

***In vivo* epigenetic editing of *Sema6a* promoter reverses transcallosal dysconnectivity caused by *C11orf46/Arl14ep* risk gene**

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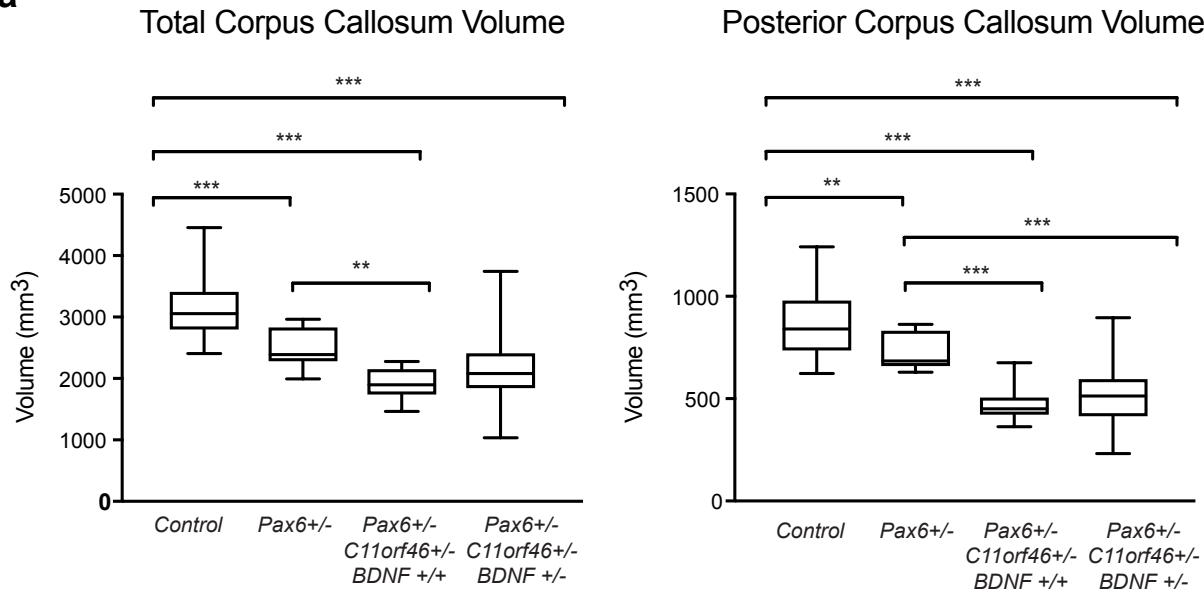
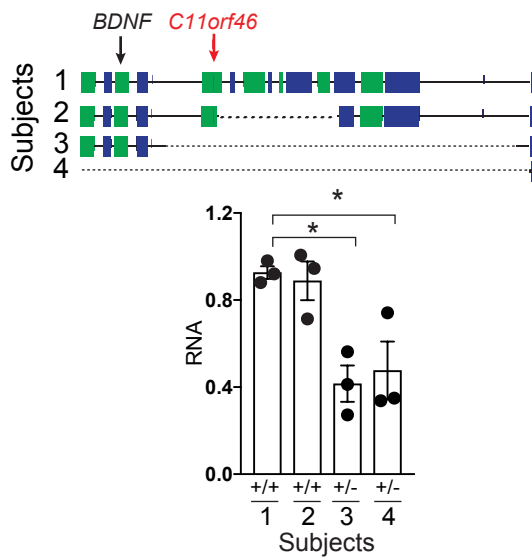
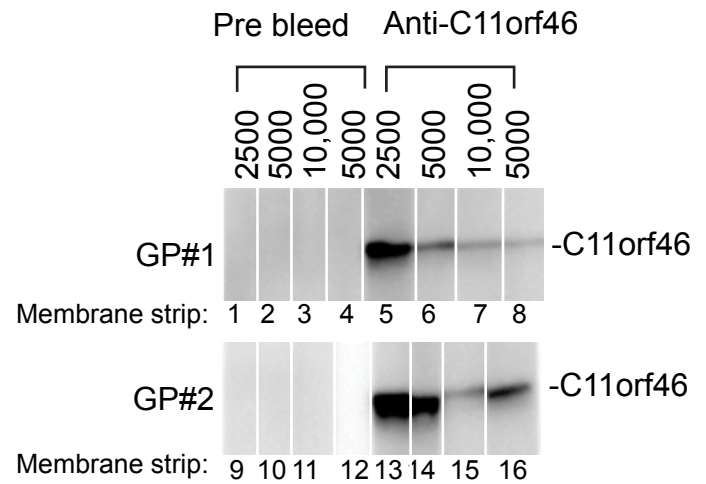
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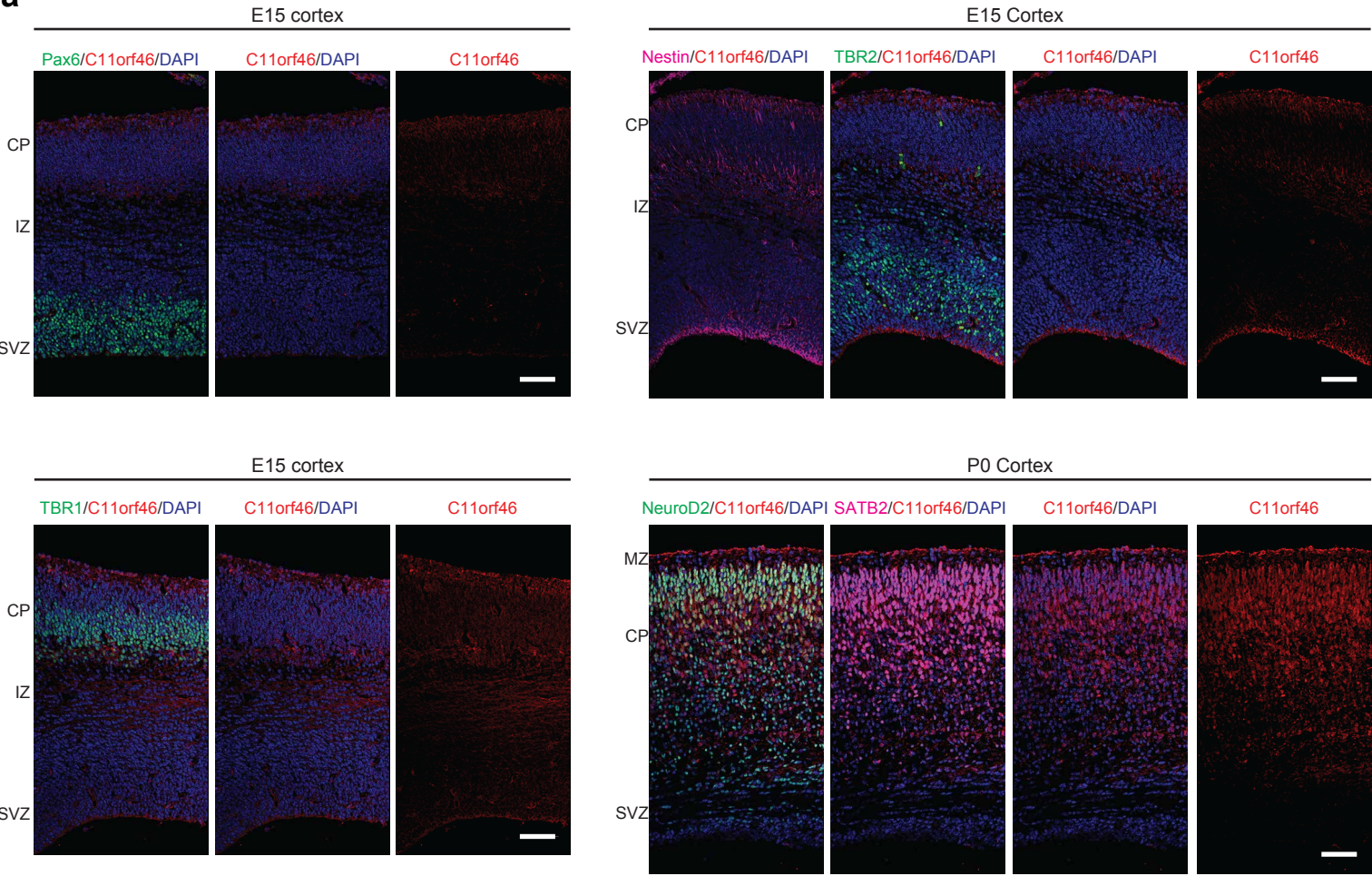
*These authors contributed equally to this work.

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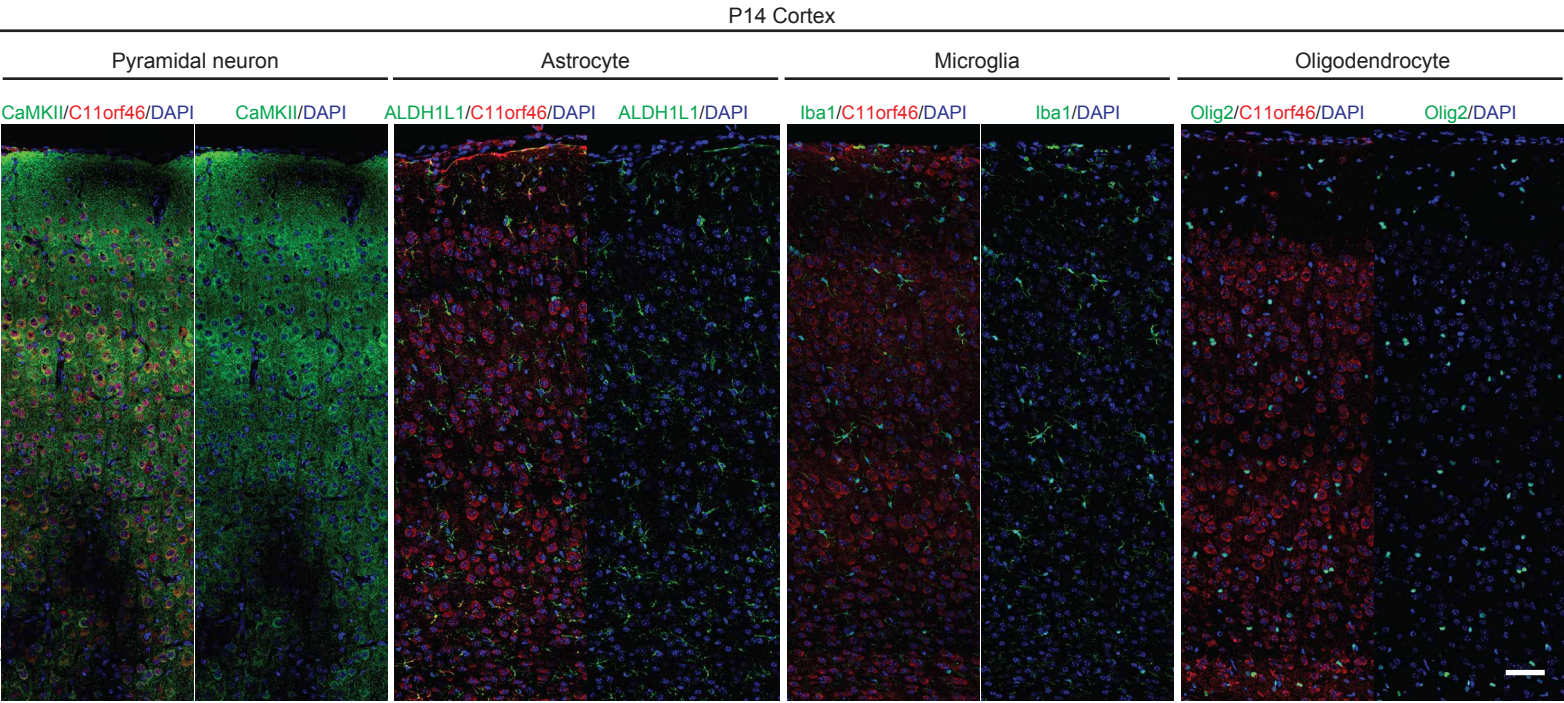
a**b****c**

