

Figure S1. *Drosophila* motor performance assay data for genes in the compensatory network.

Related to Figure 1.

Charts show motor performance as a function of age in *Drosophila* negative controls (blue dashed lines, $elav^{C155}>GAL4/w1118$), positive controls expressing HTTN231Q128 in the nervous system (black dotted line, $elav^{C155}>GAL4/w1118; UAS-HTTN231Q128/+$) and experimental animals (red line, $elav^{C155}>GAL4/w1118; UAS-HTTN231Q128/+; modifier/+$). sh: shRNA; LOF: loss of function; OE: overexpression. Error bars in motor performance charts: s.e.m. Significant differences identified using Anova followed by Tukey's post hoc test for each time point ($\alpha=0.05$).

Figure S2. *Drosophila* motor performance assay data for genes in the pathogenic networks Related to Figure 1.

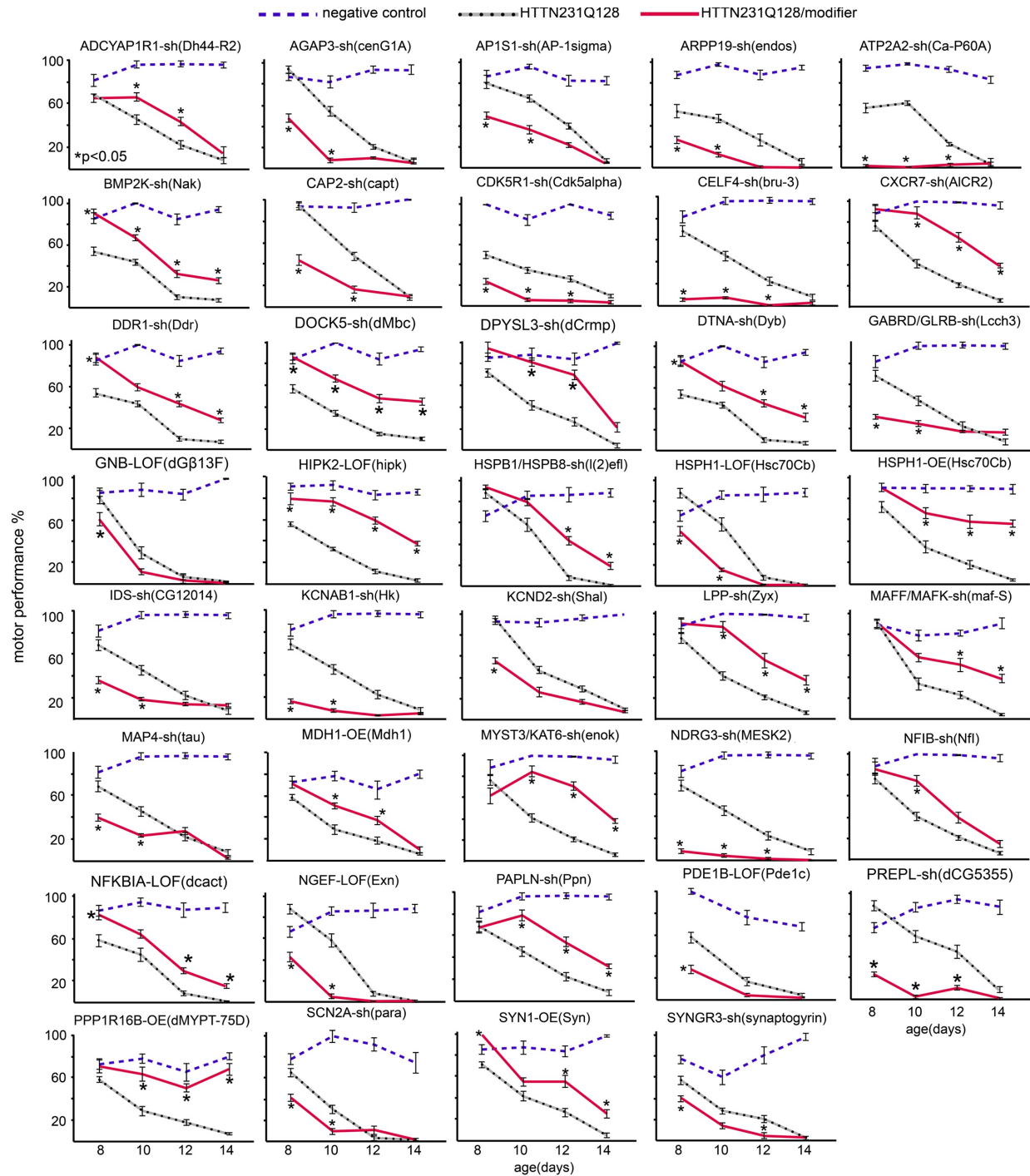


Figure S2. *Drosophila* motor performance assay data for genes in the pathogenic networks Related to Figure 1.

Charts show motor performance as a function of age in *Drosophila* negative controls (blue dashed lines, *elav^{C155}>GAL4/w1118*), positive controls expressing HTT^{N231Q128} in the nervous system (black dotted line, *elav^{C155}>GAL4/w1118; UAS-HTT^{N231Q128/+}*) and experimental animals (red line, *elav^{C155}>GAL4/w1118; UAS-HTT^{N231Q128/+}; modifier/+*). sh: shRNA; LOF: loss of function; OE: overexpression. Error bars in motor performance charts: s.e.m. Significant differences identified using Anova followed by Tukey's post hoc test for each time point ($\alpha=0.05$).

Figure S3. *Drosophila* motor performance tests for the modifier alleles of the compensatory network in control animals. Related to Figure 1.

