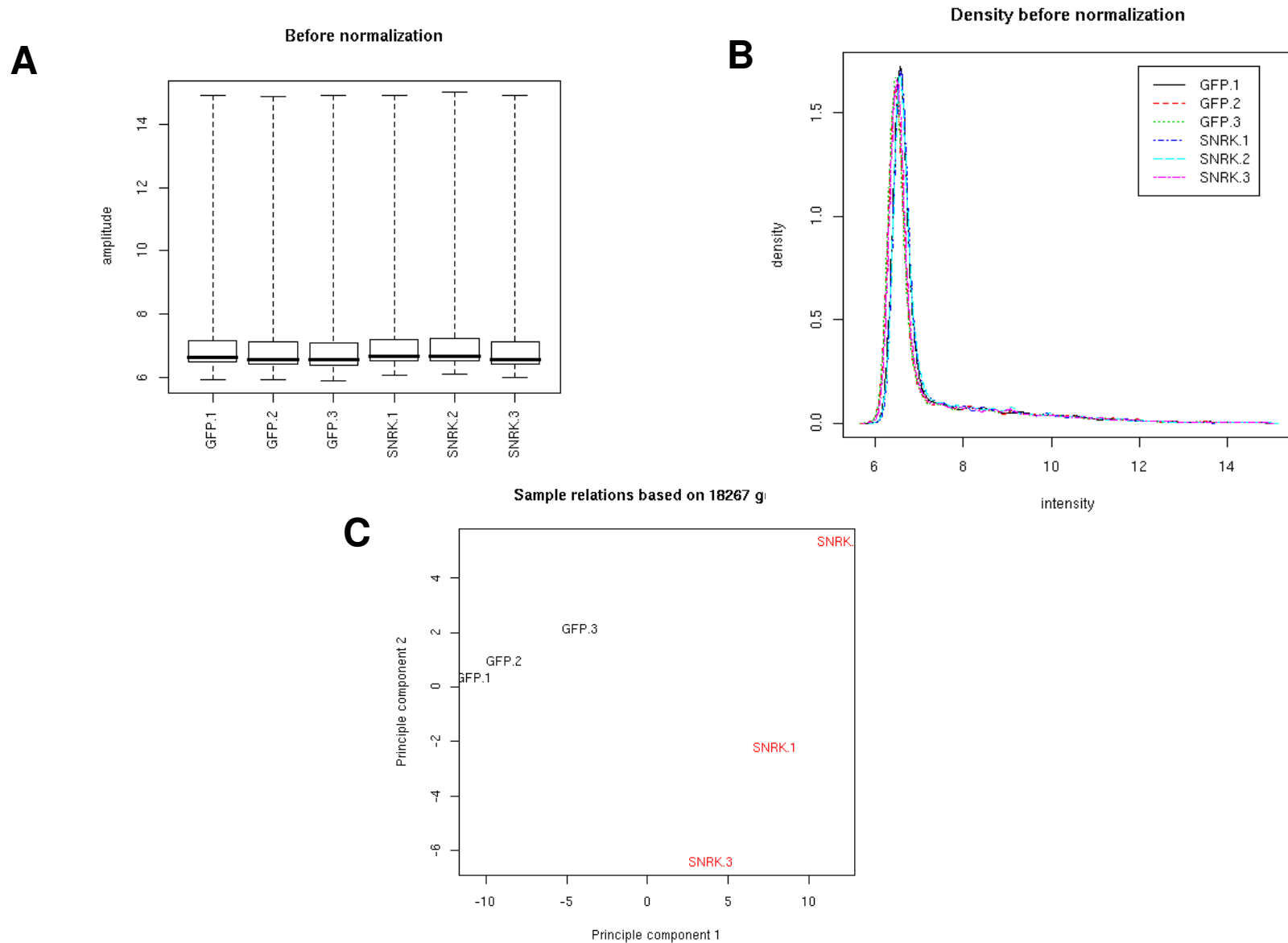
