Supplementary figures and tables

Fig S1. Schematic representation of DCLK3 sequences, regional expression of its mRNA in mouse brain, and autophosphorylation activity.

A, Schematic representation of the primary structure of DCLK3 indicating the principal predicted functional domains, with the kinase domain, the most strongly conserved across species. **B,** Northern blot analysis was performed on poly(A)$^+$ RNA purified from wild-type mouse brain regions. Same amount of RNA was loaded in all lanes. The membrane was hybridized with a probe for the DCLK3 transcript. Note that two mRNA species are produced preferentially in the striatum: the upper band corresponds to the long form of DCLK3 (L-DCLK3 mRNA), the lower fainter band corresponds to the short form of DCLK3 (S-DCLK3 mRNA). **C**, The recombinant mouse DCLK3 proteins were produced in HEK293T cells and, after immunoprecipitation with an antibody against the HA tag, they were tested for autophosphorylation activity in presence of ^{32}P-ATP. The high molecular weight forms (black arrows) of S-rDCLK3 (73 kDa) and L-rDCLK3 (90 kDa) and the 75 kDa cleavage product of L-rDCLK3 had the highest activities.

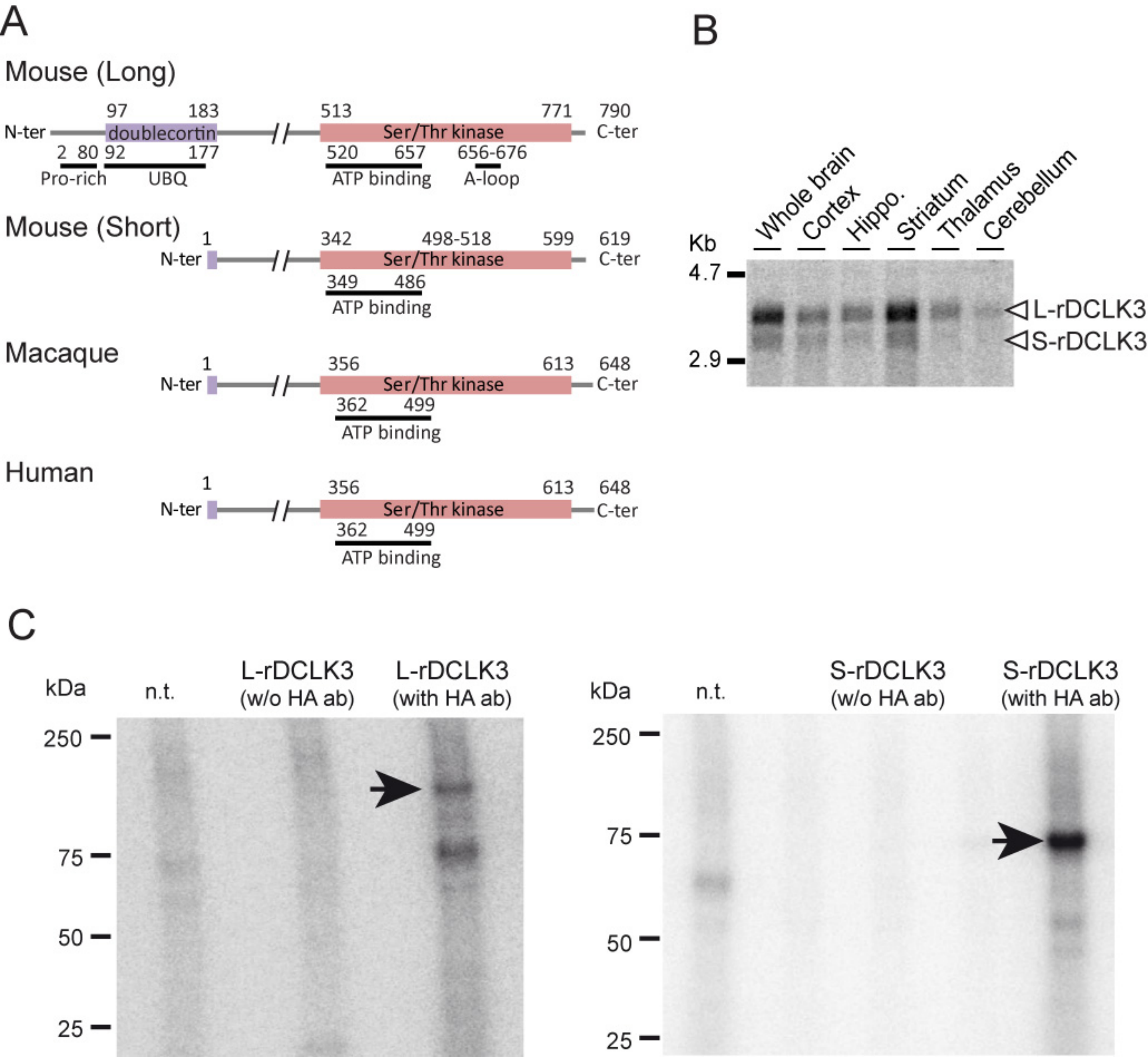

A
Mouse (Long)
97 183 513 771 790
N-ter doublecortin Ser/Thr kinase C-ter
2 80 92 177 520 657 656-676
Pro-rich UBQ ATP binding A-loop
Mouse (Short)
1 342 498-518 599 619
N-ter Ser/Thr kinase C-ter
349 486
ATP binding
Macaque
1 356 613 648
N-ter Ser/Thr kinase C-ter
362 499
ATP binding
Human
1 356 613 648
N-ter Ser/Thr kinase C-ter
362 499
ATP binding
B
Kb
Whole brain
Cortex
Hippo.
Striatum
Thalamus
Cerebellum
4.7
2.9
L-rDCLK3
S-rDCLK3
C
kDa
n.t.
L-rDCLK3 (w/o HA ab)
L-rDCLK3 (with HA ab)
250
75
50
25
kDa
n.t.
S-rDCLK3 (w/o HA ab)
S-rDCLK3 (with HA ab)
250
75
50
25

Fig S2. Efficiency of lentiviral vectors (LV) encoding rDCLK3-HA and a shRNA targeting DCLK3

A, Schematic representation of the lentiviral constructs used to overexpress S-rDCLK3-HA, L-rDCLK3-HA or to silence its expression in mice. **B,** Mice received striatal injections of LV-rDCLK3-HA (mixed with a lentiviral vector encoding GFP) or LV-shDCLK3 (bicistronic construct also encoding GFP). **C**, Six weeks later, the striatal region expressing GFP was dissected out and analyzed by RT-qPCR or western blot. **D**, LV-shDCLK3 yielded a significant ~70% decrease in DCLK3 levels. **E**, representative western blots of striatal samples showing expression of S-rDCLK3 and L-rDCLK3. Each lane represents a different striatal sample. Results are expressed as means ± the standard error of the mean (SEM). *, $p<0.01$, Unpaired Student’s *t* test.

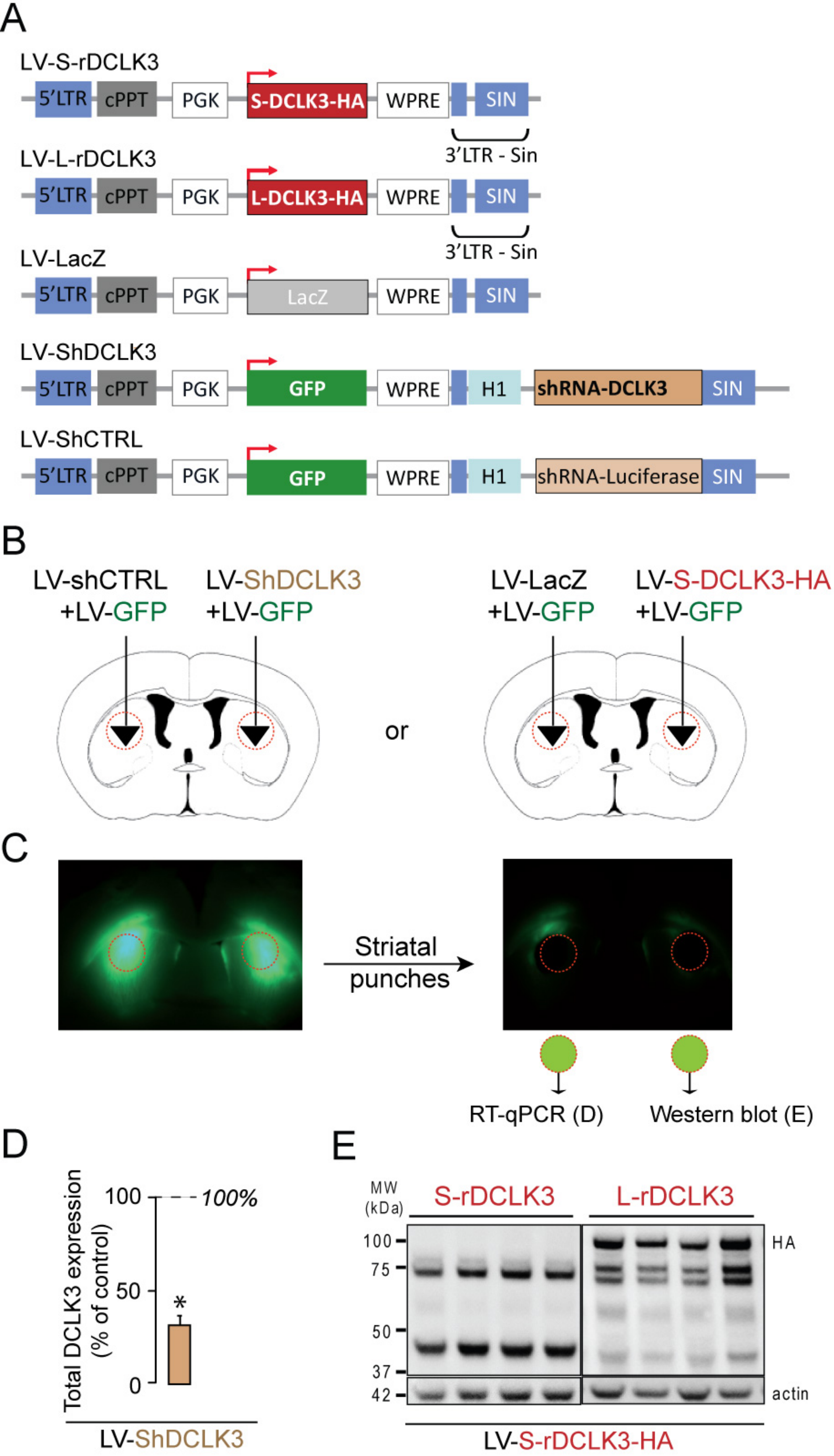

A
LV-S-rDCLK3
5'LTR
cPPT
PGK
S-DCLK3-HA
WPRE
SIN
3'LTR - Sin
LV-L-rDCLK3
5'LTR
cPPT
PGK
L-DCLK3-HA
WPRE
SIN
3'LTR - Sin
LV-LacZ
5'LTR
cPPT
PGK
LacZ
WPRE
SIN
LV-ShDCLK3
5'LTR
cPPT
PGK
GFP
WPRE
H1
shRNA-DCLK3
SIN
LV-ShCTRL
5'LTR
cPPT
PGK
GFP
WPRE
H1
shRNA-Luciferase
SIN
B
LV-shCTRL +LV-GFP
LV-ShDCLK3 +LV-GFP
or
LV-LacZ +LV-GFP
LV-S-DCLK3-HA +LV-GFP
C
Striatal punches
RT-qPCR (D)
Western blot (E)
D
Total DCLK3 expression (% of control)
100
50
0
100%
*
LV-ShDCLK3
E
MW (kDa)
S-rDCLK3
L-rDCLK3
100
75
50
37
42
HA
actin
LV-S-rDCLK3-HA

Fig S3. Gene expression changes in knock-in 140 CAG Huntington’s disease mice

Gene expression in the striatum, as assessed by RT-qPCR, in 12-month-old KI140CAG mice. Note the reduced expression of DCLK3 mRNA in heterozygous and homozygous Huntington’s disease mice. Results are presented as means ± the standard error of the mean (SEM), $n=8$ per group, One-way ANOVA and Fisher's *post hoc* PLSD test. *, $p<0.05$, **, $p<0.001$, ***, $p<0.0001$.

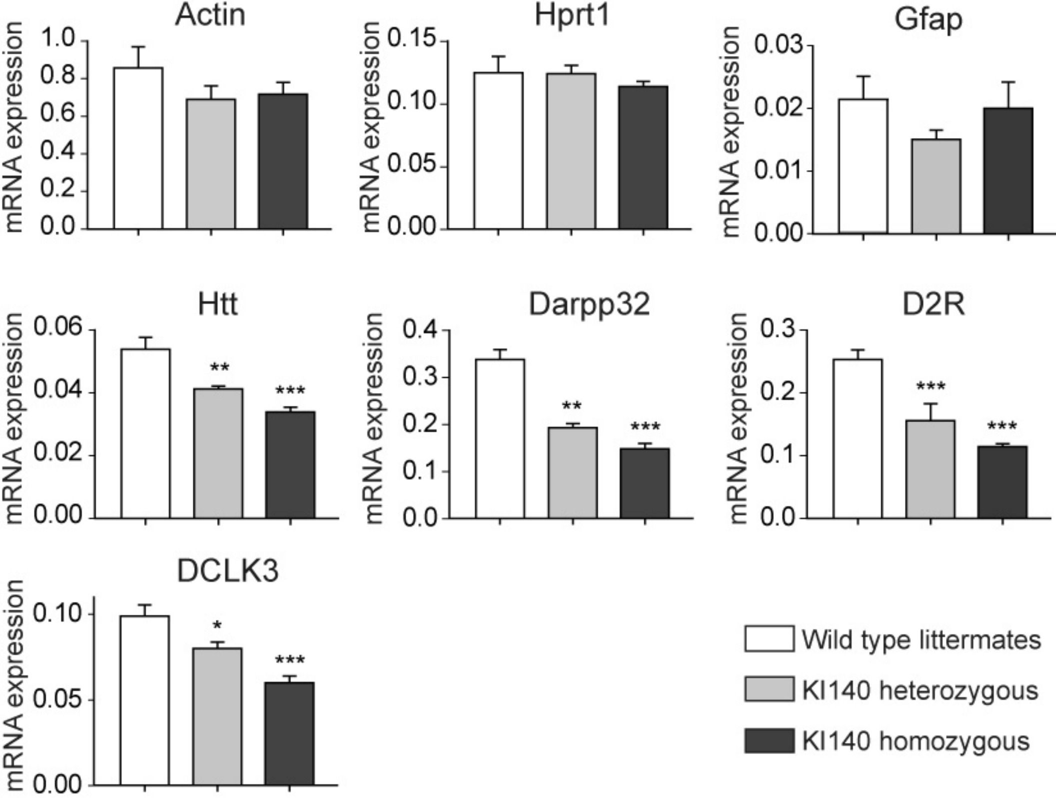

Actin
Hprt1
Gfap
Htt
Darpp32
D2R
DCLK3
mRNA expression
1.0
0.8
0.6
0.4
0.2
0.0
0.15
0.10
0.05
0.00
0.03
0.02
0.01
0.00
0.06
0.04
0.02
0.00
0.4
0.3
0.2
0.1
0.0
0.3
0.2
0.1
0.0
0.10
0.05
0.00
*
**
***
Wild type littermates
KI140 heterozygous
KI140 homozygous

Fig S4. The T286A substitution in S-rDCLK3 abolishes neuroprotective effects against Htt171-82Q

Primary cultures of striatal neurons were transfected by electroporation with plasmids encoding wild-type S-rDCLK3-HA or S-rDCLK3 with the T286→A substitution, alone or together with a plasmid encoding Htt171-82Q. Forty-eight hours later, the cells were fixed and transfected neurons with apoptotic nuclei were counted. S-rDCLK3-HA decreased rates of Htt171-82Q-induced cell death, whereas the T286A mutant had no such effect. Results are expressed as the mean ± the standard error of the mean (SEM) and correspond to three independent experiments, each including three to four slides per experimental group. The numbers in italics indicate significance levels (one-way ANOVA and Fisher's *post hoc* PLSD test).

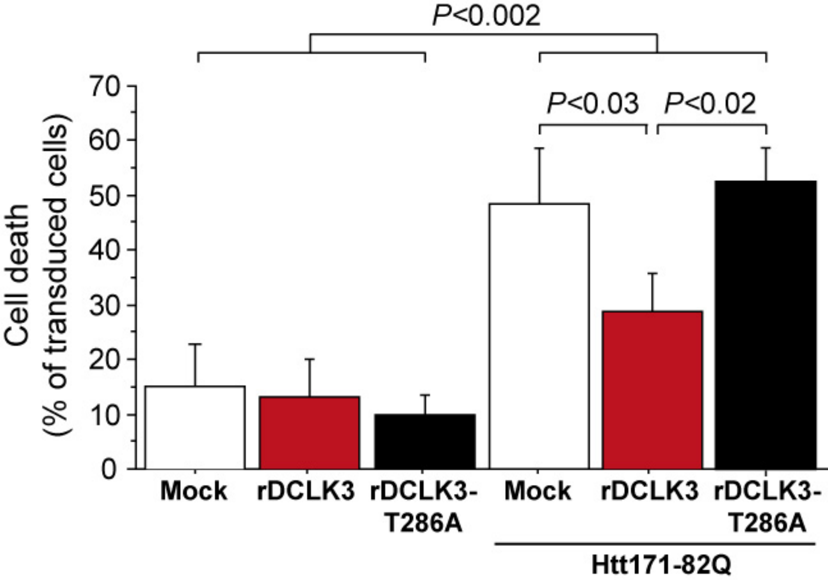

P<0.002
P<0.03
P<0.02
Cell death
(% of transduced cells)
70
60
50
40
30
20
10
0
Mock
rDCLK3
rDCLK3-
T286A
Mock
rDCLK3
rDCLK3-
T286A
Htt171-82Q

Fig S5. Identification of K543 in mouse DCLK3 for the generation of an inactive form of the kinase

An alignment of kinase sequences showed the conservation of a lysine (K) residue in all kinase domains (K in bold). The mutation of this conserved lysine in Akt1, AMPKa2, MNK1, MNK2, CAMKII, Aurora Kinase B and CAMKIV abolished kinase activity. The K543 → M substitution abolished the kinase activity of DCLK3 (see results in Figure 4).

