Identification of DISE-inducing shRNAs by monitoring cellular responses

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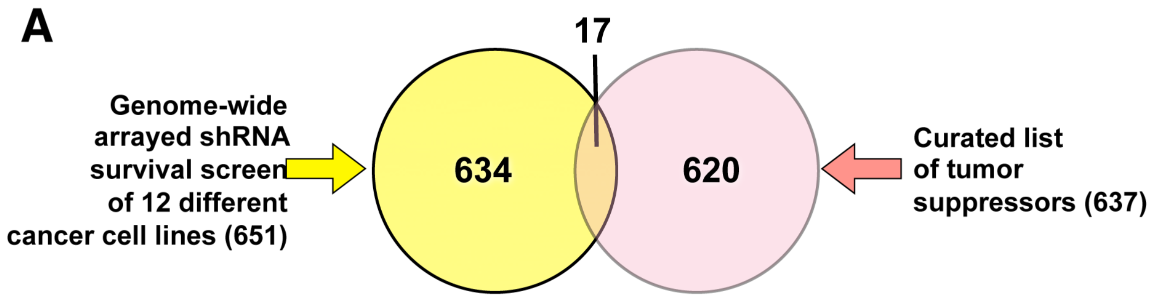
Supplementary data



B

The TS-D genes	Full name	TSG for Cancer	Kd lethal for # of cell lines	AVG H score
PAFAH1B1/LIS1	Platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	HCC [1]	12	80
NGFR	Nerve growth factor receptor	HCC [2], retinoblastoma [3], prostate cancer [4], bladder cancer [5]	11	89
ITGAV/CD51	Integrin Alpha V	Ovarian cancer [6], SCC [7]	11	76
DPP4/CD26	Dipeptidyl-peptidase 4	NSCLC [8]	10	94
EFNA5	Ephrin-A5	Glioma [9]	10	80
TMEFF1	Transmembrane protein with EGF-like and two follistatin-like domains 1	Brain cancers [10]	10	84
CHEK1	Checkpoint kinase 1	BrCa [11], Multiple cancers [12]	10	55
PTCH2	Patched 2	Basal cell carcinoma [13]	9	91
ARMC10/SVH	Armadillo repeat containing 10	Osteosarcoma [14], Leukemia [15]	9	84
BECN1/ATG6	Beclin 1	Breast cancer [16, 17, 18]	9	84
FASLG	Fas ligand	Multiple cancers [19]	9	84
DDX3X/DBX	DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked	HCC [20, 21], cutaneous squamous cell carcinoma [21]	9	80
THY1/CD90	Thy-1 cell surface antigen	Nasopharyngeal carcinoma [22], ovarian cancer [23, 24]	9	87
PHB	Prohibitin	Prostate cancer [25], liver cancer [26]	9	84
SOCS3	Suppressor of cytokine signaling 3	Breast cancer [27]	9	82
ZNF366/DC-SCRIPT	Zinc finger protein 366	Breast cancer [28]	9	80
MAPKAPK5/MK5/PRAK	Mitogen-activated protein kinase-activated protein kinase 5	Colon cancer [29], skin cancer [30]	9	68
TGFBR2	Transforming growth factor, beta receptor II (70/80kDa)	HCC [31], breast cancer [32, 33]	9	58

Figure S1: Identification of TS genes among 651 survival genes. (A) Venn diagram showing the overlap of the 651 putative survival genes we identified in 12 genome-wide shRNAs screens with a list of 637 putative tumor suppressors (http://bioinfo.mc.vanderbilt.edu/TSGene). (B) A list of the 17 genes that are putative tumor suppressors and were identified in our lethality screen. The genes are ranked first according to the number of lethality screens in which these genes were found to be survival genes, and second according to the average H score. Higher counts are indicated by darker colors. HCC, hepatocellular carcinoma. FASLG is also shown for comparison. [1], [1]; [2], [2]; [3], [3]; [4], [4]; [5], [5]; [6], [6]; [7], [7]; [8], [8]; [9], [9]; [10], [10]; [11], [11]; [12], [12]; [13], [13]; [14], [14]; [15], [15]; [16], [16]; [17], [17]; [18], [18]; [19], [19]; [20], [20]; [21], [21]; [22], [22]; [23], [23]; [24], [24]; [25], [25]; [26], [26]; [27], [27]; [28], [28]; [29], [29]; [30], [30]; [31], [31]; [32], [32]; [33], [33]. http://bioinfo.mc.vanderbilt.edu/TSGene [34].