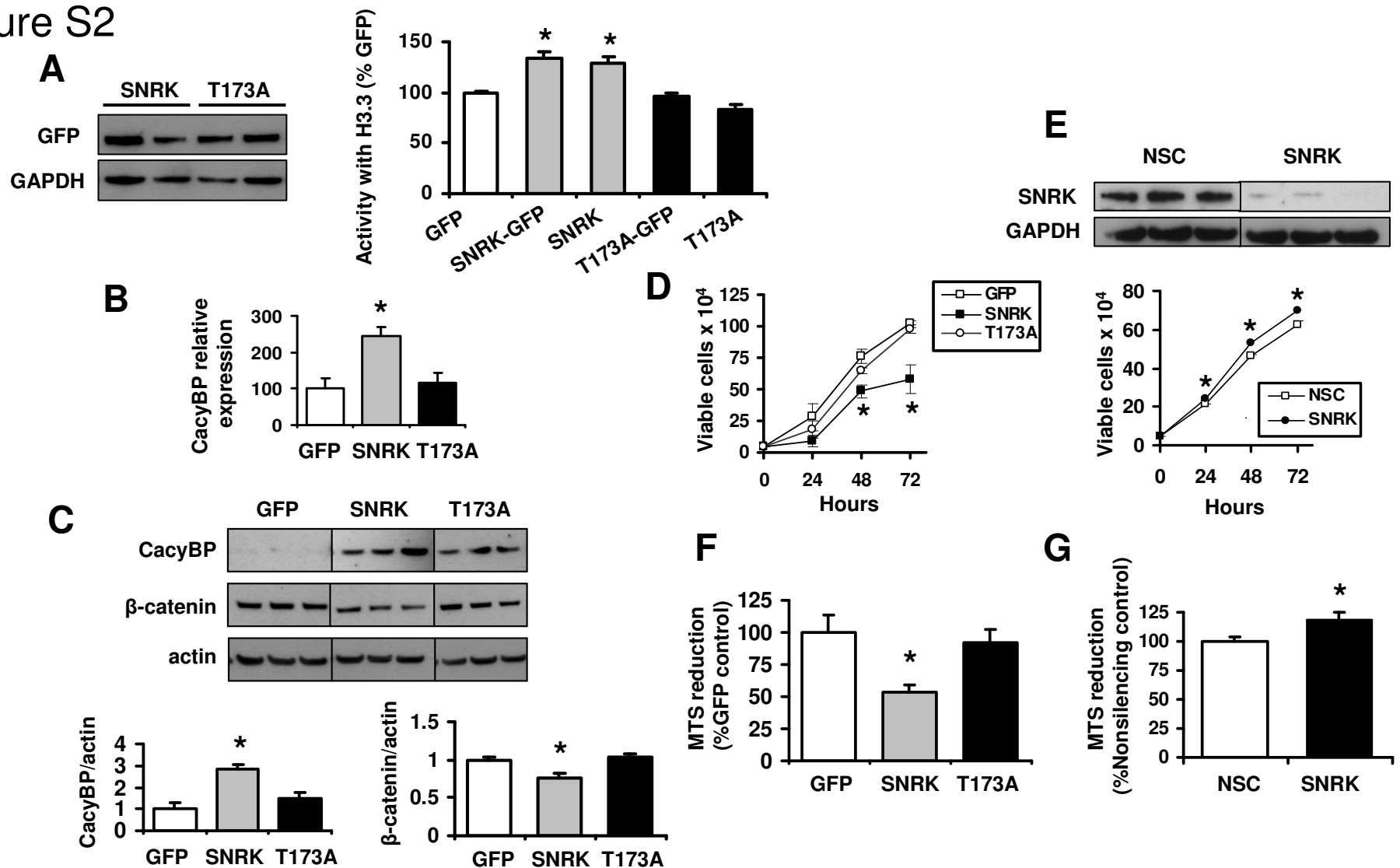