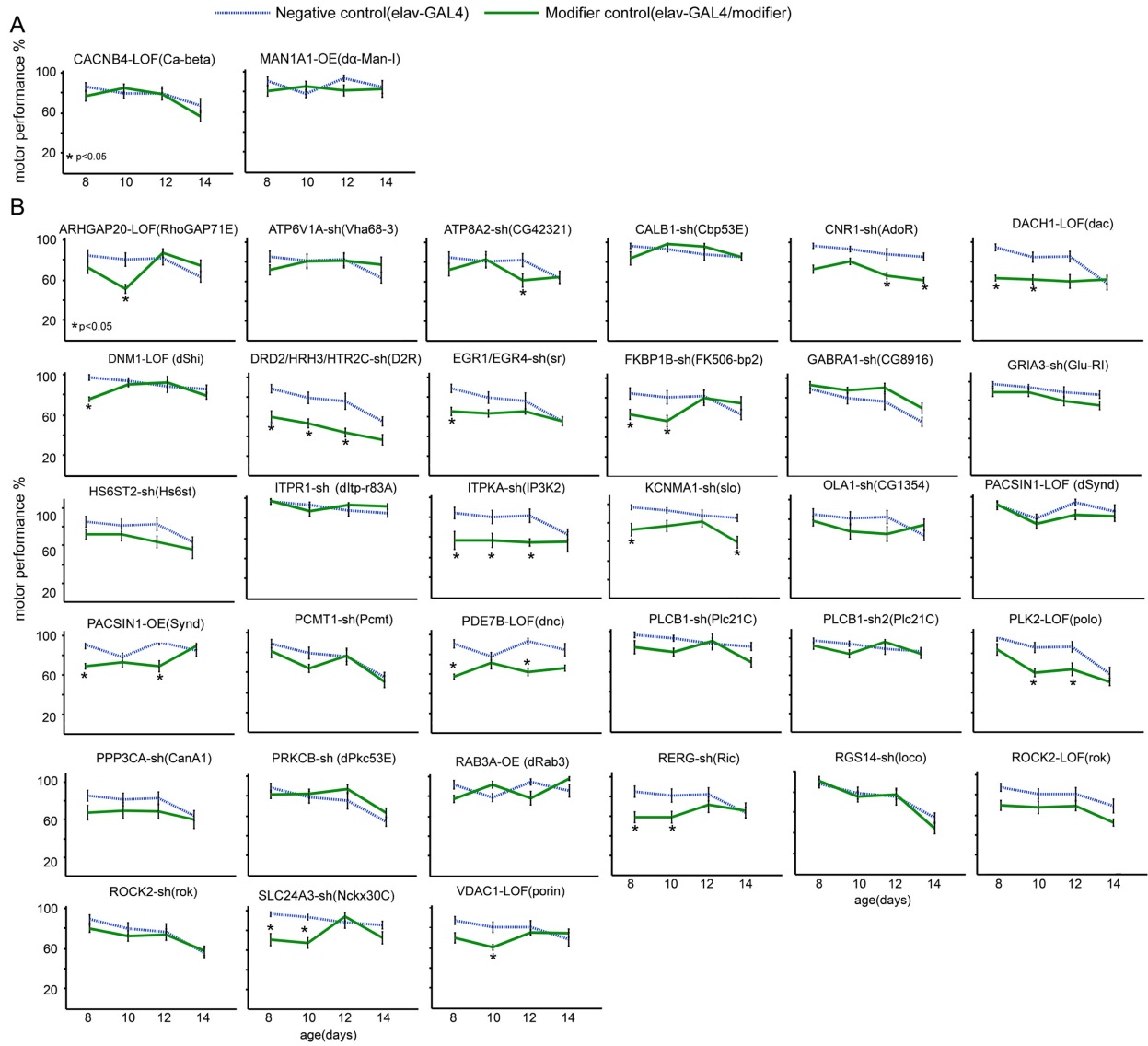


Figure S3. *Drosophila* motor performance tests for the modifier alleles of the compensatory network in control animals. Related to Figure 1.

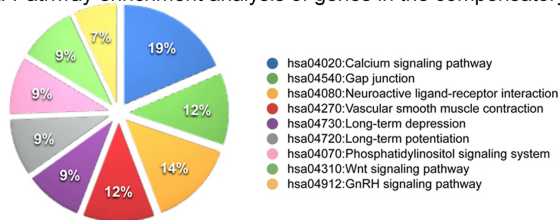
Blue lines indicate the motor performance of negative controls (*elav^{C155}/w1118*). Green line shows motor performance of animals carrying the indicated modifier alleles but not expressing HTT^{N231Q128} (*elav^{C155}/w1118; modifier/+*). Note that some modifiers impair the motor performance of the negative controls (*elav^{C155}/w1118*) but these modifiers nonetheless improve the performance of HD animals (*elav^{C155}>GAL4/w1118; UAS-HTT^{N231Q128}/+*; see **Figure S1**). sh: shRNA; LOF: loss of function; OE: overexpression. Green error bars in gene expression scatter plots: average and standard deviation. Error bars in motor performance charts: s.e.m. Significant differences identified using Anova followed by Tukey's post hoc test for each time point ($\alpha=0.05$). Panel S3A shows the control assays for the modifiers shown in Figure 1A. Panel S3B shows the control assays for the modifiers shown in Figure S1.

Figure S4. *Drosophila* motor performance tests for the modifier alleles of the pathogenic network in control animals. Related to Figure 1.

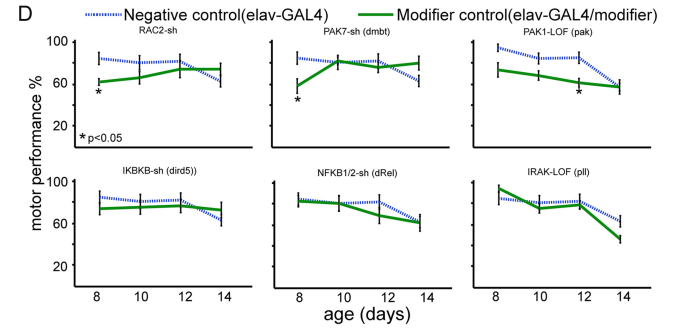
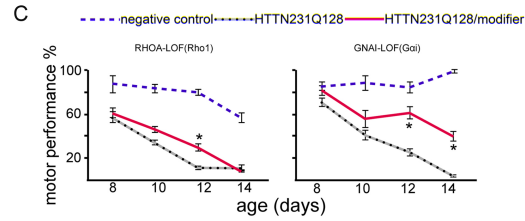
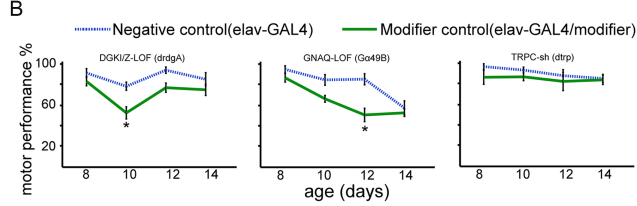
Blue lines indicate the motor performance of negative controls (*elav^{C155}/w1118*). Green line shows motor performance of animals carrying the indicated modifier alleles but not expressing HTT^{N231Q128} (*elav^{C155}/w1118; modifier/+*). Note that some modifiers impair motor performance of both the negative controls (*elav^{C155}/w1118*) and the HD animals (*elav^{C155}>GAL4/w1118; UAS-HTT^{N231Q128}/+*; see **Figure S2**); dysregulation of these genes is likely to contribute to HD pathogenesis. sh: shRNA; LOF: loss of function; OE: overexpression. Green error bars in gene expression scatter plots: average and standard deviation. Error bars in motor performance charts: s.e.m. Significant differences identified using Anova followed by Tukey's post hoc test for each time point ($\alpha=0.05$). Panel S4A shows the control assays for the modifiers shown in Figure 1C. Panel S4B shows the control assays for the modifiers shown in Figure S2.

Figure S5. Pathway enrichment, additional climbing data and additional pathway analysis related to Figure 4.

A. Pathway enrichment analysis of genes in the compensatory network.



Climbing data for controls and additional modifiers shown in Figure 4.



Additional network analysis of the pathogenic subnetwork reveals enrichment in genes involved in inflammation and actin cytoskeleton

