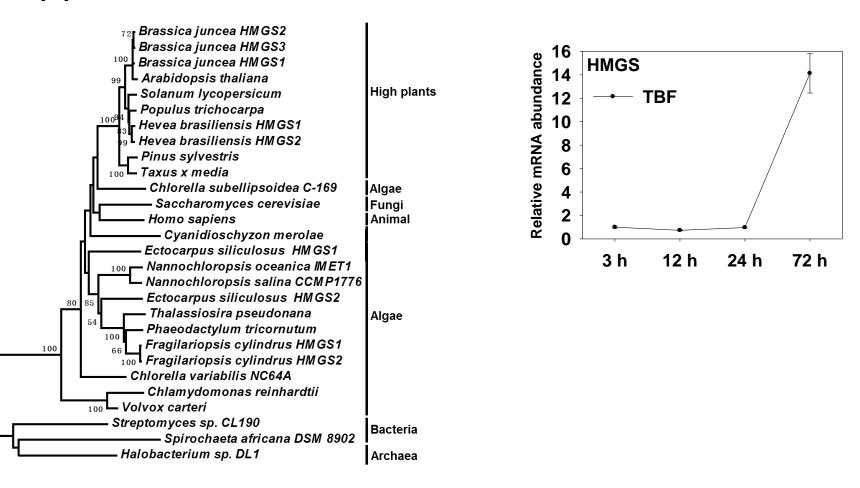
**Figure S4.** Inhibition ratio of different isoprenoid or sterol biosynthetic inhibitors. Culture in exponential phase was diluted in fresh medium and grown for 12 h. Subsequently, cultures were added with inhibitors at a gradient concentration, or an equivalent amount of DMSO (not to exceed a final concentration of 0.1%).



**Figure S5.** Changes in sterol biosynthesis induced by nitrogen depletion. (a) Changes of sterols induced by nitrogen depletion. Cells with the same initial inoculation amount were cultivated under nitrogen-replete or -deplete conditions for transcription analysis and sterol profiling (6 d). (b) Transcriptional dynamics of cholesterogenic genes of *N. oceanica* in response to nitrogen depletion. Red and green indicate up- and down-regulated genes, respectively. The time points for the cluster analysis are indicated in hours at the top. Values are the means of three replicates and are representative of a standard experiment.

## (a) HMGS omega (dN/dS) <1

**(b)** 



**Figure S6**. (a) Phylogenetic analysis of the Hydroxyl-Methyl-Glutaryl-CoA Synthase (HMGS) using Phy ML 3.0 program. Protein identity and conserved domains of proteins used to build the tree are listed in Table S3. (b) Transcriptional dynamics of *HMGS* in *N. oceanica* following TBF-induced sterol depletion.