# Figure S1



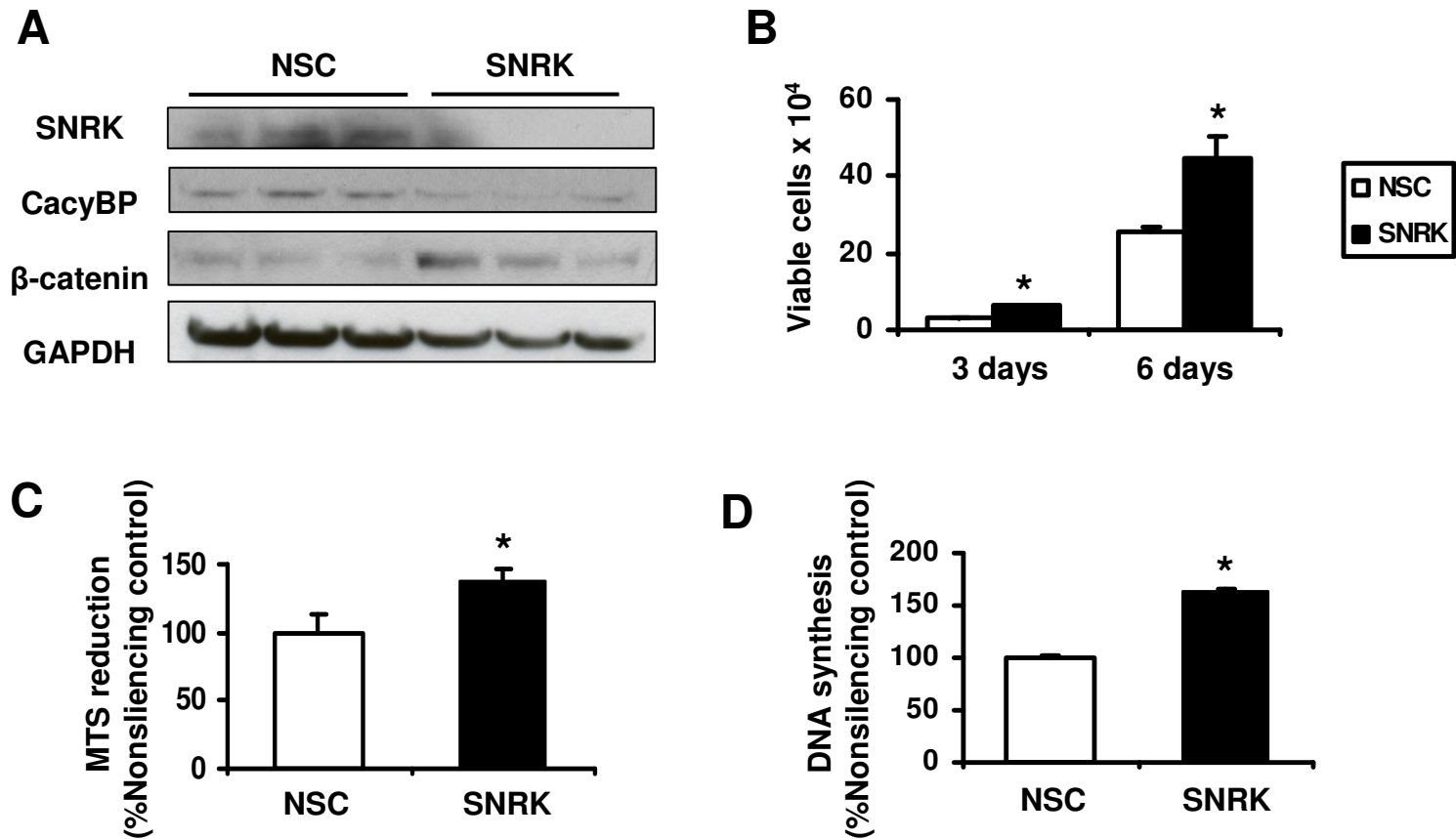
**Figure S1.** Quality control and relations of the samples used in the gene array analysis. *A* and *B*) Quality control analysis based on the control probe information and quality control plots. *C*) To illustrate the relationships among the arrays, as inferred by the distance from a genome-wide transcription survey, arrays were clustered before analysis.