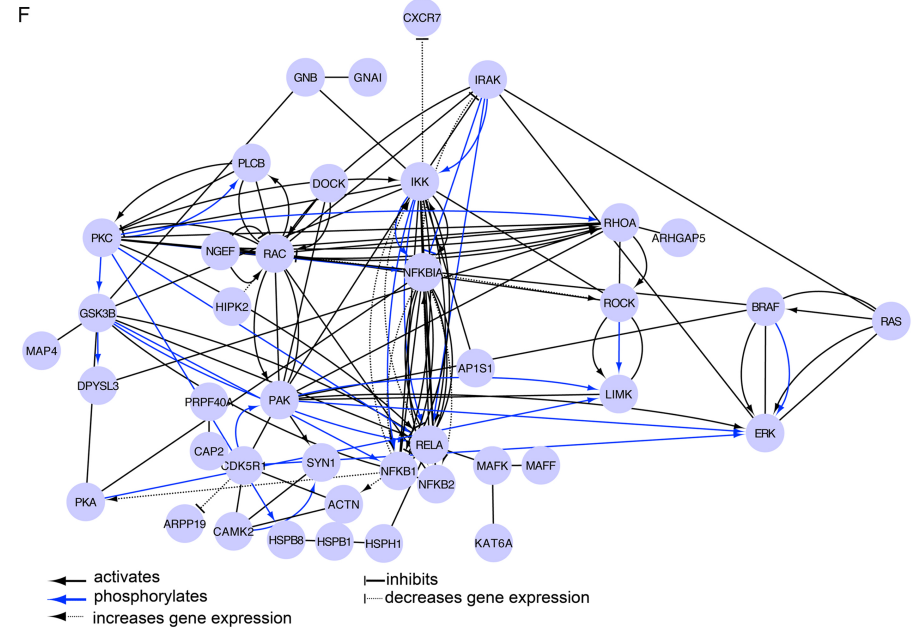
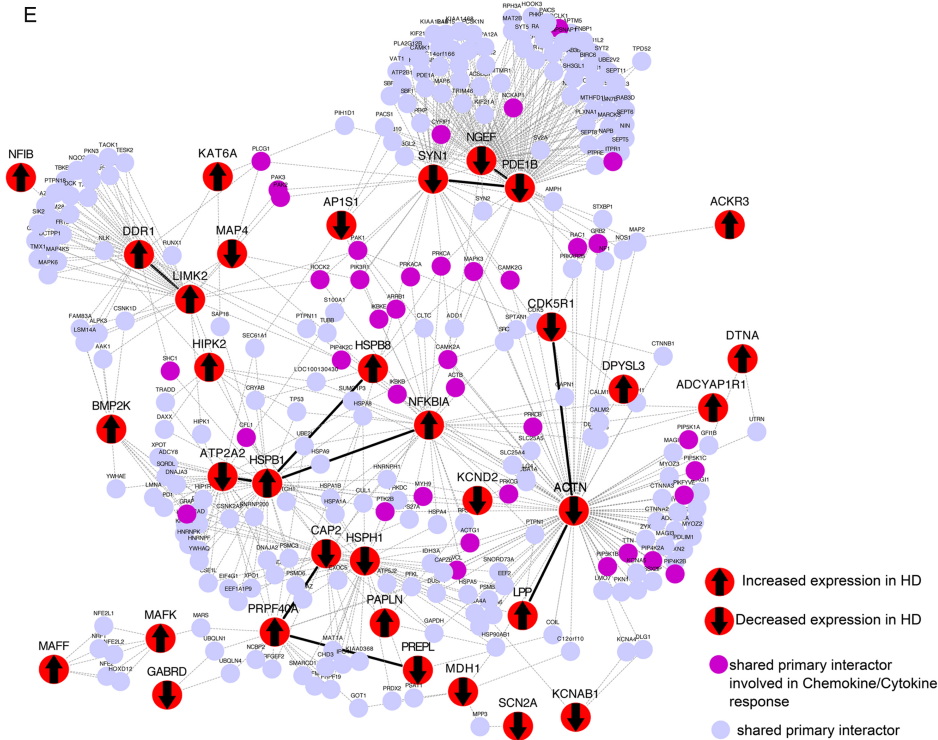


Figure S5. Pathway enrichment, additional climbing data and additional pathway analysis related to Figure 4.

(A) Pie chart illustrating the pathway enrichment within the compensatory category compared to the background of genes expressed in the striatum, using DAVID. The gene category most enriched is KEGG-hsa04020: “Ca²⁺ signaling pathway” (EASE score p=9.21E-06, Benjamini 4.70E-04). (B-D) Motor performance data for controls and additional modifiers shown in Figure 4. (B and D) Green line in charts shows motor performance of animals carrying the indicated modifier allele but not expressing HTT^{N231Q128} (*elav^{C155}/w1118; modifier/+*) compared to *elav^{C155}/w1118* negative controls (blue line). (C) Additional modifiers of HTT^{N231Q128}-induced neuronal dysfunction identified through pathway expansion in the pathogenic network. sh: shRNA; LOF: loss of function; OE: overexpression. Green error bars in gene expression scatter plots: average and standard deviation. Error bars in motor performance charts: s.e.m. Significant differences identified using Anova followed by Tukey’s post hoc test for each time point ($\alpha=0.05$). **Table S5** lists the specific modifier alleles identified through pathway expansion. (E-F) Additional network analysis of the pathogenic network reveals an enrichment in genes involved in inflammation and actin cytoskeleton regulation. (E) Network of genes categorized as pathogenic showing *Drosophila* modifiers altered in the human HD transcriptome (red circles with arrows) and their shared primary interactors. Note abundance of genes involved in inflammatory response and actin cytoskeleton regulation, downstream of chemokine/cytokine receptors (dark purple nodes). (F) Complete representation of all the interactions of the *Drosophila* modifier genes in the pathogenic network and their primary interacting partners generated using Ingenuity Pathway Analysis. This is the basis for the summary scheme shown in **Figure 4C**.

Figure S6 . Validation in iPS-derived neurons from HD patients. Related to Figure 5 .

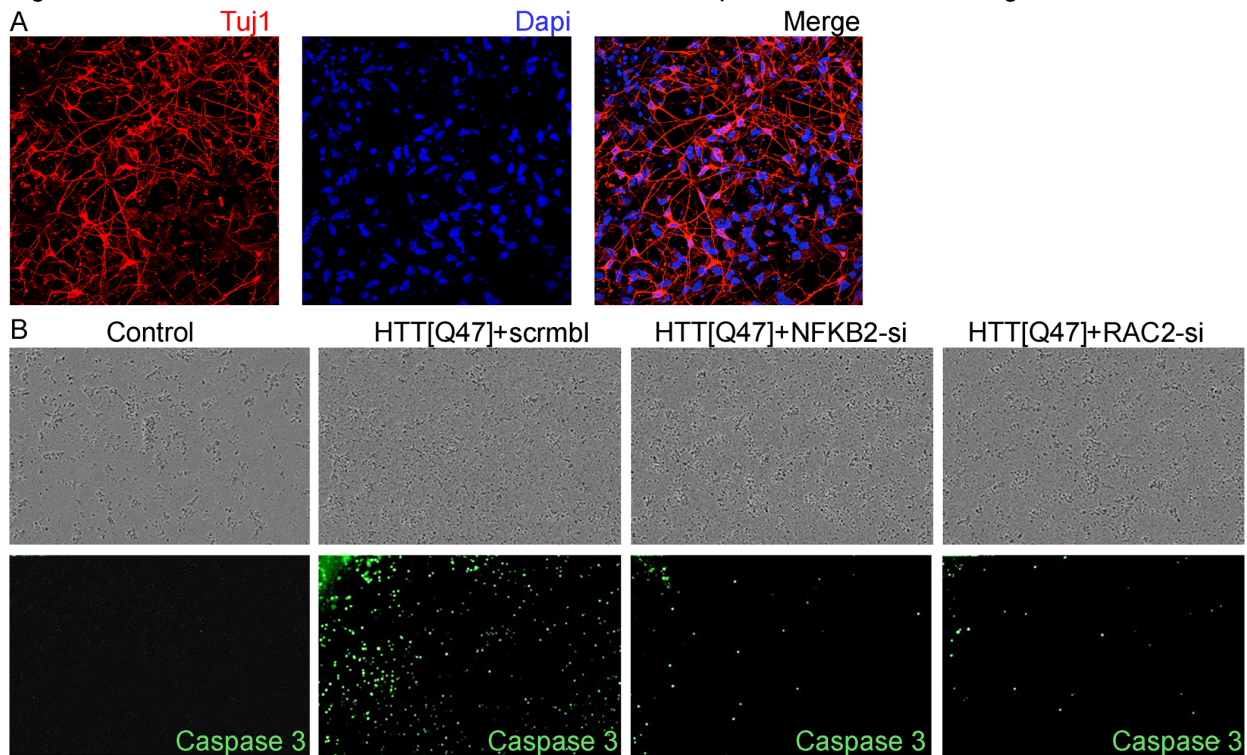


Figure S6. Validation in iPS-derived neuron-like cells from HD patients. Related to Figure 5.

