Figure S1. Sukhanova et al.
Figure S2. Sukhanova et al.
Figure S3. Sukhanova et al.
A

Sterol pathway genes

Orthology Search
Princeton Protein Orthology
Naïve Ensemble algorithm
Human orthologs

Assemble first order interactors
source: BioGRID

Subnetwork for ERG25-28
Fig.3

Searched STRING and BioGRID Databases
for interactions with EGFR

Yeast & Human networks
Fig. 4

B

Number of interacting genes

GO function enrichment, P-value

0 100 200 300

Lanosterol

4,4-dimethyl-5α-cholesta-8,14,24-trien-3β-ol

ERG11 (CYP51A1)

4,4-dimethyl-5α-cholesta-8,24-dien-3β-ol

ERG24 (TM7SF2)

Zymosterol

Squalene

(S)-2,3-Epoxysqualene

ERG7 (LSS)

4,4-dimethyl-5α-cholesta-8,14,24-trien-3β-ol

ERG1 (SQLE)

GO 6810 - Transport

GO 51179 - Localization

Figure S4. Sukhanova et al.
Figure S5. Sukhanova et al.
Figure S6. Sukhanova et al.
Figure S7. Sukhanova et al.
Figure S8. Sukhanova et al.

Figure S9. Sukhanova et al.
**Figure S10.** Sukhanova et al.