Figure S2



**Figure S2.** SNRK increases CacyBP levels and decreases  $\beta$ -catenin protein and proliferation in HEK293 cells. *A*) Expression and activity of SNRK and T173A in HEK293 cells.  $n \geq 3$ . *B*) Levels of CacyBP mRNA with overexpression of SNRK or controls in HEK293 cells.  $n = 3$ . *C*) Levels of CacyBP protein and  $\beta$ -catenin protein in HEK293 cells with overexpression of SNRK or controls. Lanes from the same gel have been rearranged for clarity.  $n = 3$ . *D*) Proliferation in transfected HEK293 cells as measured by viable cell number.  $n = 3$ . *E*) Western blots of SNRK protein, and proliferation as measured by viable cell number in HEK293 cells treated with SNRK or nonsilencing control (NSC) shRNA. Lanes from the same gel have been rearranged for clarity. *F*) Proliferation in transfected HEK293 cells as measured by MTS reduction.  $n = 7$ . *G*) Proliferation with SNRK knockdown in HEK293 cells as measured by MTS reduction.  $n = 3$ . \*  $p < 0.05$  vs. GFP and T173A or vs. NSC.

Figure S3



**Figure S3.** Stable knockdown of SNRK in RKO cells reduces CacyBP and increases  $\beta$ -catenin and cell proliferation. *A*) Western blots for SNRK, CacyBP,  $\beta$ -catenin, and GAPDH in RKO cells with stable knockdown of SNRK or with nonsilencing control (NSC) shRNA. *B*) Viable cell number in RKO cells with stable SNRK knockdown as determined by cell counting with Trypan Blue exclusion at 3 and 6 days.  $n=6$ . *C*) MTS reduction in RKO cells with stable SNRK knockdown after 6 days of growth.  $n=6$ . *D*) BrdU incorporation for 24 hours in RKO cells with stable SNRK knockdown.  $n=6$ . \*  $p < 0.05$  vs. NSC.