K543--> M

CAMKII a2	NP_803126	27	VRRCVKVL---AGQEYAAKIINTKKLS-AR---dhQKLEREARICRLLK-HPNIVRLHDSISE------EGH----HYLI	88
CAMKII g3	NP_001034228	28	VRRCVKKT---STQEYAAKIINTKKLS-AR---dhQKLEREARICRLLK-HPNIVRLHDSISE------EGF----HYLV	89
CAMKII b1	NP_001167524	28	VRRCVKLC---TGHEYAAKIINTKKLS-AR---dhQKLEREARICRLLK-HSNIVRLHDSISE------EGF----HYLV	89
CAMK1 D	NP_796317	37	VVLAEEKA---TGKLFAVKCIPKKALK--G---keSSIENEIAVLRKIK-HENIVALEDIYES------PNH----LYLV	97
CAMKIV	NP_033923	56	VYRCKQKG---TQKPYALKVLKKTV--------dkKIVRTEIGVLLRLS-HPNIIKLKEIFET------PTE----ISLV	113
CAMK1	NP_598687	34	VILAEDKR---TQKLVAIKCIAKKALE--G---keGSMENEIAVLHKIK-HPNIVALDDIYES------GGH----LYLI	94
DCLK1 i2	NP_001104521	97	VKECIERS---TAREYALKIIKKSKCRGKEHM-----IQNEVSILRRVK-HPNIVLLIEEMDV------PTE----LYLV	157
DCLK1 i3	NP_001104522	97	VKECIERS---TAREYALKIIKKSKCRGKEHM-----IQNEVSILRRVK-HPNIVLLIEEMDV------PTE----LYLV	157
DCLK1 i6	NP_001182468	113	VKECIERS---TAREYALKIIKKSKCRGKEHM-----IQNEVSILRRVK-HPNIVLLIEEMDV------PTE----LYLV	173
DCLK2 i5	NP_001182428	422	VKECVDRY---TGKEFALKIIDKAKCCGKEHL-----IENEVSILRRVK-HPNIIMLVEEMET------ATD----LFLV	482
DCLK2 i4	NP_001182427	423	VKECVDRY---TGKEFALKIIDKAKCCGKEHL-----IENEVSILRRVK-HPNIIMLVEEMET------ATD----LFLV	483
DCLK2 i2	NP_081815	407	VKECVDRY---TGKEFALKIIDKAKCCGKEHL-----IENEVSILRRVK-HPNIIMLVEEMET------ATD----LFLV	467
DCLK2 i3	NP_001182426	406	VKECVDRY---TGKEFALKIIDKAKCCGKEHL-----IENEVSILRRVK-HPNIIMLVEEMET------ATD----LFLV	466
DCLK2 i1	NP_001182425	422	VKECVDRY---TGKEFALKIIDKAKCCGKEHL-----IENEVSILRRVK-HPNIIMLVEEMET------ATD----LFLV	482
DCLK1 i1	NP_064362	420	VKECIERS---TAREYALKIIKKSKCRGKEHM-----IQNEVSILRRVK-HPNIVLLIEEMDV------PTE----LYLV	480
DAPK3 b	NP_031854	27	VRKCQQKG---TGMEYAAKFIKKRRLPSSRRGvsrEEIEREVSILREIR-HPNIITLHDVFEN------KTD----VVLI	92
DAPK3 a	NP_001177403	44	VRKCQQKG---TGMEYAAKFIKKRRLPSSRRGvsrEEIEREVSILREIR-HPNIITLHDVFEN------KTD----VVLI	109
DCLK3-L	NP_766516	528	VKECRHRE---TKQAYAMKMIDKSQLKGKEDI-----VDSEILIIQSLS-HPNIVKLHEVYET------EAE----IYLI	588
RPS6K a3	NP_683747	82	VFLVKKISgsdARQLYAMKVLKKATLKVRDRV----RTKMERDILVEVN-HPFIVKLHYAFQT------EGK----LYLI	146
RPS6K a1	NP_033123	76	VFLVRKVTrpdSGHLYAMKVLKKATLKVRDRV----RTKMERDILADVN-HPFVVKLHYAFQT------EGK----LYLI	140
MARK3 i1	NP_067491	70	VKLARHIL---TGREVAIKIIDKTQLNPTSL----QKLFREVRIMKILN-HPNIVKLFEVIET------EKT----LYLI	131
MARK3 i2	NP_073712	70	VKLARHIL---TGREVAIKIIDKTQLNPTSL----QKLFREVRIMKILN-HPNIVKLFEVIET------EKT----LYLI	131
MnK1	NP_067436	51	VQGAVNLQ---SGKEYAVKIIEKQAGH------srSRVFREVETLYQCQgNRNILELIEFFED------DTR----FYLV	111
AMPKa2	NP_835279	30	VKIGEHQL---TGHKVAVKILNRQKIRSLDVV---GKIKREIQNLKLFR-HPHIIKLYQVIST------PTD----FFMV	92
MARK4	NP_758483	73	VKLARHIL---TGREVAIKIIDKTQLNPSSL----QKLFREVRIMKGLN-HPNIVKLFEVIET------EKT----LYLV	134
MnK2	NP_067437	51	VQTCVNLI---TNQEYAVKIIEKQLGH------irSRVFREVEMLYQCQgHRNVLELIEFFEE------EDR----FYLV	111
MAPK5	NP_034895	36	VRVCVKKS---TQERFALKILLDRPKA-----------RNEVRLHMMCAtHPNIVQIIEVFANsvqfphESSprarLLIV	101
MAPK3	NP_849238	60	VLECYHRR---SGQKCALKLLYDSPKARQE---vdHHWQAS-------G-GPHIVRILDVYEN------MHHgkrcLLIV	119
Aurora KCia	NP_001074434	69	VYLARLKE---NHFIVALKVLFKSEIEKEG---leHQLRREVEIQAHLQ-HRNILRLYNYFYD------DTR----IYLI	131
Aurora KAia	NP_035627	160	VYLARERQ---SKFILALKVLFKTQLEKAN---veHQLRREVEIQSHLR-HPNILRLYGYFHD------ATR----VYLI	222
AKT1	NM_005163	163	VILVKEKA---TGRYYAMKILKKEVIVAKD	190

Fig S6. Functional enrichment analysis of DCLK3 up-regulated genes in NSCs overexpressing rDCLK3 kinase domain vs control human striatal cells differentiated from NSCs. Analysis has been performed with the tool DAVID. CC, cellular components; BP, biological processes; MF, Molecular functions. Significant terms are shown (adj. p value <0.05).

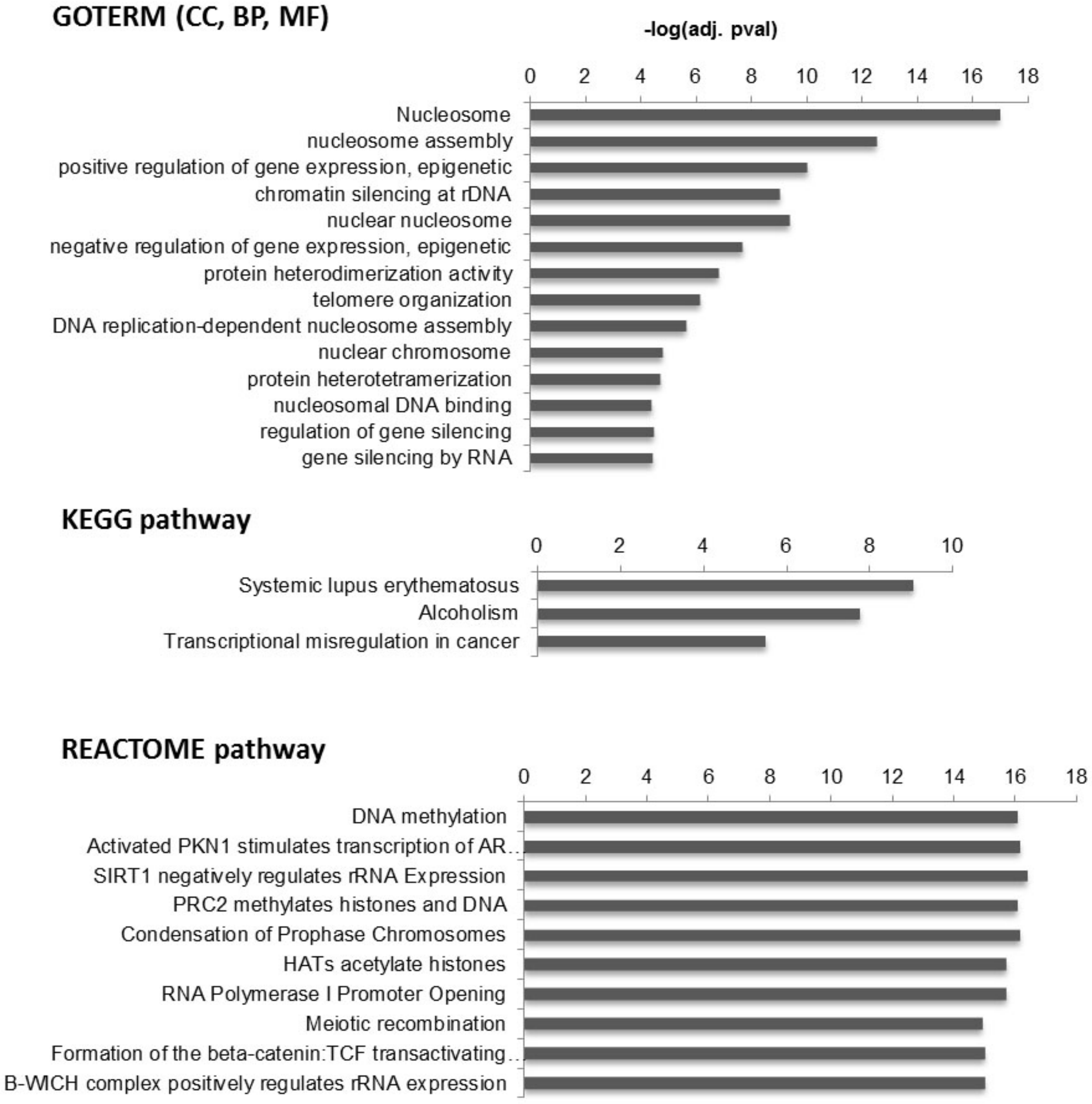

GOTERM (CC, BP, MF)
-log(adj. pval)
0
2
4
6
8
10
12
14
16
18
Nucleosome
nucleosome assembly
positive regulation of gene expression, epigenetic
chromatin silencing at rDNA
nuclear nucleosome
negative regulation of gene expression, epigenetic
protein heterodimerization activity
telomere organization
DNA replication-dependent nucleosome assembly
nuclear chromosome
protein heterotetramerization
nucleosomal DNA binding
regulation of gene silencing
gene silencing by RNA
KEGG pathway
0
2
4
6
8
10
Systemic lupus erythematosus
Alcoholism
Transcriptional misregulation in cancer
REACTOME pathway
0
2
4
6
8
10
12
14
16
18
DNA methylation
Activated PKN1 stimulates transcription of AR…
SIRT1 negatively regulates rRNA Expression
PRC2 methylates histones and DNA
Condensation of Prophase Chromosomes
HATs acetylate histones
RNA Polymerase I Promoter Opening
Meiotic recombination
Formation of the beta-catenin:TCF transactivating…
B-WICH complex positively regulates rRNA expression

Fig S7. Localization of DCLK3 in neurons and specificity of the anti-DCLK3 antibody (ab2189) with confocal microscopy. A, rat neurons (15 DIV) showing endogenous DCLK3 in cytoplasm and nucleus. B, immunoreactivity disappears when the primary ab2189 antibody was pre-incubated with purified human DCLK3 protein before incubation on methanol-fixed rat neurons. **B**, DCLK3 immunofluorescence in the striatum using floating brain sections from a non-human primate. **C**, DCLK3 immunofluorescence in the cerebral cortex (layer V) using floating brain sections from a non-human primate. Pre-incubation of the Ab2189 antibody markedly reduces the signal. Note that DCLK3 in floating sections is found both in the cytoplasm and nucleus of neurons. Scale bars, 10 µm.

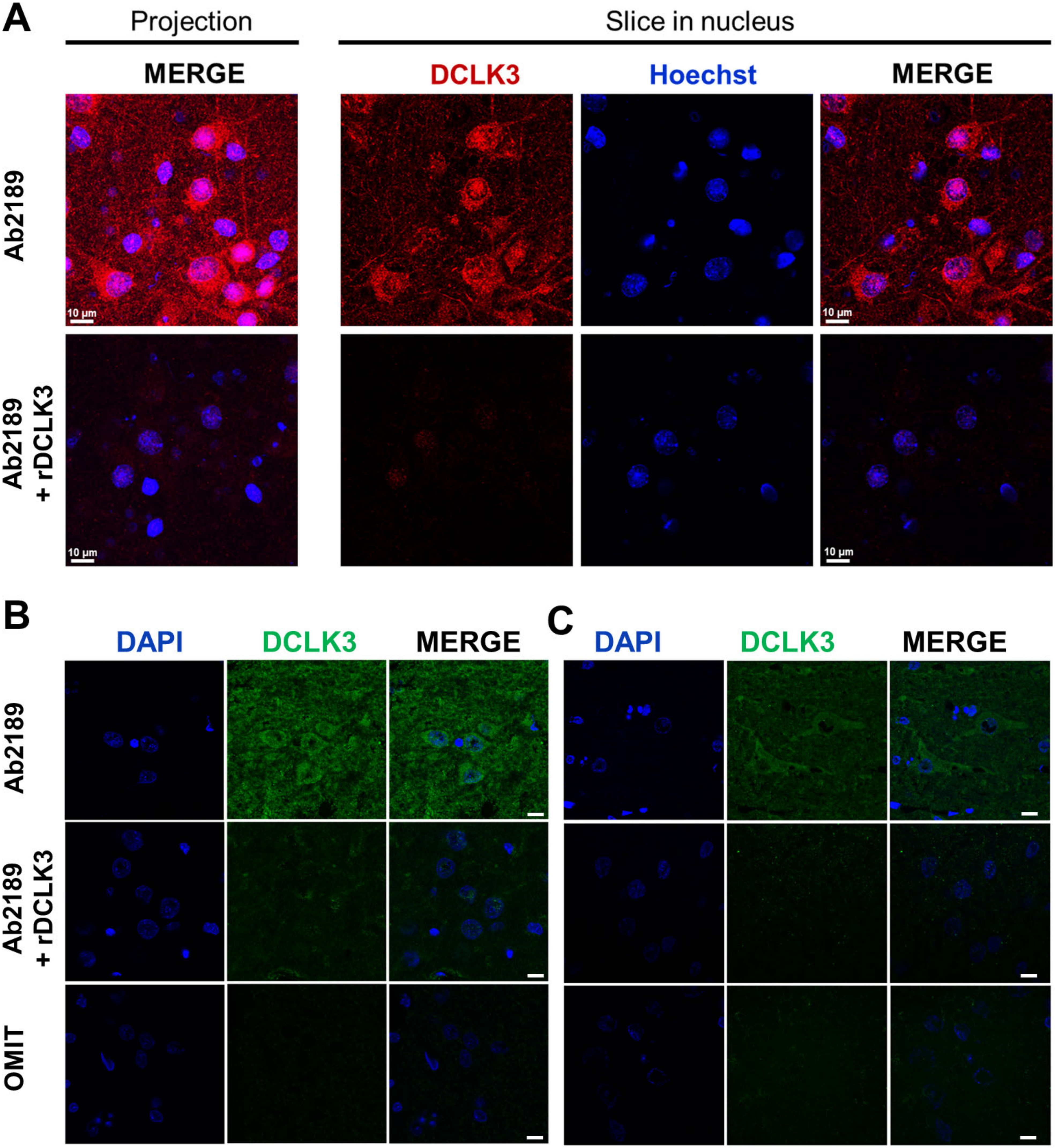

A
Projection
Slice in nucleus
MERGE
DCLK3
Hoechst
MERGE
Ab2189
Ab2189 + rDCLK3
10 µm
10 µm
10 µm
10 µm
B
DAPI
DCLK3
MERGE
Ab2189
Ab2189 + rDCLK3
OMIT
C
DAPI
DCLK3
MERGE

Fig S8. Localization of Kin-rDCLK3 in human striatal neurons expressing mHtt.

Striatal neurons were fixed in PFA 4%, at 10 days post- infection with LV-Htt171-82Q and either Kin-rDCLK3^{WT} or Kin-rDCLK3^{K543M}. DCLK3 was detected with Ab2189 and confocal imaging. Note the localization of DCLK3 in the cytoplasm and nuclei (White arrow). Scale bar, 10 µm.

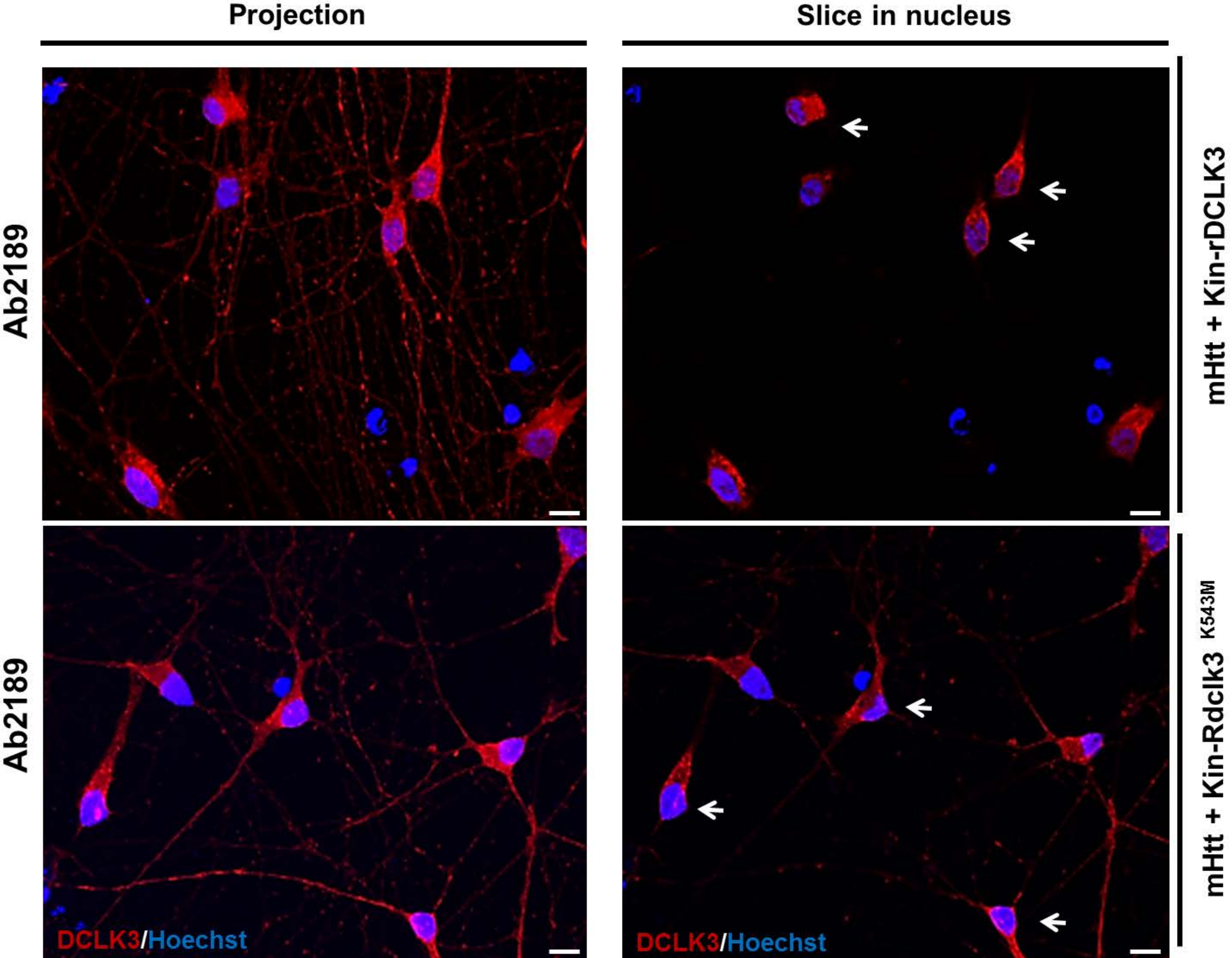
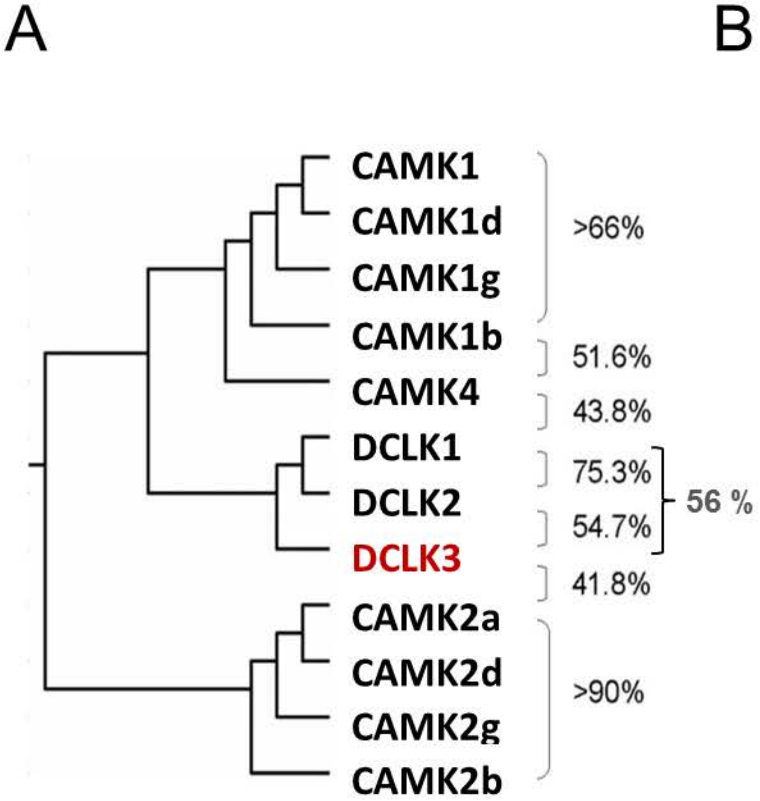

Projection
Slice in nucleus
Ab2189
mHtt + Kin-rDCLK3
Ab2189
mHtt + Kin-Rdclk3 K543M
DCLK3/Hoechst
DCLK3/Hoechst

Fig S9. Comparison of DCLK3 and DCLK1 with bioinformatics tools. A, Dendrogram showing the different kinase families related to DCLKs (after Ohmae et al. 2006). **B**, amino acids alignment of human DCLK1 and human DCLK3 showing 56% identities, with conservation of the kinase domains (pink and grey) and many differences throughout the sequences ((https://blast.ncbi.nlm.nih.gov/). **C**, DCLK1 and DCLK3 kinase domains were modeled using Phyre2 [http://www.sbg.bio.ic.ac.uk/phyre2/html;   Kelley LA et al., 2015, The Phyre2 web portal for protein modeling, prediction and analysis, Nature Protocols 10, 845-858] and visualized with NGL viewer 0.7dev (proteinformatics.charite.de/ngl-tools/ngl/). Queries were submitted through Protein Model Portal (Hass J. et al., DataBase 2013).



