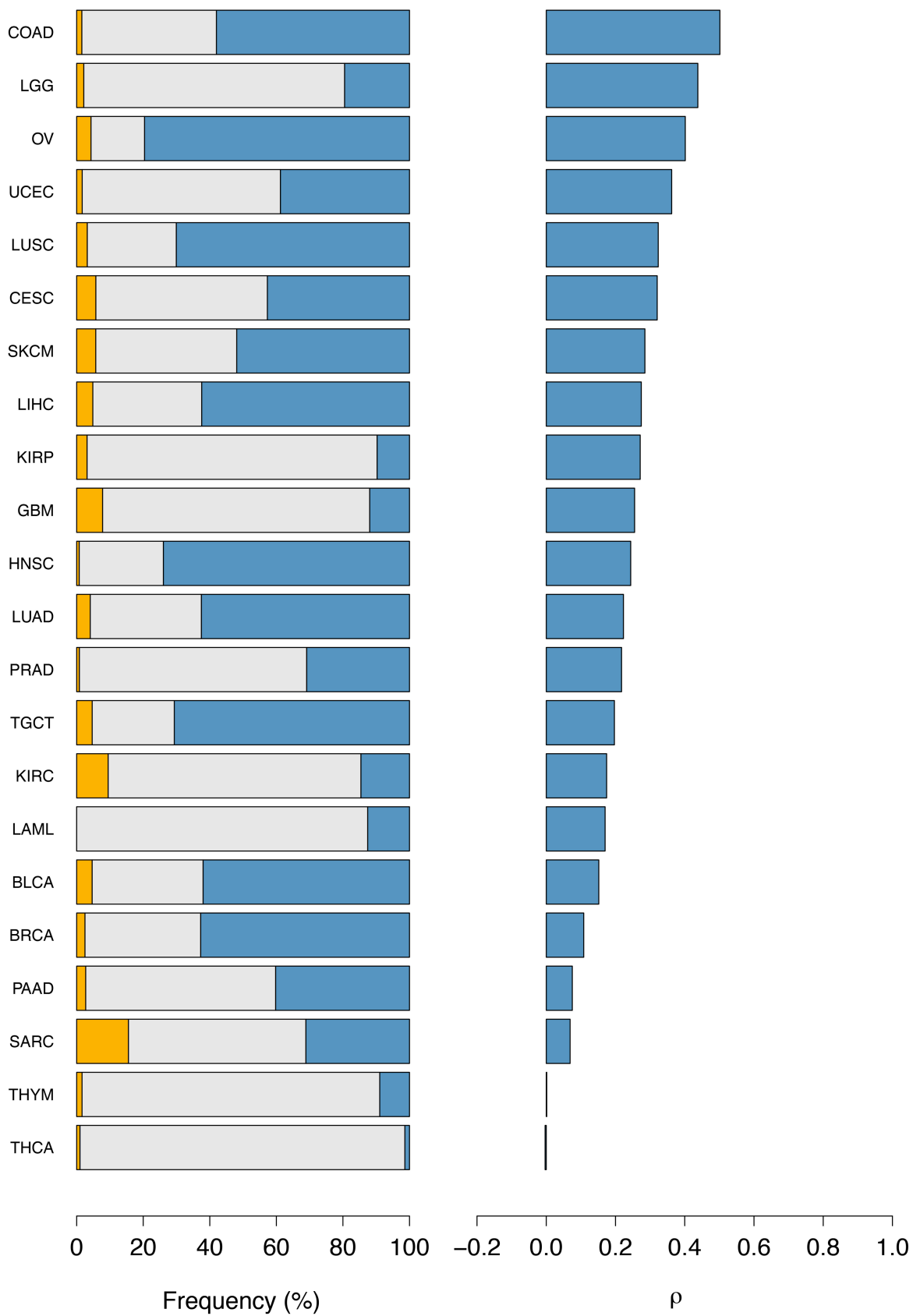


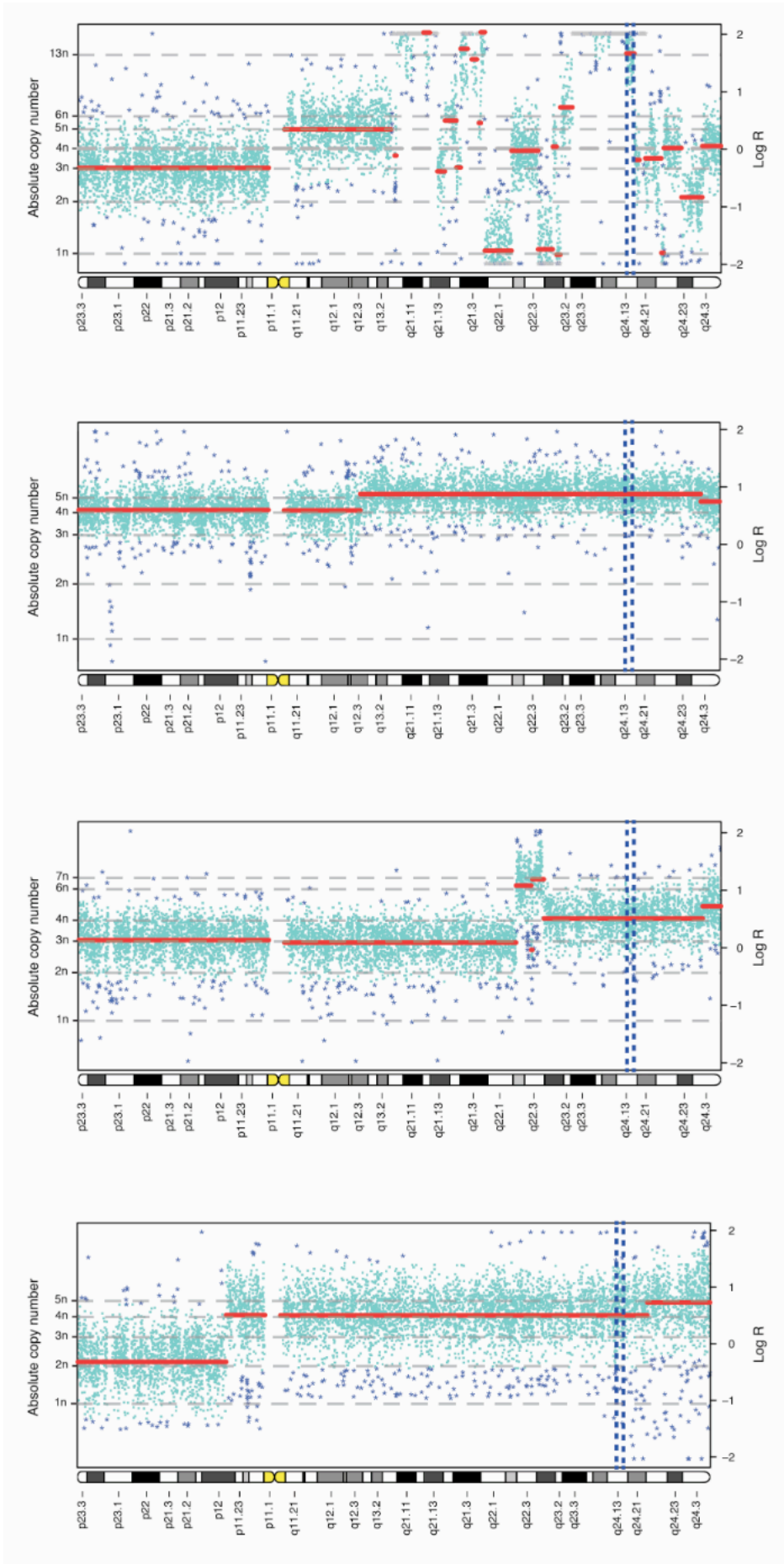
**Title:**

Squalene epoxidase is a *bona fide* oncogene by amplification with clinical relevance in breast cancer.

**Authors:**

David N Brown, Irene Caffa, Gabriella Cirmena, Daniela Piras, Anna Garuti, Maurizio Gallo, Saverio Alberti, Alessio Nencioni, Alberto Ballestrero, Gabriele Zoppoli.