# Tables S1-S3

**S1**

Genes with the smallest p-values - induction:				
Gene symbol	Gene name	Fold change	p-value	FDR
APP	amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)	2.22713289	2.37E-08	0.00014442
LOC644695	hypothetical LOC644695	1.54645886	1.56E-07	0.00015812
C6orf125	chromosome 6 open reading frame 125	1.66041491	1.61E-07	0.00015812
ARHGAP19	Rho GTPase activating protein 19	1.94579127	7.05E-07	0.00049516
C20orf52	chromosome 20 open reading frame 52	1.53865966	8.26E-07	0.00053622
WDR79	WD repeat domain 79	1.54103949	2.35E-06	0.00113898
ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	1.51397702	3.25E-06	0.00138161
CACYBP	calcyclin binding protein	1.59911286	3.97E-06	0.00154653
UNC45A	unc-45 homolog A (C. elegans)	1.60265752	4.15E-06	0.00154653
LARP5	La ribonucleoprotein domain family, member 5	1.51988305	4.90E-06	0.00162618
STX10	syntaxin 10	1.52749637	6.62E-06	0.00202089
ARID3A	AT rich interactive domain 3A (BRIGHT-like)	1.68621871	7.50E-06	0.00207596
MTF1	metal-regulatory transcription factor 1	1.90735052	1.45E-05	0.0030534
VAT1	vesicle amine transport protein 1 homolog (T. californica)	1.56974703	1.82E-05	0.00353096
ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	1.70208823	2.76E-05	0.00430463
LOC130773	similar to 60S ribosomal protein L23a	1.640351	4.05E-05	0.00506342
MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-AGT, isozyme B	1.59709588	4.82E-05	0.00550588
SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	1.77100828	5.16E-05	0.00578718
SORBS3	sorbin and SH3 domain containing 3	1.73519754	5.44E-05	0.00592268
JOSD2	Josephin domain containing 2	1.65068674	6.33E-05	0.00631489
Genes with the smallest p-values - suppression:				
Gene symbol	Gene name	Fold change	p-value	FDR
VTI1A	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	-3.0745586	2.18E-09	3.98E-05
RFX3	regulatory factor X, 3 (influences HLA class II expression)	-2.3150485	4.01E-08	0.00014532
LOC339240	keratin pseudogene	-2.1923235	6.50E-08	0.00015812
TMEM186	transmembrane protein 186	-2.0703648	1.33E-07	0.00015812
C1orf130	chromosome 1 open reading frame 130	-5.4386983	1.39E-07	0.00015812
B3GNT8	UDP-GlcNAc:betaGal beta-1,3-N-acetylgucosaminyltransferase 8	-2.1762886	1.81E-07	0.00016538
STK32B	serine/threonine kinase 32B	-2.755595	1.94E-07	0.00016887
KCNJ4	potassium inwardly-rectifying channel, subfamily J, member 4	-1.6392272	5.24E-07	0.00041643
FOXD4L4	forkhead box D4-like 4	-1.9925315	8.51E-07	0.00053622
LOC644151	similar to calpain 8	-2.3207326	1.15E-06	0.00070184
STRN	striatin, calmodulin binding protein	-1.8677273	1.55E-06	0.00091625
KIAA0774	KIAA0774	-2.0827202	1.90E-06	0.00099033
CALN1	calneuron 1	-1.5863672	2.43E-06	0.00113898
DLK2	delta-like 2 homolog (Drosophila)	-1.5245633	2.50E-06	0.00114086
ZNF180	zinc finger protein 180	-1.9272154	2.57E-06	0.00114717
SBF1	SET binding factor 1	-1.5837656	7.18E-06	0.00207596
KCNV2	potassium channel, subfamily V, member 2	-1.7284786	9.78E-06	0.00252145
CAPN6	calpain 6	-1.6409959	1.37E-05	0.00299865
SCAP	SREBF chaperone	-1.7264415	1.89E-05	0.00359919
TINF2	TERF1 (TRF1)-interacting nuclear factor 2	-1.5908685	2.53E-05	0.00416009

**S2**

GO.Term	p-value	significant gene number	increase ~ decrease
DNA binding	2.99E-05	125	71 ~ 55
transcription factor binding	3.35E-05	35	21 ~ 16
RNA polymerase II transcription factor activity	0.0002809	6	3 ~ 3
transcription coactivator activity	0.00071647	18	10 ~ 10
pyrroline-5-carboxylate reductase activity	0.00078151	3	2 ~ 1

**S3**

GO.Term	p-value	significant gene number	increase ~ decrease
nucleus	1.69E-09	188	111 ~ 80
intracellular membrane-bound organelle	4.61E-09	283	174 ~ 112
nuclear part	4.83E-08	70	39 ~ 33
intracellular part	4.92E-08	396	236 ~ 163
cell part	4.59E-07	555	304 ~ 254
intracellular organelle	4.70E-07	316	190 ~ 129
nuclear lumen	2.35E-05	42	24 ~ 20
nucleoplasm	0.00022067	31	19 ~ 14
nuclear chromosome	0.00091382	11	8 ~ 3
nucleoplasm part	0.00093084	25	15 ~ 12
intracellular organelle part	0.00095558	127	75 ~ 54

**Table S1.** List of top genes altered by SNRK-GFP vs. GFP overexpression in the microarray. Top genes were chosen from all genes with a false discovery rate (FDR) < 0.05, a p-value < 0.01 and a fold change larger than 1.5.

**Table S2.** Gene Ontology Analysis for the molecular function of genes altered in the microarray.

**Table S3.** Gene Ontology Analysis for the cellular location of genes altered in the microarray.