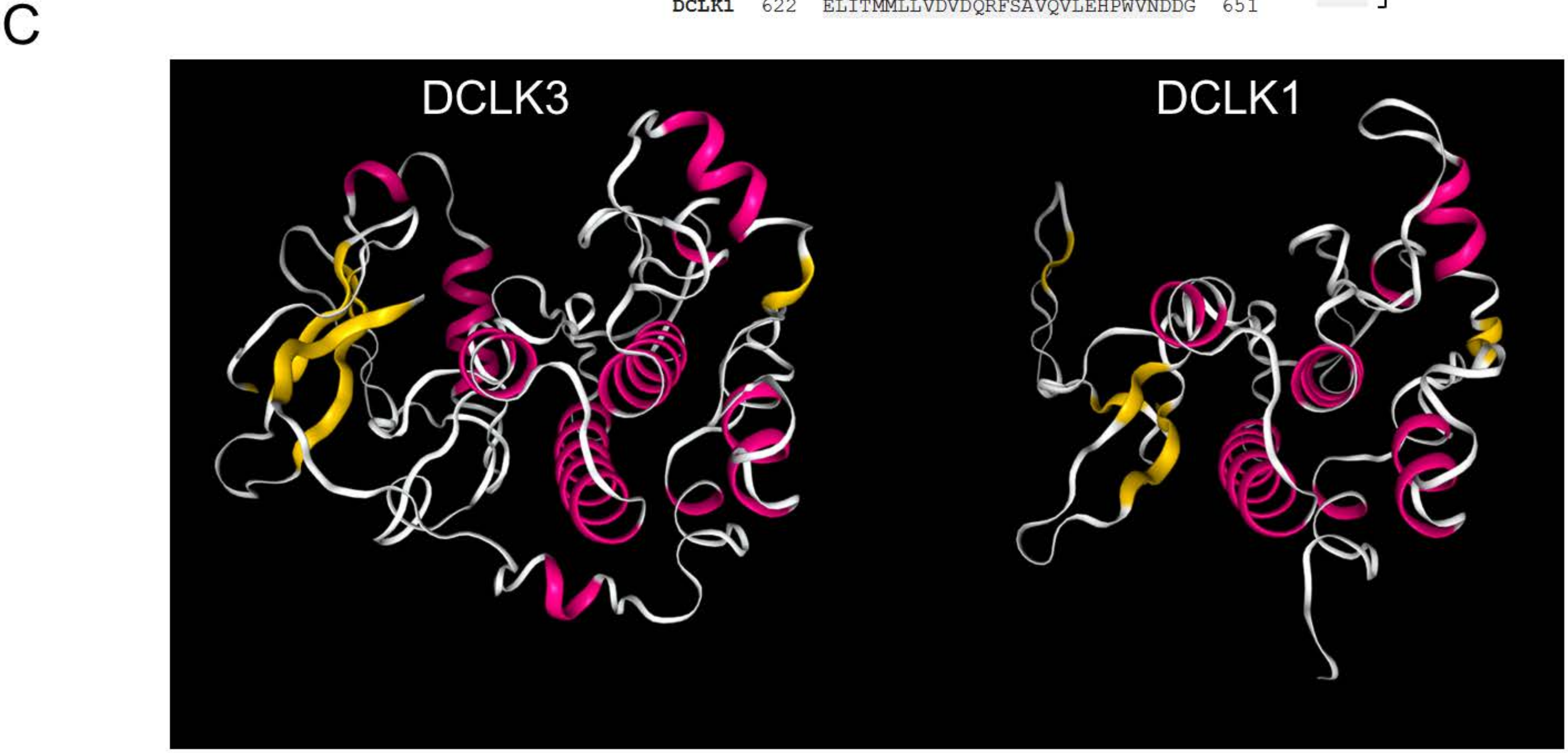
B

Alignment statistics DCLK3 / DCLK1

Score	Expect	Method	Identities	Positives	Gaps
332 bits(852)	1e-10^{8}	Compositional matrix adjust.	150/270(56%)	203/270(75%)	0/270(0%)

```
DCLK3  348  IAANVEKHYETGRVIGDGNFAVVKECRHRETRQAYAMKIIDKSRLKGKEDMVDSEILIIQ  407
            I A + + Y+ GR IGDGNFAVVKEC  R T+  YA+KII KS++ GKE M+ +E+ I++
DCLK1  382  IPATITERYKVGRTIGDGNFAVVKECVERSTAREYALKIIKKSKCRGKEHMIQNEVSILR  441

DCLK3  408  SLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAIIESVKFPEPDAALMIMDLCKALVH  467
             + HPNIV L E  +   E+YL++E V+GGDLFDAI  + K+ E DA+ M+ +L  A+ +
DCLK1  442  RVKHPNIVLLIEEMDVPTELYLVMELVKGGDLFDAITSTNKYTERDASGMLYNLASAIKY  501

DCLK3  468  MHDKSIVHRDLKPENLLVQRNEDKSTTLKLADFGLAKHVVRPIFTVCGTPTYVAPEILSE  527
            +H  +IVHRD+KPENLLV  ++D S +LKL DFGLA  V  P++TVCGTPTYVAPEI++E
DCLK1  502  LHSLNIVHRDIKPENLLVYEHQDGSKSLKLGDFGLATIVDGPLYTVCGTPTYVAPEIIAE  561

DCLK3  528  KGYGLEVDMWAAGVILYILLCGFPPFRSPERDQDELFNIIQLGHFEFLPPYWDNISDAAK  587
             GYGL+VD+WAAGVI YILLCGFPPFR    DQ+ LF+ I +G  +F  PYWDN+SD+AK
DCLK1  562  TGYGLKVDIWAAGVITYILLCGFPPFRGSGDDQEVLFDQILMGQVDFPSPYWDNVSDSAK  621

DCLK3  588  DLVSRLLVVDPKKRYTAHQVLQHPWIETAG  617
            +L++ +L+VD  +R++A QVL+HPW+   G
DCLK1  622  ELITMMLLVDVDQRFSAVQVLEHPWVNDDG  651
```

🟥 ⬜ **Kinase domain**



Legends of supplementary Tables

Table S1: Summary information relating to the protein partners of DCLK3 kinase domain identified by Y2H. Levels of confidence for each partner are indicated in B column. Putative functions have been extracted with String 10.0. The SAGE tag counts (normalized to 80,000 tags per library) indicate relative level of expression of partner RNA in the different brain regions that were investigated in (Brochier et al., 2008). Note that TADA3 expression is high in all brain regions, including the striatum.

TABLE S1
GALVAN L., et al.

Human gene	**Nb Y2H clones / Confidence**	**Gene ID**	**Summary at** http://www.ncbi.nlm.nih.gov/gene or http://string-db.org
BTBD9	**5**	Gene ID: 114781	This locus encodes a BTB/POZ domain-containing protein. This domain is known to be involved in protein-protein interactions. Polymorphisms at this locus have been reported to be associated with susceptibility to Restless Legs Syndrome and may also be associated with Tourette Syndrome. Alternatively spliced transcript variants have been described.
SALL1	**2**	Gene ID: 6299	The protein encoded by this gene is a zinc finger transcriptional repressor and may be part of the NuRD histone deacetylase complex (HDAC). Defects in this gene are a cause of Townes-Brocks syndrome (TBS) as well as bronchio-oto-renal syndrome (BOR). Two transcript variants encoding different isoforms have been found for this gene.
TRIM39	**1**	Gene ID: 56658	The protein encoded by this gene is a member of the tripartite motif (TRIM) family. The TRIM motif includes three zinc-binding domains, a RING, a B-box type 1 and a B-box type 2, and a coiled-coil region. The function of this protein has not been identified. This gene lies within the major histocompatibility complex class I region on chromosome 6. Alternate splicing results in two transcript variants encoding different isoforms
TADA3	**22**	Gene ID: 10474	DNA-binding transcriptional activator proteins increase the rate of transcription by interacting with the transcriptional machinery bound to the basal promoter in conjunction with adaptor proteins, possibly by acetylation and destabilization of nucleosomes. The protein encoded by this gene is a transcriptional activator adaptor and a component of the histone acetyl transferase (HAT) coactivator complex which plays a crucial role in chromatin modulation and cell cycle progression. Along with the other components of the complex, this protein links transcriptional activators bound to specific promoters, to histone acetylation and the transcriptional machinery. The protein is also involved in the stabilization and activation of the p53 tumor suppressor protein that plays a role in the cellular response to DNA damage. Alternate splicing results in multiple transcript variants of this gene.
ZNF12	**2**	Gene ID: 7559	This gene is a member of the krueppel C2H2-type zinc-finger protein family and encodes a protein with eight C2H2-type zinc fingers and a KRAB domain. This nuclear protein is involved in developmental control of gene expression. Alternate transcriptional splice variants, encoding different isoforms, have been characterized.
ZNF292	**2**	Gene ID: 23036	zinc finger protein 292; May be involved in transcriptional regulation
ZNF366	**1**	Gene ID: 167465	zinc finger protein 366; Has transcriptional repression activity. Acts as corepressor of ESR1; the function seems to involve CTBP1 and histone deacetylase

Mouse gene		SAGE tag count (normalized to 80,000 tags per library) (Brochier et al., 2008)												
		Sau3A I tag	Whole brain	Orbital c.	Prelimbic c.	Cingulate c.	Motor c.	Somatosensory c.	Entorhinal c.	**Striatum**	Accumbens n.	Thalamus	Substantia nigra	VTA
Btbd9		TTCCAGAGAT	0	1	1	1	0	1	1	0	1	3	0	1
Sall1		AAGAGCAGGT	1	1	0	1	1	1	1	0	3	3	1	0
Trim39		CACTAATGTG	0	2	1	1	1	1	2	1	1	0	0	0
Tada3		ATGGCTGCCC	3	4	5	2	2	4	0	3	2	1	4	1
Zfp12		TGATTTTGTT	0	0	0	0	1	0	0	1	1	0	0	0
Zfp366		TAGGCAGTTC	0	0	0	0	0	0	0	0	0	0	0	0
Zfp292		ATTCAGTAAC	0	0	0	0	0	0	0	1	1	0	2	1

Table S2: Table recapitulating the list of genes modified with high statistical confidence between GFP and Kin-rDCLK3^{WT} after infection of human striatal neurons. Transcriptomic analysis has been performed by AmpliSeq on extracts from four culture wells for each group, 12 days after infection. Filtering of data (fold-change>1.20 and adjusted p<0.0005, FDR<0.05) selected 161 genes of interest. Separate lists of down- and upregulated genes can be found by scrolling down the data sheet.

Supplemental Table S2

Galvan et al.

All genes statistically modified between GFP and Kin-DCLK3 (WT)

					fold-change>1.20 and adjusted *p* <0.0005, FDR<0.05
Gene symbol	**Total reads**	**P-value (GFP vs, KIN-WT)**	**FDR step up (GFP vs, KIN-WT)**	**Ratio (GFP vs, KIN-WT)**	**Fold change (GFP vs, KIN-WT)**
ACTR3B	9,53E+02	2,30E-04	2,87E-02	1,47E+00	1,47E+00
ALDH1B1	6,04E+02	1,49E-04	2,19E-02	1,59E+00	1,59E+00
ANK2	4,47E+04	2,05E-04	2,70E-02	1,20E+00	1,20E+00
ARF4	3,96E+04	1,86E-07	1,42E-04	7,76E-01	-1,29E+00
ATP10B	2,19E+02	1,18E-04	1,94E-02	1,65E+00	1,65E+00
ATP1A2	7,75E+03	7,83E-06	2,72E-03	1,66E+00	1,66E+00
ATP7B	5,86E+02	2,64E-04	3,11E-02	1,55E+00	1,55E+00
BASP1	4,37E+04	7,68E-07	4,97E-04	1,47E+00	1,47E+00
BBX	6,08E+03	8,46E-12	2,59E-08	7,20E-01	-1,39E+00
BIVM	5,11E+03	8,04E-05	1,47E-02	1,76E+00	1,76E+00
BSX	1,00E+01	5,48E-04	4,95E-02	7,42E-04	-1,35E+03
BTN2A1	4,82E+03	4,71E-04	4,46E-02	8,29E-01	-1,21E+00
C1orf213	9,11E+02	6,96E-05	1,33E-02	5,08E-01	-1,97E+00
C21orf91	2,56E+03	4,08E-06	1,56E-03	7,14E-01	-1,40E+00
C4orf48	2,99E+03	3,68E-04	3,92E-02	1,56E+00	1,56E+00
C9orf172	2,03E+03	1,06E-10	2,72E-07	1,66E+00	1,66E+00
CCNB1IP1	2,66E+03	1,06E-07	1,02E-04	7,13E-01	-1,40E+00
CCND2	8,43E+03	3,64E-05	8,32E-03	1,36E+00	1,36E+00
CHMP1B	1,88E+04	5,34E-05	1,09E-02	7,75E-01	-1,29E+00
CHRD	3,73E+02	2,35E-04	2,90E-02	1,57E+00	1,57E+00
CPNE5	1,54E+03	4,97E-04	4,67E-02	1,39E+00	1,39E+00
CRCP	5,84E+02	6,16E-05	1,21E-02	5,74E-01	-1,74E+00
DANCR	4,70E+02	3,19E-04	3,54E-02	6,21E-01	-1,61E+00
DCAF16	2,55E+03	2,05E-05	5,71E-03	7,40E-01	-1,35E+00
DHRS2	4,79E+03	2,16E-04	2,76E-02	7,95E-01	-1,26E+00
DLGAP1	6,40E+02	1,06E-04	1,81E-02	1,62E+00	1,62E+00
DUSP5P1	1,61E+03	4,39E-04	4,27E-02	7,76E-01	-1,29E+00
EDN1	3,29E+02	3,67E-04	3,92E-02	5,85E-01	-1,71E+00
EDNRB	1,43E+03	1,68E-05	5,15E-03	1,66E+00	1,66E+00
EEF1G	3,09E+03	7,33E-05	1,35E-02	6,67E-01	-1,50E+00
EFNB2	6,58E+03	9,82E-05	1,73E-02	1,28E+00	1,28E+00
ELP5	9,19E+03	4,44E-04	4,28E-02	8,02E-01	-1,25E+00
EMID2	4,57E+03	1,84E-06	9,10E-04	1,28E+00	1,28E+00
ENDOD1	1,40E+03	2,30E-06	1,02E-03	1,53E+00	1,53E+00
EWSR1	2,39E+03	6,61E-05	1,28E-02	7,84E-01	-1,28E+00
EZR	2,23E+03	2,42E-04	2,91E-02	1,26E+00	1,26E+00
FAM109A	4,24E+02	1,14E-04	1,90E-02	1,87E+00	1,87E+00
FAM222A	2,49E+03	1,32E-04	2,03E-02	1,38E+00	1,38E+00
FAM89B	2,34E+03	8,52E-07	5,22E-04	1,37E+00	1,37E+00
FBXW7	9,20E+03	4,55E-05	9,69E-03	8,15E-01	-1,23E+00
FGGY	3,60E+03	8,39E-06	2,86E-03	7,93E-01	-1,26E+00
FKBP14	4,48E+03	3,96E-04	3,99E-02	8,07E-01	-1,24E+00
FRMD3	5,19E+02	1,44E-04	2,14E-02	1,77E+00	1,77E+00
FRMD6	1,08E+03	3,32E-08	3,64E-05	1,86E+00	1,86E+00
FTH1	2,31E+03	2,28E-05	5,82E-03	6,92E-01	-1,44E+00
FZD10	8,70E+02	3,79E-04	3,96E-02	2,06E+00	2,06E+00
FZD8	6,18E+02	2,14E-04	2,75E-02	1,72E+00	1,72E+00

G6PC3	2,94E+04	5,25E-04	4,82E-02	8,22E-01	-1,22E+00
GAPDH	5,57E+04	1,34E-07	1,08E-04	8,17E-01	-1,22E+00
GEMIN4	8,10E+01	2,69E-04	3,14E-02	3,05E+00	3,05E+00
GFOD2	4,05E+02	2,37E-04	2,90E-02	1,70E+00	1,70E+00
GNB4	4,01E+03	2,49E-05	6,14E-03	1,28E+00	1,28E+00
GRHL1	1,14E+03	1,22E-04	1,97E-02	7,17E-01	-1,39E+00
GUSBP9	1,42E+04	2,44E-04	2,92E-02	7,56E-01	-1,32E+00
HES1	7,57E+02	3,41E-06	1,39E-03	1,96E+00	1,96E+00
HIST1H1D	1,02E+04	2,13E-04	2,75E-02	7,42E-01	-1,35E+00
HIST1H2BC	2,45E+03	3,14E-06	1,34E-03	2,25E+00	2,25E+00
HIST1H2BD	3,58E+04	1,21E-42	1,85E-38	7,25E-01	-1,38E+00
HIST1H2BK	4,45E+02	1,50E-04	2,19E-02	5,74E-01	-1,74E+00
HIST1H3D	2,24E+02	5,07E-04	4,74E-02	4,71E-01	-2,12E+00
HIST1H3F	4,28E+03	3,11E-08	3,64E-05	1,99E+00	1,99E+00
HIST1H3G	2,42E+03	1,67E-04	2,32E-02	1,78E+00	1,78E+00
HIST1H3I	3,39E+04	1,92E-08	2,68E-05	6,29E-01	-1,59E+00
HIST1H3J	2,18E+04	6,19E-20	4,74E-16	6,78E-01	-1,48E+00
HIST1H4B	1,09E+04	4,23E-10	8,10E-07	6,14E-01	-1,63E+00
HIST2H3D	3,34E+02	1,94E-05	5,49E-03	4,79E-01	-2,09E+00
HSPB1	4,94E+03	2,83E-04	3,28E-02	1,26E+00	1,26E+00
HTRA2	1,08E+04	1,40E-08	2,14E-05	7,47E-01	-1,34E+00
IFT43	8,13E+03	1,92E-05	5,49E-03	6,48E-01	-1,54E+00
INPP5K	4,98E+03	2,32E-06	1,02E-03	7,52E-01	-1,33E+00
INSM2	8,71E+02	1,63E-04	2,29E-02	6,71E-01	-1,49E+00
INSRR	6,70E+01	2,18E-04	2,76E-02	3,39E-01	-2,95E+00
IRAK1BP1	1,49E+03	7,28E-05	1,35E-02	7,26E-01	-1,38E+00
JPH1	4,45E+02	1,77E-04	2,42E-02	1,87E+00	1,87E+00
KBTBD10	1,60E+04	1,52E-04	2,19E-02	7,75E-01	-1,29E+00
KCNK1	1,69E+03	1,33E-07	1,08E-04	6,63E-01	-1,51E+00
KRTAP19-7	1,30E+01	4,81E-09	8,19E-06	6,60E-04	-1,52E+03
KRTAP5-2	9,88E+02	1,16E-07	1,04E-04	1,72E+00	1,72E+00
LAMC2	5,21E+02	3,10E-04	3,46E-02	6,39E-01	-1,57E+00
LAMP1	1,42E+03	4,32E-04	4,24E-02	1,31E+00	1,31E+00
LOC10049940	1,04E+03	1,09E-06	6,16E-04	6,10E-01	-1,64E+00
LOC254100	7,54E+02	2,13E-05	5,71E-03	6,24E-01	-1,60E+00
LOC645513	1,16E+03	2,22E-05	5,82E-03	6,66E-01	-1,50E+00
LOC646471	1,69E+03	8,26E-05	1,49E-02	7,51E-01	-1,33E+00
LOC728392	1,36E+04	3,09E-05	7,40E-03	1,39E+00	1,39E+00
LUC7L	1,19E+04	6,00E-05	1,20E-02	7,23E-01	-1,38E+00
MATK	1,88E+03	3,24E-04	3,57E-02	1,27E+00	1,27E+00
MESDC1	9,91E+02	1,28E-04	2,00E-02	1,45E+00	1,45E+00
MGST3	3,69E+04	1,03E-04	1,80E-02	8,23E-01	-1,22E+00
MIR600HG	5,40E+03	6,03E-05	1,20E-02	1,35E+00	1,35E+00
MLL5	2,30E+04	3,95E-17	2,02E-13	7,89E-01	-1,27E+00
MXI1	1,52E+03	2,61E-04	3,10E-02	6,83E-01	-1,46E+00
MYEOV2	1,40E+03	2,30E-04	2,87E-02	7,42E-01	-1,35E+00
NAPEPLD	1,43E+03	3,84E-04	3,96E-02	7,65E-01	-1,31E+00
NENF	3,13E+03	2,30E-06	1,02E-03	1,31E+00	1,31E+00
NFIC	2,88E+03	3,41E-10	7,46E-07	1,56E+00	1,56E+00
NNAT	7,27E+03	2,29E-06	1,02E-03	6,96E-01	-1,44E+00
NOP10	2,06E+03	7,29E-05	1,35E-02	7,45E-01	-1,34E+00
NUSAP1	3,44E+02	3,86E-05	8,33E-03	2,23E+00	2,23E+00
OTUB2	3,41E+03	2,87E-04	3,28E-02	1,28E+00	1,28E+00
PALM3	6,60E+02	1,42E-04	2,13E-02	1,79E+00	1,79E+00
PCP4	5,43E+02	3,46E-04	3,75E-02	5,94E-01	-1,68E+00
PDE10A	2,45E+03	5,42E-04	4,94E-02	1,25E+00	1,25E+00
PEX13	4,88E+02	1,19E-04	1,94E-02	5,74E-01	-1,74E+00
PI4K2A	2,40E+03	1,06E-04	1,81E-02	1,33E+00	1,33E+00