(A) Immunofluorescence staining of iPS-derived cells showing positive signal for the TuJ1 neuronal marker (red), which also highlights their neuron-like morphology. **(B)** Bright field and fluorescence images of control and HTT[Q47] iPS-derived neuron-like cells transfected with a scramble, RAC2 and NFKB2 targeting siRNAs 12 hours after BDNF deprivation. Caspase-3 activation signal is shown in green.

Supplementary Tables.

Table S1. Genes considered for this study because their expression is altered early during human HD progression (Vonsattel grade 0-2 patients) and in at least one HD mouse model. Related to Figure 1. For the majority of these genes (67%), the direction of the transcriptional alteration (up or down) is the same between HD patients and at least one of the mouse HD models, i.e., not all models show transcriptional change in the same direction.

Table S2. Human genes whose expression alterations in HD we categorized as compensatory. Related to Figure 1. Also shown: the *Drosophila* homolog, blast e-value, direction of transcriptomic change in human, class of the modifier allele and specific allele that modified the HTT^{N231Q128}-induced behavioral deficits.

Table S3. Human genes whose expression alterations in HD we categorized as pathogenic. Related to Figure 1. Also shown: the *Drosophila* homolog, blast e-value, direction of transcriptomic change in human, class of the modifier allele and specific allele that modified the HTT^{N231Q128}-induced behavioral deficits.

Table S4. Pathways enriched in the compensatory and pathogenic networks. Related to Figure 4. Analysis performed using primary modifier genes from the screen and shared primary protein interactors using either Inweb or STRING databases. Query performed using DAVID/KEGG databases. P-value represents EASE enrichment score.

Table S5. Additional modifiers identified through pathway analysis. Related to Figure 4.

Table S6. Complete list of siRNAs used for the HTRF screen in human HD fibroblasts. Related to Figures 5 and 6.

Table S2. Human genes whose gene expression alterations in HD are categorized as compensatory. Related to Figure 1.

Human/ Mouse Gene Symbol	Drosophila Homologous Gene	Protein Blast e-value	Transcriptomic change in human	Allele Class	Modifier Allele	Effect on <i>Drosophila</i> HD model	Effect of allele on control motor performance
ARHGAP20	RhoGAP71E	9E-22	DOWN	LOF	RhoGAP71E[j6b9]	S	N
ATP6V1A	Vha68-3	0	DOWN	shRNA*	Vha68-3[GD11527]-v34926	S	N
ATP6V1A	Vha68-3	0	DOWN	shRNA	Vha68-3[GD11527]-v41646	S	N
ATP8A2	CG42321	0	DOWN	LOF	CG42321[KG03082]	S	N
ATP8A2	CG42321	0	DOWN	LOF*	CG42321[KG05950]	S	N
CACNA1B	cac	0	DOWN	LOF*	cac[HC129]	S	N
CACNB4	Ca-beta	6E-178	DOWN	LOF	Ca-beta[(2)04008]	S	N
CALB1	Cbp53E	1E-68	DOWN	shRNA	Cbp53E[GD10584]	S	N
CNR1	AdoR	4E-21	DOWN	shRNA	AdoR[GD380]	S	I
DACH1	dac	1E-54	DOWN	LOF	dac[9]	S	I
DNM1	shi	0	DOWN	LOF	shi[1]	S	N
DRD2	D2R	2E-79	DOWN	shRNA	D2R[GD732]	S	I
EGR1	sr	1E-64	DOWN	shRNA	sr[KK107677]	S	N
EGR4	sr	1E-46	DOWN	shRNA	sr[KK107677]	S	N
FKBP1B	FK506-bp2	3E-54	DOWN	shRNA*	FK506-bp2[GD6658]-v45014	S	N
FKBP1B	FK506-bp2	3E-54	DOWN	shRNA	FK506-bp2[GD6658]-v45015	S	N
GABRA1	CG8916	4E-96	DOWN	shRNA	CG8916[GD3383]	S	N
GRIA3	Glu-RI	0	DOWN	shRNA	Glu-RI[KK101533]	S	N
GRIA3	Glu-RI	0	DOWN	shRNA*	Glu-RI[GD3582]	S	N
HRH3	D2R	3E-37	DOWN	shRNA	D2R[GD732]	S	I
HS6ST2	Hs6st	6E-108	DOWN	shRNA	Hs6st[KK101636]	S	N
HTR2C	D2R	1E-54	DOWN	shRNA	D2R[GD732]	S	I
ITPKA	IP3K2	7E-120	DOWN	shRNA	IP3K2[GD8778]	S	I
ITPR1	ltp-r83A	0	DOWN	shRNA	ltp-r83A[GD1676]	S	N
KCNMA1	slo	0	DOWN	shRNA	slo[GD244]	S	I
MAN1A1	alpha-Man-I	0	DOWN	OE	alpha-Man-I[EY00697]	E	N
OLA1	CG1354	4E-113	DOWN	shRNA	CG1354[GD8048]	S	N
PACSIN1	Synd	2E-121	DOWN	LOF	Synd[EY07010]	S	N
PACSIN1	Synd	2E-121	DOWN	OE	Synd[EP877]	E	N
PCMT1	Pcmt	4E-83	DOWN	shRNA	Pcmt[GD8637]	S	N
PDE7B	dnc	2E-52	DOWN	LOF	dnc[M14]	S	N
PLCB1	Plc21C	1E-145	DOWN	shRNA	Plc21C[GD11359]-v26557	S	N
PLCB1	Plc21C	1E-145	DOWN	shRNA	Plc21C[GD11359]-v26558	S	N
PLK2	polo	3E-132	DOWN	LOF	polo[01673]	S	I
PPP3CA	CanA1	0	DOWN	shRNA	CanA1[GD8366]	S	N
PRKCB	Pkc53E	0	DOWN	shRNA	Pkc53E[GD11984]	S	N
RAB3A	Rab3	1E-125	DOWN	OE	P{UASp-YFP.Rab3.Q80L}11	E	N
RERG	Ric	2E-35	DOWN	RNAi	Ric[GD13919]	S	I
RGS14	loco	4E-37	DOWN	shRNA	loco[GD1282]	S	N
ROCK2	rok	0	DOWN	shRNA	rok[GD1522]	S	N
ROCK2	rok	0	DOWN	LOF	rok[1]	S	N
SLC24A3	Nckx30C	2E-114	DOWN	shRNA	Nckx30C[GD1040]	S	N
STXBP1	Rop	0	DOWN	OE*	Rop[G4478]	E	N
STXBP1	Rop	0	DOWN	LOF*	Rop[G27]	S	N
SYNE1	Msp-300	0	DOWN	LOF	Msp-300[DG03312]	S	N
VDAC1	porin	5E-121	DOWN	LOF	porin[k05123]	S	N

LOF: loss of function; OE: overexpression; shRNA: inducible hairpin RNAi; S: suppressor; E: enhancer; N: no effect; I: impaired; * data not shown

Table S3. Human genes whose gene expression alterations in HD are categorized as pathogenic. Related to Figure 1.

