### **Supplementary Figure Legends**

Supplementary Figure 1. Evidence of protein-protein interaction of yeast ergosterol synthetic enzymes. (A) Table compiled using data from the STRING database (http://string-db.org/) based on experimental evidence, where '+' indicates high confidence for interaction, with scores of at least 0.7. (B) Yeast ergosterol synthesis protein network compiled using the high-confidence yeast protein-protein interaction dataset updated from [1] as described in [2]. The pink nodes are the ergosterol synthesis enzymes, and the grey nodes are their interaction partners.

Supplementary Figure 2. Ion *m/z* values monitored during selective ion monitoring (SIM) analysis of the *N*,*O*-bis(trimethylsilyl)trifluoroacetamide derivatives. (A) A simplified schematic illustrating our metabolic labelling strategy. (B) Chromatograms and mass spectra of the  $[^{2}D_{6}]$ -desmosterol and  $[^{2}D_{7}]$ -7DHC standards, and their relative retention times with respect to the 5 $\alpha$ -cholestane internal standard (IS). (C) The SIM ions for 5 $\alpha$ -cholestane were monitored from 27 to 32 min (width 0.1 Da, dwell 120 ms); for  $[^{2}D_{6}]$ -cholesterol and  $[^{2}D_{7}]$ -cholesterol from 32 to 35.5 min (width 0.1 Da, dwell 120 ms); for  $[^{2}D_{6}]$ -desmosterol and  $[^{2}D_{7}]$ -7DHC from 35.5 to 38 min (width 0.1 Da, Dwell 200 ms).

# **Supplementary Figures**

# **Supplementary Figure 1**



# **Supplementary Figure 2**



С

Compound	Retention time (min)	Quantification/ confirmation ion <i>m</i> /z	Molecular ion m/z
5α-Cholestane (IS)	28.92	217	372
[ <sup>2</sup> D <sub>6</sub> ]-Cholesterol	34.57	374	464
[ <sup>2</sup> D <sub>6</sub> ]-Desmosterol	37.08	333	462
[ <sup>2</sup> D <sub>7</sub> ]-Cholesterol	34.53	336	465
[ <sup>2</sup> D <sub>7</sub> ]-7-Dehydrocholesterol	36.58	358	463
Cholesterol	34.04	368	458
Desmosterol	37.37	327	456

### References

1. Bertin N, Simonis N, Dupuy D, Cusick ME, Han JD, Fraser HB, Roth FP, Vidal M (2007) Confirmation of organized modularity in the yeast interactome. PLoS biology 5 (6):e153. doi:10.1371/journal.pbio.0050153

2. Erce MA, Pang CN, Hart-Smith G, Wilkins MR (2012) The methylproteome and the intracellular methylation network. Proteomics 12 (4-5):564-586. doi:10.1002/pmic.201100397