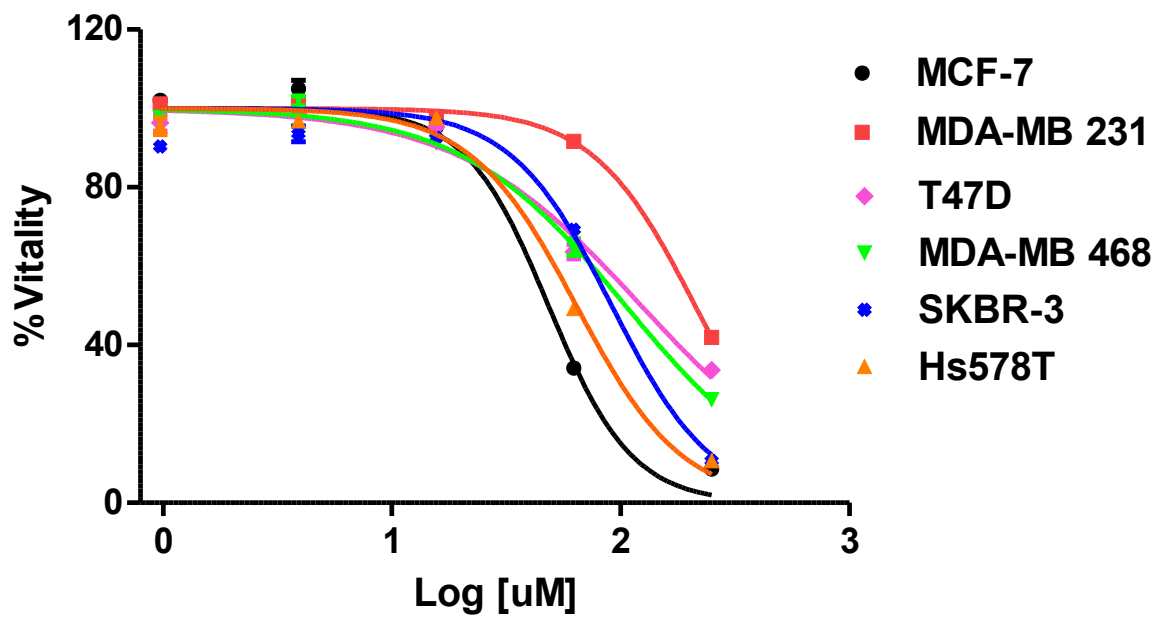


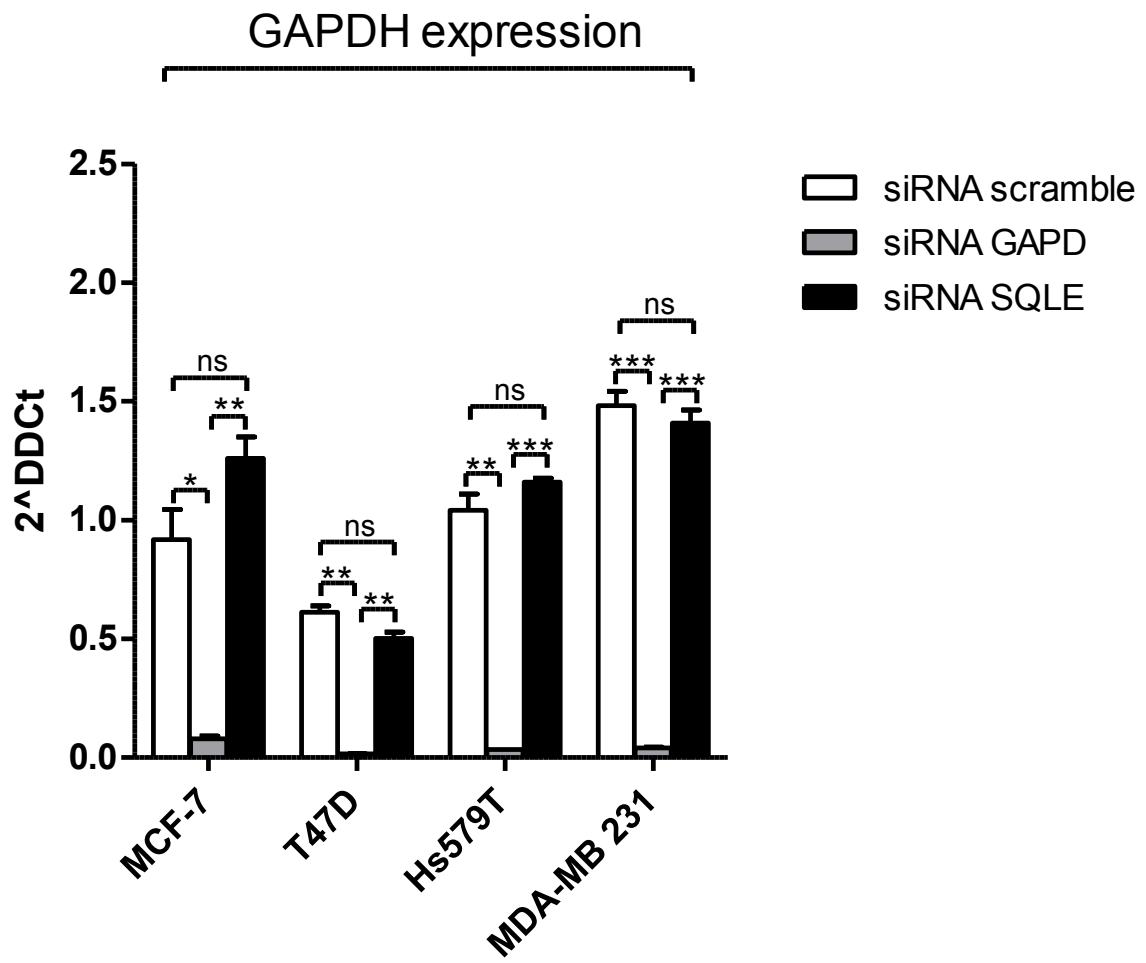
Set	N	Loss <sup>A</sup>	Gain <sup>A</sup>	$\rho^B$	P	FDR
COAD	323	0.02	0.58	0.5	5.50E-22	< 10E-6
LGG	526	0.02	0.19	0.44	4.80E-26	< 10E-6
OV	258	0.04	0.8	0.4	2.03E-11	< 10E-6
UCEC	196	0.02	0.39	0.36	1.81E-07	< 10E-5
LUSC	548	0.03	0.7	0.32	8.10E-15	< 10E-6
CESC	295	0.06	0.43	0.32	1.82E-08	< 10E-6
SKCM	470	0.06	0.52	0.28	3.14E-10	< 10E-6
LIHC	411	0.05	0.62	0.27	1.54E-08	< 10E-6
KIRP	319	0.03	0.1	0.27	8.60E-07	<10E-4
GBM	158	0.08	0.12	0.26	1.21E-03	< 0.001
HNSC	554	0.01	0.74	0.24	5.98E-09	< 10E-6
LUAD	560	0.04	0.63	0.22	9.63E-08	< 10E-5
PRAD	540	0.01	0.31	0.22	3.28E-07	< 10E-5
TGCT	150	0.05	0.71	0.2	1.57E-02	<0.05
KIRC	595	0.09	0.15	0.17	1.89E-05	< 0.0001
LAML	157	0	0.13	0.17	3.33E-02	<0.05
BLCA	419	0.05	0.62	0.15	1.84E-03	<0.01
BRCA	1178	0.03	0.63	0.11	1.95E-04	< 0.001
PAAD	181	0.03	0.4	0.08	3.14E-01	0.3452
SARC	260	0.16	0.31	0.07	2.68E-01	0.3106
THCA	564	0.01	0.01	0	9.37E-01	0.9817
THYM	121	0.02	0.09	0	9.88E-01	0.9876