Human/ Mouse Gene Symbol	Drosophila Homologous Gene	Protein Blast e-value	Transcriptomic change in human	Allele Class	Modifier Allele	Effect on <i>Drosophila</i> HD model	Effect of allele on control motor performance
ACTN1	Actn	0	DOWN	shRNA	Actn[GD7761]	E	I
ACTN2	Actn	0	DOWN	shRNA	Actn[GD7761]	E	I
ADCYAP1R1	Dh44-R2	2E-47	UP	shRNA	Dh44-R2[GD15731]	S	N
AGAP3	cenG1A	8E-121	DOWN	shRNA	cenG1A[KK104806]	E	I
AP1S1	AP-1sigma	1E-86	DOWN	shRNA	AP-1sigma[KK108869]	E	I
ARPP19	endos	9E-20	DOWN	shRNA	endos[KK108642]	E	N
ARPP19	endos	9E-20	DOWN	shRNA*	endos[GD10576]	E	N
ATP2A2	Ca-P60A	0	DOWN	shRNA	Ca-P60A[KK107371]	E	I
BMP2K	Nak	6E-136	UP	shRNA	Nak[GD12597]	S	N
CAP2	capt	5E-134	DOWN	shRNA	capt[KK103925]	E	N
CDK5R1	Cdk5alpha	8E-71	DOWN	shRNA	Cdk5alpha[KK100567]	E	N
CELF4	bru-3	1E-110	DOWN	shRNA	bru-3[KK111663]	E	N
CXCR7	AICR2	2E-32	UP	shRNA	AICR2[GD17055]	S	N
DDR1	Ddr	8E-64	UP	shRNA	Ddr[GD7334]	S	N
DOCK5	mbc	0	UP	shRNA	mbc[GD6965]	S	N
DPYSL3	CRMP	0	UP	LOF	CRMP[sup12]	S	N
DPYSL3	CRMP	0	UP	shRNA*	CRMP[GD4716]	S	N
DTNA	Dyb	2E-137	UP	shRNA	Dyb[KK109268]	S	N
GABRD	Lcch3	1E-98	DOWN	shRNA	Lcch3[KK100854]	E	I
GLRB	Lcch3	2E-80	DOWN	shRNA	Lcch3[KK100854]	E	I
HIPK2	hipk	0	UP	LOF	hipk[EY12599]	S	N
HSPB1	l(2)efl	1E-28	UP	shRNA	l(2)efl[GD11341]	S	N
HSPB8	l(2)efl	4E-24	UP	shRNA	l(2)efl[KK108279]	S	N
HSPB8	l(2)efl	4E-24	UP	shRNA	l(2)efl[GD11341]	S	N
HSPH1	Hsc70Cb	0	DOWN	LOF	Hsc70Cb[00082]	E	N
HSPH1	Hsc70Cb	0	DOWN	OE	Hsc70Cb[EY00671]	S	N
IDS	CG12014	6E-140	DOWN	shRNA	CG12014[KK101391]	E	N
KCNAB1	Hk	1E-112	DOWN	shRNA	Hk[KK109058]	E	I
KCND2	Shal	0	DOWN	shRNA	Shal[KK100264]	E	I
LIMK2	LIMK1	2E-148	UP	shRNA	LIMK1[GD9586]-v25343	S	N
LIMK2	LIMK1	2E-148	UP	shRNA	LIMK1[GD9586]-v25344	S	N
LPP	Zyx	6E-92	UP	shRNA	Zyx[GD10696]	S	N
MAFF	maf-S	1E-26	UP	shRNA	maf-S[KK102044]	S	N
MAFK	maf-S	3E-30	UP	shRNA	maf-S[KK102044]	S	N
MAP4	tau	8E-29	DOWN	shRNA	tau[KK109359]	E	I
MDH1	Mdh1	6E-150	DOWN	OE	Mdh1[EY08761]	S	N
MYST3/KAT6	enok	2E-111	UP	shRNA	enok[GD4037]	S	I
NDRG3	MESK2	9E-79	DOWN	shRNA	MESK2[GD9083]	E	I
NFIB	Nfl	2E-92	UP	shRNA	Nfl[GD4283]	S	I
NFKBIA	cact	2E-35	UP	LOF*	cact[KG00376]	S	N
NFKBIA	cact	2E-35	UP	LOF	cact[KG07677]	S	N
NGEF	Exn	7E-76	DOWN	LOF	Exn[EP3042]	E	N
PAPLN	Ppn	4E-89	UP	shRNA	Ppn[KK101228]	S	N
PDE1B	Pde1c	3E-161	DOWN	LOF	Pde1c[c04487]*	E	N
PPP1R16B	MYPT-75D	4E-102	DOWN	OE	UAS-MYPT-75D.HM}B9	S	I
PREPL	CG5355	5E-23	DOWN	shRNA	CG5355[KK100768]	E	I
PRPF40A	CG3542	6E-172	UP	OE	CG3542[EP719]	E	I
SCN2A	para	0	DOWN	shRNA	para[GD3392]	E	I
SYN1	Syn	7E-118	DOWN	OE	Syn[EY01930]	S	N
SYNGR3	synaptogyrin	1E-41	DOWN	shRNA	synaptogyrin[KK108648]	E	I

LOF: loss of function; OE: overexpression; shRNA: inducible hairpin RNAi; S: suppressor; E: enhancer; N: no effect; I: impaired; * data not shown

Table S4. Pathways enriched in the compensatory and pathogenic networks. Related to Figure 4.

Compensatory						
	David Source	Pathway	Gene Count	%	P-Value	Benjamini
Inweb	KEGG_PATHWAY	hsa04720:Long-term potentiation	4	44.44	4.45E-05	8.00E-04
	KEGG_PATHWAY	hsa04070:Phosphatidylinositol signaling system	4	44.44	5.74E-05	6.88E-04
	KEGG_PATHWAY	hsa04020:Calcium signaling pathway	6	66.67	2.74E-07	9.87E-06
Pathogenic						
	David Source	Pathway	Gene Count	%	P-Value	Benjamini
Inweb	KEGG_PATHWAY	Regulation of actin cytoskeleton	26	8.4	7.4E-09	2.9E-07
	PANTHER_PATHWAY	P00031:Inflammation mediated by chemokine and cytokine signaling pathway	25	8.1	1.8E-03	3.9E-02
	KEGG_PATHWAY	MAPK signaling pathway	22	7.1	7.2E-05	5.3E-04
	KEGG_PATHWAY	Tight junction	21	6.8	3.7E-09	2.2E-07
	KEGG_PATHWAY	Calcium signaling pathway	21	6.8	4E-07	6.8E-06
	KEGG_PATHWAY	Focal adhesion	21	6.8	3.4E-06	3.6E-05
	PANTHER_PATHWAY	P00005:Angiogenesis	19	6.1	5.3E-03	6.6E-02
	KEGG_PATHWAY	Pathways in cancer	19	6.1	1.3E-02	4.7E-02
	KEGG_PATHWAY	Adherens junction	18	5.8	1.1E-10	1.3E-08
	KEGG_PATHWAY	Leukocyte transendothelial migration	18	5.8	1E-07	2.4E-06
STRING	David Source	Pathway	Gene Count	%	P-Value	Benjamini
	KEGG_PATHWAY	Regulation of actin cytoskeleton	57	11	2.1E-23	9E-22
	KEGG_PATHWAY	Focal adhesion	56	10.8	3.9E-24	2.5E-22
	KEGG_PATHWAY	Pathways in cancer	56	10.8	1.2E-13	2.2E-12
	PANTHER_PATHWAY	P00031:Inflammation mediated by chemokine and cytokine signaling pathway	52	10	3.3E-07	1.1E-05
	KEGG_PATHWAY	MAPK signaling pathway	45	8.7	8.8E-11	1.3E-09
	PANTHER_PATHWAY	P00034:Integrin signalling pathway	45	8.7	1E-08	5E-07
	KEGG_PATHWAY	Dilated cardiomyopathy	42	8.1	1.9E-27	2.5E-25
	KEGG_PATHWAY	Chemokine signaling pathway	34	6.6	4.3E-09	3.1E-08
	KEGG_PATHWAY	Hypertrophic cardiomyopathy (HCM)	32	6.2	7.3E-18	1.9E-16
KEGG_PATHWAY	Tight junction	32	6.2	1E-11	1.7E-10	

Table S5. Additional modifiers identified through pathway analysis. Related to Figure 4.