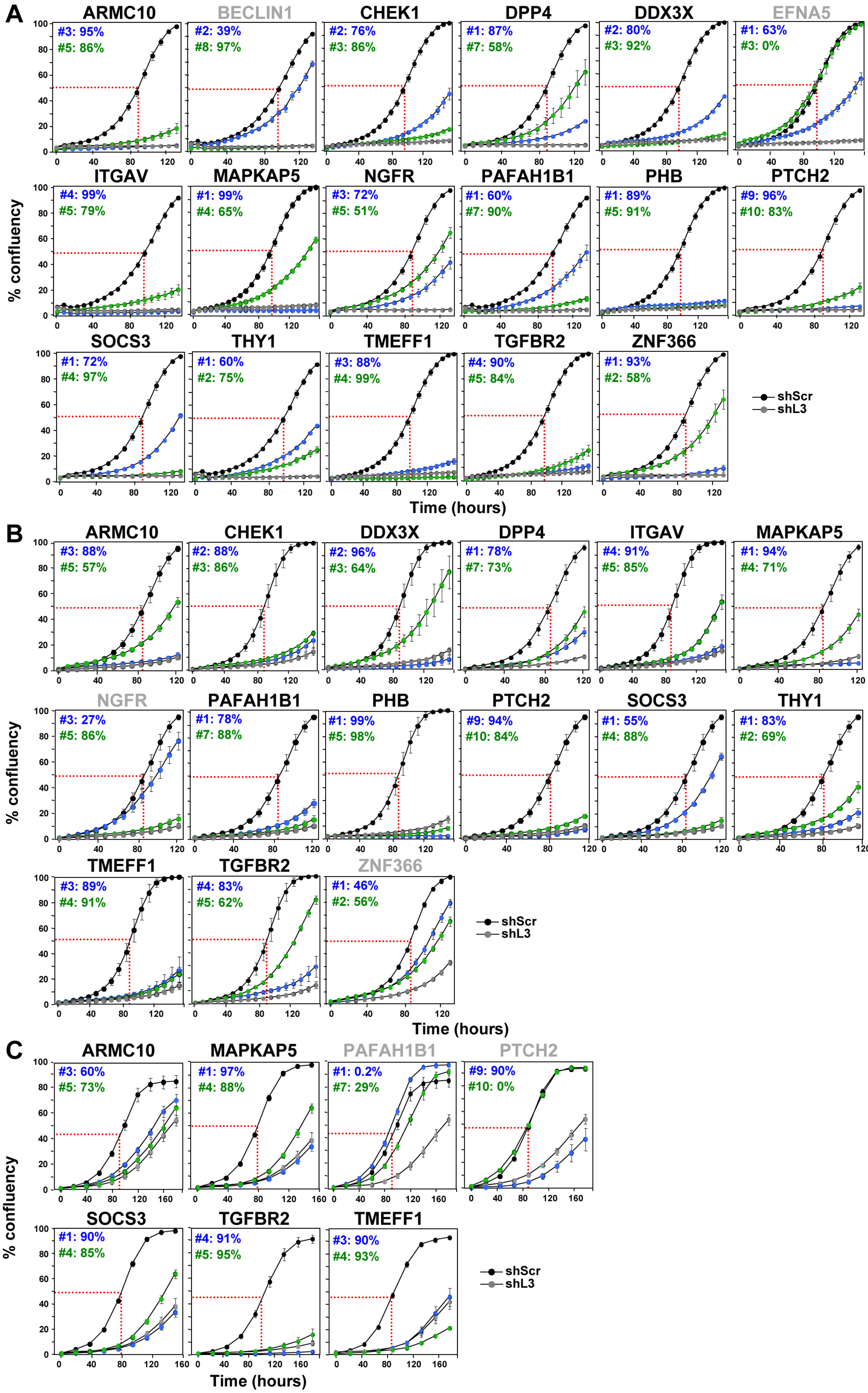

A
ARMC10
#3: 95%
#5: 86%
BECLIN1
#2: 39%
#8: 97%
CHEK1
#2: 76%
#3: 86%
DPP4
#1: 87%
#7: 58%
DDX3X
#2: 80%
#3: 92%
EFNA5
#1: 63%
#3: 0%
ITGAV
#4: 99%
#5: 79%
MAPKAP5
#1: 99%
#4: 65%
NGFR
#3: 72%
#5: 51%
PAFAH1B1
#1: 60%
#7: 90%
PHB
#1: 89%
#5: 91%
PTCH2
#9: 96%
#10: 83%
SOCS3
#1: 72%
#4: 97%
THY1
#1: 60%
#2: 75%
TMEFF1
#3: 88%
#4: 99%
TGFBR2
#4: 90%
#5: 84%
ZNF366
#1: 93%
#2: 58%
shScr
shL3
% confluency
Time (hours)
B
ARMC10
#3: 88%
#5: 57%
CHEK1
#2: 88%
#3: 86%
DDX3X
#2: 96%
#3: 64%
DPP4
#1: 78%
#7: 73%
ITGAV
#4: 91%
#5: 85%
MAPKAP5
#1: 94%
#4: 71%
NGFR
#3: 27%
#5: 86%
PAFAH1B1
#1: 78%
#7: 88%
PHB
#1: 99%
#5: 98%
PTCH2
#9: 94%
#10: 84%
SOCS3
#1: 55%
#4: 88%
THY1
#1: 83%
#2: 69%
TMEFF1
#3: 89%
#4: 91%
TGFBR2
#4: 83%
#5: 62%
ZNF366
#1: 46%
#2: 56%
shScr
shL3
% confluency
Time (hours)
C
ARMC10
#3: 60%
#5: 73%
MAPKAP5
#1: 97%
#4: 88%
PAFAH1B1
#1: 0.2%
#7: 29%
PTCH2
#9: 90%
#10: 0%
SOCS3
#1: 90%
#4: 85%
TGFBR2
#4: 91%
#5: 95%
TMEFF1
#3: 90%
#4: 93%
shScr
shL3
% confluency
Time (hours)

Figure S2. Toxic shRNAs cause growth reduction in T98G, HCT116 and Hap1 cells.
Percent cell confluency over time of T98G (A), HCT116 (B) and Hap1 (C) cells infected with shScr, shL3, and two shRNAs derived from each TS gene. The curves for cells infected with two independent shRNA for each TS gene and their specific ID number and respective growth reduction caused by each shRNA are shown in blue and green. Percent growth reduction values (as shown in Table 1) were calculated using STATA1C software when cells infected with shScr reached half maximal confluency as indicated by the red dotted line. Names of genes for which only one of the two shRNAs reduced growth more than 50% are shown in grey.

Supplementary references

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