



S7 Fig. t-SNE analysis of cholesterol-related transcripts identifies distinct tumor cohorts that correlate with patient survival. t-SNE patterns for the transcripts listed in Fig. 2J were calculated from TCGA expression profiles and displayed as previously described (blue dots) [17]. Where available, t-SNE patterns for matched normal human tissues were similarly calculated and plotted (red dots). Kaplan-Meier survival data for each of the tumor cohorts were then plotted as shown in Fig. 4E.