PIK3CD	1,09E+03	4,02E-04	4,02E-02	1,39E+00	1,39E+00
PION	1,18E+02	3,51E-04	3,78E-02	3,36E-01	-2,97E+00
PITPNM3	2,30E+03	3,73E-05	8,33E-03	1,30E+00	1,30E+00
PNPLA3	9,26E+02	5,11E-04	4,75E-02	1,39E+00	1,39E+00
PRPF31	1,77E+02	3,87E-04	3,96E-02	4,29E-01	-2,33E+00
PSMD8	1,23E+03	3,08E-04	3,46E-02	7,31E-01	-1,37E+00
PSMF1	6,00E+02	1,56E-04	2,21E-02	5,92E-01	-1,69E+00
PXDC1	7,84E+02	2,00E-04	2,69E-02	1,69E+00	1,69E+00
RAB2B	1,69E+04	6,45E-06	2,30E-03	7,36E-01	-1,36E+00
RAB3B	1,98E+04	3,88E-04	3,96E-02	1,28E+00	1,28E+00
RAB6A	3,76E+04	2,44E-05	6,12E-03	8,18E-01	-1,22E+00
REM2	4,16E+03	5,06E-07	3,69E-04	5,89E-01	-1,70E+00
RET	7,76E+02	3,76E-04	3,96E-02	1,36E+00	1,36E+00
RGS8	1,32E+03	2,28E-08	2,91E-05	2,03E+00	2,03E+00
RHOB	4,78E+04	3,77E-05	8,33E-03	1,21E+00	1,21E+00
RIMKLB	1,14E+02	3,93E-04	3,99E-02	3,42E-01	-2,93E+00
RMRP	9,52E+05	5,26E-04	4,82E-02	1,67E+00	1,67E+00
RNF157	9,99E+03	6,13E-07	4,27E-04	1,28E+00	1,28E+00
RNU12	7,42E+02	2,03E-04	2,70E-02	5,41E-01	-1,85E+00
RPS11	2,96E+03	4,40E-04	4,27E-02	7,31E-01	-1,37E+00
RUSC1	3,20E+03	1,14E-04	1,90E-02	1,25E+00	1,25E+00
SCARNA7	1,39E+05	1,54E-04	2,21E-02	7,16E-01	-1,40E+00
SCARNA9	5,32E+04	2,35E-16	9,01E-13	7,23E-01	-1,38E+00
SDC2	6,96E+02	1,29E-04	2,00E-02	6,25E-01	-1,60E+00
SDHAP1	2,12E+03	3,86E-05	8,33E-03	7,90E-01	-1,27E+00
SIPA1L3	4,33E+03	1,80E-05	5,41E-03	1,28E+00	1,28E+00
SLC1A3	1,26E+03	7,79E-07	4,97E-04	1,75E+00	1,75E+00
SLC4A4	1,10E+03	3,44E-06	1,39E-03	1,68E+00	1,68E+00
SLC7A5	1,65E+04	1,74E-04	2,41E-02	1,29E+00	1,29E+00
SMA5	1,75E+03	3,29E-05	7,64E-03	6,86E-01	-1,46E+00
SNRPA1	2,45E+02	1,27E-04	2,00E-02	4,56E-01	-2,19E+00
SNRPN	4,25E+04	1,01E-05	3,29E-03	8,28E-01	-1,21E+00
SORD	1,81E+03	2,41E-04	2,91E-02	1,29E+00	1,29E+00
SOX4	1,37E+04	2,28E-05	5,82E-03	1,36E+00	1,36E+00
SOX9	1,01E+03	3,85E-04	3,96E-02	1,79E+00	1,79E+00
ST18	1,68E+03	9,55E-06	3,18E-03	6,31E-01	-1,58E+00
STC1	1,10E+03	2,71E-05	6,59E-03	6,14E-01	-1,63E+00
STX4	1,24E+04	4,05E-04	4,03E-02	8,28E-01	-1,21E+00
SUPT3H	1,78E+03	3,31E-04	3,62E-02	7,86E-01	-1,27E+00
TAC1	3,86E+03	1,29E-06	6,82E-04	4,88E-01	-2,05E+00
TAF7	3,77E+04	1,04E-06	6,14E-04	8,29E-01	-1,21E+00
TBC1D13	1,11E+03	4,95E-05	1,04E-02	5,84E-01	-1,71E+00
TMEM201	1,16E+03	2,85E-04	3,28E-02	1,43E+00	1,43E+00
TMEM234	1,89E+03	4,47E-04	4,28E-02	7,47E-01	-1,34E+00
TNFRSF12A	2,40E+03	3,20E-05	7,54E-03	1,34E+00	1,34E+00
TNRC18	4,58E+03	1,90E-05	5,49E-03	1,27E+00	1,27E+00
TPP2	1,45E+04	2,09E-05	5,71E-03	8,30E-01	-1,20E+00
TTC3P1	5,12E+03	1,24E-05	3,96E-03	7,60E-01	-1,32E+00
TUBB	1,26E+04	1,28E-04	2,00E-02	1,53E+00	1,53E+00
UPF3B	5,55E+03	1,23E-06	6,72E-04	7,80E-01	-1,28E+00
UQCR10	3,94E+02	1,40E-04	2,12E-02	1,77E+00	1,77E+00
WBP2	8,17E+02	3,09E-04	3,46E-02	6,79E-01	-1,47E+00
ZC3H10	1,64E+02	4,14E-04	4,09E-02	3,97E-01	-2,52E+00
ZNF480	3,25E+03	5,32E-05	1,09E-02	7,72E-01	-1,29E+00
ZNF768	1,39E+02	2,13E-04	2,75E-02	1,88E+00	1,88E+00
ZNRF3	7,38E+02	1,43E-05	4,47E-03	1,67E+00	1,67E+00

DOWN-REGULATED GENES

Gene symbol	Total reads	P-value (GFP vs, DKIN-WT)	FDR step up (GFP vs, DKIN-WT)	Ratio (GFP vs, DKIN-WT)	Fold change (GFP vs, DKIN-WT)
ACTR3B	9,53E+02	2,30E-04	2,87E-02	1,47E+00	1,47E+00
ALDH1B1	6,04E+02	1,49E-04	2,19E-02	1,59E+00	1,59E+00
ANK2	4,47E+04	2,05E-04	2,70E-02	1,20E+00	1,20E+00
ATP10B	2,19E+02	1,18E-04	1,94E-02	1,65E+00	1,65E+00
ATP1A2	7,75E+03	7,83E-06	2,72E-03	1,66E+00	1,66E+00
ATP7B	5,86E+02	2,64E-04	3,11E-02	1,55E+00	1,55E+00
BASP1	4,37E+04	7,68E-07	4,97E-04	1,47E+00	1,47E+00
BIVM	5,11E+03	8,04E-05	1,47E-02	1,76E+00	1,76E+00
C4orf48	2,99E+03	3,68E-04	3,92E-02	1,56E+00	1,56E+00
C9orf172	2,03E+03	1,06E-10	2,72E-07	1,66E+00	1,66E+00
CCND2	8,43E+03	3,64E-05	8,32E-03	1,36E+00	1,36E+00
CHRD	3,73E+02	2,35E-04	2,90E-02	1,57E+00	1,57E+00
CPNE5	1,54E+03	4,97E-04	4,67E-02	1,39E+00	1,39E+00
DLGAP1	6,40E+02	1,06E-04	1,81E-02	1,62E+00	1,62E+00
EDNRB	1,43E+03	1,68E-05	5,15E-03	1,66E+00	1,66E+00
EFNB2	6,58E+03	9,82E-05	1,73E-02	1,28E+00	1,28E+00
EMID2	4,57E+03	1,84E-06	9,10E-04	1,28E+00	1,28E+00
ENDOD1	1,40E+03	2,30E-06	1,02E-03	1,53E+00	1,53E+00
EZR	2,23E+03	2,42E-04	2,91E-02	1,26E+00	1,26E+00
FAM109A	4,24E+02	1,14E-04	1,90E-02	1,87E+00	1,87E+00
FAM222A	2,49E+03	1,32E-04	2,03E-02	1,38E+00	1,38E+00
FAM89B	2,34E+03	8,52E-07	5,22E-04	1,37E+00	1,37E+00
FRMD3	5,19E+02	1,44E-04	2,14E-02	1,77E+00	1,77E+00
FRMD6	1,08E+03	3,32E-08	3,64E-05	1,86E+00	1,86E+00
FZD10	8,70E+02	3,79E-04	3,96E-02	2,06E+00	2,06E+00
FZD8	6,18E+02	2,14E-04	2,75E-02	1,72E+00	1,72E+00
GEMIN4	8,10E+01	2,69E-04	3,14E-02	3,05E+00	3,05E+00
GFOD2	4,05E+02	2,37E-04	2,90E-02	1,70E+00	1,70E+00
GNB4	4,01E+03	2,49E-05	6,14E-03	1,28E+00	1,28E+00
HES1	7,57E+02	3,41E-06	1,39E-03	1,96E+00	1,96E+00
HIST1H2BC	2,45E+03	3,14E-06	1,34E-03	2,25E+00	2,25E+00
HIST1H3F	4,28E+03	3,11E-08	3,64E-05	1,99E+00	1,99E+00
HIST1H3G	2,42E+03	1,67E-04	2,32E-02	1,78E+00	1,78E+00
HSPB1	4,94E+03	2,83E-04	3,28E-02	1,26E+00	1,26E+00
JPH1	4,45E+02	1,77E-04	2,42E-02	1,87E+00	1,87E+00
KRTAP5-2	9,88E+02	1,16E-07	1,04E-04	1,72E+00	1,72E+00
LAMP1	1,42E+03	4,32E-04	4,24E-02	1,31E+00	1,31E+00
LOC728392	1,36E+04	3,09E-05	7,40E-03	1,39E+00	1,39E+00
MATK	1,88E+03	3,24E-04	3,57E-02	1,27E+00	1,27E+00
MESDC1	9,91E+02	1,28E-04	2,00E-02	1,45E+00	1,45E+00
MIR600HG	5,40E+03	6,03E-05	1,20E-02	1,35E+00	1,35E+00
NENF	3,13E+03	2,30E-06	1,02E-03	1,31E+00	1,31E+00
NFIC	2,88E+03	3,41E-10	7,46E-07	1,56E+00	1,56E+00
NUSAP1	3,44E+02	3,86E-05	8,33E-03	2,23E+00	2,23E+00
OTUB2	3,41E+03	2,87E-04	3,28E-02	1,28E+00	1,28E+00
PALM3	6,60E+02	1,42E-04	2,13E-02	1,79E+00	1,79E+00
PDE10A	2,45E+03	5,42E-04	4,94E-02	1,25E+00	1,25E+00
PI4K2A	2,40E+03	1,06E-04	1,81E-02	1,33E+00	1,33E+00
PIK3CD	1,09E+03	4,02E-04	4,02E-02	1,39E+00	1,39E+00
PITPNM3	2,30E+03	3,73E-05	8,33E-03	1,30E+00	1,30E+00
PNPLA3	9,26E+02	5,11E-04	4,75E-02	1,39E+00	1,39E+00
PXDC1	7,84E+02	2,00E-04	2,69E-02	1,69E+00	1,69E+00
RAB3B	1,98E+04	3,88E-04	3,96E-02	1,28E+00	1,28E+00
RET	7,76E+02	3,76E-04	3,96E-02	1,36E+00	1,36E+00

RGS8	1,32E+03	2,28E-08	2,91E-05	2,03E+00	2,03E+00
RHOB	4,78E+04	3,77E-05	8,33E-03	1,21E+00	1,21E+00
RMRP	9,52E+05	5,26E-04	4,82E-02	1,67E+00	1,67E+00
RNF157	9,99E+03	6,13E-07	4,27E-04	1,28E+00	1,28E+00
RUSC1	3,20E+03	1,14E-04	1,90E-02	1,25E+00	1,25E+00
SIPA1L3	4,33E+03	1,80E-05	5,41E-03	1,28E+00	1,28E+00
SLC1A3	1,26E+03	7,79E-07	4,97E-04	1,75E+00	1,75E+00
SLC4A4	1,10E+03	3,44E-06	1,39E-03	1,68E+00	1,68E+00
SLC7A5	1,65E+04	1,74E-04	2,41E-02	1,29E+00	1,29E+00
SORD	1,81E+03	2,41E-04	2,91E-02	1,29E+00	1,29E+00
SOX4	1,37E+04	2,28E-05	5,82E-03	1,36E+00	1,36E+00
SOX9	1,01E+03	3,85E-04	3,96E-02	1,79E+00	1,79E+00
TMEM201	1,16E+03	2,85E-04	3,28E-02	1,43E+00	1,43E+00
TNFRSF12A	2,40E+03	3,20E-05	7,54E-03	1,34E+00	1,34E+00
TNRC18	4,58E+03	1,90E-05	5,49E-03	1,27E+00	1,27E+00
TUBB	1,26E+04	1,28E-04	2,00E-02	1,53E+00	1,53E+00
UQCR10	3,94E+02	1,40E-04	2,12E-02	1,77E+00	1,77E+00
ZNF768	1,39E+02	2,13E-04	2,75E-02	1,88E+00	1,88E+00
ZNRF3	7,38E+02	1,43E-05	4,47E-03	1,67E+00	1,67E+00

UP REGULATED GENES

Gene symbol	Total reads	P-value (GFP vs, DKIN-WT)	FDR step up (GFP vs, DKIN-WT)	Ratio (GFP vs, DKIN-WT)	Fold change (GFP vs, DKIN-WT)
ARF4	3,96E+04	1,86E-07	1,42E-04	7,76E-01	-1,29E+00
BBX	6,08E+03	8,46E-12	2,59E-08	7,20E-01	-1,39E+00
BSX	1,00E+01	5,48E-04	4,95E-02	7,42E-04	-1,35E+03
BTN2A1	4,82E+03	4,71E-04	4,46E-02	8,29E-01	-1,21E+00
C1orf213	9,11E+02	6,96E-05	1,33E-02	5,08E-01	-1,97E+00
C21orf91	2,56E+03	4,08E-06	1,56E-03	7,14E-01	-1,40E+00
CCNB1IP1	2,66E+03	1,06E-07	1,02E-04	7,13E-01	-1,40E+00
CHMP1B	1,88E+04	5,34E-05	1,09E-02	7,75E-01	-1,29E+00
CRCP	5,84E+02	6,16E-05	1,21E-02	5,74E-01	-1,74E+00
DANCR	4,70E+02	3,19E-04	3,54E-02	6,21E-01	-1,61E+00
DCAF16	2,55E+03	2,05E-05	5,71E-03	7,40E-01	-1,35E+00
DHRS2	4,79E+03	2,16E-04	2,76E-02	7,95E-01	-1,26E+00
DUSP5P1	1,61E+03	4,39E-04	4,27E-02	7,76E-01	-1,29E+00
EDN1	3,29E+02	3,67E-04	3,92E-02	5,85E-01	-1,71E+00
EEF1G	3,09E+03	7,33E-05	1,35E-02	6,67E-01	-1,50E+00
ELP5	9,19E+03	4,44E-04	4,28E-02	8,02E-01	-1,25E+00
EWSR1	2,39E+03	6,61E-05	1,28E-02	7,84E-01	-1,28E+00
FBXW7	9,20E+03	4,55E-05	9,69E-03	8,15E-01	-1,23E+00
FGGY	3,60E+03	8,39E-06	2,86E-03	7,93E-01	-1,26E+00
FKBP14	4,48E+03	3,96E-04	3,99E-02	8,07E-01	-1,24E+00
FTH1	2,31E+03	2,28E-05	5,82E-03	6,92E-01	-1,44E+00
G6PC3	2,94E+04	5,25E-04	4,82E-02	8,22E-01	-1,22E+00
GAPDH	5,57E+04	1,34E-07	1,08E-04	8,17E-01	-1,22E+00
GRHL1	1,14E+03	1,22E-04	1,97E-02	7,17E-01	-1,39E+00
GUSBP9	1,42E+04	2,44E-04	2,92E-02	7,56E-01	-1,32E+00
HIST1H1D	1,02E+04	2,13E-04	2,75E-02	7,42E-01	-1,35E+00
HIST1H2BD	3,58E+04	1,21E-42	1,85E-38	7,25E-01	-1,38E+00
HIST1H2BK	4,45E+02	1,50E-04	2,19E-02	5,74E-01	-1,74E+00
HIST1H3D	2,24E+02	5,07E-04	4,74E-02	4,71E-01	-2,12E+00
HIST1H3I	3,39E+04	1,92E-08	2,68E-05	6,29E-01	-1,59E+00

