Extended data Figure 5: TECR and lipid metabolism. a, *TECR* gene dependency correlations from the DepMap resource (24Q2). **b**, Gene expression determined using reverse transcription coupled to quantitative polymerase chain reaction. **c**, Cell death determined by imaging of live (nuclear mKate2-positive) and dead (SYTOX Green-positive) cells. Live and dead cell counts were integrated into the lethal fraction score (0 = all cells in the population alive, 1 = all cells in the population dead). Results in **b** and **c** are individual datapoints from independent experiments.