Human/Mouse Gene Symbol	Drosophila Homologous Gene	Protein Blast e-value	Allele Class	Modifier Allele
GRM3	mGluR4	0	shRNA	GD707
GNAQ	Gα49B	0	LOF	KG07290
TRPC4/5	trp	1.46288E-172	shRNA	GD372
DGKI/Z	rdgA	0	LOF	EY11543
IKKB	ird5	8.11278E-47	shRNA	GD11248
NFKB1/2	rel	7E-56	shRNA	HM05154
IRAK	pll	1.5784E-39	LOF	pll ²
PAK1	pak	0	LOF	pak ¹¹
PAK7	mbt	2E-176	shRNA	GD9608
RAC2	Rac2	4.47228E-99	shRNA	GD17536

Gene Symbol	siRNA	Source
B4GALT6	SI03150259	Qiagen
B4GALT6	SI04226747	Qiagen
B4GALT6	SI04238962	Qiagen
B4GALT6	SI04330508	Qiagen
BMP2K	J-005071-05	Dharmacon
BMP2K	J-005071-06	Dharmacon
BMP2K	J-005071-07	Dharmacon
BMP2K	J-005071-08	Dharmacon
BMP2K	SI02224803	Qiagen
BMP2K	SI02224810	Qiagen
BMP2K	SI04440051	Qiagen
BMP2K	SI04901757	Qiagen
CA11	J-009336-09	Dharmacon
CA11	J-009336-10	Dharmacon
CA11	J-009336-11	Dharmacon
CA11	J-009336-12	Dharmacon
CA11	SI00023548	Qiagen
CA11	SI00023555	Qiagen
CA11	SI03047877	Qiagen
CA11	SI03062206	Qiagen
CA12	J-003634-06	Dharmacon
CA12	J-003634-07	Dharmacon
CA12	J-003634-08	Dharmacon
CA12	J-003634-09	Dharmacon
CA12	SI00023583	Qiagen
CA12	SI03041913	Qiagen
CA12	SI03106306	Qiagen
CA12	SI03115273	Qiagen
CACNA1B	J-006122-07	Dharmacon
CACNA1B	J-006122-08	Dharmacon
CACNA1B	J-006122-09	Dharmacon
CACNA1B	J-006122-10	Dharmacon
CACNA1B	SI00337141	Qiagen
CACNA1B	SI00337148	Qiagen
CACNA1B	SI00337155	Qiagen
CACNA1B	SI00337162	Qiagen
CACNB4	J-009062-05	Dharmacon
CACNB4	J-009062-06	Dharmacon
CACNB4	J-009062-07	Dharmacon
CACNB4	J-009062-08	Dharmacon
CACNB4	SI00014294	Qiagen
CACNB4	SI00014308	Qiagen
CACNB4	SI00014315	Qiagen
CACNB4	SI03113719	Qiagen
CALB1	J-011989-05	Dharmacon
CALB1	J-011989-06	Dharmacon
CALB1	J-011989-07	Dharmacon
CALB1	J-011989-08	Dharmacon
CALB1	SI04132933	Qiagen
CALB1	SI04308087	Qiagen
CALB1	SI04329143	Qiagen
CALB1	SI04362183	Qiagen
CAP2	J-012211-05	Dharmacon
CAP2	J-012211-06	Dharmacon
CAP2	J-012211-07	Dharmacon
CAP2	J-012211-08	Dharmacon
CAP2	SI00337939	Qiagen
CAP2	SI04226663	Qiagen
CAP2	SI04235490	Qiagen
CAP2	SI04237331	Qiagen
CDHR1	J-013677-09	Dharmacon
CDHR1	J-013677-10	Dharmacon
CDHR1	J-013677-11	Dharmacon
CDHR1	J-013677-12	Dharmacon
CDHR1	SI00678867	Qiagen
CDHR1	SI00678874	Qiagen
CDHR1	SI00678881	Qiagen
CDHR1	SI00678888	Qiagen
CDK5R1	J-008988-05	Dharmacon
CDK5R1	J-008988-06	Dharmacon
CDK5R1	J-008988-07	Dharmacon
CDK5R1	J-008988-08	Dharmacon
CDK5R1	SI00057372	Qiagen
CDK5R1	SI00057393	Qiagen
CDK5R1	SI02659580	Qiagen
CDK5R1	SI04379543	Qiagen
CELFA	J-013824-18	Dharmacon
CELFA	J-013824-19	Dharmacon
CELFA	J-013824-20	Dharmacon
CELFA	J-013824-21	Dharmacon
CELFA	SI00313621	Qiagen
CELFA	SI00313628	Qiagen
CELFA	SI04159463	Qiagen
CELFA	SI04162179	Qiagen
CH3L1	J-012568-09	Dharmacon
CH3L1	J-012568-10	Dharmacon
CH3L1	J-012568-11	Dharmacon
CH3L1	J-012568-12	Dharmacon
CH3L1	SI00345821	Qiagen
CH3L1	SI00345842	Qiagen
CH3L1	SI03125227	Qiagen
CH3L1	SI04254187	Qiagen
CLMN	J-017131-18	Dharmacon
CLMN	J-017131-19	Dharmacon
CLMN	J-017131-20	Dharmacon
CLMN	J-017131-21	Dharmacon
CLMN	SI00348418	Qiagen
CLMN	SI04201498	Qiagen
CLMN	SI04256875	Qiagen
CLMN	SI04320848	Qiagen
CNR1	J-004711-09	Dharmacon
CNR1	J-004711-10	Dharmacon
CNR1	J-004711-12	Dharmacon
CNR1	SI00113162	Qiagen
CNR1	SI00113169	Qiagen
CNR1	SI00113176	Qiagen
CNR1	SI00113183	Qiagen
CORO1C	J-017331-05	Dharmacon
CORO1C	J-017331-06	Dharmacon
CORO1C	J-017331-07	Dharmacon
CORO1C	J-017331-08	Dharmacon
CORO1C	SI00351918	Qiagen