HIST1H3J	2,18E+04	6,19E-20	4,74E-16	6,78E-01	-1,48E+00
HIST1H4B	1,09E+04	4,23E-10	8,10E-07	6,14E-01	-1,63E+00
HIST2H3D	3,34E+02	1,94E-05	5,49E-03	4,79E-01	-2,09E+00
HTRA2	1,08E+04	1,40E-08	2,14E-05	7,47E-01	-1,34E+00
IFT43	8,13E+03	1,92E-05	5,49E-03	6,48E-01	-1,54E+00
INPP5K	4,98E+03	2,32E-06	1,02E-03	7,52E-01	-1,33E+00
INSM2	8,71E+02	1,63E-04	2,29E-02	6,71E-01	-1,49E+00
INSRR	6,70E+01	2,18E-04	2,76E-02	3,39E-01	-2,95E+00
IRAK1BP1	1,49E+03	7,28E-05	1,35E-02	7,26E-01	-1,38E+00
KBTBD10	1,60E+04	1,52E-04	2,19E-02	7,75E-01	-1,29E+00
KCNK1	1,69E+03	1,33E-07	1,08E-04	6,63E-01	-1,51E+00
KRTAP19-7	1,30E+01	4,81E-09	8,19E-06	6,60E-04	-1,52E+03
LAMC2	5,21E+02	3,10E-04	3,46E-02	6,39E-01	-1,57E+00
LOC10049940	1,04E+03	1,09E-06	6,16E-04	6,10E-01	-1,64E+00
LOC254100	7,54E+02	2,13E-05	5,71E-03	6,24E-01	-1,60E+00
LOC645513	1,16E+03	2,22E-05	5,82E-03	6,66E-01	-1,50E+00
LOC646471	1,69E+03	8,26E-05	1,49E-02	7,51E-01	-1,33E+00
LUC7L	1,19E+04	6,00E-05	1,20E-02	7,23E-01	-1,38E+00
MGST3	3,69E+04	1,03E-04	1,80E-02	8,23E-01	-1,22E+00
MLL5	2,30E+04	3,95E-17	2,02E-13	7,89E-01	-1,27E+00
MXI1	1,52E+03	2,61E-04	3,10E-02	6,83E-01	-1,46E+00
MYEOV2	1,40E+03	2,30E-04	2,87E-02	7,42E-01	-1,35E+00
NAPEPLD	1,43E+03	3,84E-04	3,96E-02	7,65E-01	-1,31E+00
NNAT	7,27E+03	2,29E-06	1,02E-03	6,96E-01	-1,44E+00
NOP10	2,06E+03	7,29E-05	1,35E-02	7,45E-01	-1,34E+00
PCP4	5,43E+02	3,46E-04	3,75E-02	5,94E-01	-1,68E+00
PEX13	4,88E+02	1,19E-04	1,94E-02	5,74E-01	-1,74E+00
PION	1,18E+02	3,51E-04	3,78E-02	3,36E-01	-2,97E+00
PRPF31	1,77E+02	3,87E-04	3,96E-02	4,29E-01	-2,33E+00
PSMD8	1,23E+03	3,08E-04	3,46E-02	7,31E-01	-1,37E+00
PSMF1	6,00E+02	1,56E-04	2,21E-02	5,92E-01	-1,69E+00
RAB2B	1,69E+04	6,45E-06	2,30E-03	7,36E-01	-1,36E+00
RAB6A	3,76E+04	2,44E-05	6,12E-03	8,18E-01	-1,22E+00
REM2	4,16E+03	5,06E-07	3,69E-04	5,89E-01	-1,70E+00
RIMKLB	1,14E+02	3,93E-04	3,99E-02	3,42E-01	-2,93E+00
RNU12	7,42E+02	2,03E-04	2,70E-02	5,41E-01	-1,85E+00
RPS11	2,96E+03	4,40E-04	4,27E-02	7,31E-01	-1,37E+00
SCARNA7	1,39E+05	1,54E-04	2,21E-02	7,16E-01	-1,40E+00
SCARNA9	5,32E+04	2,35E-16	9,01E-13	7,23E-01	-1,38E+00
SDC2	6,96E+02	1,29E-04	2,00E-02	6,25E-01	-1,60E+00
SDHAP1	2,12E+03	3,86E-05	8,33E-03	7,90E-01	-1,27E+00
SMA5	1,75E+03	3,29E-05	7,64E-03	6,86E-01	-1,46E+00
SNRPA1	2,45E+02	1,27E-04	2,00E-02	4,56E-01	-2,19E+00
SNRPN	4,25E+04	1,01E-05	3,29E-03	8,28E-01	-1,21E+00
ST18	1,68E+03	9,55E-06	3,18E-03	6,31E-01	-1,58E+00
STC1	1,10E+03	2,71E-05	6,59E-03	6,14E-01	-1,63E+00
STX4	1,24E+04	4,05E-04	4,03E-02	8,28E-01	-1,21E+00
SUPT3H	1,78E+03	3,31E-04	3,62E-02	7,86E-01	-1,27E+00
TAC1	3,86E+03	1,29E-06	6,82E-04	4,88E-01	-2,05E+00
TAF7	3,77E+04	1,04E-06	6,14E-04	8,29E-01	-1,21E+00
TBC1D13	1,11E+03	4,95E-05	1,04E-02	5,84E-01	-1,71E+00
TMEM234	1,89E+03	4,47E-04	4,28E-02	7,47E-01	-1,34E+00
TPP2	1,45E+04	2,09E-05	5,71E-03	8,30E-01	-1,20E+00
TTC3P1	5,12E+03	1,24E-05	3,96E-03	7,60E-01	-1,32E+00
UPF3B	5,55E+03	1,23E-06	6,72E-04	7,80E-01	-1,28E+00
WBP2	8,17E+02	3,09E-04	3,46E-02	6,79E-01	-1,47E+00
ZC3H10	1,64E+02	4,14E-04	4,09E-02	3,97E-01	-2,52E+00
ZNF480	3,25E+03	5,32E-05	1,09E-02	7,72E-01	-1,29E+00

Table S3: Table showing the list of genes whose expression changes were linked to the kinase activity. To this purpose, genes with modified expression between [GFP and Kin-rDCLK3^{WT}] and [Kin-rDCLK3 ^{WT} and Kin-rDLK3^{K543M}] were selected. Filtering of data from comparison between GFP and Kin-rDCLK3^{WT} (FC>1.1, adjusted p<0.0009, FDR<0.05) selected 275 genes of interest. This list of significantly changed genes was crossed with the list of genes (Table S4) also changed between Kin-rDCLK3^{WT} and Kin-rDCLK3^{K543M} after infection of human striatal neurons (FC>1.1, adjusted p<0.002, FDR<0.05; 371 genes). These genes were considered to be regulated through a kinase –dependent mechanism (see Table S5).

Supplemental Table S3

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list of genes from GFP vs, kin-DCLK3 (WT) for search of kinase specific effects

					FC>1.1, adjusted p<0.0009, FDR<0.05, 275 genes	FC>1.1, adjusted p<0.002, FDR<0.05; 371 genes
Gene symbol	Total reads	P-value (GFP vs, KIN-WT)	FDR step up (GFP vs, KIN-WT)	Ratio (GFP vs, KIN-WT)	Fold change (GFP vs, KIN-WT)	**Fold change (KIN-WT vs, KIN-K543M) [see table S4]**
ABTB2	1,04E+03	9,09E-05	1,24E-02	1,46E+00	1,46E+00	not found
ACAD9	1,87E+03	6,03E-05	1,00E-02	7,51E-01	-1,33E+00	1,37E+00
ADAMTS6	3,20E+03	6,19E-05	1,01E-02	7,27E-01	-1,38E+00	1,38E+00
AKAP12	6,55E+03	6,55E-04	4,26E-02	1,27E+00	1,27E+00	not found
ALDH1B1	1,09E+03	7,54E-04	4,61E-02	1,46E+00	1,46E+00	not found
ANK2	8,29E+04	4,46E-04	3,38E-02	1,23E+00	1,23E+00	-1,22E+00
APBB3	4,35E+03	2,08E-06	1,05E-03	7,87E-01	-1,27E+00	1,19E+00
ARID2	5,05E+03	2,14E-05	4,84E-03	8,35E-01	-1,20E+00	not found
ATF2	1,40E+04	3,76E-04	3,07E-02	8,09E-01	-1,24E+00	not found
ATP1A2	1,50E+04	4,35E-04	3,36E-02	1,62E+00	1,62E+00	not found
ATP5E	2,68E+04	5,26E-04	3,73E-02	8,16E-01	-1,23E+00	not found
ATP7B	1,07E+03	6,02E-06	2,21E-03	1,51E+00	1,51E+00	not found
BASP1	4,14E+04	8,06E-07	4,65E-04	1,48E+00	1,48E+00	not found
BBX	9,98E+03	4,45E-18	1,80E-14	7,41E-01	-1,35E+00	1,44E+00
BLCAP	1,67E+03	7,33E-06	2,42E-03	6,98E-01	-1,43E+00	not found
BMF	1,15E+03	1,36E-08	1,38E-05	5,78E-01	-1,73E+00	1,52E+00
BOD1L1	5,93E+03	3,21E-06	1,37E-03	1,21E+00	1,21E+00	1,18E+00
BTBD9	2,32E+03	5,29E-04	3,74E-02	5,11E-01	-1,96E+00	2,38E+00
C10orf88	2,43E+03	5,20E-04	3,70E-02	8,22E-01	-1,22E+00	not found
C17orf49	7,61E+03	1,90E-05	4,58E-03	8,31E-01	-1,20E+00	not found
C1orf213	8,87E+02	4,60E-04	3,39E-02	5,06E-01	-1,98E+00	-1,84E+00
C20orf112	4,14E+04	2,51E-04	2,42E-02	8,41E-01	-1,19E+00	not found
C21orf91	4,94E+03	2,70E-09	3,96E-06	7,33E-01	-1,36E+00	not found
C22orf32	1,12E+04	1,18E-05	3,35E-03	6,84E-01	-1,46E+00	not found
C4orf48	3,47E+03	2,78E-04	2,51E-02	1,58E+00	1,58E+00	not found
C9orf172	1,87E+03	2,44E-09	3,95E-06	1,66E+00	1,66E+00	not found
CCDC144C	4,37E+02	8,15E-04	4,89E-02	6,04E-01	-1,65E+00	not found
CCND2	1,32E+04	3,19E-05	6,29E-03	1,31E+00	1,31E+00	not found
CD27-AS1	2,42E+02	7,28E-04	4,47E-02	5,09E-01	-1,96E+00	not found
CD3EAP	1,36E+03	2,80E-04	2,51E-02	1,43E+00	1,43E+00	not found
CDIPT	2,32E+04	9,65E-05	1,25E-02	7,98E-01	-1,25E+00	not found
CDKN3	2,21E+03	6,44E-04	4,21E-02	1,27E+00	1,27E+00	not found
CEP44	5,72E+02	1,39E-04	1,58E-02	5,85E-01	-1,71E+00	not found
CHMP1B	1,87E+04	4,45E-05	8,00E-03	7,74E-01	-1,29E+00	not found
CLK4	8,03E+02	5,43E-04	3,77E-02	7,67E-01	-1,30E+00	not found
CLN3	2,02E+03	1,21E-04	1,42E-02	7,61E-01	-1,31E+00	not found
COL6A2	1,03E+04	5,66E-04	3,90E-02	1,35E+00	1,35E+00	not found
COX17	8,74E+03	6,80E-04	4,35E-02	7,27E-01	-1,38E+00	not found
CPSF6	1,09E+04	1,14E-04	1,38E-02	1,62E-01	-6,19E+00	not found
CREBRF	5,48E+03	2,70E-04	2,51E-02	7,15E-01	-1,40E+00	not found
CRMP1	1,14E+05	3,93E-05	7,38E-03	1,22E+00	1,22E+00	not found
DAGLA	4,56E+03	4,90E-04	3,55E-02	1,22E+00	1,22E+00	not found
DCAF13P3	4,81E+03	1,26E-04	1,48E-02	8,08E-01	-1,24E+00	1,24E+00
DCAF16	4,87E+03	3,16E-05	6,29E-03	8,34E-01	-1,20E+00	not found
DDT	2,05E+03	8,23E-05	1,18E-02	7,40E-01	-1,35E+00	not found

DHRS2	4,78E+03	1,73E-05	4,30E-03	7,74E-01	-1,29E+00	not found
DLG5	3,03E+04	7,03E-04	4,45E-02	1,18E+00	1,18E+00	not found
DLGAP1	6,11E+02	1,05E-04	1,30E-02	1,62E+00	1,62E+00	not found
DNAJC12	1,63E+04	1,76E-12	4,73E-09	8,26E-01	-1,21E+00	not found
DOK3	1,26E+02	1,16E-04	1,38E-02	2,41E+00	2,41E+00	not found
DPY30	8,92E+03	3,13E-04	2,66E-02	7,49E-01	-1,34E+00	not found
DYNC1H1	2,21E+04	2,86E-04	2,54E-02	1,25E+00	1,25E+00	not found
DZIP3	3,53E+04	1,46E-05	3,70E-03	8,08E-01	-1,24E+00	not found
E2F7	8,40E+01	6,72E-04	4,34E-02	3,43E+00	3,43E+00	not found
EDC3	5,85E+03	2,98E-04	2,58E-02	8,71E-01	-1,15E+00	not found
EDNRB	2,81E+03	4,39E-04	3,36E-02	1,66E+00	1,66E+00	not found
EFNB2	7,45E+03	4,20E-05	7,80E-03	1,26E+00	1,26E+00	1,24E+00
ELP5	8,95E+03	1,71E-04	1,85E-02	7,96E-01	-1,26E+00	not found
ENDOD1	2,47E+03	4,08E-07	2,44E-04	1,51E+00	1,51E+00	not found
ENTPD2	1,10E+02	4,45E-05	8,00E-03	4,52E+00	4,52E+00	-4,88E+00
ERH	1,39E+04	1,65E-04	1,81E-02	5,92E-01	-1,69E+00	not found
EZR	4,75E+03	2,08E-06	1,05E-03	1,26E+00	1,26E+00	1,31E+00
F2R	2,66E+03	6,83E-05	1,05E-02	1,31E+00	1,31E+00	not found
FAM109A	7,82E+02	1,44E-04	1,61E-02	1,64E+00	1,64E+00	not found
FAM163A	2,18E+02	4,11E-04	3,27E-02	4,55E-01	-2,20E+00	not found
FAM89B	4,56E+03	8,29E-05	1,18E-02	1,35E+00	1,35E+00	not found
FARP2	1,11E+03	2,11E-07	1,31E-04	6,08E-01	-1,64E+00	not found
FBLN1	4,19E+02	4,91E-05	8,55E-03	2,19E+00	2,19E+00	not found
FBXW7	1,69E+04	6,50E-06	2,28E-03	7,96E-01	-1,26E+00	not found
FEZF1-AS1	1,33E+03	2,24E-06	1,07E-03	6,01E-01	-1,66E+00	1,56E+00
FGD5	1,25E+03	4,13E-04	3,27E-02	1,33E+00	1,33E+00	-1,32E+00
FGFBP3	1,61E+03	4,80E-04	3,51E-02	1,77E+00	1,77E+00	not found
FGGY	7,02E+03	9,12E-06	2,78E-03	8,13E-01	-1,23E+00	not found
FHOD3	5,23E+03	1,97E-04	2,05E-02	1,38E+00	1,38E+00	not found
FKBP14	4,43E+03	2,76E-04	2,51E-02	8,14E-01	-1,23E+00	1,43E+00
FLJ43663	9,75E+02	5,75E-04	3,90E-02	6,58E-01	-1,52E+00	not found
FRMD6	1,75E+03	5,42E-04	3,77E-02	1,71E+00	1,71E+00	not found
FZD10	8,70E+02	2,98E-04	2,58E-02	2,06E+00	2,06E+00	not found
FZD4	6,72E+02	5,75E-04	3,90E-02	1,47E+00	1,47E+00	not found
FZD7	2,71E+03	8,17E-04	4,89E-02	1,41E+00	1,41E+00	not found
FZD8	6,24E+02	2,54E-04	2,43E-02	1,74E+00	1,74E+00	not found
G6PC3	2,92E+04	3,30E-04	2,80E-02	8,19E-01	-1,22E+00	not found
GABBR1	1,44E+05	2,04E-04	2,07E-02	8,43E-01	-1,19E+00	not found
GNAI3	5,17E+03	4,70E-35	3,80E-31	8,73E+00	8,73E+00	-1,46E+00
GOLGA1	3,22E+03	7,85E-05	1,15E-02	8,15E-01	-1,23E+00	not found
GRHL1	1,97E+03	4,92E-05	8,55E-03	7,21E-01	-1,39E+00	not found
GUSBP4	1,29E+03	1,32E-05	3,56E-03	6,61E-01	-1,51E+00	not found
HAPLN3	6,35E+02	3,43E-04	2,83E-02	1,58E+00	1,58E+00	not found
HES1	1,14E+03	1,47E-05	3,70E-03	1,79E+00	1,79E+00	not found
HIP1R	5,73E+03	2,89E-04	2,55E-02	7,80E-01	-1,28E+00	not found
HIST1H1D	1,01E+04	2,01E-04	2,06E-02	7,43E-01	-1,35E+00	1,69E+00
HIST1H2AG	6,16E+03	7,11E-04	4,45E-02	1,39E+00	1,39E+00	2,23E+00
HIST1H2BC	2,41E+03	1,61E-06	8,98E-04	2,31E+00	2,31E+00	not found
HIST1H2BD	3,52E+04	6,77E-42	1,09E-37	7,25E-01	-1,38E+00	4,67E+00
HIST1H2BN	1,23E+04	4,85E-04	3,53E-02	8,19E-01	-1,22E+00	not found
HIST1H3F	4,28E+03	4,24E-08	3,42E-05	1,98E+00	1,98E+00	not found
HIST1H3G	2,41E+03	2,20E-04	2,20E-02	1,75E+00	1,75E+00	4,32E+00
HIST1H3I	3,32E+04	1,81E-08	1,62E-05	6,29E-01	-1,59E+00	1,333020769
HIST1H3J	2,16E+04	1,49E-20	8,03E-17	6,78E-01	-1,47E+00	1,40E+00
HIST1H4B	1,04E+04	3,14E-09	4,16E-06	6,22E-01	-1,61E+00	1,60E+00
HIST2H3D	3,26E+02	9,88E-05	1,26E-02	4,95E-01	-2,02E+00	1,81E+00

HMG20A	2,34E+04	2,22E-04	2,20E-02	9,23E-01	-1,08E+00	not found	
HNRNPH1	1,09E+04	1,23E-05	3,42E-03	1,40E+00	1,40E+00	not found	
HS3ST3A1	3,52E+02	5,71E-04	3,90E-02	2,12E+00	2,12E+00	not found	
HSD17B7	1,18E+04	2,36E-06	1,09E-03	8,35E-01	-1,20E+00		-1,21E+00
HTRA2	1,05E+04	1,28E-07	8,59E-05	7,48E-01	-1,34E+00	not found	
IFI27L2	5,83E+02	7,26E-04	4,47E-02	6,35E-01	-1,58E+00	not found	
IFT43	7,90E+03	1,36E-05	3,59E-03	6,41E-01	-1,56E+00	not found	
ING3	3,48E+03	2,78E-04	2,51E-02	7,90E-01	-1,27E+00	not found	
INSM2	8,58E+02	1,31E-04	1,52E-02	6,64E-01	-1,51E+00		1,42E+00
IQCB1	3,95E+03	1,42E-04	1,60E-02	7,35E-01	-1,36E+00	not found	
ITGA6	5,93E+02	6,28E-05	1,01E-02	2,05E+00	2,05E+00	not found	
ITGAV	5,24E+03	9,07E-05	1,24E-02	1,24E+00	1,24E+00	not found	
JHDM1D	2,34E+03	5,11E-05	8,78E-03	7,41E-01	-1,35E+00		1,30E+00
KBTBD10	1,52E+04	1,10E-04	1,35E-02	7,68E-01	-1,30E+00	not found	
KIAA1161	1,02E+03	1,16E-04	1,38E-02	1,45E+00	1,45E+00	not found	
KIAA1324	3,08E+03	3,89E-05	7,38E-03	7,63E-01	-1,31E+00	not found	
KLHL3	3,47E+03	3,19E-05	6,29E-03	7,70E-01	-1,30E+00	not found	
KRTAP5-2	6,22E+02	1,77E-04	1,91E-02	1,63E+00	1,63E+00	not found	
LAMC1	1,08E+04	4,24E-04	3,32E-02	1,41E+00	1,41E+00	not found	
LANCL3	8,03E+02	2,40E-04	2,35E-02	1,48E+00	1,48E+00	not found	
LATS2	7,41E+02	6,81E-04	4,35E-02	1,47E+00	1,47E+00	not found	
LGR4	2,75E+03	2,77E-06	1,24E-03	1,41E+00	1,41E+00	not found	
LHX8	1,05E+04	1,25E-07	8,59E-05	7,68E-01	-1,30E+00		1,20E+00
LMBR1L	8,35E+03	8,49E-04	4,99E-02	7,50E-01	-1,33E+00	not found	
LOC100133985	4,90E+02	9,22E-05	1,24E-02	5,84E-01	-1,71E+00	not found	
LOC100499405	3,34E+03	1,03E-04	1,29E-02	6,19E-01	-1,61E+00	not found	
LOC254100	7,50E+02	2,13E-05	4,84E-03	6,24E-01	-1,60E+00		1,55E+00
LOC388796	4,43E+03	1,29E-08	1,38E-05	7,12E-01	-1,40E+00	not found	
LOC389023	7,37E+02	1,83E-04	1,95E-02	7,02E-01	-1,42E+00	not found	
LOC642852	5,68E+03	3,44E-04	2,83E-02	1,20E+00	1,20E+00	not found	
LOC646471	1,71E+03	9,35E-05	1,24E-02	7,41E-01	-1,35E+00		1,41E+00
LPL	1,53E+03	6,70E-05	1,05E-02	1,52E+00	1,52E+00	not found	
LPP	1,03E+03	7,47E-05	1,11E-02	1,49E+00	1,49E+00	not found	
LUC7L	1,03E+04	1,45E-04	1,61E-02	7,17E-01	-1,39E+00	not found	
MAGI1	1,48E+03	5,70E-04	3,90E-02	1,44E+00	1,44E+00	not found	
MAGOHB	1,83E+03	3,61E-05	7,03E-03	6,85E-01	-1,46E+00	not found	
MARCKS	1,20E+04	5,81E-05	9,78E-03	1,35E+00	1,35E+00	not found	
MARVELD1	1,02E+03	7,05E-04	4,45E-02	1,41E+00	1,41E+00	not found	
MATK	3,70E+03	4,50E-04	3,39E-02	1,19E+00	1,19E+00		-1,48E+00
MATN2	1,32E+03	4,34E-04	3,36E-02	1,36E+00	1,36E+00		1,64E+00
MAX	1,56E+04	4,18E-06	1,65E-03	7,18E-01	-1,39E+00	not found	
MCM2	2,99E+02	4,33E-04	3,36E-02	1,80E+00	1,80E+00	not found	
MDGA1	7,83E+03	9,24E-05	1,24E-02	6,75E-01	-1,48E+00		1,62E+00
MESDC1	9,32E+02	3,04E-05	6,29E-03	1,50E+00	1,50E+00	not found	
METRNL	2,87E+03	2,08E-04	2,08E-02	1,30E+00	1,30E+00	not found	
MIR600HG	5,21E+03	6,79E-05	1,05E-02	1,35E+00	1,35E+00	not found	
MNT	6,04E+03	4,06E-04	3,25E-02	1,23E+00	1,23E+00	not found	
MOCS1	1,00E+02	3,48E-04	2,85E-02	1,44E-01	-6,96E+00	not found	
MOXD1	2,86E+03	1,45E-07	9,36E-05	1,38E+00	1,38E+00	not found	
MTSS1L	2,58E+04	1,29E-05	3,52E-03	1,26E+00	1,26E+00	not found	
MXI1	1,22E+04	3,44E-06	1,42E-03	7,56E-01	-1,32E+00	not found	
MYLIP	1,08E+02	1,35E-04	1,55E-02	3,20E+00	3,20E+00	not found	
MYT1L	2,68E+04	5,98E-04	3,99E-02	8,32E-01	-1,20E+00	not found	
NDUFB5	1,47E+04	2,31E-04	2,28E-02	7,65E-01	-1,31E+00	not found	
NENF	3,07E+03	7,99E-06	2,56E-03	1,30E+00	1,30E+00	not found	
NFIC	2,82E+03	1,75E-08	1,62E-05	1,56E+00	1,56E+00	not found	