Supplementary Fig. 1 The critical role of C11orf46 for interhemispheric connectivity and knockdown effect of C11orf46. **a** Total (left) or posterior (right) CC volumes in participants with BDNF and without BDNF. ANCOVA including age and sex as covariates, compared corpus callosum volumes of healthy control (n = 23), isolated *PAX6*^{+/-} (n = 12), *PAX6*^{+/-} *C11orf46*^{+/-} without *BDNF* haploinsufficiency (n = 7) and *PAX6*^{+/-} and *C11orf46*^{+/-} with *BDNF* haploinsufficiency (n = 10). No significant differences in the CC volumes of *PAX6*^{+/-}*C11orf46*^{+/-} patients with and without *BDNF*^{+/-} ($P = 0.19$ and 0.47 , for unadjusted comparisons; $P = 0.13$ and 0.37 respectively on ANCOVA adjusting for age and sex). Box and whisker plots represent the distribution of corpus callosum volume from each participant. The inner bar in the box indicates average value. The upper and lower box ends represent first and third quantile, respectively. The upper and lower whisker ends represent the maximum and minimum values in the group, respectively. **b** Schematic illustration of genetic map highlighting various types of micro deletions at 11p13 WAGR locus (dotted lines) including *C11orf46*; one control and three different types of microdeletion in WAGR patients are indicated. mRNA levels of *C11orf46* in WAGR patients lymphoblastoid cells were quantified. Bar graphs represent the averages of mRNA expression in three independent experiments per patient. n = 3, 1 (*C11orf46* ^{+/+}) versus 3 (*C11orf46* ^{+/-}) $P = 0.0139$, 1 (*C11orf46* ^{+/+}) versus 4 (*C11orf46* ^{+/-}) $P = 0.0239$. Error bars indicate S.E.M. **c** Immunoblot with affinity purified guinea pig (GP) anti-*C11orf46* antibodies detecting full-length human *C11orf46*. Note the pre-immune IgG from same animals (GP#1 & GP#2) did not detect *C11orf46* (negative control). Antibody dilutions 1:5000 were used.

a

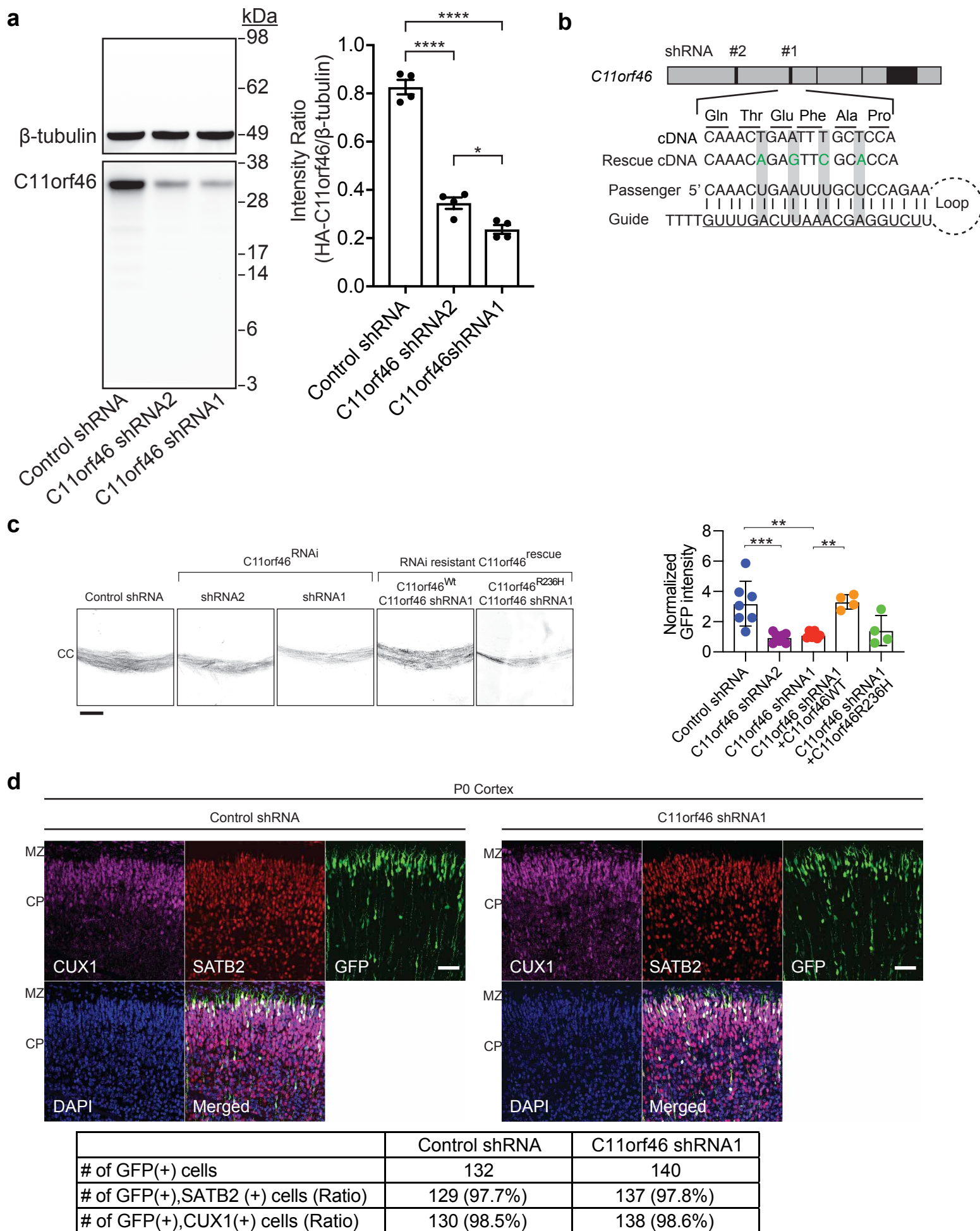


b



Cell-type	Pyramidal neuron	Astrocyte	Microglia	Oligodendrocyte
C11orf46(+) cells/Cell-type marker(+) cells	339/393	42/93	2/42	9/58
Ratio	86.3%	42.2%	4.8%	15.5%

Supplementary Fig. 2 C11orf46 is highly expressed in the neuronal cells in cortical plate and pyramidal neuron after differentiation. a (Upper left) Low magnification images of C11orf46 (red) protein staining with Pax6 (green) in the cerebral cortex at E15. (Upper right) Low magnification images of C11orf46 (red) protein staining with Nestin (magenta) and TBR2 (green) in the cerebral cortex at E15. (Lower left) Low magnification images of C11orf46 (red) protein staining with TBR1(green) in the cerebral cortex at E15. (Lower right) Low magnification images of C11orf46 (red) protein staining with NeuroD2 (green) and SATB2 (magenta) in the cerebral cortex at P0. Nuclear and cytoplasmic distribution of C11orf46 are shown in higher magnification images in **Fig. 1f**. Blue, nucleus counterstained by DAPI. Scale bar, 100 μ m. **b** Low magnification images of C11orf46 protein staining (red) with cell type-specific markers (green) in the cortex. C11orf46 is predominantly expressed in CaMKII-positive pyramidal neurons, but not in ALDH1L1 (astrocyte), Iba-1 (microglia), or Olig2 (oligodendrocyte)-positive cells in the cerebral cortex at P14. (Bottom) Ratio of the number of nuclear C11orf46-positive cells in each specific marker-positive cells are shown in the table. Higher magnification images are shown in **Fig. 1g**. Scale bar, 100 μ m.



Supplementary Fig. 3. Knockdown plasmids against *C11orf46* and its effects on midline crossing of callosal projections and neuronal marker expression. **a** (Left) Western blot analysis of whole cell extract derived from HEK293 cells cotransfected with HA-C11orf46 and shRNA (C11orf46 or Control) plasmids blotted with anti-HA antibody. Endogenous β -tubulin was used as a loading control. (Right) Exogenous C11orf46 protein expression was strongly suppressed by shRNA1, compared with shRNA2. $F(2, 9) = 166.4$, $P < 0.0001$ was determined by one-way ANOVA with post hoc Bonferroni test. **b** Nucleotide sequence targeted by C11orf46 shRNA1. Four synonymous mutations were added within shRNA1 (bottom) target sequence in the rescue plasmids (green). **c** Knockdown of C11orf46 show impaired midline crossing of callosal projections at P14. Normalized GFP intensity at corpus callosum was decreased by delivery of C11orf46 shRNA1 and shRNA2 when compared with control shRNA (first 3 panels). These deficits were partially rescued by co-expressing RNAi resistant wild type C11orf46 (C11orf46^{WT}), but not by R236H mutant (C11orf46^{R236H}) (last 2 panels). (Right) Quantitative data are shown in the graph. $F(4, 23) = 9.9$, $P < 0.0001$ was determined by one-way ANOVA with *post hoc* Bonferroni test. Scale bar, 100 μ m. **d** CUX1 (magenta) and SATB2 (red) expression in the P0 brains after C11orf46 knockdown. Knockdown of C11orf46 does not affect the percentage of SATB2 and CUX1-positive cells in GFP-labeled neurons, compared to those in controls. Scale bar, 50 μ m. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, and **** $P < 0.0001$. Bar graphs indicate mean $\pm$ S.E.M (a,c).

