**Supplementary Methods**

**Analysis of patient survival based on gene signatures.** UCSC Cancer Genomic Browserwas used to analyze the TCGA data. A gene signature consists of 7 cholesterol synthesis genes [MVK+PMVK+MVD+FDPS+FDFT1+SQLE+LSS] or 2 mitochondrial cholesterol transport genes [STAR+STARD3] was used to represent the activity of cholesterol synthesis and mitochondrial cholesterol import pathways, respectively. In each cancer type, patients were divided into 3 relatively equal sized groups based on the expression of these signatures. Cancers with significant overall patient survival difference for the high and low expressing groups were plotted. The Kaplan-Meir curves were drawn and statistical calculations were performed using Prism software (version 6.05, GraphPad software, La Jolla, CA). Please note that, the survival curves and patient numbers in the study is slightly different than the data available through UCSC Cancer Genomic Browser as control subjects (normal samples) are eliminated during data processing.

**Analysis of expression of cholesterol synthesis genes according to p53 mutational status of breast tumors.** The p53 mutational status and gene expression data for the breast cancer cohort of the TCGA database was obtained through the Regulome Explorer (explorer.cancerregulome.org) tool (Institute for Systems Biology, Seattle ,WA)

**Analysis of copy number variation for cholesterol synthesis genes.** Copy number and gene expression status of cholesterol synthesis genes and various oncogenes were plotted using the cBioPortal for Cancer GenomicsPortal (www.cbioportal.org) (1).

1. Cerami E, Gao J, Dogrusoz U, Gross BE, Sumer SO, Aksoy BA, et al. The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. Cancer discovery 2012;2(5):401-4.