NGFR	5,30E+02	4,92E-04	3,55E-02	1,81E+00	1,81E+00	not found
NGFRAP1	5,53E+04	2,16E-05	4,84E-03	8,46E-01	-1,18E+00	not found
NKD1	1,29E+03	6,40E-04	4,21E-02	1,36E+00	1,36E+00	not found
NOP10	4,09E+04	8,08E-06	2,56E-03	7,30E-01	-1,37E+00	not found
NOTCH3	5,85E+03	4,46E-06	1,72E-03	1,62E+00	1,62E+00	not found
NSUN6	1,05E+03	3,15E-05	6,29E-03	6,66E-01	-1,50E+00	not found
NTSR1	3,66E+03	1,01E-05	2,98E-03	1,85E+00	1,85E+00	-1,62E+00
OLFM3	4,94E+03	5,79E-05	9,78E-03	7,88E-01	-1,27E+00	not found
OR4F17	1,80E+01	7,75E-04	4,69E-02	3,28E-04	-3,05E+03	not found
OTUB2	3,34E+03	7,21E-05	1,09E-02	1,30E+00	1,30E+00	-1,34E+00
PACSIN2	1,88E+03	6,95E-04	4,42E-02	1,35E+00	1,35E+00	not found
PALD1	6,77E+02	7,26E-04	4,47E-02	1,43E+00	1,43E+00	not found
PCSK1	7,25E+04	2,01E-05	4,78E-03	8,59E-01	-1,16E+00	not found
PDE10A	4,64E+03	6,29E-05	1,01E-02	1,32E+00	1,32E+00	not found
PFN2	6,99E+04	9,88E-05	1,26E-02	8,83E-01	-1,13E+00	1,11E+00
PGPEP1	2,17E+03	1,13E-04	1,38E-02	1,33E+00	1,33E+00	not found
PHF20L1	6,22E+03	9,56E-05	1,25E-02	6,80E-01	-1,47E+00	1,43E+00
PHF8	4,46E+03	1,66E-04	1,81E-02	7,45E-01	-1,34E+00	not found
PIP5K1C	1,26E+04	2,42E-05	5,22E-03	1,17E+00	1,17E+00	not found
PLAGL1	1,11E+02	7,21E-05	1,09E-02	3,72E-01	-2,69E+00	not found
PLXNB1	7,86E+03	2,67E-04	2,51E-02	8,26E-01	-1,21E+00	1,26E+00
POLE3	3,10E+03	3,98E-04	3,20E-02	1,24E+00	1,24E+00	not found
POLR2B	2,12E+04	5,83E-04	3,92E-02	9,11E-01	-1,10E+00	not found
POLR2H	3,26E+03	6,97E-06	2,35E-03	7,89E-01	-1,27E+00	not found
PPARA	1,07E+03	7,70E-04	4,67E-02	1,31E+00	1,31E+00	not found
PPP1R14C	6,89E+03	2,42E-05	5,22E-03	1,53E+00	1,53E+00	not found
PPP1R17	3,05E+03	3,35E-04	2,80E-02	7,44E-01	-1,34E+00	not found
PRR12	8,83E+03	2,52E-04	2,42E-02	1,21E+00	1,21E+00	not found
PRRC2A	3,94E+04	2,73E-04	2,51E-02	1,16E+00	1,16E+00	not found
PSME2	1,43E+02	4,55E-04	3,39E-02	4,04E-01	-2,47E+00	not found
PTN	2,94E+04	2,65E-04	2,50E-02	1,21E+00	1,21E+00	1,57E+00
R3HDM1	2,97E+04	7,84E-04	4,73E-02	8,45E-01	-1,18E+00	not found
RAD21	4,83E+04	3,78E-05	7,28E-03	8,14E-01	-1,23E+00	not found
RAD54B	1,58E+03	4,54E-04	3,39E-02	7,14E-01	-1,40E+00	not found
RASGEF1B	5,80E+03	1,33E-08	1,38E-05	6,90E-01	-1,45E+00	not found
RBM44	7,40E+01	7,57E-04	4,62E-02	2,41E-01	-4,15E+00	not found
RBMX	4,57E+03	6,41E-04	4,21E-02	7,53E-01	-1,33E+00	not found
REEP1	3,49E+04	2,73E-04	2,51E-02	1,18E+00	1,18E+00	not found
REM2	5,77E+03	3,51E-06	1,42E-03	5,87E-01	-1,70E+00	not found
RET	1,45E+03	9,38E-05	1,24E-02	1,36E+00	1,36E+00	-1,44E+00
RGS8	2,23E+03	1,10E-09	1,98E-06	2,03E+00	2,03E+00	not found
RIPK1	3,51E+02	3,34E-04	2,80E-02	1,97E+00	1,97E+00	not found
RMRP	9,42E+05	5,34E-04	3,75E-02	1,67E+00	1,67E+00	not found
RNF112	2,28E+02	7,24E-04	4,47E-02	1,92E+00	1,92E+00	not found
RNU12	7,27E+02	6,21E-05	1,01E-02	5,39E-01	-1,85E+00	2,18E+00
ROMO1	4,43E+03	6,88E-06	2,35E-03	8,01E-01	-1,25E+00	not found
RPL8	2,39E+03	2,85E-04	2,54E-02	1,83E+00	1,83E+00	not found
RTN3	1,67E+03	2,92E-04	2,55E-02	1,32E+00	1,32E+00	not found
SBDSP1	5,66E+03	3,79E-04	3,07E-02	7,88E-01	-1,27E+00	not found
SCARNA7	1,38E+05	1,27E-04	1,48E-02	7,14E-01	-1,40E+00	not found
SCARNA9	5,29E+04	7,15E-17	2,31E-13	7,21E-01	-1,39E+00	not found
SCN8A	2,50E+03	1,81E-04	1,93E-02	1,40E+00	1,40E+00	not found
SERF2	2,58E+02	1,01E-04	1,27E-02	4,74E-01	-2,11E+00	not found
SFMBT2	1,60E+04	2,65E-04	2,50E-02	7,69E-01	-1,30E+00	not found
SGK223	1,41E+03	2,23E-05	4,93E-03	1,49E+00	1,49E+00	not found
SHFM1	1,11E+04	5,34E-06	2,00E-03	8,20E-01	-1,22E+00	not found

SKP2	1,45E+03	2,78E-04	2,51E-02	1,40E+00	1,40E+00	not found
SLC16A9	2,73E+03	5,02E-04	3,61E-02	8,00E-01	-1,25E+00	1,35E+00
SLC1A3	2,20E+03	1,16E-10	2,67E-07	1,70E+00	1,70E+00	2,22E+00
SLC25A23	1,47E+04	5,40E-04	3,77E-02	1,24E+00	1,24E+00	not found
SLC43A2	6,71E+03	2,08E-06	1,05E-03	1,22E+00	1,22E+00	not found
SLC4A4	1,79E+03	1,18E-07	8,59E-05	1,68E+00	1,68E+00	not found
SLC7A11	2,23E+03	8,75E-06	2,72E-03	1,37E+00	1,37E+00	not found
SMG9	3,70E+03	7,21E-04	4,47E-02	1,18E+00	1,18E+00	not found
SMIM7	5,72E+03	4,40E-04	3,36E-02	8,48E-01	-1,18E+00	1,25E+00
SNRPN	5,15E+04	1,14E-04	1,38E-02	7,77E-01	-1,29E+00	not found
SOX4	1,37E+04	1,84E-05	4,51E-03	1,35E+00	1,35E+00	not found
SOX9	2,96E+03	2,26E-06	1,07E-03	1,95E+00	1,95E+00	not found
SPRED1	6,61E+03	8,38E-05	1,18E-02	1,21E+00	1,21E+00	not found
SST	1,06E+04	3,41E-04	2,83E-02	7,74E-01	-1,29E+00	not found
ST18	3,05E+03	3,02E-08	2,57E-05	7,05E-01	-1,42E+00	not found
STAC2	1,12E+03	2,42E-04	2,35E-02	1,39E+00	1,39E+00	not found
STAU2	7,26E+03	5,93E-04	3,98E-02	8,34E-01	-1,20E+00	not found
STIP1	2,68E+04	2,71E-05	5,68E-03	8,02E-01	-1,25E+00	not found
STX4	1,23E+04	7,48E-05	1,11E-02	8,25E-01	-1,21E+00	not found
SULT1C4	8,44E+02	1,63E-04	1,81E-02	6,59E-01	-1,52E+00	1,56E+00
SYMPK	2,28E+04	6,75E-04	4,34E-02	8,18E-01	-1,22E+00	not found
SYNDIG1L	1,84E+03	8,73E-05	1,22E-02	1,32E+00	1,32E+00	not found
SYNGR3	3,73E+02	3,89E-04	3,14E-02	1,96E+00	1,96E+00	not found
SYPL2	1,20E+01	8,43E-04	4,97E-02	5,83E-04	-1,72E+03	not found
TAF7	3,50E+04	3,23E-06	1,37E-03	8,38E-01	-1,19E+00	not found
TIMM17B	8,97E+03	2,00E-04	2,06E-02	8,58E-01	-1,17E+00	not found
TIMP4	2,69E+02	8,11E-05	1,18E-02	2,09E+00	2,09E+00	not found
TMEM106C	3,60E+04	6,77E-05	1,05E-02	8,11E-01	-1,23E+00	not found
TNFRSF12A	3,74E+03	4,34E-05	7,97E-03	1,27E+00	1,27E+00	not found
TNNI1	1,64E+03	1,13E-05	3,27E-03	6,46E-01	-1,55E+00	not found
TNRC18	4,07E+03	3,35E-09	4,16E-06	1,34E+00	1,34E+00	1,20E+00
TPP2	1,42E+04	9,89E-06	2,96E-03	8,25E-01	-1,21E+00	not found
TPRN	2,00E+03	6,43E-06	2,28E-03	1,38E+00	1,38E+00	not found
TPT1-AS1	3,16E+03	3,02E-04	2,60E-02	7,02E-01	-1,43E+00	not found
TRA2A	4,21E+03	9,44E-05	1,24E-02	7,58E-01	-1,32E+00	1,39E+00
TRIM11	2,99E+03	4,59E-04	3,39E-02	1,23E+00	1,23E+00	not found
TSPAN31	6,68E+03	3,08E-04	2,63E-02	6,80E-01	-1,47E+00	not found
TSPAN4	2,35E+03	8,33E-05	1,18E-02	1,30E+00	1,30E+00	not found
TTC21A	2,65E+02	5,20E-04	3,70E-02	5,21E-01	-1,92E+00	not found
TTC3P1	4,98E+03	2,50E-05	5,31E-03	7,58E-01	-1,32E+00	1,37E+00
TULP3	4,63E+03	4,19E-04	3,30E-02	8,46E-01	-1,18E+00	1,24E+00
UBE2V2	2,80E+04	8,31E-04	4,92E-02	8,89E-01	-1,12E+00	not found
UBL4A	1,59E+03	5,82E-04	3,92E-02	1,31E+00	1,31E+00	not found
USH1G	1,23E+02	6,04E-04	4,02E-02	2,12E+00	2,12E+00	not found
VPS72	2,63E+04	4,41E-04	3,36E-02	8,28E-01	-1,21E+00	not found
VSNL1	8,81E+04	1,87E-04	1,98E-02	7,33E-01	-1,36E+00	not found
YPEL3	5,69E+03	4,67E-04	3,43E-02	8,50E-01	-1,18E+00	not found
ZDHHC16	6,72E+03	8,26E-04	4,92E-02	8,49E-01	-1,18E+00	not found
ZFAND1	6,41E+03	2,92E-04	2,55E-02	8,18E-01	-1,22E+00	not found
ZFP36L1	2,77E+03	6,32E-04	4,18E-02	1,67E+00	1,67E+00	not found
ZFP62	3,52E+02	1,45E-05	3,70E-03	2,13E+00	2,13E+00	not found
ZIC3	1,35E+04	2,08E-04	2,08E-02	8,88E-01	-1,13E+00	1,13E+00
ZNF114	3,90E+02	2,01E-04	2,06E-02	1,77E+00	1,77E+00	not found
ZNF33A	3,67E+03	4,91E-05	8,55E-03	7,85E-01	-1,27E+00	not found
ZNF394	3,21E+02	8,19E-08	6,30E-05	6,23E-02	-1,61E+01	9,45E+00
ZNF490	5,15E+03	7,09E-04	4,45E-02	8,78E-01	-1,14E+00	1,16E+00

ZNF491	2,23E+03	6,62E-04	4,29E-02	8,04E-01	-1,24E+00	not found
ZNF571	5,84E+03	8,31E-04	4,92E-02	8,35E-01	-1,20E+00	not found
ZNF689	2,15E+03	4,60E-04	3,39E-02	1,41E+00	1,41E+00	not found
ZNF710	1,84E+03	2,13E-05	4,84E-03	1,37E+00	1,37E+00	not found
ZNF98	1,44E+01	8,03E-10	1,62E-06	7,80E-04	-1,28E+03	not found
ZNRF3	1,12E+03	1,95E-04	2,04E-02	1,66E+00	1,66E+00	not found

Table S4: Table showing the list of genes statistically modified between Kin-rDCLK3^{WT} and Kin-rDCLK3$^{K543M.}$ Transcriptomic analysis has been performed by AmpliSeq on extracts from four culture wells for each group, 12 days after infection. Filtering of data (FC>1.1, adjusted p<0.002, FDR<0.05); identified 371 genes of interest.

Supplemental Table S4

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List of genes from kin-DCLK3 (WT) vs kin-DCLK3 Dead Kinase (K543M)

					FC>1.1, adjusted p<0.0009, FDR<0.05, 275 genes
Gene symbol	Total reads	P-value (KIN-WT vs, KIN-K543M)	FDR step up (KIN-WT vs, KIN-K543M)	Ratio (KIN-WT vs, KIN-K543M)	Fold change (KIN-WT vs, KIN-K543M)
A2M	4,71E+02	2,98E-05	3,62E-03	4,67E+00	4,67E+00
A4GALT	1,07E+03	8,70E-04	4,05E-02	6,83E-01	-1,46E+00
AARS	2,69E+04	1,59E-04	1,23E-02	8,14E-01	-1,23E+00
ABHD6	7,49E+03	3,58E-04	2,23E-02	8,70E-01	-1,15E+00
ACAD9	1,87E+03	1,39E-05	1,96E-03	1,37E+00	1,37E+00
ADAM17	3,10E+03	6,35E-04	3,26E-02	1,54E+00	1,54E+00
ADAMTS6	3,20E+03	4,88E-05	5,19E-03	1,38E+00	1,38E+00
ADCY7	3,66E+03	2,35E-04	1,67E-02	6,58E-01	-1,52E+00
ADHFE1	1,27E+02	4,22E-04	2,47E-02	3,08E+00	3,08E+00
ADNP2	1,68E+03	4,79E-04	2,69E-02	8,99E-02	-1,11E+01
AHSA2	9,50E+02	2,25E-07	7,74E-05	1,98E+00	1,98E+00
AKR7A2	2,52E+03	2,75E-05	3,39E-03	1,35E+00	1,35E+00
ALPL	3,11E+02	4,86E-04	2,70E-02	1,02E-01	-9,81E+00
ANK2	8,29E+04	6,04E-04	3,14E-02	8,17E-01	-1,22E+00
ANKRD34C	1,99E+02	1,12E-03	4,85E-02	8,63E-02	-1,16E+01
ANTXR1	2,09E+03	1,11E-03	4,85E-02	1,91E+00	1,91E+00
ANXA5	6,18E+03	2,09E-06	4,50E-04	2,03E+00	2,03E+00
AP1M1	1,87E+04	8,36E-04	3,93E-02	8,17E-01	-1,22E+00
APBB3	4,35E+03	7,33E-04	3,60E-02	1,19E+00	1,19E+00
APP	5,55E+03	5,12E-04	2,79E-02	1,86E+00	1,86E+00
ARGLU1	4,77E+03	2,87E-04	1,87E-02	1,48E+00	1,48E+00
ARHGAP29	2,96E+03	4,09E-05	4,59E-03	1,61E+00	1,61E+00
ARHGEF1	8,23E+02	1,17E-05	1,76E-03	1,65E+00	1,65E+00
ARL13B	8,07E+02	4,59E-05	4,95E-03	1,63E+00	1,63E+00
ARL6IP6	3,12E+03	2,16E-05	2,77E-03	1,28E+00	1,28E+00
ATG16L2	2,83E+02	4,77E-04	2,69E-02	2,03E+00	2,03E+00
ATXN10	2,68E+04	4,98E-04	2,73E-02	1,25E+00	1,25E+00
B2M	7,76E+03	6,87E-08	3,26E-05	1,73E+00	1,73E+00
BAZ1A	3,49E+02	4,00E-06	7,69E-04	2,41E+00	2,41E+00
BBX	9,98E+03	1,32E-24	5,33E-21	1,44E+00	1,44E+00
BCAP29	3,66E+03	5,67E-04	3,00E-02	1,32E+00	1,32E+00
BIRC5	2,93E+02	3,14E-07	1,02E-04	6,95E+00	6,95E+00
BIVM-ERCC5	7,64E+03	9,10E-04	4,20E-02	1,39E+00	1,39E+00
BMF	1,15E+03	4,64E-06	8,46E-04	1,52E+00	1,52E+00
BOD1L1	5,93E+03	5,97E-05	6,05E-03	1,18E+00	1,18E+00
BTBD9	2,32E+03	1,62E-05	2,24E-03	2,38E+00	2,38E+00
C14orf1	4,23E+04	1,27E-11	1,46E-08	7,44E-01	-1,34E+00
C16orf3	3,31E+02	5,40E-04	2,91E-02	1,82E+00	1,82E+00
C17orf59	1,57E+03	2,47E-04	1,67E-02	7,59E-01	-1,32E+00