a

Human **MMDPCSVGVQLRT**TTNECHKTYTTRHTGFK**TLQELSSNDMLLLQLRTGMTL** 50
 Mouse -MDPCSVGVQLRTTHDCHKTFYTRHTGFKTLKELSSNDMLLLQLRTGMTL 49
 Chicken -MDPCSVGVQLQATNECHKTYTTRHTGFKTKEDISSFDLLLLQLRTGMTL 49
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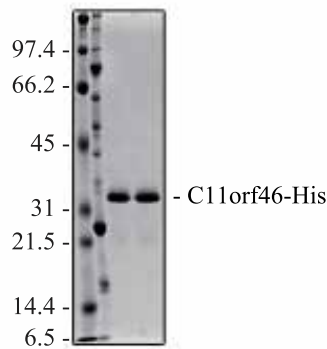
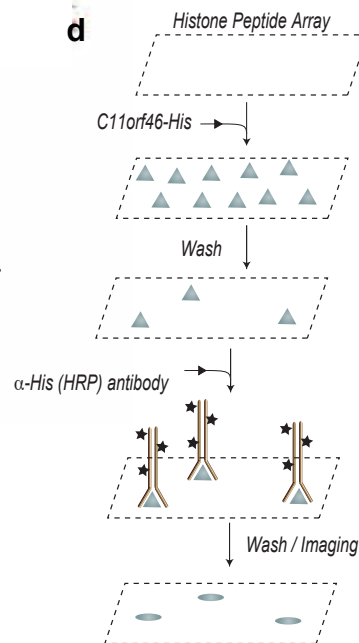
Human **SGNNTICFHHVKIYIDRFEDLQKSCCDPFNIHKKLAKKNLHVIDLDDATF** 100
 Mouse SGNNTICLHHVKIYIDRFEDLQKSCCDPFNIHKKLAKKNLHVIDLDDATF 99
 Chicken SENDTICFHHAKIYIERFEDLQKSCCDPFNMHRKLSKKNLRAIDLHDATF 99
 *:::*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****

Human **LSAKFGRQLVPGWKLC**PK**CTQIINGSVDVDTEDRQ**KRPESDGRTAKALR 150
 Mouse LSAKFGRQLVPGWKLC**PKCTQIINGSVDVSDDRQRKPDSDGRTAKALR** 149
 Chicken LTAKFGRQFVPGWKLC**PKCMQVINGSVDVEAERQRKLDSDGRTAKALK** 149
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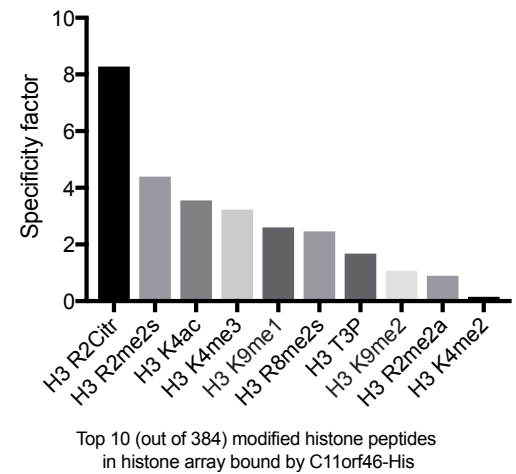
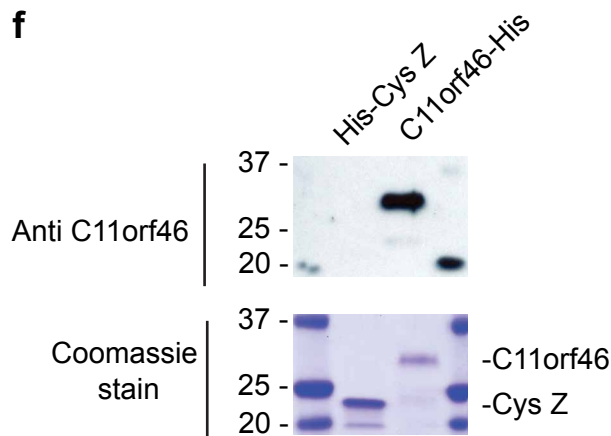
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 Mouse SLQFTNPGKQTEFAPEGGKREKRRL-TKATSAASDRQIIPAKSKVYDSQG 198
 Chicken SLQFTNPGRQTEFTPETSKREKRRLQTKNPSFNSDRQVIPAKSKVYDSQG 199
 *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****

Human LLIFSGMDLCDLDEDC**LGCFYAC**PACG**STK GAEC**CDR**KWLYEQIEIE** 249
 Mouse LLIFSGMDLCDLDEDC**LGCFYAC**PTCG**STKCGAEC**CDR**KWLYEQIEIE** 248
 Chicken LLLYSGMDLCDLDEDC**LGCFYAC**PKCGSNKCGTE**CDR**KWLYEQIEIE 249
 :***:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****

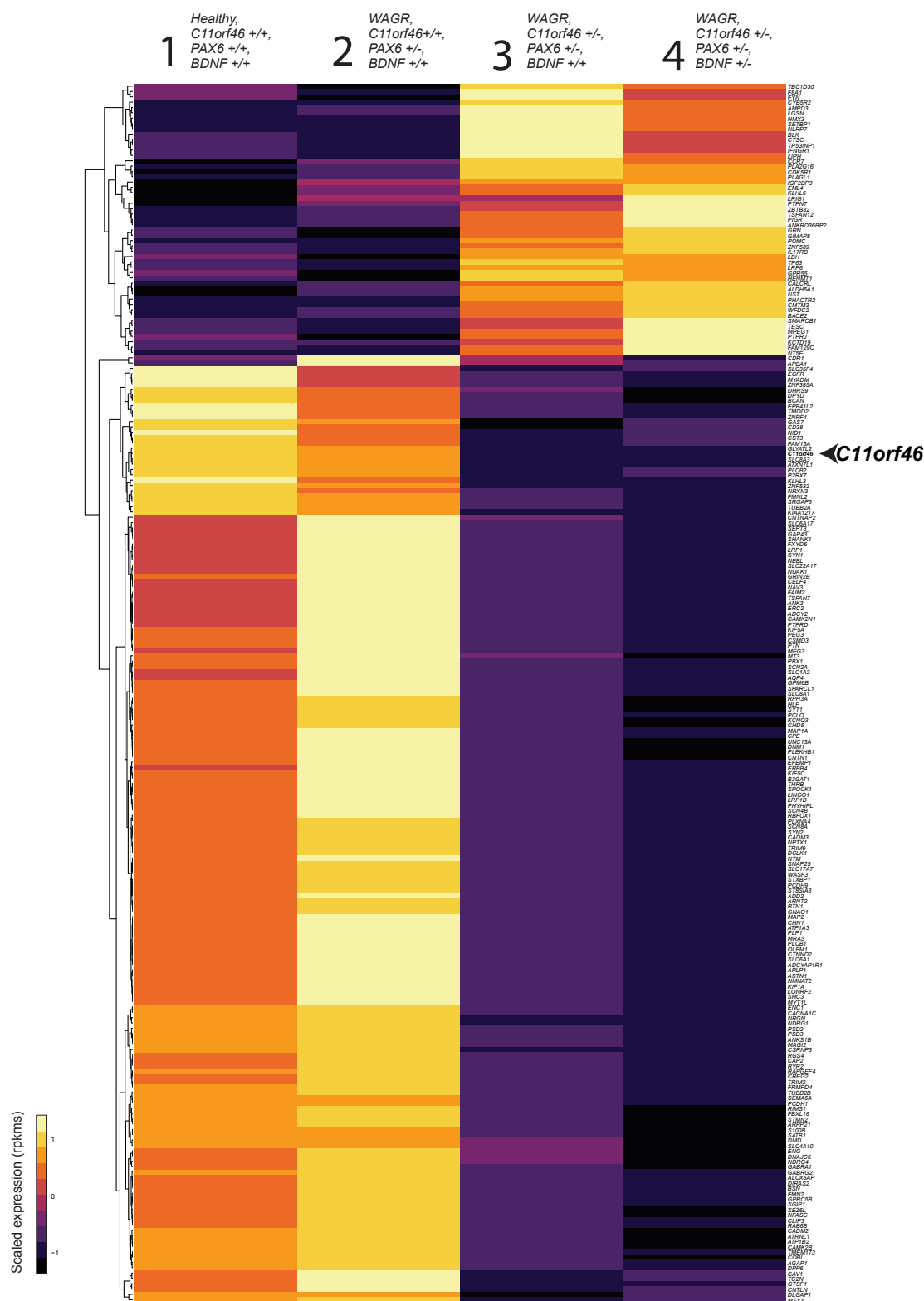
Human **GGEIIHNKHAG**----- 260
 Mouse GGEIIHNKHAGKAYGLLSPCHPYDILQK 276
 Chicken GGEIIRNKHVG----- 276
 *****:*****:*****