<b>Doubling time measurements (h)</b>		
	<b><u>siRNA Scramble</u></b>	<b><u>siRNA SQLE</u></b>
MCF-7	56,5+/-2,6	98,5+/-3,4
Hs578T	134,6+/-2,7	178,2+/-2,6
T47D	55,5+/-3,1	115,9+/-4,2
MDA-MB231	42,2+/-3,2	42,9+/-4,1

Terbinafine titration					
IC50			IC50		
MCF-7	46,5uM		MDA-MB 468	105uM	
Hs578T	64,05uM		T47D	123,6uM	
SKBR-3	91,4uM		MDA-MB 231	211,9uM	

### Terbinafin titration





**Supplemental figure 1 (page 2): Correlation of MYC CN and GE in TCGA.** All cancer histotypes with at least 100 cases collected by the TCGA were assessed for the presence of MYC copy number gains and losses (blue and orange respectively, left bar chart), and  $\log_2$  ratios were correlated with normalized MYC gene expression using the Spearman's correlation coefficient ( $\rho$  value on the  $x$ -axis, decreasing from highest to lowest, right bar chart). Full definitions of the TCGA acronyms can be found at <https://tcga-data.nci.nih.gov/tcga>.

**Supplemental figure 2 (page 3): Chromosome 8 karyogram of (top to bottom) SK-BR-3, Hs 578T, MDA-MB-468, and T-47D.** Left  $y$ -axis: absolute copy numbers. Right  $y$ -axis:  $\log_2$  ratio.  $x$ -axis: chromosome 8 cytobands. Thick horizontal red lines represent segmented regions, turquoise dots are individual probes, whereas blue asterisks are outlier probes excluded from segmentation analysis. Dashed blue boxes enclose the SQLE locus.

**Supplementary Table S1 (page 4): TCGA cancer sets and MYC CN/GE.** <sup>A</sup>SQLE fraction of losses and gains defined by GISTIC 2.0. <sup>B</sup>Spearman's correlation coefficient. Full definitions of the TCGA acronyms can be found at <https://tcga-data.nci.nih.gov/tcga>.

**Supplementary Table S2 (page 5): Second biological replicate of siRNA doubling time measurements in hours.** Time is expressed in hours (h) for doubling time of cell lines treated with scramble or targeting siRNA.

**Supplementary figure 3 (page 6): Second biological replicate of terbinafine titration in the six-cell line set.** IC50 = terbinafine concentration inhibiting 50% of cell growth.  $\mu\text{M}$  = micromolar concentration.  $y$ -axis: Percent of cells viable by MTT assay,  $x$ -axis: micromolar concentration of terbinafine. Whiskers represent standard error of the means (S.E.M.).



***Supplementary figure 4 (page 7): GAPDH expression in scramble, GAPDH, and SQLE siRNA treated cells.*** \*\*=  $P < 0.01$ , \*\*\* =  $P < 0.001$ , NS = non significant. Whiskers represent S.E.M. P values are calculated by ANOVA with contrasts with the Bonferroni correction for multiple testing. Data are normalized using the median of scramble siRNA.