C1orf106	2,11E+02	6,25E-06	1,04E-03	3,52E+00	3,52E+00
C1orf213	8,87E+02	9,97E-04	4,48E-02	5,43E-01	-1,84E+00
C2orf72	2,46E+03	3,70E-05	4,24E-03	7,68E-01	-1,30E+00
C7orf50	5,53E+03	8,27E-04	3,91E-02	3,89E-01	-2,57E+00
CA14	1,81E+03	3,89E-07	1,21E-04	1,57E+00	1,57E+00
CCDC109B	5,47E+02	6,49E-05	6,51E-03	1,76E+00	1,76E+00
CCDC113	4,43E+02	7,93E-04	3,84E-02	1,67E+00	1,67E+00
CCDC117	1,61E+03	2,24E-08	1,26E-05	2,01E+01	2,01E+01
CCDC152	1,94E+03	6,47E-04	3,30E-02	2,04E+00	2,04E+00
CCDC8	1,51E+03	5,24E-07	1,51E-04	1,61E+00	1,61E+00
CCDC85B	8,45E+03	1,32E-04	1,11E-02	8,66E-01	-1,15E+00
CCNC	7,24E+03	9,61E-07	2,50E-04	1,57E+00	1,57E+00
CCNE2	8,10E+01	5,08E-04	2,78E-02	3,79E+00	3,79E+00
CDC45	1,73E+02	2,58E-05	3,23E-03	3,70E+00	3,70E+00
CDCA8	9,20E+01	3,03E-04	1,94E-02	3,81E+00	3,81E+00
CDK10	1,68E+03	2,51E-04	1,68E-02	1,43E+00	1,43E+00
CDK2	3,68E+02	1,03E-07	4,27E-05	2,57E+00	2,57E+00
CDKN1A	3,45E+04	2,03E-04	1,51E-02	7,23E-01	-1,38E+00
CDKN2C	1,73E+02	1,08E-07	4,27E-05	4,39E+00	4,39E+00
CDT1	2,93E+02	1,50E-04	1,19E-02	2,01E+00	2,01E+00
CEBPG	4,63E+02	1,49E-04	1,19E-02	1,85E+00	1,85E+00
CENPF	4,16E+02	3,56E-07	1,13E-04	4,02E+00	4,02E+00
CHKB	1,01E+03	1,17E-04	1,01E-02	1,54E+00	1,54E+00
CHPF	1,98E+04	1,52E-04	1,20E-02	1,27E+00	1,27E+00
CNOT8	4,10E+02	2,42E-04	1,67E-02	1,68E+00	1,68E+00
COL3A1	1,09E+04	9,57E-04	4,34E-02	3,79E+00	3,79E+00
COL5A2	9,96E+03	4,12E-05	4,60E-03	1,59E+00	1,59E+00
CPSF4	3,83E+03	2,49E-04	1,67E-02	1,48E+00	1,48E+00
CRISPLD1	5,09E+03	1,04E-03	4,64E-02	1,40E+00	1,40E+00
CRYAB	2,05E+03	1,12E-04	9,70E-03	2,43E+00	2,43E+00
CTNNA1	7,08E+03	9,98E-06	1,54E-03	1,60E+00	1,60E+00
CTSC	1,90E+03	1,74E-06	3,98E-04	1,43E+00	1,43E+00
CXCR4	4,52E+03	4,23E-04	2,47E-02	1,83E+00	1,83E+00
CYB5B	3,45E+04	1,77E-07	6,66E-05	7,87E-01	-1,27E+00
CYR61	1,44E+03	2,91E-04	1,87E-02	2,14E+00	2,14E+00
DARS2	5,26E+02	3,75E-04	2,28E-02	1,55E+00	1,55E+00
DCAF13P3	4,81E+03	8,12E-05	7,65E-03	1,24E+00	1,24E+00
DIS3L2	6,28E+03	2,67E-04	1,78E-02	1,19E+00	1,19E+00
DMTF1	5,30E+03	3,44E-04	2,15E-02	1,58E+00	1,58E+00
DTL	1,11E+02	3,03E-05	3,63E-03	5,77E+00	5,77E+00
DTWD2	1,17E+03	1,68E-05	2,27E-03	1,47E+00	1,47E+00
E2F1	1,17E+03	5,01E-09	3,24E-06	1,76E+00	1,76E+00
ECM2	1,82E+02	1,50E-04	1,19E-02	2,57E+00	2,57E+00
EDN1	6,52E+02	1,37E-04	1,13E-02	1,66E+00	1,66E+00
EFNB2	7,45E+03	1,88E-04	1,42E-02	1,24E+00	1,24E+00
EGR1	7,77E+02	2,73E-04	1,80E-02	1,51E+00	1,51E+00
EGR3	8,09E+02	5,65E-04	2,99E-02	1,66E+00	1,66E+00
EIF3H	2,52E+04	1,66E-05	2,27E-03	1,30E+00	1,30E+00
ENTPD2	1,10E+02	3,09E-05	3,64E-03	2,05E-01	-4,88E+00
EPHB4	9,11E+02	4,36E-07	1,30E-04	1,85E+00	1,85E+00

EPS8	4,11E+03	7,78E-04	3,78E-02	1,24E+00	1,24E+00
ERBB2	8,53E+02	1,04E-03	4,62E-02	1,56E+00	1,56E+00
ERBB2IP	3,12E+03	4,54E-04	2,60E-02	1,25E+00	1,25E+00
ERBB4	3,64E+03	2,25E-04	1,61E-02	1,34E+00	1,34E+00
EZR	4,75E+03	2,32E-07	7,80E-05	1,31E+00	1,31E+00
FABP3	8,17E+03	1,36E-05	1,94E-03	6,70E-01	-1,49E+00
FAM49A	2,97E+04	9,61E-04	4,35E-02	8,50E-01	-1,18E+00
FBLN5	8,38E+03	2,37E-04	1,67E-02	1,65E+00	1,65E+00
FEZF1-AS1	1,33E+03	4,46E-05	4,89E-03	1,56E+00	1,56E+00
FGD5	1,25E+03	5,54E-04	2,96E-02	7,57E-01	-1,32E+00
FKBP14	4,43E+03	4,27E-10	3,63E-07	1,43E+00	1,43E+00
FLJ20021	3,10E+02	1,08E-03	4,80E-02	1,81E+00	1,81E+00
FLNA	1,02E+04	7,85E-08	3,62E-05	1,69E+00	1,69E+00
FOSB	1,63E+02	8,95E-04	4,14E-02	2,12E+00	2,12E+00
FOXC1	2,65E+02	6,60E-04	3,34E-02	2,17E+00	2,17E+00
FOXN2	7,54E+02	2,06E-04	1,51E-02	1,50E+00	1,50E+00
FREM1	3,22E+02	6,87E-07	1,92E-04	2,53E+00	2,53E+00
FRZB	1,44E+03	3,09E-08	1,66E-05	1,81E+00	1,81E+00
FZD2	1,10E+03	7,56E-04	3,70E-02	2,57E+00	2,57E+00
GADD45G	4,50E+03	2,37E-04	1,67E-02	6,77E-01	-1,48E+00
GAS1	1,27E+03	3,60E-08	1,87E-05	1,73E+00	1,73E+00
GFPT2	1,94E+03	2,27E-05	2,88E-03	1,58E+00	1,58E+00
GNAI3	5,17E+03	1,14E-35	9,19E-32	1,12E-01	-8,93E+00
GNG5	1,44E+03	8,42E-05	7,77E-03	1,96E+00	1,96E+00
GOLIM4	1,84E+03	8,24E-04	3,91E-02	1,81E+00	1,81E+00
GPSM2	6,65E+02	2,35E-05	2,96E-03	1,63E+00	1,63E+00
GTSE1	2,01E+02	5,97E-04	3,11E-02	2,53E+00	2,53E+00
HACE1	1,69E+03	5,62E-06	9,66E-04	1,48E+00	1,48E+00
HEG1	4,79E+03	8,29E-05	7,69E-03	1,65E+00	1,65E+00
HELLS	3,99E+02	4,56E-04	2,60E-02	2,40E+00	2,40E+00
HIATL1	2,23E+03	2,88E-05	3,53E-03	1,39E+00	1,39E+00
HIST1H1B	5,46E+02	2,91E-04	1,87E-02	3,26E+00	3,26E+00
HIST1H1C	3,72E+03	1,06E-04	9,22E-03	1,78E+00	1,78E+00
HIST1H1D	1,01E+04	5,90E-10	4,77E-07	1,69E+00	1,69E+00
HIST1H1E	1,82E+04	2,27E-08	1,26E-05	1,58E+00	1,58E+00
HIST1H2AB	9,78E+02	4,06E-13	5,96E-10	2,19E+00	2,19E+00
HIST1H2AG	6,16E+03	9,17E-10	7,05E-07	2,23E+00	2,23E+00
HIST1H2AH	3,62E+03	5,75E-05	5,96E-03	1,81E+00	1,81E+00
HIST1H2AI	2,55E+02	1,75E-06	3,98E-04	2,77E+00	2,77E+00
HIST1H2AJ	4,21E+03	9,88E-21	2,28E-17	2,47E+00	2,47E+00
HIST1H2AL	1,49E+03	1,90E-07	6,98E-05	1,87E+00	1,87E+00
HIST1H2AM	8,60E+03	1,54E-06	3,71E-04	1,56E+00	1,56E+00
HIST1H2BD	3,52E+04	4,77E-57	7,71E-53	1,46E+00	1,46E+00
HIST1H2BH	2,14E+03	8,79E-05	8,02E-03	1,92E+00	1,92E+00
HIST1H2BI	1,81E+03	1,24E-08	7,41E-06	1,94E+00	1,94E+00
HIST1H2BM	2,83E+03	3,82E-05	4,35E-03	1,60E+00	1,60E+00
HIST1H2BO	2,47E+03	1,98E-06	4,37E-04	1,96E+00	1,96E+00
HIST1H3B	3,90E+03	1,94E-11	1,96E-08	3,81E+00	3,81E+00
HIST1H3C	1,69E+03	1,51E-05	2,10E-03	2,74E+00	2,74E+00
HIST1H3E	1,32E+04	4,16E-06	7,73E-04	1,43E+00	1,43E+00

HIST1H3G	2,41E+03	1,03E-07	4,27E-05	4,32E+00	4,32E+00
HIST1H3I	3,32E+04	4,15E-04	2,45E-02	1,33E+00	1,33E+00
HIST1H3J	2,16E+04	4,47E-16	8,02E-13	1,40E+00	1,40E+00
HIST1H4A	3,86E+03	7,39E-21	1,99E-17	1,86E+00	1,86E+00
HIST1H4B	1,04E+04	4,30E-09	2,89E-06	1,60E+00	1,60E+00
HIST1H4H	1,85E+04	6,70E-05	6,64E-03	1,35E+00	1,35E+00
HIST1H4L	7,83E+02	8,19E-04	3,91E-02	2,50E+00	2,50E+00
HIST2H3D	3,26E+02	3,76E-04	2,28E-02	1,81E+00	1,81E+00
HIVEP2	2,90E+03	1,57E-04	1,22E-02	1,49E+00	1,49E+00
HJURP	3,61E+02	9,02E-13	1,13E-09	4,36E+00	4,36E+00
HK2	5,75E+02	6,07E-06	1,02E-03	2,06E+00	2,06E+00
HMG20B	1,04E+03	6,42E-04	3,28E-02	1,49E+00	1,49E+00
HSD17B7	1,18E+04	1,11E-06	2,84E-04	8,29E-01	-1,21E+00
HSPG2	5,19E+02	7,16E-07	1,96E-04	2,19E+00	2,19E+00
IER5L	4,20E+03	1,09E-03	4,81E-02	8,15E-01	-1,23E+00
IFI44L	1,17E+02	1,50E-04	1,19E-02	3,91E+00	3,91E+00
IFITM10	3,04E+03	1,41E-05	1,98E-03	7,17E-01	-1,40E+00
IFITM3	3,25E+03	2,08E-06	4,50E-04	2,30E+00	2,30E+00
ILDR2	1,91E+03	1,37E-04	1,13E-02	1,38E+00	1,38E+00
INHBA	4,90E+02	2,88E-04	1,87E-02	3,28E+00	3,28E+00
INSM2	8,58E+02	5,15E-04	2,79E-02	1,42E+00	1,42E+00
INTS7	3,00E+03	1,31E-04	1,11E-02	1,28E+00	1,28E+00
JAZF1	2,40E+04	9,71E-04	4,38E-02	8,36E-01	-1,20E+00
JHDM1D	2,34E+03	4,87E-04	2,70E-02	1,30E+00	1,30E+00
KANSL1	1,47E+04	3,25E-04	2,07E-02	1,29E+00	1,29E+00
KCNH8	1,04E+03	2,78E-04	1,82E-02	2,93E+00	2,93E+00
KCNJ5	6,81E+02	8,14E-05	7,65E-03	6,16E-01	-1,62E+00
KIAA0101	5,88E+02	1,64E-04	1,27E-02	2,70E+00	2,70E+00
KIAA0895L	1,24E+04	1,72E-04	1,31E-02	1,33E+00	1,33E+00
KIAA1009	1,53E+03	8,23E-05	7,69E-03	1,46E+00	1,46E+00
KIAA1024	3,19E+03	7,33E-04	3,60E-02	2,96E-01	-3,38E+00
KIAA1045	5,88E+03	9,70E-05	8,70E-03	7,41E-01	-1,35E+00
KIF11	1,47E+02	2,44E-04	1,67E-02	3,74E+00	3,74E+00
KIF15	4,36E+02	2,15E-04	1,55E-02	2,33E+00	2,33E+00
KIF20A	1,34E+02	5,47E-06	9,54E-04	5,98E+00	5,98E+00
KIF4A	7,23E+02	1,68E-04	1,29E-02	1,64E+00	1,64E+00
LAMB2	3,73E+03	4,09E-10	3,63E-07	1,81E+00	1,81E+00
LAPTM4B	3,01E+04	2,40E-04	1,67E-02	1,20E+00	1,20E+00
LBR	4,13E+03	5,89E-06	1,00E-03	1,86E+00	1,86E+00
LENG8	1,12E+04	4,85E-04	2,70E-02	1,72E+00	1,72E+00
LHX8	1,05E+04	2,08E-04	1,51E-02	1,20E+00	1,20E+00
LINC00086	1,18E+03	3,99E-04	2,38E-02	7,21E-01	-1,39E+00
LINC00473	3,08E+02	3,78E-04	2,28E-02	2,18E+00	2,18E+00
LINC00630	4,00E+03	7,84E-05	7,50E-03	7,81E-01	-1,28E+00
LOC254100	7,50E+02	4,26E-05	4,71E-03	1,55E+00	1,55E+00
LOC283922	1,24E+03	5,59E-04	2,97E-02	1,40E+00	1,40E+00
LOC441155	8,27E+03	1,32E-04	1,11E-02	1,21E+00	1,21E+00
LOC646471	1,71E+03	9,02E-06	1,42E-03	1,41E+00	1,41E+00
LRIG1	9,69E+03	3,39E-04	2,13E-02	1,39E+00	1,39E+00
LRP2	2,46E+03	2,63E-05	3,27E-03	1,51E+00	1,51E+00

MALAT1	2,71E+05	1,25E-05	1,84E-03	1,70E+00	1,70E+00
MATK	3,70E+03	9,05E-13	1,13E-09	6,77E-01	-1,48E+00
MATN2	1,32E+03	4,07E-08	2,06E-05	1,64E+00	1,64E+00
MCM3	1,41E+03	1,19E-04	1,02E-02	2,88E+00	2,88E+00
MCM3AP	3,44E+03	1,10E-03	4,81E-02	1,16E+00	1,16E+00
MDGA1	7,83E+03	3,12E-06	6,30E-04	1,62E+00	1,62E+00
MDM1	3,88E+02	7,71E-04	3,76E-02	1,84E+00	1,84E+00
MED20	1,01E+03	5,89E-04	3,09E-02	1,32E+00	1,32E+00
MELK	2,30E+02	1,74E-06	3,98E-04	3,09E+00	3,09E+00
METTL10	1,29E+03	4,55E-04	2,60E-02	1,32E+00	1,32E+00
MFF	1,80E+03	8,07E-04	3,88E-02	1,49E+00	1,49E+00
MGST1	1,28E+03	1,11E-03	4,85E-02	2,16E+00	2,16E+00
MIS18BP1	4,05E+02	8,27E-07	2,19E-04	2,26E+00	2,26E+00
MLC1	1,60E+02	4,31E-04	2,49E-02	2,47E+00	2,47E+00
MLF1IP	2,72E+02	8,12E-04	3,88E-02	3,06E+00	3,06E+00
MRC2	1,03E+04	2,11E-07	7,46E-05	1,63E+00	1,63E+00
MSH5	1,25E+02	5,93E-04	3,10E-02	2,53E+00	2,53E+00
MT3	5,09E+03	4,14E-04	2,45E-02	7,71E-01	-1,30E+00
MYO10	8,16E+02	4,58E-05	4,95E-03	1,56E+00	1,56E+00
NCBP2	1,35E+04	1,95E-05	2,52E-03	1,39E+00	1,39E+00
NDN	5,15E+04	6,63E-04	3,34E-02	8,77E-01	-1,14E+00
NDRG1	6,53E+03	8,56E-04	4,01E-02	7,23E-01	-1,38E+00
NECAB2	7,16E+03	8,53E-06	1,35E-03	7,56E-01	-1,32E+00
NEFM	2,48E+05	3,27E-04	2,07E-02	7,11E-01	-1,41E+00
NEK2	1,53E+02	2,47E-04	1,67E-02	3,19E+00	3,19E+00
NFATC3	1,46E+03	3,73E-04	2,28E-02	1,47E+00	1,47E+00
NFATC4	5,32E+02	1,42E-04	1,16E-02	2,42E+00	2,42E+00
NFIB	5,78E+02	4,48E-05	4,89E-03	1,91E+00	1,91E+00
NFKB2	4,49E+02	2,42E-04	1,67E-02	2,34E+00	2,34E+00
NGEF	9,25E+03	1,35E-04	1,12E-02	8,55E-01	-1,17E+00
NIPA2	3,18E+03	9,34E-04	4,26E-02	1,90E+00	1,90E+00
NKAIN1	4,37E+04	5,49E-06	9,54E-04	8,33E-01	-1,20E+00
NOD1	1,78E+02	1,38E-04	1,13E-02	2,46E+00	2,46E+00
NOTCH2NL	2,50E+03	3,11E-05	3,64E-03	1,59E+00	1,59E+00
NPC2	7,17E+03	1,14E-08	7,11E-06	1,31E+00	1,31E+00
NR2C1	8,94E+02	1,09E-03	4,81E-02	1,51E+00	1,51E+00
NR2F2	5,62E+02	3,80E-04	2,28E-02	1,68E+00	1,68E+00
NRTN	3,97E+02	6,71E-04	3,36E-02	5,03E-01	-1,99E+00
NTMT1	6,73E+02	5,81E-05	5,98E-03	5,99E-01	-1,67E+00
NTSR1	3,66E+03	7,30E-04	3,60E-02	6,18E-01	-1,62E+00
NUF2	1,73E+02	1,74E-05	2,30E-03	4,91E+00	4,91E+00
NUSAP1	1,86E+02	9,75E-05	8,70E-03	2,94E+00	2,94E+00
NXF1	7,21E+03	4,66E-06	8,46E-04	1,29E+00	1,29E+00
OTUB2	3,34E+03	1,03E-05	1,57E-03	7,48E-01	-1,34E+00
OXLD1	4,32E+02	6,99E-04	3,46E-02	1,57E+00	1,57E+00
PAK6	7,98E+03	1,22E-05	1,81E-03	1,26E+00	1,26E+00
PAQR6	1,68E+02	8,73E-04	4,05E-02	2,29E+00	2,29E+00
PAR-SN	3,10E+04	1,10E-03	4,81E-02	8,52E-01	-1,17E+00
PCDHAC2	1,32E+04	8,48E-05	7,78E-03	7,31E-01	-1,37E+00
PCM1	9,06E+03	7,87E-04	3,82E-02	1,38E+00	1,38E+00