c**d****b**

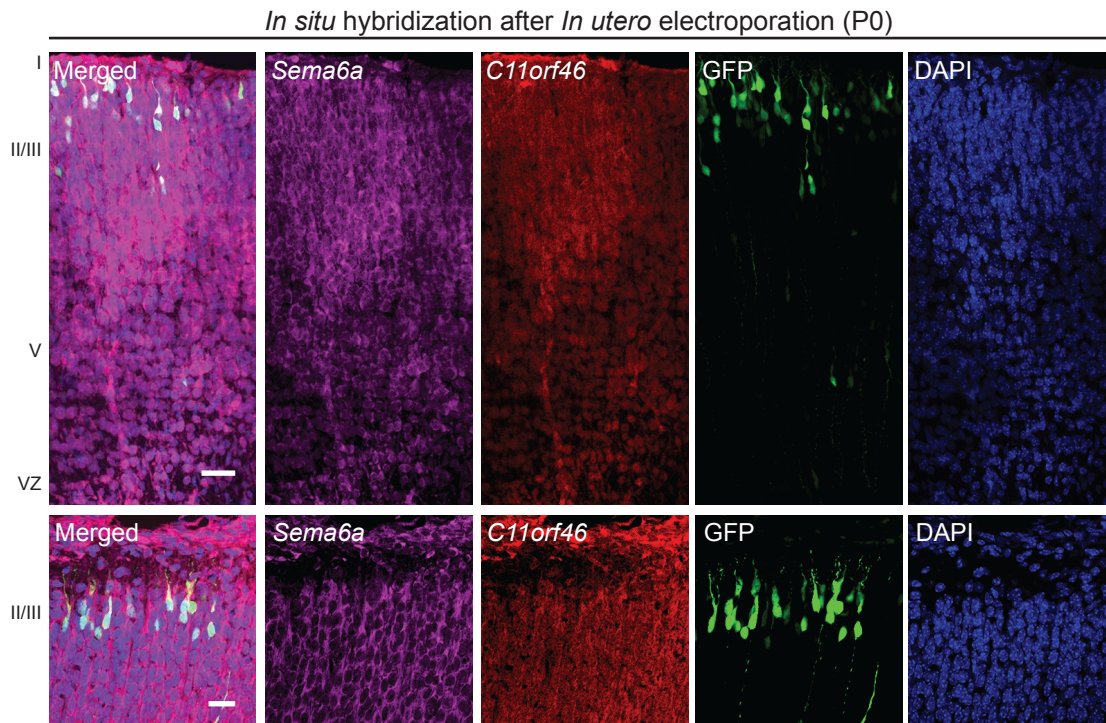
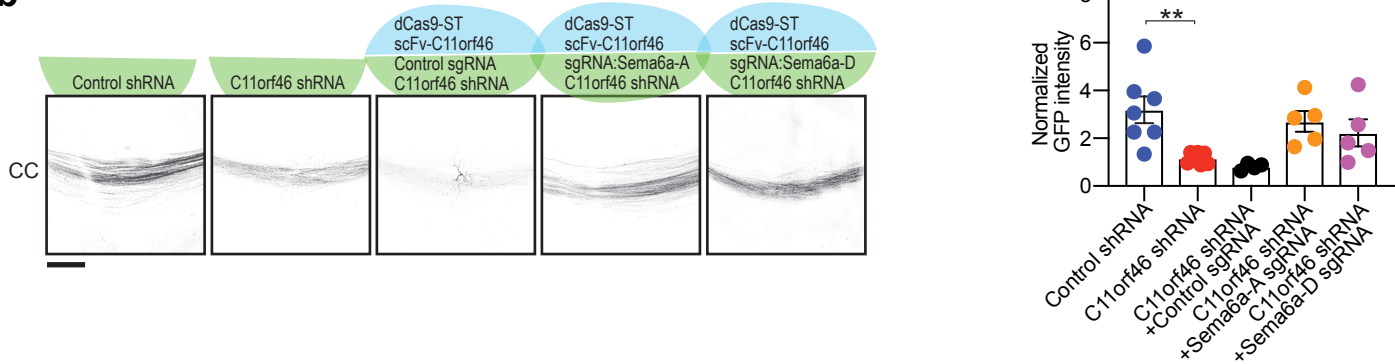
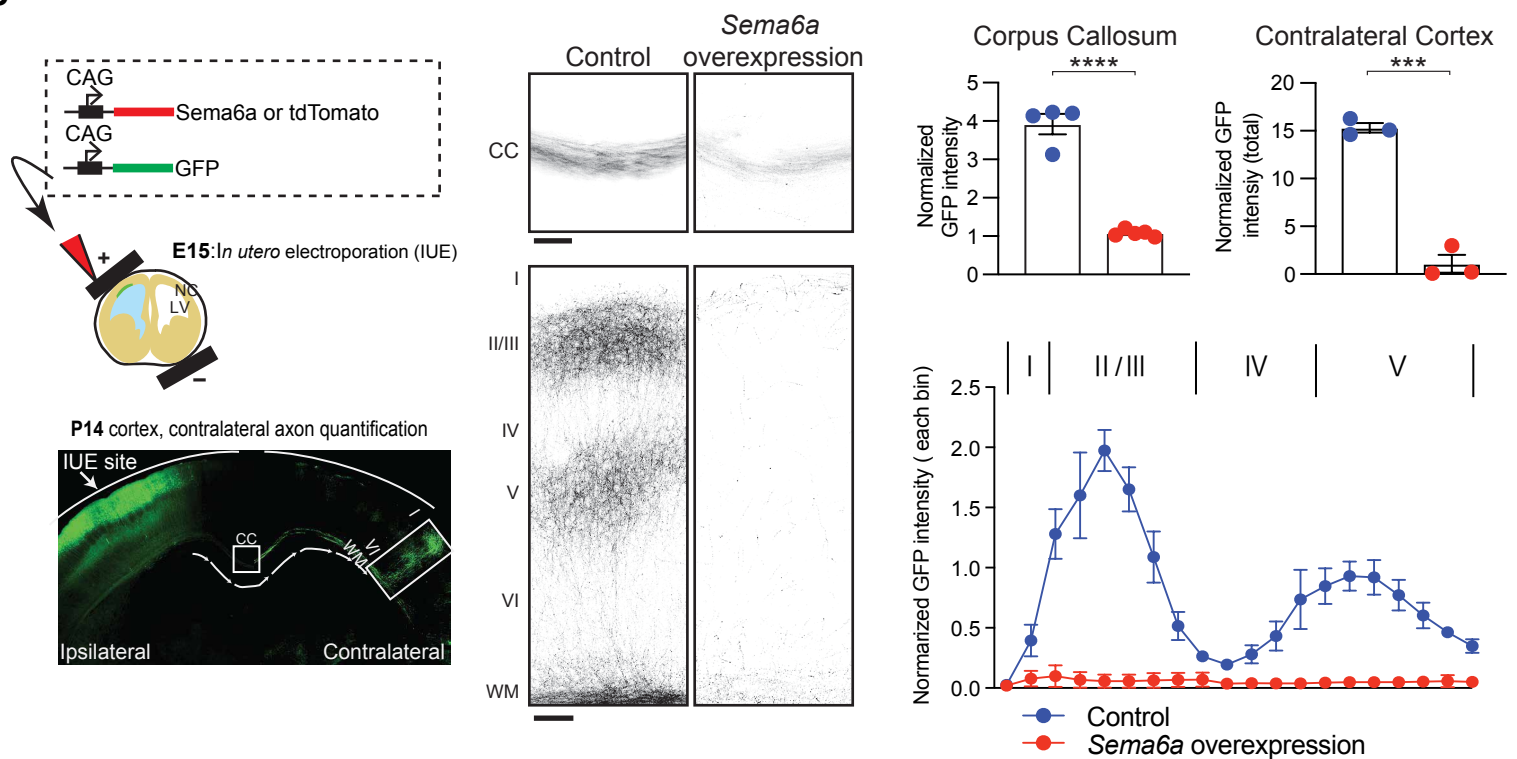
#	C11orf46 Peptides Identified by mass spectrometry	Clone-8 (C11orf46 ▲)	
1	MMDPCSVGVQLRT	+	+
2	KTLQELSSNDmLLLQLRT	+	+
3	RTGMTLSGNNTICFHHVKI	+	+
4	KIYIDRFEDLQKS	+	+
5	KSCCDPFNIHKKL	+	+
6	KKNLHVIDLDDATFLSAKF	+	+
7	TQIINGSVDVDTEDRQK	+	+
8	RSLQFTNPGRQ	+	+
9	RQTEFAPETGKRE	+	+
10	KWLYEQIEIEGGEIIHNKH	-	+

e**f**

Supplementary Fig. 4 C11orf46 is a chromatin regulator. a, b C11orf46 is a conserved molecule. CLUSTAL W multiple sequence alignment of human C11orf46 protein and mouse and chicken *orthologs*. Identical (*), similar (:) critical point mutation associated with cognitive diseases (see text) marked in red. C11orf46 peptides present in C11orf46 complexes purified from clones 8 & 10 are highlighted (bold and underlined) (**a**) and detailed in the table (**b**). Note absence of carboxyl terminal peptide (marked in green) in clone 8 expressing truncated C11orf46. **c** Immunoblot showing recombinant protein load (250ng each). **d** Purified C11orf46-His incubated with Histone peptide array followed by HRP labeled anti-Histidine antibody detection and imaging analysis. **e** Histone peptide array showing purified C11orf46 binding to histone H3 N-terminal tail including its modifications. Top ten histone H3 peptides (out of >300 on the array) detected by C11orf46 includes H3K9me2/3. **f** Immunoblot showing mouse anti-C11orf46 detecting *E. coli* derived histidine-tagged full-length human C11orf46 but not the control protein CysZ; coomassie stained gel (bottom).



Supplementary Fig. 5 RNA-seq dataset obtained from lymphoblastoid cell lines of the WAGR cases and controls. **a** Genes differentially expressed in *C11orf46* haploinsufficient WAGR lymphoblastoid cells. **b** Pair-end (50bp) RNA sequenced libraries were mapped to human (GRCh38.p10_v26) with STAR (v2.5.3a) using a two-method step protocol following tool specifications. Reads were counted in exon regions using featureCounts tool (subread v1.5.2) producing a table that was normalized to rpkm (Supplementary Table 3). Heatmaps were produced scaling rpkm values by scale function (base v3.5.1).

a**b****c**

Supplementary Fig. 6 Sema6a plays critical roles for axonal development. a *In situ* hybridization of *C11orf46* and *Sema6a* in the electroporated brains. *C11orf46* (red) and *Sema6a* (magenta) are highly expressed in the upper cortical layers II/III in the cerebral cortex at P0. Scale bar, 50 μ m (upper panels) and 20 μ m (lower panels). **b** The midline crossing of callosal projections was disrupted by *C11orf46* knockdown, but restored by dCas9-ST mediated recruitment of *C11orf46* to two different part of *Sema6a* promoter (*Sema6a*-), using specific sgRNAs *Sema6a*-A, *Sema6a*-D, but not with non-targeting control sgRNA. Normalized GFP intensity at corpus callosum was shown in the graph. Control shRNA and *C11orf46* shRNA samples were shared with Supplementary Fig. 3c. $F(4, 23) = 5.633$, $P = 0.0026$ was determined by one-way ANOVA with *post hoc* Bonferroni test. Scale bar, 100 μ m. **c** (Left) Schematic diagram of *Sema6a* overexpression into transcallosal projection neurons by *in utero* electroporation. *Sema6a* or tdTomato overexpression plasmid together with GFP expression construct were delivered in the developing cerebral cortex at E15, followed by analysis of corpus callosum (CC) formation and axonal arborization at P14. (Middle) Overexpression of *Sema6a* in pyramidal neurons of layer II/III (Ipsilateral) impaired midline crossing of callosal projections and axon terminal arborization across all cortical layers in the contralateral somatosensory cortex at P14. (Upper right) Normalized GFP intensity at corpus callosum and total GFP intensity (axonal density) in contralateral cortex were shown in brains with overexpression of *Sema6a* and controls. $P < 0.0001$ (corpus callosum) and $P = 0.0002$ (contralateral cortex) were determined by Student's t-test. (Lower right) Layer distributions of callosal axons in the contralateral site of the electroporated brains were shown as normalized immunofluorescence intensities of callosal axons. Scale bar, 100 μ m. $**P < 0.01$, $***P < 0.001$, and $****P < 0.0001$. Bar graphs indicate mean $\pm$ S.E.M (b,c).

Supplementary Table 1. The complete list of proteins identified by mass spectrometry analysis of purified Flag-C11orf46 complexes.