Gene Symbol	siRNA	Source
GABRD	J-006171-08	Dharmacon
GABRD	SI00016233	Qiagen
GABRD	SI00016240	Qiagen
GABRD	SI00016247	Qiagen
GADP1	SI00016254	Qiagen
GADP1	J-021225-05	Dharmacon
GADP1	J-021225-06	Dharmacon
GADP1	J-021225-07	Dharmacon
GADP1	J-021225-08	Dharmacon
GADP1	J-021225-09	Dharmacon
GADP1	J-021225-10	Dharmacon
GADP1	SI00123445	Qiagen
GADP1	SI00123466	Qiagen
GADP1	SI02777831	Qiagen
GADP1	SI02777838	Qiagen
GLRB	J-006183-05	Dharmacon
GLRB	J-006183-06	Dharmacon
GLRB	J-006183-07	Dharmacon
GLRB	J-006183-08	Dharmacon
GLRB	J-006183-09	Dharmacon
GLRB	SI00016436	Qiagen
GLRB	SI00016443	Qiagen
GLRB	SI00016450	Qiagen
GLRB	SI03077263	Qiagen
GNB5	J-017235-05	Dharmacon
GNB5	J-017235-06	Dharmacon
GNB5	J-017235-07	Dharmacon
GNB5	J-017235-08	Dharmacon
GNB5	J-017235-09	Dharmacon
GNB5	J-017235-10	Dharmacon
GNB5	SI02637607	Qiagen
GNB5	SI03025876	Qiagen
GNB5	SI03049242	Qiagen
GNB5	SI03073973	Qiagen
GPR155	J-005494-05	Dharmacon
GPR155	J-005494-06	Dharmacon
GPR155	J-005494-08	Dharmacon
GPR155	SI04903682	Qiagen
GPR155	SI04903689	Qiagen
GPR155	SI04903696	Qiagen
GPR155	SI04903703	Qiagen
GRIA3	J-006186-07	Dharmacon
GRIA3	J-006186-08	Dharmacon
GRIA3	J-006186-09	Dharmacon
GRIA3	J-006186-10	Dharmacon
GRIA3	SI00016541	Qiagen
GRIA3	SI03043642	Qiagen
GRIA3	SI03046967	Qiagen
GRIA3	SI03111024	Qiagen
HIPK2	J-003266-10	Dharmacon
HIPK2	J-003266-11	Dharmacon
HIPK2	J-003266-12	Dharmacon
HIPK2	SI00134330	Qiagen
HIPK2	SI00134337	Qiagen
HIPK2	SI04439386	Qiagen
HIPK2	SI04439393	Qiagen
HS6ST2	J-015558-05	Dharmacon
HS6ST2	J-015558-06	Dharmacon
HS6ST2	J-015558-07	Dharmacon
HS6ST2	J-015558-08	Dharmacon
HS6ST2	J-015558-09	Dharmacon
HS6ST2	SI04145414	Qiagen
HS6ST2	SI04269020	Qiagen
HS6ST2	SI04296208	Qiagen
HS6ST2	SI04335051	Qiagen
HSPB1	J-005269-06	Dharmacon
HSPB1	J-005269-07	Dharmacon
HSPB1	J-005269-08	Dharmacon
HSPB1	J-005269-09	Dharmacon
HSPB1	SI02650585	Qiagen
HSPB1	SI02650606	Qiagen
HSPB1	SI04231129	Qiagen
HSPB1	SI04354490	Qiagen
HSPB8	J-005006-05	Dharmacon
HSPB8	J-005006-06	Dharmacon
HSPB8	J-005006-07	Dharmacon
HSPB8	J-005006-08	Dharmacon
HSPB8	J-005006-09	Dharmacon
HSPB8	SI02224502	Qiagen
HSPB8	SI03021921	Qiagen
HSPB8	SI03100083	Qiagen
HSPB8	SI04900854	Qiagen
HSPH1	J-004972-05	Dharmacon
HSPH1	J-004972-06	Dharmacon
HSPH1	J-004972-07	Dharmacon
HSPH1	J-004972-08	Dharmacon
HSPH1	J-004972-09	Dharmacon
HSPH1	SI03158281	Qiagen
HSPH1	SI04159764	Qiagen
HSPH1	SI04314905	Qiagen
HSPH1	SI04367643	Qiagen
HTR2C	J-005640-05	Dharmacon
HTR2C	J-005640-06	Dharmacon
HTR2C	J-005640-07	Dharmacon
HTR2C	J-005640-08	Dharmacon
HTR2C	J-005640-09	Dharmacon
HTR2C	SI00017367	Qiagen
HTR2C	SI00017374	Qiagen
HTR2C	SI03083164	Qiagen
HTR2C	SI04896927	Qiagen
IDS	J-009254-05	Dharmacon
IDS	J-009254-06	Dharmacon
IDS	J-009254-07	Dharmacon
IDS	J-009254-08	Dharmacon
IDS	J-009254-09	Dharmacon
IDS	SI00004368	Qiagen
IDS	SI03033149	Qiagen
IDS	SI03054345	Qiagen
IDS	SI03098753	Qiagen
IGDCC4	J-014170-09	Dharmacon
IGDCC4	J-014170-10	Dharmacon
IGDCC4	J-014170-11	Dharmacon
IGDCC4	J-014170-12	Dharmacon
IGDCC4	SI00660380	Qiagen
IGDCC4	SI04181996	Qiagen
IGDCC4	SI04242833	Qiagen
IGDCC4	SI04275558	Qiagen
IKBKAP	J-009371-05	Dharmacon
IKBKAP	J-009371-06	Dharmacon
IKBKAP	J-009371-07	Dharmacon
IKBKAP	J-009371-08	Dharmacon

Gene Symbol	siRNA	Source
LIX1	SI04318069	Qiagen
LIX1	SI04335863	Qiagen
LPP	J-020012-05	Dharmacon
LPP	J-020012-06	Dharmacon
LPP	J-020012-07	Dharmacon
LPP	J-020012-08	Dharmacon
LPP	SI00623119	Qiagen
LPP	SI03687439	Qiagen
LPP	SI04173659	Qiagen
LPP	SI04264022	Qiagen
LPP	SI04300114	Qiagen
LPP	SI04371129	Qiagen
LRIG1	J-013940-05	Dharmacon
LRIG1	J-013940-06	Dharmacon
LRIG1	J-013940-07	Dharmacon
LRIG1	J-013940-08	Dharmacon
LRIG1	SI04295767	Qiagen
LRIG1	SI04316767	Qiagen
LRIG1	SI04341022	Qiagen
LRIG1	SI04363667	Qiagen
LTBP3	J-014144-05	Dharmacon
LTBP3	J-014144-06	Dharmacon
LTBP3	J-014144-07	Dharmacon
LTBP3	J-014144-08	Dharmacon
LTBP3	SI00625121	Qiagen
LTBP3	SI04204613	Qiagen
LTBP3	SI04274158	Qiagen
LTBP3	SI04285505	Qiagen
MAFF	J-003903-05	Dharmacon
MAFF	J-003903-06	Dharmacon
MAFF	J-003903-07	Dharmacon
MAFF	J-003903-08	Dharmacon
MAFF	SI02662058	Qiagen
MAFF	SI03026611	Qiagen
MAFF	SI03067372	Qiagen
MAFF	SI03116456	Qiagen
MAFK	J-008580-05	Dharmacon
MAFK	J-008580-06	Dharmacon
MAFK	J-008580-07	Dharmacon
MAFK	J-008580-08	Dharmacon
MAFK	SI00036715	Qiagen
MAFK	SI02628416	Qiagen
MAFK	SI02628423	Qiagen
MAFK	SI02628430	Qiagen
MAN1A1	J-012174-05	Dharmacon
MAN1A1	J-012174-06	Dharmacon
MAN1A1	J-012174-07	Dharmacon
MAN1A1	J-012174-08	Dharmacon
MAN1A1	SI04172826	Qiagen
MAN1A1	SI04273689	Qiagen
MAN1A1	SI04341316	Qiagen
MAN1A1	SI04364815	Qiagen
MAPA	SI03153612	Qiagen
MAPA	SI04239214	Qiagen
MAPA	SI04315731	Qiagen
MAPA	SI04337053	Qiagen
MDH1	J-009264-09	Dharmacon
MDH1	J-009264-10	Dharmacon
MDH1	J-009264-11	Dharmacon
MDH1	J-009264-12	Dharmacon
MDH1	SI00082649	Qiagen
MDH1	SI00082656	Qiagen
MDH1	SI00082663	Qiagen
MDH1	SI03092761	Qiagen
MYLK	J-005351-18	Dharmacon
MYLK	J-005351-19	Dharmacon
MYLK	J-005351-20	Dharmacon
MYLK	J-005351-21	Dharmacon
MYLK	SI00083202	Qiagen
MYLK	SI00083209	Qiagen
MYLK	SI02224040	Qiagen
MYLK	SI03067960	Qiagen
MYST3	J-019849-05	Dharmacon
MYST3	J-019849-06	Dharmacon
MYST3	J-019849-07	Dharmacon
MYST3	J-019849-08	Dharmacon
MYST3	SI00091714	Qiagen
MYST3	SI03020836	Qiagen
MYST3	SI04388293	Qiagen
MYST3	SI04388300	Qiagen
MYST3	J-012835-18	Dharmacon
MYST3	J-012835-19	Dharmacon
MYST3	J-012835-20	Dharmacon
MYST3	J-012835-21	Dharmacon
MYST3	SI00655683	Qiagen
MYST3	SI00655690	Qiagen
MYST3	SI04227167	Qiagen
MYST3	SI04282285	Qiagen
NDRG3	J-013533-09	Dharmacon
NDRG3	J-013533-10	Dharmacon
NDRG3	J-013533-11	Dharmacon
NDRG3	J-013533-12	Dharmacon
NDRG3	SI00656124	Qiagen
NDRG3	SI04152099	Qiagen
NDRG3	SI04222645	Qiagen
NDRG3	SI04322192	Qiagen
NECAP1	J-017872-09	Dharmacon
NECAP1	J-017872-10	Dharmacon
NECAP1	J-017872-11	Dharmacon
NECAP1	J-017872-12	Dharmacon
NECAP1	SI04155732	Qiagen
NECAP1	SI04159008	Qiagen
NECAP1	SI04334869	Qiagen
NECAP1	SI04358333	Qiagen
NEK7	J-003795-11	Dharmacon
NEK7	J-003795-12	Dharmacon
NEK7	J-003795-13	Dharmacon
NEK7	J-003795-14	Dharmacon
NEK7	SI00287966	Qiagen
NEK7	SI04903552	Qiagen
NEK7	SI04903542	Qiagen
NELL2	J-012185-09	Dharmacon

