

Table S1 Genes selected for the study

| Gene symbol | Official gene name | RNA Refseq |
|--------------------------|---|------------|
| Cholesterol biosynthesis | | |
| <i>FDFT1</i> | Farnesyl-diphosphate farnesyltransferase 1 | NM_004462 |
| <i>FDPS</i> | Farnesyl diphosphate synthase | NM_002004 |
| <i>GGPS1</i> | Geranylgeranyl diphosphate synthase 1 | NM_004837 |
| <i>HMGCR</i> | 3-hydroxy-3-methylglutaryl-coenzyme-A reductase | NM_000859 |
| <i>INSIG1</i> | Insulin-induced gene 1 | NM_005542 |
| <i>LSS</i> | Lanosterol synthase | NM_002340 |
| <i>NSDHL</i> | NAD(P) dependent steroid dehydrogenase-like | NM_015922 |
| <i>SQLE</i> | Squalene epoxidase | NM_003129 |
| Hippo signaling pathway | | |
| <i>LATS1</i> | Large tumor suppressor kinase 1 | NM_004690 |
| <i>MOB1A</i> | MOB (Mps one binder) kinase activator 1A | NM_018221 |
| <i>SAV1</i> | Salvador family WW domain containing protein 1 | NM_021818 |
| <i>STK3</i> | Serine/threonine kinase 3 | NM_006281 |
| <i>WWTR1</i> | WW domain containing transcription regulator 1 | NM_015472 |
| <i>YAP1</i> | Yes1 associated transcriptional regulator | NM_006106 |
| YAP/TAZ-regulated genes | | |
| <i>BIRC5</i> | Baculoviral IAP repeat containing 5 | NM_001168 |
| <i>CDK6</i> | Cyclin dependent kinase 6 | NM_001259 |

Refseq, reference sequence; YAP, Yes-associated protein; TAZ, transcriptional coactivator with PDZ-binding motif.

Table S2 Correlation among the genes involved in cholesterol biosynthesis

| Gene | HN | | DCIS | |
|----------------------------|-------|---------|-------|---------|
| | r | P value | r | P value |
| <i>HMGCR</i> * | | | | |
| <i>FDPS</i> | 0.23 | 0.5517 | 0.20 | 0.6044 |
| <i>FDFT1</i> | 0.10 | 0.7963 | 0.24 | 0.5422 |
| <i>GGPS1</i> [†] | 0.64 | 0.0610 | 0.18 | 0.6354 |
| <i>SQLE</i> [†] | 0.69 | 0.0412 | -0.06 | 0.8805 |
| <i>LSS</i> [†] | -0.65 | 0.0666 | 0.44 | 0.2396 |
| <i>NSDHL</i> | -0.06 | 0.8810 | 0.13 | 0.7313 |
| <i>INSIG1</i> [†] | 0.85 | 0.0061 | 0.10 | 0.8038 |
| <i>FDPS</i> * | | | | |
| <i>FDFT1</i> | -0.58 | 0.1017 | 0.85 | 0.0034 |
| <i>GGPS1</i> | 0.26 | 0.5003 | 0.20 | 0.6134 |
| <i>SQLE</i> | 0.33 | 0.3786 | 0.34 | 0.3660 |
| <i>LSS</i> | 0.28 | 0.4630 | 0.48 | 0.1942 |
| <i>NSDHL</i> | 0.82 | 0.0068 | -0.25 | 0.5206 |
| <i>INSIG1</i> [†] | 0.25 | 0.5206 | 0.61 | 0.0843 |
| <i>FDFT1</i> * | | | | |
| <i>GGPS1</i> | -0.06 | 0.8715 | 0.21 | 0.5890 |
| <i>SQLE</i> | 0.11 | 0.7787 | 0.32 | 0.3957 |
| <i>LSS</i> | -0.24 | 0.5274 | 0.47 | 0.2057 |
| <i>NSDHL</i> | -0.73 | 0.0269 | -0.49 | 0.1854 |
| <i>INSIG1</i> [†] | 0.19 | 0.6183 | 0.62 | 0.0773 |
| <i>GGPS1</i> * | | | | |
| <i>SQLE</i> | 0.49 | 0.1832 | -0.69 | 0.0412 |
| <i>LSS</i> | -0.54 | 0.1301 | 0.22 | 0.5739 |
| <i>NSDHL</i> | 0.05 | 0.9060 | 0.12 | 0.7756 |
| <i>INSIG1</i> [†] | 0.61 | 0.0805 | 0.07 | 0.8636 |
| <i>SQLE</i> * | | | | |
| <i>LSS</i> | -0.46 | 0.2125 | -0.01 | 0.9914 |
| <i>NSDHL</i> | 0.12 | 0.7548 | -0.01 | 0.9830 |
| <i>INSIG1</i> [†] | 0.89 | 0.0014 | 0.51 | 0.1643 |
| <i>LSS</i> * | | | | |
| <i>NSDHL</i> | 0.33 | 0.3914 | -0.09 | 0.8138 |
| <i>INSIG1</i> [†] | -0.60 | 0.0968 | 0.53 | 0.1407 |
| <i>NSDHL</i> * | | | | |
| <i>INSIG1</i> | 0.07 | 0.8641 | -0.24 | 0.5422 |

The asterisks indicate the correlation between a given gene and the other genes involved in the biosynthetic pathway. [†], the associations reported in *Figure 4*. HN, histologically normal; DCIS, ductal carcinoma in situ.