S.No	Protein ID	Description	Sequence Coverage (%)			Exclusive Unique Peptide Count			Total Spectrum Count		
			HEK293 (Wt; +Dox)	HEK293 (Tet-ON Flag-C11orf46; clone #10; +Dox)	HEK293 (Tet-ON Flag-C11orf46Δ; clone #8; +Dox)	HEK293 (Wt; +Dox)	HEK293 (Tet-ON Flag-C11orf46; clone #10; +Dox)	HEK293 (Tet-ON Flag-C11orf46Δ; clone #8; +Dox)	HEK293 (Wt; +Dox)	HEK293 (Tet-ON Flag-C11orf46; clone #10; +Dox)	HEK293 (Tet-ON Flag-C11orf46Δ; clone #8; +Dox)
1	RS27A	Ubiquitin-40S ribosomal protein S27a (RPS27A)	8.30%	47%	31%	1	5	3	1	6	3
2	C11orf46	Uncharacterized protein C11orf46 (C11orf46)		45%	41%		10	9		20	19
3	SETDB1	Histone-lysine N-methyltransferase SETDB1 (SETDB1)		40%	28%		42	108		8	0
4	H2A1D	Histone H2A type 1-D (HIST1H2AD)	15%	35%	28%	1	4	5	5	8	11
5	MCAF1	Activating transcription factor 7-interacting protein 1 (ATF7IP)		34%			26			63	0
6	EIF6	Eukaryotic translation initiation factor 6 (EIF6)	5.70%	33%	43%	1	5	6	1	8	14
7	H12	Histone H1.2 (HIST1H1C)		26%	6.10%		4		1	4	1
8	RS11	40S ribosomal protein S11 (RPS11)		25%	32%	2	4	5	2	4	5
9	PABP4	Polyadenylate-binding protein 4 (PABPC4)	13%	24%	20%	1	6		8	15	12
10	DDX21	Nucleolar RNA helicase 2 (DDX21)	7.80%	23%	26%	1	12	15	3	15	22
11	EIF3K	Eukaryotic translation initiation factor 3 subunit K (EIF3K)	5.00%	23%	13%	2	4	2	2	4	4
12	RL8	60S ribosomal protein L8 (RPL8)	6.40%	18%	23%	1	2	4	2	4	5
13	KAP1	Transcription intermediary factor 1-beta (TRIM28)	12%	18%	24%	1	9		2	14	17
14	RS9	40S ribosomal protein S9 (RPS9)	6.70%	18%		2	4	10	2	3	6
15	RL7A	60S ribosomal protein L7a (RPL7A)	4.60%	16%	21%	1	3	6	1	4	0
16	LMNB1	Lamin-B1 (LMNB1)	7.50%	16%	20%	1	7	8	1	8	11
17	CKAP4	Cytoskeleton-associated protein 4 (CKAP4)	5.50%	12%	9.60%	3	5	4	3	6	4
18	DDX1	ATP-dependent RNA helicase DDX1 (DDX1)	1.20%	7.20%	13%	1	3	5	1	4	5
19	HS90A	Heat shock protein HSP 90-alpha (HSP90AA1)	3.80%	6.40%	9.40%	1	2	4	3	4	6
20	LAP2A	nuclear lamina-heterochromatin anchoring protein		6.10%	11%		2	5		2	6
21	C1TC	C-1-tetrahydrofolate synthase, cytoplasmic (MTHFD1)		5.80%	9.20%		4	7		4	8
22	SYLC	Leucyl-RNA synthetase, cytoplasmic (LARS)		3.10%	9.10%		2	6		3	8
23	NSUN2	RNA (cytosine(34)-C(5))-methyltransferase (NSUN2)		3.00%	8.90%		2	4		3	5
24	NMD3	60S ribosomal export protein NMD3 (NMD3)		2.80%	12%		1	4		1	4
25	NOP56	Nucleolar protein 56 (NOP56)			12%			4			5
26	SRP68	Signal recognition particle 68 kDa protein (SRP68)			11%			5			6

Known of the (SETDB-MCAF1-KAP1) and C11orf46 in magenta

Protein ID UniProt Protein ID

Description HUGO Gene Symbol and gene name

Sequence Coverage (%) Percent of the residues in each protein sequence that have been identified.

total number of unique peptides Number of unique peptides obtained for each protein

Spectral counts Number of spectral counts adjusted for shared peptides

References
SETDB1
MCAF1
KAP1
Schultz et al, Genes and development, 2002 (PMID: 11959841)
Ivanov et al, Molecular Cell, 2007 (PMID: 18082607)

Supplementary Table 2. The complete list of proteins identified by mass spectrometry analysis of purified Flag-SETDB1 complexes

S.No	Protein ID	Description	Percent Sequence coverage (%)		Exclusive Unique Peptide Count		Total Spectrum count	
			HEK293 (Wt; +Dox)	HEK293 (Tet-ON SETDB1; clone #1; +Dox)	HEK293 (Wt; +Dox)	HEK293 (Tet-ON SETDB1; clone #1; +Dox)	HEK293 (Wt; +Dox)	HEK293 (Tet-ON SETDB1; clone #1; +Dox)
1	SETDB1	Histone-lysine N-methyltransferase SETDB1 (SETDB1)	17%	72%	14	96	28	550
2	KAP1	Transcription intermediary factor 1-beta (TRIM28)		62%		32		95
3	C11orf46	Uncharacterized protein C11orf46 (C11orf46)		53%		15		53
4	MCAF1	Activating transcription factor 7-interacting protein 1 (ATF7IP)		51%		46		127
5	RL38	60S ribosomal protein L38 (RPL38)		50%		4		5
6	C1140	Protein C9orf140 (C9orf140)		49%		16		21
7	CDK1	Cyclin-dependent kinase 1 (CDK1)		47%		12		15
8	HSP7C	Heat shock cognate 71 kDa protein (HSPA8)		46%		24		39
9	RL40	Ubiquitin-60S ribosomal protein L40 (UBA52)		45%		7		28
10	HSP71	Heat shock 70 kDa protein 1A/1B (HSPA1A)		41%		18		24
11	RL23	60S ribosomal protein L23 (RPL23)		38%		4		7
12	FHL1	Four and a half LIM domains protein 1 (FHL1)		36%		9		12
13	GRP78	78 kDa glucose-regulated protein (HSPA5)		33%		15		20
14	HP1-γ	Heterochromatin protein 1-gamma		30%		5		13
15	PRDX4	Peroxisomal protein 4 (PRDX4)		30%		6		8
16	CDC23	Cell division cycle protein 23 homolog (CDC23)		28%		11		16
17	E2F7	Transcription factor E2F7 (E2F7)		27%		17		23
18	EFTU	Elongation factor Tu, mitochondrial (TUFM)		27%		9		10
19	ADT2	ADP/ATP translocase 2 (SLC25A5)		27%		8		8
20	POGZ	Pogo transposable element with ZNF domain (POGZ)		25%		24		35
21	RL3	60S ribosomal protein L3 (RPL3)		24%		7		8
22	PCM1	Pericentriolar material 1 protein (PCM1)		24%		37		52
23	SERA	D-3-phosphoglycerate dehydrogenase (PHGDH)		23%		9		9
24	MCAF2	Activating transcription factor 7-interacting protein 2 (ATF7IP2)		23%		11		13
25	ZN828	Zinc finger protein 828 (ZNF828)		23%		16		19
26	ADNP	Activity-dependent neuroprotector homeobox protein (ADNP)		19%		17		23
27	CAMP3	Calmodulin-regulated spectrin-associated protein 3 (KIAA1543)		18%		13		16
28	NAMPT	Nicotinamide phosphoribosyltransferase (NAMPT)		18%		6		7
29	ATPA	ATP synthase subunit alpha, mitochondrial (ATP5A1)		17%		7		7
30	RLA0	60S acidic ribosomal protein P0 (RPLP0)		17%		4		6
31	TIM50	Mitochondrial import inner membrane translocase subunit TIM50 (TIMM50)		17%		5		6
32	IQGA3	Ras GTPase-activating-like protein IQGAP3 (IQGAP3)		17%		20		24
33	EXOC4	Exocyst complex component 4 (EXOC4, SEC8)		17%		12		15
34	ST38L	Serine/threonine-protein kinase 38-like (STK38L)		16%		4		7
35	EF1A1	Elongation factor 1-alpha 1 (EEF1A1)		14%		5		6
36	PYR1	CAD protein (CAD)		13%		24		26
37	SPAG5	Sperm-associated antigen 5 (SPAG5)		12%		10		11
38	MYO5C	Myosin-Vc (MYO5C)		12%		17		19
39	RUVB1	RuvB-like 1 (RUVBL1, Pontin)		12%		4		4
40	IRS4	Insulin receptor substrate 4 (IRS4)		12%		11		13
41	GRP75	Stress-70 protein, mitochondrial (HSPA9)		9.90%		6		6
42	CC123	Coiled-coil domain-containing protein 123, mitochondrial (CCDC123, CEP89)		9.70%		7		7
43	RFB2	DNA-directed RNA polymerase II subunit RPB2 (POLR2B)		9.50%		9		9
44	EXOC5	Exocyst complex component 5 (EXOC5, SEC10)		7.60%		5		5
45	UBP7	Ubiquitin carboxyl-terminal hydrolase 7 (USP7)		5.50%		4		6
46	UBR5	E3 ubiquitin-protein ligase UBR5 (UBR5)		5.40%		9		12
47	PRKDC	DNA-dependent protein kinase catalytic subunit (PRKDC)		5.30%		18		20
48	IQGA1	Ras GTPase-activating-like protein IQGAP1 (IQGAP1)		5.20%		6		8
49	EF2	Elongation factor 2 (EEF2)		4.80%		4		5
50	GCN1L	Translational activator GCN1 (GCN1L1)		4.60%		8		15
51	AZI1	5-azacytidine-induced protein 1 (AZI1)		4.00%		4		4
52	SYEP			3.40%		4		4

Known of the (SETDB1-MCAF1-KAP1) and C11orf46 in magenta

Protein ID UniProt Protein ID

Description HUGO Gene Symbol and gene name

Sequence Coverage (%) Percent of the residues in each protein sequence that have been identified.

total number of unique peptides Number of unique peptides obtained for each protein

Spectral counts Number of spectral counts adjusted for shared peptides

References

SETDB1
MCAF1
KAP1 Schultz et al, Genes and development, 2002 (PMID:)
Ivanov et al, Molecular Cell, 2007 (PMID:)

Supplementary Table 3. Differentially expressed genes in lymphoblastoid cells in WAGR patients with *C11orf46* haploinsufficiency