Gene Symbol	siRNA	Source
PLK2	J-003325-20	Dharmacon
PLK2	J-003325-21	Dharmacon
PLK2	SI00090363	Qiagen
PLK2	SI00288386	Qiagen
PLK2	SI04438770	Qiagen
PLK2	SI04438777	Qiagen
PPP		

Gene Symbol	siRNA	Source
CORO1C	SI03168578	Qiagen
CORO1C	SI04138631	Qiagen
CORO1C	SI04310481	Qiagen
CRISPLD1	J-016681-17	Dharmacon
CRISPLD1	J-016681-18	Dharmacon
CRISPLD1	J-016681-19	Dharmacon
CRISPLD1	J-016681-20	Dharmacon
CRISPLD1	SI04179049	Qiagen
CRISPLD1	SI04248986	Qiagen
CRISPLD1	SI04295774	Qiagen
CRISPLD1	SI04339370	Qiagen
CXCR7	J-013212-10	Dharmacon
CXCR7	J-013212-11	Dharmacon
CXCR7	J-013212-12	Dharmacon
CXCR7	J-013212-13	Dharmacon
CXCR7	SI00125790	Qiagen
CXCR7	SI02660644	Qiagen
CXCR7	SI04901925	Qiagen
CXCR7	SI04901932	Qiagen
DACH1	J-013222-05	Dharmacon
DACH1	J-013222-06	Dharmacon
DACH1	J-013222-07	Dharmacon
DACH1	J-013222-08	Dharmacon
DACH1	J-013222-09	Dharmacon
DACH1	SI00359212	Qiagen
DACH1	SI03649107	Qiagen
DACH1	SI04175073	Qiagen
DACH1	SI04200553	Qiagen
DACH1	SI04238255	Qiagen
DDR1	J-003111-12	Dharmacon
DDR1	J-003111-13	Dharmacon
DDR1	J-003111-14	Dharmacon
DDR1	J-003111-15	Dharmacon

Gene Symbol	siRNA	Source
IKBKAP	SI00287462	Qiagen
IKBKAP	SI03045749	Qiagen
IKBKAP	SI04899181	Qiagen
IKBKAP	SI04899188	Qiagen
IKBKB	J-003503-11	Dharmacon
IKBKB	J-003503-12	Dharmacon
IKBKB	J-003503-13	Dharmacon
IKBKB	J-003503-14	Dharmacon
IKBKB	SI00300545	Qiagen
IKBKB	SI02626442	Qiagen
IKBKB	SI02626456	Qiagen
IKBKB	SI02777376	Qiagen
IKBKE	J-003723-09	Dharmacon
IKBKE	J-003723-10	Dharmacon
IKBKE	J-003723-11	Dharmacon

Gene Symbol	siRNA	Source
NELL2	J-012185-10	Dharmacon
NELL2	J-012185-11	Dharmacon
NELL2	J-012185-12	Dharmacon
NELL2	SI04167205	Qiagen
NELL2	SI04205565	Qiagen
NELL2	SI04292183	Qiagen
NELL2	SI04352901	Qiagen
NFIB	J-008456-05	Dharmacon
NFIB	J-008456-06	Dharmacon
NFIB	J-008456-07	Dharmacon
NFIB	J-008456-08	Dharmacon
NFIB	SI00079352	Qiagen
NFIB	SI00079359	Qiagen
NFIB	SI03032197	Qiagen
NFIB	SI03101140	Qiagen
NFIB	SI04300947	Qiagen
NFKB1	J-003520-06	Dharmacon
NFKB1	J-003520-07	Dharmacon
NFKB1	J-003520-08	Dharmacon
NFKB1	J-003520-09	Dharmacon
NFKB1	SI02654932	Qiagen
NFKB1	SI02654939	Qiagen
NFKB1	SI02662618	Qiagen
NFKB2	J-003918-05	Dharmacon
NFKB2	J-003918-06	Dharmacon
NFKB2	J-003918-07	Dharmacon
NFKB2	J-003918-08	Dharmacon
NFKB2	SI00300965	Qiagen
NFKB2	SI02650949	Qiagen
NFKB2	SI04219852	Qiagen
NFKB2	SI04224290	Qiagen
NFKB2	SI04245318	Qiagen

Gene Symbol	siRNA	Source
RERG	SI03068107	Qiagen
RGS14	J-008826-05	Dharmacon
RGS14	J-008826-06	Dharmacon
RGS14	J-008826-07	Dharmacon
RGS14	J-008826-08	Dharmacon
RGS14	J-022559-18	Dharmacon
RGS14	SI00088879	Qiagen
RGS14	SI00088886	Qiagen
RGS14	SI03054737	Qiagen
RGS14	SI03076367	Qiagen
ROCK1	J-003536-06	Dharmacon
ROCK1	J-003536-07	Dharmacon
ROCK1	J-003536-08	Dharmacon
ROCK1	J-003536-09	Dharmacon
ROCK1	SI02622095	Qiagen
ROCK1	SI02622102	Qiagen
ROCK1	SI03095484	Qiagen
ROCK1	SI04898362	Qiagen
ROCK2	J-004610-06	Dharmacon
ROCK2	J-004610-07	Dharmacon
ROCK2	J-004610-08	Dharmacon
ROCK2	J-004610-09	Dharmacon
ROCK2	SI02223753	Qiagen
ROCK2	SI04899720	Qiagen
ROCK2	SI04899727	Qiagen
TBK1	J-003788-08	Dharmacon
TBK1	J-003788-09	Dharmacon
TBK1	J-003788-10	Dharmacon
TBK1	J-003788-11	Dharmacon
TBK1	SI00100961	Qiagen
TBK1	SI02224411	Qiagen
TBK1	SI04379606	Qiagen
TBK1	SI04901169	Qiagen