PFKFB2	7,36E+02	1,19E-30	6,41E-27	3,75E-02	-2,67E+01
PFN2	6,99E+04	6,87E-04	3,42E-02	1,11E+00	1,11E+00
PHF20L1	6,22E+03	2,48E-04	1,67E-02	1,43E+00	1,43E+00
PHF21B	1,40E+03	9,77E-04	4,40E-02	1,43E+00	1,43E+00
PIP4K2C	6,30E+03	5,49E-04	2,95E-02	8,85E-01	-1,13E+00
PLEKHG1	8,42E+03	2,06E-04	1,51E-02	1,21E+00	1,21E+00
PLS3	1,07E+04	1,57E-06	3,73E-04	1,52E+00	1,52E+00
PLXNA2	5,34E+04	1,84E-04	1,39E-02	8,63E-01	-1,16E+00
PLXNB1	7,86E+03	8,08E-06	1,31E-03	1,26E+00	1,26E+00
PNPLA3	6,94E+03	1,05E-04	9,22E-03	6,61E-01	-1,51E+00
POLH	2,59E+03	9,51E-04	4,33E-02	1,21E+00	1,21E+00
POLR3E	2,57E+03	5,72E-04	3,01E-02	1,25E+00	1,25E+00
PRKD3	2,73E+03	1,06E-09	7,80E-07	1,58E+00	1,58E+00
PSMD6	3,80E+03	1,57E-04	1,22E-02	1,25E+00	1,25E+00
PTK7	5,10E+03	3,45E-04	2,15E-02	1,53E+00	1,53E+00
PTN	2,94E+04	1,82E-14	2,94E-11	1,57E+00	1,57E+00
PTPRD	2,22E+03	8,67E-08	3,89E-05	1,82E+00	1,82E+00
PTTG1	5,79E+02	1,38E-06	3,42E-04	1,86E+00	1,86E+00
PXDN	6,41E+03	5,76E-05	5,96E-03	1,52E+00	1,52E+00
RAB11FIP1	5,97E+03	1,86E-05	2,44E-03	8,23E-01	-1,22E+00
RAB13	1,27E+03	9,53E-06	1,48E-03	2,39E+00	2,39E+00
RAB38	1,39E+02	4,53E-04	2,60E-02	2,43E+00	2,43E+00
RAD51AP1	1,09E+02	5,56E-04	2,96E-02	3,09E+00	3,09E+00
RASGEF1C	1,06E+03	1,20E-05	1,80E-03	6,35E-01	-1,58E+00
RASGRP2	6,07E+03	9,28E-04	4,26E-02	6,92E-01	-1,45E+00
RBM12B-AS1	1,45E+03	3,76E-04	2,28E-02	1,30E+00	1,30E+00
RCAN1	1,05E+04	5,14E-04	2,79E-02	7,17E-01	-1,40E+00
RENBP	3,82E+02	2,04E-04	1,51E-02	1,77E+00	1,77E+00
RET	1,45E+03	3,63E-06	7,15E-04	6,93E-01	-1,44E+00
RFTN2	7,49E+02	4,63E-04	2,61E-02	2,07E+00	2,07E+00
RFX4	1,60E+03	6,58E-07	1,86E-04	1,84E+00	1,84E+00
RFXANK	2,86E+03	7,90E-05	7,51E-03	1,39E+00	1,39E+00
RHOB	2,10E+04	2,12E-07	7,46E-05	7,32E-01	-1,37E+00
RNF169	2,77E+03	6,87E-04	3,42E-02	1,27E+00	1,27E+00
RNF175	2,11E+03	6,65E-06	1,09E-03	6,80E-01	-1,47E+00
RNU12	7,27E+02	4,90E-07	1,44E-04	2,18E+00	2,18E+00
RPS12	2,59E+04	1,06E-04	9,22E-03	1,22E+00	1,22E+00
RPS20	2,39E+04	1,70E-05	2,27E-03	1,30E+00	1,30E+00
RPS6	5,17E+04	9,08E-05	8,19E-03	1,30E+00	1,30E+00
RRM2	3,92E+02	4,01E-09	2,82E-06	4,11E+00	4,11E+00
RRP7B	4,04E+03	1,89E-04	1,42E-02	1,67E+00	1,67E+00
RSPH4A	4,86E+02	4,89E-04	2,71E-02	1,58E+00	1,58E+00
RTTN	8,09E+02	6,97E-05	6,79E-03	1,83E+00	1,83E+00
SATB1	2,56E+03	1,50E-11	1,62E-08	1,59E+00	1,59E+00
SCAF11	2,64E+03	1,91E-04	1,43E-02	1,23E+00	1,23E+00
SCO1	2,12E+03	2,33E-04	1,66E-02	1,31E+00	1,31E+00
SDHAP2	2,66E+03	5,41E-04	2,91E-02	1,42E+00	1,42E+00
SEC61G	1,69E+04	8,10E-04	3,88E-02	1,25E+00	1,25E+00
SEMA6D	1,26E+03	1,57E-04	1,22E-02	1,39E+00	1,39E+00
SENP7	4,21E+03	7,36E-07	1,98E-04	1,26E+00	1,26E+00

SFSWAP	4,35E+03	4,32E-04	2,49E-02	1,40E+00	1,40E+00
SGSH	1,62E+03	8,62E-04	4,03E-02	1,31E+00	1,31E+00
SH2D3A	5,79E+02	2,16E-04	1,55E-02	6,36E-01	-1,57E+00
SH3BGRL	1,57E+04	8,25E-04	3,91E-02	1,25E+00	1,25E+00
SH3BGRL3	2,59E+04	6,68E-05	6,64E-03	8,86E-01	-1,13E+00
SKA3	2,03E+02	6,73E-04	3,36E-02	2,25E+00	2,25E+00
SLC15A2	4,21E+02	3,43E-05	3,99E-03	1,80E+00	1,80E+00
SLC16A3	1,11E+03	3,83E-06	7,45E-04	5,90E-01	-1,69E+00
SLC16A9	2,73E+03	3,10E-06	6,30E-04	1,35E+00	1,35E+00
SLC1A3	2,20E+03	1,22E-21	3,94E-18	2,22E+00	2,22E+00
SLC2A6	5,35E+03	1,10E-03	4,81E-02	6,85E-01	-1,46E+00
SLC35B3	4,74E+02	2,74E-04	1,80E-02	1,88E+00	1,88E+00
SMAD3	2,26E+03	1,02E-03	4,59E-02	1,32E+00	1,32E+00
SMARCA2	2,03E+03	7,07E-05	6,84E-03	1,32E+00	1,32E+00
SMIM7	5,72E+03	4,10E-06	7,73E-04	1,25E+00	1,25E+00
SNAP25	1,46E+04	3,97E-05	4,48E-03	1,33E+00	1,33E+00
SNRPB	9,66E+03	1,35E-05	1,94E-03	1,18E+00	1,18E+00
SOX21	9,37E+02	6,38E-11	6,06E-08	2,64E+00	2,64E+00
SP1	1,21E+03	3,77E-04	2,28E-02	1,48E+00	1,48E+00
SPATA6	9,30E+02	5,99E-05	6,05E-03	1,60E+00	1,60E+00
SPC24	3,56E+02	1,89E-05	2,47E-03	4,52E+00	4,52E+00
SPDL1	2,90E+03	1,77E-06	3,98E-04	1,31E+00	1,31E+00
SPINT1	1,38E+03	2,30E-06	4,80E-04	6,54E-01	-1,53E+00
SPTLC2	1,16E+04	1,01E-07	4,27E-05	8,44E-01	-1,18E+00
SPTLC3	8,20E+01	9,18E-04	4,23E-02	4,01E+00	4,01E+00
SRSF8	1,07E+04	1,20E-04	1,02E-02	8,52E-01	-1,17E+00
ST18	3,05E+03	3,60E-05	4,16E-03	1,30E+00	1,30E+00
STK3	3,40E+02	5,22E-05	5,48E-03	2,01E+00	2,01E+00
STK33	3,95E+03	8,38E-04	3,93E-02	1,28E+00	1,28E+00
SULT1C4	8,44E+02	4,94E-05	5,22E-03	1,56E+00	1,56E+00
SUSD1	2,79E+03	4,20E-04	2,47E-02	7,98E-01	-1,25E+00
SYN1	1,21E+04	7,50E-05	7,21E-03	1,39E+00	1,39E+00
SYNRG	8,73E+02	4,32E-04	2,49E-02	1,60E+00	1,60E+00
SYT1	6,53E+04	1,13E-06	2,84E-04	1,22E+00	1,22E+00
SYT16	1,26E+04	6,36E-04	3,26E-02	7,48E-01	-1,34E+00
TACC3	6,96E+02	3,53E-06	7,05E-04	1,73E+00	1,73E+00
TANC1	7,82E+02	6,29E-06	1,04E-03	2,23E+00	2,23E+00
TARS2	2,78E+03	6,11E-04	3,16E-02	1,22E+00	1,22E+00
TBC1D15	2,52E+01	6,50E-04	3,30E-02	4,05E+00	4,05E+00
TCF3	8,87E+02	1,39E-04	1,14E-02	1,68E+00	1,68E+00
TFPI2	2,41E+03	1,08E-07	4,27E-05	3,10E+00	3,10E+00
TGFB1I1	3,28E+02	4,98E-04	2,73E-02	1,74E+00	1,74E+00
TMEM214	2,90E+03	1,47E-04	1,19E-02	1,34E+00	1,34E+00
TMEM45A	1,83E+03	4,02E-07	1,22E-04	1,43E+00	1,43E+00
TMEM98	3,62E+03	2,80E-07	9,23E-05	1,72E+00	1,72E+00
TMPO	6,92E+02	3,66E-04	2,25E-02	1,61E+00	1,61E+00
TNC	6,24E+03	9,85E-05	8,74E-03	2,25E+00	2,25E+00
TNFRSF10B	1,43E+04	3,05E-05	3,63E-03	1,43E+00	1,43E+00
TNFRSF19	2,17E+03	4,07E-04	2,42E-02	1,80E+00	1,80E+00
TNRC18	4,07E+03	1,04E-04	9,15E-03	1,20E+00	1,20E+00

TOB2	2,55E+03	4,87E-06	8,75E-04	1,40E+00	1,40E+00
TOB2P1	2,45E+03	3,27E-04	2,07E-02	1,35E+00	1,35E+00
TOP2A	1,40E+03	2,17E-20	4,38E-17	4,05E+00	4,05E+00
TP53	4,04E+03	6,62E-04	3,34E-02	1,57E+00	1,57E+00
TPRG1L	1,06E+04	4,70E-05	5,03E-03	8,53E-01	-1,17E+00
TRA2A	4,21E+03	5,49E-06	9,54E-04	1,39E+00	1,39E+00
TRIM59	3,05E+02	2,10E-04	1,52E-02	1,59E+00	1,59E+00
TSPAN3	3,05E+04	6,32E-04	3,26E-02	1,18E+00	1,18E+00
TST	5,85E+02	9,00E-05	8,17E-03	1,63E+00	1,63E+00
TTC17	3,74E+03	5,86E-05	6,00E-03	1,44E+00	1,44E+00
TTC3P1	4,98E+03	1,46E-06	3,57E-04	1,37E+00	1,37E+00
TTC7B	1,01E+04	1,70E-05	2,27E-03	8,45E-01	-1,18E+00
TTK	3,87E+02	9,33E-04	4,26E-02	1,81E+00	1,81E+00
TUBB4B	3,89E+04	1,31E-05	1,91E-03	8,25E-01	-1,21E+00
TULP3	4,63E+03	8,32E-06	1,33E-03	1,24E+00	1,24E+00
UACA	9,38E+02	2,32E-06	4,80E-04	2,03E+00	2,03E+00
UBR2	5,09E+03	4,61E-04	2,61E-02	8,48E-01	-1,18E+00
UBXN1	9,73E+03	1,99E-04	1,48E-02	1,18E+00	1,18E+00
VARS	1,80E+04	2,68E-04	1,78E-02	8,83E-01	-1,13E+00
WDR24	1,61E+03	2,39E-04	1,67E-02	1,34E+00	1,34E+00
WNT5A	5,09E+02	6,92E-05	6,78E-03	1,81E+00	1,81E+00
XKR4	1,37E+04	3,64E-04	2,25E-02	7,74E-01	-1,29E+00
ZBTB38	2,11E+04	3,85E-04	2,31E-02	8,51E-01	-1,17E+00
ZEB2	1,75E+03	2,31E-06	4,80E-04	1,63E+00	1,63E+00
ZIC3	1,35E+04	2,48E-04	1,67E-02	1,13E+00	1,13E+00
ZNF12	2,03E+03	3,04E-04	1,94E-02	1,28E+00	1,28E+00
ZNF238	1,39E+03	6,86E-05	6,76E-03	1,35E+00	1,35E+00
ZNF394	3,21E+02	3,00E-05	3,62E-03	9,45E+00	9,45E+00
ZNF449	1,81E+03	5,10E-08	2,50E-05	1,49E+00	1,49E+00
ZNF490	5,15E+03	2,43E-04	1,67E-02	1,16E+00	1,16E+00
ZNF833P	3,96E+02	8,05E-04	3,88E-02	7,13E-01	-1,40E+00
ZNHIT2	2,55E+03	4,13E-06	7,73E-04	7,57E-01	-1,32E+00
ZWINT	4,77E+02	1,30E-07	4,99E-05	2,49E+00	2,49E+00

Table S5: Table showing the raw data of expression for the genes whose expression change was statistically linked to the kinase activity. Raw expression data (n=4 wells per condition) for the 53 genes regulated by a kinase-dependent mechanism [i.e., differentially expressed between (GFP and Kin-rDCLK3WT) and (Kin-rDCLK3WT and Kin-rDCLK3K543M)].

Supplemental Table S5

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Genes differentially regulated in a kinase dependent manner (see figure 6) [i.e., significant (GFP vs kin-DCLK3) and significant (kin-Dclk3 vs kin-DCLK3-K543M"Dead-kinase")]

Expression data in all samples

Reads/million	GFP n1	GFP n2	GFP n3	GFP n4	KIN-WT n1	KIN-WT n2	KIN-WT n3	KIN-WT n4	KIN-K543M n1	KIN-K543M n2	KIN-K543M n3	KIN-K543M n4
ACAD9	12,6640	13,1454	10,2026	11,0819	14,7880	15,4246	17,5382	14,9538	11,3495	10,3331	11,1212	13,0331
ADAMTS6	20,5290	18,6703	21,4348	18,4088	30,8808	28,6168	26,7649	22,4306	20,5608	21,6467	17,2379	19,3635
ANK2	652,9299	640,3144	594,2776	595,1273	500,7046	486,6884	463,9246	571,6605	669,5407	522,3113	615,9312	667,8921
APBB3	23,5951	30,4821	26,7701	27,2927	35,4913	31,9994	36,4490	33,5391	29,6898	29,1892	27,8958	28,8963
BBX	59,5875	60,9644	65,6148	67,4075	90,0338	83,9561	87,3862	80,8571	58,3103	61,2442	60,7961	57,8671
BMF	6,1320	5,9694	6,8329	6,1363	10,5256	9,6742	9,6842	13,4584	6,0037	7,2407	7,5068	7,7454
BOD1L1	48,9231	51,0575	51,9490	45,8847	41,6674	43,4326	37,8979	39,9479	33,0617	33,3374	37,5342	34,0351
BTBD9	11,7309	14,4790	15,0699	8,8839	14,5270	29,2934	35,6102	18,6922	7,3196	10,1068	12,3260	11,3947
C1orf213	1,5997	3,7468	2,3400	3,1139	4,5781	5,7504	6,3290	4,6998	10,1981	10,4085	8,2483	10,5010
DCAF13P3	30,6602	28,8227	32,0118	33,2458	40,1886	41,5383	35,2290	37,4791	29,1140	28,3530	34,6612	32,0893
EFNB2	73,9845	60,4561	65,2404	60,9964	53,2368	50,6713	47,8108	55,2221	41,8617	43,0671	44,1142	38,2802
ENTPD2	0,9331	1,2701	0,9360	0,8243	0,2610	0,2030	0,3050	0,1068	1,3981	0,9051	0,9268	1,0427
EZR	39,1918	44,1353	44,0864	39,3821	32,0117	31,6611	33,5514	35,1413	24,8374	25,4179	25,0228	25,7684
FEZF1-AS1	6,5320	9,0176	5,9905	7,9680	12,7873	11,0719	14,5644	10,6813	7,9776	8,2966	8,5263	6,6283
FGD5	9,8646	10,6052	8,5178	9,1586	6,5241	8,0506	7,3966	6,6224	9,2112	9,3526	10,4725	8,7136
FKBP14	30,1162	27,3704	29,0165	33,7952	38,8838	36,2616	38,2791	34,3935	25,3309	29,3400	24,5595	24,2043
GNAI3	61,9870	46,1677	47,7369	51,7462	5,1323	4,8709	7,4728	6,3019	69,3309	42,3883	53,0112	47,6640
HIST1H1D	57,1880	76,1417	65,4276	69,6971	84,3786	82,9413	99,8155	94,2086	59,9552	54,4561	45,5971	53,5476
HIST1H2AG	75,1629	50,2135	65,0192	71,0625	46,6824	43,1319	54,6237	43,5611	15,8445	24,9230	25,6223	17,9471
HIST1H2BD	223,8198	215,6811	228,4435	219,2098	308,4344	292,5123	323,9832	299,4606	213,7620	203,3748	211,7363	208,3119
HIST1H3G	27,8608	30,9901	27,5189	35,0775	16,0058	14,4775	18,9108	20,0808	4,6879	5,8831	3,3364	2,1598
HIST1H3I	131,7760	212,3681	190,6621	190,0625	283,1504	268,4411	315,5572	284,6137	242,3308	221,8680	183,4754	216,3515
HIST1H3J	127,1027	128,3106	127,9349	127,7811	206,2953	191,6466	176,7336	178,9526	134,4205	142,8825	135,1091	125,6193
HIST1H4B	49,5896	71,7599	61,4964	55,2216	92,0336	93,0215	101,0355	96,5585	64,1496	57,0960	58,3865	59,2821
HIST2H3D	1,4664	1,9691	1,3104	1,7401	3,4795	3,1812	3,6602	2,7771	1,5626	2,2627	1,8535	1,5696
HSD17B7	63,6669	74,8272	66,8640	63,4964	81,1131	77,4981	82,9483	80,5265	101,6845	98,7941	93,2516	94,7792
INSM2	5,7321	4,9533	4,6801	4,8541	6,6111	7,3741	7,3966	9,0791	5,7570	4,9780	5,1899	5,5856
JHDM1D	13,3305	13,4629	14,6955	15,9360	21,7471	21,5133	17,9195	16,3423	14,4748	15,9899	15,4771	13,8524
LHX8	67,5858	63,5044	65,3340	61,0880	77,7675	90,1801	86,6237	80,6434	67,8505	77,9130	68,2099	65,1657
LOC254100	4,3991	3,6833	4,4929	4,5793	6,7851	7,2388	7,3966	6,0883	3,6187	5,5814	3,9851	4,5430
LOC646471	10,5311	12,0658	10,3898	9,9829	15,8319	12,5833	16,0894	13,4584	10,1347	10,2577	9,0823	11,7671
MATK	24,2616	26,6718	25,5532	23,5376	21,2251	21,6486	19,3683	21,8966	33,4728	33,2619	28,7298	28,7473
MATN2	10,6644	12,2563	11,7002	16,3939	9,7427	9,6742	9,1504	9,0791	5,7570	5,6568	5,8386	5,6601
MDGA1	58,5211	44,3260	40,6232	50,4640	93,4254	74,3495	59,0200	60,6695	41,7795	40,5781	51,2504	44,3871
NTSR1	38,7919	34,5464	28,9229	25,3694	17,5716	16,6424	17,0807	17,7309	33,3084	27,9823	20,4816	29,8635

OTUB2	26,7944	24,1317	26,4893	22,3470	17,8326	19,8220	20,8934	18,3718	27,7982	26,6247	21,7791	26,6621
PFN2	466,9595	473,3850	460,6134	451,0475	560,0037	525,3995	538,6909	474,2561	483,2322	482,3584	466,8352	450,2589
PHF20L1	37,4588	35,6259	37,6279	37,2756	66,8070	53,6480	54,5973	42,6182	34,7888	43,0671	36,4220	37,6844
PLXNB1	49,3231	57,1539	50,2640	50,8301	67,9373	57,3010	60,7734	65,1552	53,6221	50,9863	48,0991	46,0997
PTN	291,8055	222,1382	280,7117	274,3923	213,5563	208,3005	232,1148	230,3946	152,2319	114,9462	141,0544	154,6102
RET	12,1308	9,9702	11,4194	9,9829	7,4810	9,1330	8,5404	6,9428	10,3626	11,2382	12,8821	11,8415
RNU12	3,4659	3,3657	4,4929	5,1288	5,5673	6,8329	9,9892	8,1178	4,2766	3,0170	3,7071	2,9790
SLC16A9	18,6628	19,7499	16,8483	16,3939	21,3121	23,6105	21,8084	22,8579	17,6823	17,7246	17,2379	13,7779
SLC1A3	26,1279	22,6711	26,9573	26,3768	13,4832	15,0864	16,1657	15,2742	7,3196	8,0704	5,9313	5,7346
SMIM7	34,3928	36,7055	39,3127	42,4044	45,8428	44,7856	47,4295	42,1909	37,0916	37,4857	36,6074	33,5138
SULT1C4	4,5324	4,7628	5,8969	5,1288	8,6118	6,2916	8,4641	7,4769	4,8523	3,9220	6,2094	4,8409
TNRC18	33,0597	38,9282	37,7215	34,4364	25,4876	27,8726	28,5187	25,4214	21,3010	21,7975	23,8180	22,5659
TRA2A	23,5951	25,4017	28,8293	29,4908	39,0577	32,6759	38,7366	31,0824	23,9327	26,4738	26,2276	25,5449
TTC3P1	34,2011	30,6277	28,5671	33,8205	40,3707	42,5529	43,4807	41,4380	26,5658	30,2082	35,6837	30,0379
TULP3	28,3941	31,5617	31,7310	31,2309	36,3611	35,7202	39,6517	33,5391	26,4823	30,6221	29,2859	31,2050
ZIC3	91,3142	95,6376	92,3849	81,4202	99,7756	105,4018	99,5867	101,4719	92,3589	89,3775	91,1015	87,8805
ZNF394	0,2666	0,3175	0,6552	0,1832	8,1769	7,3741	0,9913	6,3019	0,9047	0,4525	0,4634	0,5958
ZNF490	34,1694	36,0773	34,1503	33,7252	38,5383	40,1911	38,7210	39,8594	35,1844	31,7679	35,8199	32,8102

Recapitulative counts

	down/up	up/down	more reduced	more increased	total
n	34	8	2	9	53
% total	12,36	2,91	0,73	3,27	
%relatif	64,15	15,09	3,77	16,98	