Cell line genotypes-->	Healthy (C11orf46 +/+, PAX6 +/+, BDNF +/+)	WAGR (C11orf46 +/+, PAX6 +/-, BDNF +/-)	WAGR (C11orf46 +/-, PAX6 +/-, BDNF +/-)	WAGR (C11orf46 +/-, PAX6 +/-, BDNF +/-)
	1	2	3	4
APBA1	0	0.037939914	0.013183187	0
SLC35F4	0.893425838	0.483859175	0.017697806	0.031326568
EFEMP1	0.354116473	0.626822534	0.018939601	0
B3GAT1	0.241510017	0.415841381	0.029555724	0.004650316
CACNA1C	0.144440766	0.155439845	0.033388941	0.01251554
CNTNAP2	0.067339067	0.148996333	0.033764714	0.003187537
FRMPD4	0.209618462	0.26745894	0.035403963	0
MAGI2	0.169096259	0.203768949	0.035699847	0.007582999
CSMD3	0.134159184	0.223125506	0.03830925	0.005166515
EGFR	0.511706458	0.280269334	0.03895468	0.00424326
ERBB4	0.255125296	0.456299248	0.040358886	0.006123303
TC2N	0.502134508	0.772895359	0.048829477	0.138291482
GABRG2	0.216343725	0.273311761	0.049121956	0
SHANK1	0.259576219	0.577913082	0.049582859	0
PLXNA4	0.285652224	0.412201452	0.050416913	0.009735498
COBL	0.202073517	0.252089297	0.057524963	0.003702687
RIMS1	0.255996931	0.287083033	0.061612945	0
NDRG1	0.49990157	0.527628602	0.064932194	0.035156681
SCN4B	0.364267519	0.61165938	0.066417684	0.009405179
CREG2	0.444776893	0.581414588	0.068216999	0.014861499
RBFOX1	0.4156812	0.624486455	0.068524321	0
MSX1	1.764971779	2.03730179	0.070791226	0.275673795
ADCY2	0.223995125	0.394031684	0.072736794	0
SLC6A17	0.549040429	1.105122765	0.073412334	0
LRP1B	0.293665909	0.46574584	0.074862552	0.024943596
CDR1	0.037914051	0.262611256	0.07604246	0
NAV3	0.300603594	0.524980857	0.077295735	0.008756466
SCN2A	0.230923693	0.366834694	0.079171449	0
DPP6	0.330752194	0.385802582	0.088449918	0.017613405
ATXN7L1	1.127594506	1.04136945	0.090462567	0.096075694
PLCB1	0.298135482	0.461996676	0.090501533	0.015256679
DCLK1	0.422936186	0.604671171	0.09135146	0.00739198
PSD2	0.632126282	0.72973595	0.091449778	0.011772625
CSRP3	0.461528515	0.567169253	0.092566641	0.078225419
P2RX7	2.184033245	1.878791923	0.094711665	0.335294817
PBX1	0.244300203	0.376031701	0.095347776	0.022503117
NUAK1	0.400402244	0.708753105	0.096368193	0.015162631
ASTN1	0.391376766	0.621973778	0.097865927	0.011548714
GRIN2B	0.405079061	0.696209252	0.098221367	0.001717135
ARPP21	0.426333963	0.449369182	0.104096491	0
SLC22A17	0.470074856	0.845542152	0.105243618	0.012419322
NEBL	0.260311311	0.486347238	0.107166738	0.007782314
RYR2	0.428813528	0.570953339	0.107638344	0.05080765
RGS4	0.754306164	1.04940421	0.10861681	0
NRXN3	0.590043676	0.455261871	0.108681734	0.00684002
CELF4	0.443899708	0.768666605	0.109134667	0.008133781
SGIP1	0.437450057	0.561682373	0.11014588	0
MYT1L	0.504100947	0.771794895	0.111861068	0
NFASC	0.373766488	0.497472874	0.114651767	0.008742161
SLC8A1	0.313600327	0.502401855	0.114670031	0
KCNQ3	0.373514566	0.520844274	0.115708891	0
DLGAP1	1.846573391	1.80169775	0.117770964	0.5178691
AGAP1	0.453885161	0.547259392	0.118680905	0.024827037
THRB	0.708834728	1.091052422	0.120627143	0.036603416
GLYATL2	4.172897211	4.02416983	0.122478835	0.404688804
LRP1	0.291746614	0.518148639	0.124230295	0.028044937
ADCYAP1R1	0.438098193	0.695402192	0.131800994	0
ANKS1B	0.511970039	0.605679334	0.132385292	0.057681924
ADD2	0.435453633	0.639017961	0.133225814	0.008384733
PCDH1	0.649651455	0.649361904	0.139831559	0.018000969
CADM2	0.46813796	0.5404254	0.142716245	0.005318304
SEZGL	0.49063137	0.641911076	0.146949474	0
RAPGEF4	0.924974679	1.188973783	0.147361732	0.022357915
SCN8A	0.482230683	0.66514118	0.148218388	0.042688872
CNTLN	1.576652598	2.322715544	0.149209272	0.261711614
FXYD6	0.427885568	0.78822996	0.153378692	0.010342585
TRIM9	0.517599914	0.712201531	0.155194627	0.071275383
CADM3	0.69293423	0.982374531	0.156046164	0
SHC3	0.763042714	1.174490426	0.158708096	0
FMN2	0.588749543	0.774368088	0.158734221	0.016447175
FAM13A	1.397878014	1.062202749	0.158992325	0.410082905
ERC2	0.506991109	0.898333753	0.160803969	0.006697322
PTPRD	0.464947158	0.822037131	0.161301279	0.014275824
LONRF2	0.627677145	0.929967658	0.161570443	0.041945629
LINGO1	0.849094535	1.321627844	0.168385494	0.086707236
SATB1	0.509208695	0.491207151	0.173480474	0.04358479
SRGAP3	0.58817067	0.499259514	0.17645435	0.082822386
DNM1	0.490456518	0.73654841	0.177585785	0.009861691
CHD5	0.477600121	0.698738895	0.182095934	0.005372079
PHYHIP1L	1.039774096	1.714758042	0.183334228	0.025961328
CAP2	1.028693586	1.395358471	0.185688285	0.043824464
ST8SIA3	0.651048475	0.952896085	0.18653969	0
WASF3	0.715728708	1.045883329	0.18897774	0.005146247
BSN	0.758071883	0.978281556	0.191932575	0.044206662
PCDH9	0.590934915	0.856655644	0.196423689	0.024037552
DIRAS2	0.958094385	1.244293155	0.200167252	0
MRAS	0.705362182	1.085707411	0.200417579	0
KIF5C	0.776489232	1.224481385	0.203577589	0.121077269
ANK3	0.608003633	1.072856453	0.206536593	0.030076636
NTM	0.860577015	1.272874292	0.210358631	0.00763799
CAMK2B	0.653442329	0.774194656	0.211532061	0.02604724
BACE2	0	0.044901547	0.218430563	0.29274171
UNC13A	0.564313782	0.844475067	0.224686846	0.028492952
HLF	0.658789661	0.899535704	0.227321113	0
GNAO1	0.76141031	1.087889705	0.227356795	0.019394706
SLC4A10	0.668984645	0.693627053	0.228594713	0
PSD3	1.039061327	1.263386911	0.231829282	0.073340369
SYN2	0.847615548	1.168499944	0.237673163	0.060767919
GABRA1	0.687848908	0.887482149	0.238046343	0

RPH3A	0.712622546	0.978863682	0.238815419	0.010247827
CTNND2	0.851795537	1.337322536	0.240543696	0.007741492
SLC6A1	0.829675254	1.299070697	0.244824468	0
PCLO	0.856702904	1.182539991	0.262453371	0.015098329
SPOCK1	0.901966869	1.336263035	0.265244877	0.18785871
NPTX1	1.158185743	1.610875651	0.268675039	0.063410245
ARNT2	0.942468572	1.31815347	0.27142276	0.010295154
KIF1A	1.154319783	1.730148497	0.273265475	0.058044274
KCTD19	0	0	0.274420274	0.726820497
CAV1	1.649790649	2.341000501	0.275742403	0.546657047
RAB6B	0.817740737	1.078870889	0.281160822	0.084052233
PLCB2	2.736027527	2.166885271	0.285861712	0.513227207
LRIG1	0.066505947	0.26871408	0.298788905	0.536436287
SLC17A7	1.135536237	1.661046403	0.299505868	0.008835832
LRP6	0.108581559	0.083565441	0.312147051	0.305816639
FBXL16	1.019986826	1.109816192	0.319793905	0.039957277
KIAA1217	1.164089775	1.084066248	0.329817546	0.253186613
ZNF532	1.616162968	1.323623943	0.335919205	0.295635144
CNTN1	0.998760964	1.484467495	0.3455466	0
TRIM2	1.166073295	1.46642497	0.350313291	0.18602497
ATRNLI	0.999701369	1.192539082	0.351361988	0.040561272
PEG3	1.335767436	2.275221222	0.351819726	0.005726434
RTN1	1.333186639	1.912944022	0.362564178	0.008556911
APLP1	1.215225193	1.860653905	0.36944655	0.108991778
PLP1	1.315754187	2.01635224	0.370378575	0.013112009
TSPAN7	1.323310106	2.37827143	0.386051186	0.034167112
OLFM1	1.252618826	1.939812091	0.392166973	0.069416768
ZNRF1	1.505192989	1.040122911	0.39684822	0.267937298
NLRP7	0	0	0.421781141	0.271486248
GPRC5B	1.592336126	2.056858909	0.42207158	0.00796908
SLC8A3	2.453549632	2.365673146	0.43100153	0.446733772
FAIM2	1.544229228	2.789895938	0.433606485	0
DNAJC6	0.98860316	1.350876985	0.437024349	0.053481307
PLEKH81	1.175573847	1.729207905	0.456347249	0.053851468
GAP43	1.747879544	3.673390817	0.467418827	0.152745162
NMNAT2	1.736220133	2.622190803	0.481755781	0.059321545
SYN1	1.370461016	2.472000798	0.530100702	0.013901062
NDRG4	1.231347929	1.49983594	0.579494465	0.154207116
ATP1A3	1.781095474	2.707567933	0.580050278	0.110186359
STMN2	2.395768349	2.514282268	0.603613585	0
DHRS9	2.04527602	1.497280995	0.630325074	0.056671849
BCAN	1.65974891	1.35765031	0.646754152	0.285528545
CST3	4.505831028	3.448250445	0.649861537	1.380369807
MEG3	2.061199353	3.522998532	0.65668974	0.020215559
ZNF385A	2.75099895	1.613371266	0.660925946	0.409462579
SYT1	2.066849997	2.943013257	0.664417187	0
GTSF1	26.9225139	41.58226585	0.713521705	0.631495944
S100B	2.48691825	2.38623193	0.725512286	0
AQP4	2.020458445	3.368089748	0.725979076	0
LGSN	0	0.03708638	0.73453647	0.428834511
STXBP1	2.518994103	3.637851543	0.801110578	0.068407543
FMNL2	2.948493583	2.509359521	0.840286095	0.48492508
SEMA6A	2.5184848	2.562433248	0.859561589	0.458266854
CHN1	2.66245342	4.06189862	0.860431676	0.080159714
PTN	2.73012155	4.56995454	0.876108574	0
CPE	2.561274885	3.814603097	0.91324989	0.089807063
MT3	2.138501089	3.379791619	0.939515561	0
NID1	13.82911785	9.703935247	0.940543042	3.316085998
CAMK2N1	3.07606919	5.450463985	1.047385287	0.040634691
CLIP3	3.087215948	4.007629714	1.104095391	0.366218538
KLHL3	3.661191112	2.823761465	1.259718337	1.142914963
TMEM173	3.194731508	3.800229299	1.266887132	0.607198385
DMD	2.411306589	2.481015561	1.291649743	0.619520563
MAP1A	3.977547452	6.008880653	1.362542946	0.079977208
DPYD	4.311592022	3.360140846	1.368469218	0.383445356
ENG	2.923679189	3.882781391	1.382542745	0.364550492
ATP1B2	4.482549572	5.372481734	1.431599117	0.186505914
GAS7	8.015212486	6.815379626	1.519347922	3.33245203
NRGN	7.431269892	8.290059574	1.547780659	1.217643821
MAP2	5.336590489	8.178376935	1.577507045	0
TMOD2	4.493424377	3.354562018	1.657351816	1.287609158
GPM6B	3.304592043	4.851829725	1.732170857	0.875355382
KIF5A	6.162395828	10.29584187	1.761809424	0.101830108
ENC1	5.316969975	5.70482757	1.863798353	1.315095513
TUBB2A	7.446971681	6.940038465	2.585293926	1.507448221
SNAP25	10.49018098	15.1495873	2.626466241	0.031653178
MYADM	19.80120387	11.17965892	2.797361036	0.643341146
SLC1A2	8.954411229	14.99558865	3.371295064	0
CD38	30.33884313	22.87915172	3.497427343	10.41283227
SPARCL1	14.95682604	24.23814912	5.600386102	0.091682241
TUBB2B	22.36033012	23.18011147	5.848503913	1.380310824
EPB41L2	20.82308944	15.42229558	7.954683825	5.153390367
ALOX5AP	24.40609273	29.78024406	9.75721863	5.669250231
CALCRL	0.137012643	0.351487613	0.977066398	1.214965031
TBC1D30	0.529968114	0.206015312	1.11499455	0.847816895
NTSE	0.381729173	0.369213197	1.158771002	1.763962881
TESC	0.534202288	0.224251287	1.499994769	2.662010056
PTPRJ	0.792413523	0.190811737	1.630258645	2.534990141
TSPAN12	0.347142088	0.689283073	1.648712515	2.358347351
PHACTR2	0.354169056	0.452148856	1.86861337	2.082781347
HENMT1	0.674709141	0.111270605	2.22703477	1.828665789
ANKRD36BP2	0.023261369	0.624338505	2.27672751	3.7326996
KLHL6	0.221728533	1.31054953	2.348072329	3.078166478
UST	0.297226054	0.899216701	2.540758064	3.004055128
CMTM3	0.266141536	0.290168971	2.633353028	3.653412669
FAM129C	0.635037476	0.358402819	2.694509723	4.484936022
POMC	0.243261286	0	2.781018116	3.229936145
GIMAP8	1.67663655	0.825827877	3.237209663	3.904739856
CYBSR2	0.505971305	0.389400517	3.247370423	2.385775415
HMX3	0.0797391	0	3.454466977	2.060876873
TP53INP1	1.244153331	1.13189415	3.496782236	2.377551818
SETBP1	1.123984505	1.108722618	3.509342813	2.62290263
AMPD3	1.487070241	1.669009931	3.562487934	2.784370632
LBH	2.186240401	0.761910438	3.574059329	3.555658682