Table S3 Correlation among the genes involved in cholesterol biosynthesis and the Hippo signaling pathway

| Gene | HN | | DCIS | |
|---------------------------|-------|---------|-------|---------|
| | r | P value | r | P value |
| <i>HMGCR</i> * | | | | |
| <i>LATS1</i> | -0.19 | 0.6183 | -0.24 | 0.5257 |
| <i>MOB1A</i> [†] | 0.64 | 0.0656 | 0.28 | 0.4720 |
| <i>SAV1</i> | -0.04 | 0.9149 | -0.04 | 0.9149 |
| <i>STK3</i> | 0.10 | 0.8100 | -0.02 | 0.9659 |
| <i>WWTR1</i> [†] | 0.83 | 0.0083 | -0.21 | 0.5890 |
| <i>YAP1</i> | 0.47 | 0.2125 | -0.09 | 0.8138 |
| <i>FDPS</i> * | | | | |
| <i>LATS1</i> | 0.20 | 0.6028 | -0.45 | 0.2296 |
| <i>MOB1A</i> [†] | 0.02 | 0.9489 | 0.62 | 0.0857 |
| <i>SAV1</i> | -0.17 | 0.6669 | 0.40 | 0.2912 |
| <i>STK3</i> | 0.42 | 0.2696 | -0.18 | 0.6436 |
| <i>WWTR1</i> | 0.05 | 0.9116 | 0.53 | 0.1475 |
| <i>YAP1</i> | -0.13 | 0.7435 | 0.33 | 0.3853 |
| <i>FDFT1</i> * | | | | |
| <i>LATS1</i> | -0.07 | 0.8624 | -0.45 | 0.2274 |
| <i>MOB1A</i> | 0.01 | 0.9742 | 0.27 | 0.4860 |
| <i>SAV1</i> | 0.39 | 0.3019 | 0.45 | 0.2220 |
| <i>STK3</i> | -0.37 | 0.3274 | -0.24 | 0.5292 |
| <i>WWTR1</i> | 0.20 | 0.6028 | 0.57 | 0.1098 |
| <i>YAP1</i> | 0.20 | 0.6028 | 0.28 | 0.4720 |
| <i>GGPS1</i> * | | | | |
| <i>LATS1</i> [†] | -0.24 | 0.5257 | -0.87 | 0.0026 |
| <i>MOB1A</i> | 0.11 | 0.7797 | 0.25 | 0.5206 |
| <i>SAV1</i> | 0.36 | 0.3454 | -0.27 | 0.4933 |
| <i>STK3</i> [†] | 0.70 | 0.0347 | -0.85 | 0.0061 |
| <i>WWTR1</i> [†] | 0.76 | 0.0171 | -0.47 | 0.2125 |
| <i>YAP1</i> | 0.50 | 0.1684 | 0.37 | 0.3363 |
| <i>SQLE</i> * | | | | |
| <i>LATS1</i> | 0.34 | 0.3680 | 0.60 | 0.0854 |
| <i>MOB1A</i> | 0.23 | 0.5497 | 0.14 | 0.7150 |
| <i>SAV1</i> | 0.34 | 0.3765 | 0.18 | 0.6511 |
| <i>STK3</i> [†] | 0.43 | 0.2520 | 0.71 | 0.0317 |
| <i>WWTR1</i> | 0.61 | 0.0805 | 0.60 | 0.0860 |
| <i>YAP1</i> | 0.13 | 0.7476 | -0.51 | 0.1603 |
| <i>LSS</i> * | | | | |
| <i>LATS1</i> | 0.16 | 0.6816 | -0.57 | 0.1062 |
| <i>MOB1A</i> | -0.07 | 0.8641 | 0.42 | 0.2624 |
| <i>SAV1</i> | -0.37 | 0.3296 | 0.37 | 0.3296 |
| <i>STK3</i> | -0.15 | 0.7081 | -0.48 | 0.1942 |
| <i>WWTR1</i> [†] | -0.77 | 0.0214 | 0.31 | 0.4175 |
| <i>YAP1</i> [†] | -0.65 | 0.0666 | 0.14 | 0.7150 |
| <i>NSDHL</i> * | | | | |
| <i>LATS1</i> | 0.05 | 0.8885 | 0.17 | 0.6656 |
| <i>MOB1A</i> | -0.10 | 0.8047 | 0.03 | 0.9484 |
| <i>SAV1</i> [†] | 0.02 | 0.9658 | -0.68 | 0.0503 |
| <i>STK3</i> | 0.44 | 0.2318 | 0.10 | 0.8100 |
| <i>WWTR1</i> | -0.03 | 0.9316 | -0.32 | 0.4101 |
| <i>YAP1</i> | -0.40 | 0.2839 | -0.63 | 0.0760 |
| <i>INSIG1</i> * | | | | |
| <i>LATS1</i> | -0.12 | 0.7631 | -0.20 | 0.5997 |
| <i>MOB1A</i> | 0.42 | 0.2624 | 0.63 | 0.0688 |
| <i>SAV1</i> | 0.35 | 0.3537 | 0.39 | 0.2928 |
| <i>STK3</i> | 0.30 | 0.4366 | -0.13 | 0.7466 |
| <i>WWTR1</i> [†] | 0.78 | 0.0172 | 0.36 | 0.3393 |
| <i>YAP1</i> | 0.37 | 0.3363 | 0.02 | 0.9658 |

The asterisks indicate the correlation between a given gene and the other genes involved in the biosynthetic pathway. [†], the associations reported in Figure 6. HN, histologically normal; DCIS, ductal carcinoma in situ.