PIGR	0.096184378	1.073354496	4.038302946	6.805138441
GPR55	1.78914847	0.549035567	4.16074144	3.923633635
FYN	1.937317976	0.998033214	4.348822205	3.05043245
ALDH5A1	1.362802557	2.257256634	4.617766113	5.409148513
PLAGL1	1.249765666	1.938112134	4.625909037	4.14972288
LIPH	1.350138495	0.864444646	4.842380889	3.248113634
BLK	1.791614557	1.573680958	5.077571785	3.053058715
IGF2BP3	1.357237057	3.888491238	5.752878782	6.155098191
ZBTB32	2.633808381	3.761653431	5.824303378	7.969478809
PLA2G16	0.690398324	1.836579181	6.140843495	5.831325958
TP63	1.305008356	0.333172911	6.306915097	5.716413563
SMARCB1	5.014114169	4.156309153	6.956429201	9.293977705
PTPN7	4.497738887	6.261788137	8.042583251	10.79059694
CDK5R1	2.270766764	3.707418205	8.2932944	7.511886384
ZNF589	5.082446892	4.635129103	8.453916136	9.719463379
IL17RB	3.479044755	2.683430912	8.546211313	10.06459305
F8A1	3.767567739	1.76494796	9.680999739	5.815439878
EMIL4	4.448935122	8.236847459	10.80639879	13.50021
WFDCC2	0.541441183	2.031405113	11.3481101	15.7236702
GRN	12.56862645	9.829427521	17.93384132	20.8332571
MPEG1	11.5917261	6.854910524	22.39166951	32.60513167
IFNGR1	10.25926796	6.845682676	36.06002062	22.34925796
CTSC	13.7708923	12.33306977	48.21569872	31.70532809
CCR7	3.337834851	24.60480565	48.78413049	39.69910496

Lymphocyte Sample Information:

NIH ID	Manuscript ID	Diagnosis	Age (years)	Sex	Race/Ethnicity	Chr	Cytoband	Start (Hg18, March 2006, Build 36)	Stop (Hg18, March 2006, Build 36)	SizeMb	BDNF	C11orf46	PAX6	
H23.3	1	Healthy	29	M	White/Non-Hispanic	no deletion	N/A	N/A	N/A	N/A	+/+	+/+	+/+	
W42.3	2	WAGR	13	M	White/Non-Hispanic	chr11	p14.1 - p13	30,406,179	35,176,519	4.77	+/+	+/+	+/-	
W39.3	3	WAGR	12	M	White/Non-Hispanic	chr11	p14.1 - p12	28,901,513	39,755,713	10.85	+/+	+/-	+/-	
W15.3	4	WAGR	17	M	White/Non-Hispanic	chr11	p14.2 - p12	26,005,134	40,174,102	14.17	+/-	+/-	+/-	
824.3	A	Healthy	8	M	Asian	no deletion	N/A	N/A	N/A	N/A	+/+	+/+	+/+	
A4.3	B	Aniridia	8	M	White/Non-Hispanic									heterozygous W266X (premature stop-codon in exon 10)
W45.3	C	WAGR	7	M	White/Hispanic	chr11	p15.1 - p13	19,309,352	32,405,969	13.10	+/-	+/-	+/-	
H24.3	D	Healthy	24	F	Asian	no deletion	N/A	N/A	N/A	N/A	+/+	+/+	+/+	
A5.3	E	Aniridia	28	F	White/Non-Hispanic									heterozygous deletion of exons 1-4
W8.3	F	WAGR	25	F	White/Non-Hispanic	chr11	p14.1 - p12	30232199	37070116	6.837917	+/+	+/-	+/-	

Supplementary Table 4. Genes with KAP1 binding sites

#	GENE	KAP1 Binding SITES					
		Chr	Start	End	Strand	Annotation	Distance to TSS
1	DCLK1	chr13	36429427	36429776	+	promoter-TSS (NM_001195415)	-203
		chr13	36430027	36430376	+	intron (NM_004734, intron 5 of 17)	397
		chr13	36428827	36429176	+	intron (NM_004734, intron 5 of 17)	997
2	SEMA6A	chr5	115883857	115884206	+	promoter-TSS (NM_020796)	-652
		chr5	115882030	115882775	+	intron (NM_020796, intron 1 of 18)	26520
		chr5	115880296	115881879	+	intron (NM_020796, intron 1 of 18)	28149
		chr5	115910979	115911428	+	intron (NM_020796, intron 1 of 18)	29464
3	GAP43	chr3	115342328	115342777	+	exon (NM_002045, exon 1 of 3)	401
		chr3	115580855	115581204	+	Intergenic	161810
		chr3	115503737	115504186	+	Intergenic	167517
		chr3	115509294	115510043	+	intron (NM_002338, intron 3 of 6)	238878
4	PLXNA4	chr7	132330825	132331512	+	intron (NM_181775, intron 1 of 4)	2279
		chr7	132249535	132250369	+	intron (NM_181775, intron 2 of 4)	11371
		chr7	132321034	132321383	+	intron (NM_181775, intron 2 of 4)	12239
		chr7	132172893	132173342	+	intron (NM_181775, intron 4 of 4)	88206
		chr7	132159928	132160277	+	intron (NM_001105543, intron 3 of 3)	101221
		chr7	132088492	132089041	+	intron (NM_001105543, intron 3 of 3)	172557
		chr7	132086292	132086941	+	intron (NM_001105543, intron 3 of 3)	174707
		chr7	132064009	132065211	+	intron (NM_020911, intron 3 of 31)	196713
		chr7	131908018	131908567	+	exon (NM_020911, exon 9 of 32)	353031
		chr7	131871293	131872898	+	intron (NM_020911, intron 15 of 31)	389228
		chr7	131831114	131831463	+	exon (NM_020911, exon 28 of 32)	430035
		chr7	131760741	131761090	+	Intergenic	500408
5	NUAK1	chr12	106413007	106413716	+	intron (NM_014840, intron 1 of 6)	7159
		chr12	106409791	106410440	+	intron (NM_014840, intron 1 of 6)	32756
		chr12	106386100	106386549	+	Intergenic	120450
		chr12	106500881	106501230	+	Intergenic	123696
		chr12	106526389	106526915	+	Intergenic	147487
6	ATXN7L1	chr7	105305401	105306250	+	intron (NM_020725, intron 3 of 11)	13784
		chr7	105353769	105354703	+	intron (NM_020725, intron 3 of 11)	-34627
		chr7	105278867	105279216	+	exon (NM_138495, exon 5 of 10)	40568
		chr7	105331052	105331901	+	intron (NM_020725, intron 3 of 11)	-11867
7	CAP2	chr6	17394551	17394900	+	intron (NM_006366, intron 1 of 12)	989
8	CD38	chr4	15742959	15743628	+	Intergenic	-36638
9	CTNND2	chr5	11589741	11590090	+	promoter-TSS (NM_001288716)	-886
10	CTSC	chr11	88034855	88035255	+	intron (NM_001814, intron 4 of 6)	35886
11	DPP6	chr7	153126424	153126873	+	Intergenic	-457771
12	ENC1	chr5	73839508	73840057	+	Intergenic	97467
13	EPB41L2	chr6	131375467	131376410	+	intron (NM_001431, intron 1 of 19)	8524
14	ERC2	chr3	56317713	56318062	+	intron (NM_015576, intron 3 of 16)	184504
		chr3	56322578	56322927	+	intron (NM_015576, intron 3 of 16)	179639
15	FMNL2	chr2	153193442	153193891	+	intron (NM_052905, intron 1 of 25)	1915
		chr2	153311507	153311956	+	intron (NM_052905, intron 1 of 25)	119980
		chr2	153290131	153290480	+	intron (NM_052905, intron 1 of 25)	98554
		chr2	153308234	153308583	+	intron (NM_052905, intron 1 of 25)	116657
16	GPR55	chr2	231801432	231802499	+	Intergenic	-12024
17	KIAA1217	chr10	24849930	24850661	+	Intergenic	94861
		chr10	24848655	24849779	+	Intergenic	93783
		chr10	23982588	23983337	+	promoter-TSS (NM_001098500)	-713
		chr10	24495830	24496179	+	intron (NM_001098500, intron 2 of 18)	-1716
		chr10	24160260	24160609	+	intron (NM_001098500, intron 1 of 18)	176759
18	MEG3	chr14	101299332	101300245	+	intron (NR_033360, intron 4 of 6)	7319
19	MSX1	chr4	4727235	4727993	+	Intergenic	-133778
		chr4	4858104	4858453	+	Intergenic	-3114

20	NDRG1	chr8	134415298	134415847	+	Intergenic	-106025
21	NID1	chr1	236139620	236140869	+	3' UTR (NM_002508, exon 20 of 20)	88237
22	NMNAT2	chr1	183395942	183397220	+	Intergenic	-8947
		chr1	183398905	183399377	+	Intergenic	-11507
23	NRXN3	chr14	79747740	79748289	+	intron (NM_001272020, intron 1 of 5)	2332
		chr14	79115279	79115628	+	intron (NR_073547, intron 5 of 20)	245379
		chr14	78459136	78461053	+	Intergenic	-176622
24	PSD3	chr8	18870380	18870929	+	intron (NM_015310, intron 1 of 15)	542
		chr8	18473281	18473630	+	intron (NM_206909, intron 8 of 12)	192950
25	RAPGEF4	chr2	173865496	173866245	+	intron (NM_001282901, intron 10 of 24)	72937
		chr2	173538960	173539409	+	Intergenic	-61341
26	SLC8A3	chr14	70656506	70657019	+	promoter-TSS (NM_058240)	-975
27	SPOCK1	chr5	136368969	136369429	+	intron (NM_004598, intron 6 of 10)	465819
28	SRGAP3	chr3	9289652	9290101	+	intron (NM_001033117, intron 1 of 21)	1493
		chr3	9290556	9290905	+	5' UTR (NM_014850, exon 1 of 22)	639
29	TC2N	chr14	92363123	92363616	+	intron (NM_006329, intron 4 of 10)	-29489
30	TRIM9	chr14	51615755	51616104	+	Intergenic	-53507
31	PTN	chr7	137027601	137028150	+	intron (NM_002825, intron 1 of 4)	671
		chr7	137028301	137028685	+	promoter-TSS (NM_002825)	53
32	MAP2	chr2	210479508	210481177	+	intron (NM_002374, intron 2 of 14)	35939
		chr2	210361422	210365296	+	intron (NM_001039538, intron 1 of 14)	74588
33	PLEKHB1	chr11	73344057	73344406	+	Intergenic	-12992
34	SLC6A1	chr3	10948383	10949867	+	intron (NM_014229, intron 6 of 13)	-85295
35	COBL	chr7	51215907	51216456	+	intron (NM_001287436, intron 5 of 13)	168334
		chr7	51459755	51460104	+	Intergenic	-75414
		chr7	51147851	51148200	+	intron (NM_001287438, intron 7 of 7)	236490
		chr7	51213617	51214566	+	intron (NM_001287436, intron 5 of 13)	170424
36	DNAJC6	chr1	65730594	65730943	+	intron (NM_014787, intron 1 of 18)	391
37	DPP6	chr7	153126424	153126873	+	Intergenic	-457771
38	EGFR	chr7	55134099	55134548	+	intron (NM_201282, intron 1 of 15)	47598
39	ERBB4	chr2	213586438	213587195	+	Intergenic	-183464
		chr2	213401560	213402130	+	intron (NM_001042599, intron 1 of 26)	1507
40	SHC3	chr9	91725340	91726189	+	intron (NM_016848, intron 2 of 11)	67918
41	SYN1	chrX	47467934	47468372	+	intron (NM_006950, intron 1 of 12)	11103

Supplementary Table 5. sgRNA sequences

HUMAN sgRNAs		sgRNAs score	sgRNA Sequence (5' to 3')	Total no. of offtarget sites (hg19)	off-target sites in exons (mm9)	score	mismatches	UCSC gene	locus
Gene	Promoter location								
DCLK1	GRCh38: 13:35788052:36131906:-1 chr13:-36705474	73	TTGGCAGGGCGCACCCACCA C GG	125 (17 are in genes)	TTGGTGGGGGGGCCACCCACGAG TTGGGTAGAGCCACCCACCGAGG TGCTCGGGGGCGCACCCGCGCAGG TTGGCCGTGTGGCACCACCGAGG CTGCCAGGGCGGCCCCACGAGG TTGGCAGTGAAGACCCACGAGAG CAGGCAGGCTGGACCGACCGAGAG TTGGCACTGAGCACCCACGAAAG CAGGCCAGGGCCCCACCGACATGG GTGGCAGGGTGCACTACCCCGGG TTGGCAGGGCCACGACGACCGAGG GTGGCAGGCCACGACGACCGAGG GTGGCAGGCCACCGACGACCGAGG TTGGCGAGGACCGACCTCCAGAG CTGGCGGGGGCGCACTCACCAAG TTGGCGCGGGCGGCCACCCAGG TTGGCAGGCGCACGCCCTCCAGAG	1.4 0.8 0.4 0.3 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1	3MMs [5:6:10] 4MMs [2:5:8:11] 4MMs [2:4:6:17] 4MMs [6:7:9:10] 4MMs [1:4:12:13] 4MMs [8:10:12:19] 4MMs [1:2:10:14] 4MMs [7:8:10:18] 4MMs [1:2:11:18] 4MMs [1:10:15:20] 4MMs [2:9:11:15] 4MMs [1:8:11:14] 4MMs [6:9:11:17] 4MMs [1:6:15:20] 4MMs [1:6:11:13] 4MMs [6:12:13:20] 4MMs [9:11:13:17]	NM_001869027 NR_048548 NM_139057 NM_00252617 NM_016621 NM_00189320 NM_133476 NM_015299 NM_013433 NM_00171611 NR_027033 NR_024369 NM_004260 NM_00146657 NM_012188 NR_046363	chr17:-37816592 chr1:-44476336 chr15:-100881552 chr9:-138418498 chr11:-45951948 chr15:-26961770 chr12:-6797421 chr14:-24901106 chr19:-12822337 chr10:-88428532 chr22:-46508498 chr9:-34568012 chr8:-14574111 chr1:-21995727 chr5:-169532831 chr11:-113857828
	chr13:-36705605	66	TCTCCAGAGGAGGGCGGG C GG	300 (64 are in genes)	TCTCGAGGGGAGGGCGGGCGTGG TCTCAGGGGAGGGCGGGCGGGAG ACGCCCTGGGAGGGCGGGCGGAG GCACCAAGCGGTGGCGGGCGCGG GCCCCGGAGCAGGGCGGGCGGAG TCTTGAGTGGCGGGCGGGCGGAG CCTCCAGAGGAGGGCGGGCGGAG CCTGCAGCGGAGTGTGGGGCGGG CCTCCAGAGGACCGGGCGGGGG TCTATAAAGGGCGGGCGGGCGAG GCCCCACAGGAAGCGGGCGGTGG GCACCGGAGGTGGGGCGGGCGGG CATCTGAGGAGGGCGGGCGGAG TCTTCAGGGAGGGCGGGCGGGG TCTTCAAGGGAGGGCGGACGGGG TCTCCAGGGCAGGGCGGGCGGGG TCTGCTGAGAAAGCGGGCGGAG TGTCAGAGCTGTGGGGCGGGAG TCTCCAGAAATGGCGGGGTGGAG TCTCCGGCTGGGGCGGGCGGGG TGTTCAGAGGAGCGGGCGCTGG CCTCCAGGGGATGGGGCGCCGAG TCTCGCTGGAGGGGGCGGGGGG TCAGCAGAGGAGGGCGGGCGGG TCTCCGGGAAAGGGCGGTGGAG TCTCTAGAGTAGGGGGCGGCTAG TCACCAAGCAGAGGGCAGCGGAGG TCTATAGGAGGAGAGGGCGGAGG TCTCAAGAGCTGGGGCGGTGGTG GTTCAGAGGAGGAGGAGCGGGG CCTCCAAAGAGGGCAGCAGAGG TCTCTCGCGAGGTGGGGCGGTGG TCATCAGAGGAGGGCGAAGGCGAG GCTCCCAAGGAGGCGACGGGGGG TCTCCCCAGAGCGGGCGGTGGG TCTCCCAAGAGGGCGGGCGGGG GCTCCAGAGAAAGCGGGTGGAG CTTCCAGAGGAGGGCTGCTGGAG CCTCCAGAGGGCGGGCGGGGAG TCTCCCCAGGGCGGTGGCGGAG TCTCCAGGTGAGCGGGGGCGGAG TCTCCAGAGGAGGGCGGGCGGG TCTCAGAGGGGTGGGGCGGGG TGCGCCGAGGAGCGGGTGGCGG TCTGCAGGGAGGGGAAGCGGAGG TCTCCAGCTGGCGCGGGCGGAG TCTCCCAAGTGGGGCGGGGCGG TCTCCAGAAATGGCGGTCCAG TCTCCCGAGGGGGAGCGCTGG TCTCGACAGGAGGCGACGAGTGG TCTCAGGAGGGAGGGTGGGAG TCTCCGAGGTGGGGCGGGACAG GCTCCAGAGGAGGGGAGGAGG CCTCCAGAGGAGGGCGGGTGG TCCCCAGAGGATGACGGCCGAG TCTCCGGGGAGGAGGGCGGGCG TGTCAGAGGAGCGCGCCGAGG TCTACTGAGGAGGGCTGTGGCAG TCTCCAGAGGAGGGCGGGTGGAG TCTCCAGAGGAGCGCTGTGGGG TCTCCAGAGGAGCGCTGTGGGG TCTCCAGAGGAGCGAGCTGGAGG TCTCTGAGGATGGCAGAGGTGG TCTTCCAGAGGAGGACTGCAGAA TCTCCAGAGGAATGCAGGGGAGG TCTCCAGAGCAGGGCGGGGCGG	1 0.8 0.8 0.8 0.8 0.8 0.8 0.6 0.6 0.5 0.5 0.5 0.4 0.4 0.3 0			

SEMA6A	chr3:115342101	86	GGGGGCGACTGTCTAGAATGGGG	78 (5 are in genes)	GGGGGTGTCTGGCTAGCATGGGG GCGGGTGACTGCTAGAGAGGGGG GGGGGCGCTGCTGCTGCTGGGG GGGGGCGCTGCTCAGAGTGCAAG	0.2 0.2 0.1 0	4MMs [8:8-12:17] 4MMs [2:6-12:19] 4MMs [8:12-17:18] 4MMs [8:14-16:18]	NM_025029 NM_001040107 NM_00146028 NM_023058	chr2:-130940041 chr12:-111099240 chr19:-14168122 chr20:-3677444
	chr3:115342020	77	ATCATATCTCTGGATTGACTGG	161 (12 are in genes)	TATTGCACTGGAAAAGTAGTGG TACTTCAGTGGCAAGTCGGGG CAAAGCAATGAAAAGTCTGTGG CGAGGCAAGAGGAGTGGGAG AGCTGCAGTGGAAAAGTTGGAG CAATGCAGCGGAGGAGCGGCGAG AAATGAAGGGGAAAAGTCAGAA CAATCTCTGTGAAAAGTCAATGG CAATGCAGTGATAAAGTCTGTGG CAAAGCAGTGGAGAGCTGGGGG CAAAGGAGTGGAAAATTTGGTAG CAATGCATGGAAAATCTGGCTGG	0.7 0.6 0.5 0.3 0.3 0.2 0.2 0.1 0.1 0 0 0	3MMs [1:3-18] 4MMs [1:3-5:13] 4MMs [4:8-10:19] 4MMs [2:4-9:13] 4MMs [1:2-3:18] 3MMs [9:13-17] 4MMs [1:6-9:19] 4MMs [5:7-19:20] 4MMs [11:12-19:20] 4MMs [4:13-17:18] 4MMs [4:6-16:18] 4MMs [8:16-18:20]	NM_014831 NR_024453 NM_022340 NM_031419 NM_015180 NM_0014699 NM_018723 NM_00110421 NM_006379 NM_212481 NM_005657 NM_00113498	chr3:-36876240 chr16:-433349 chr3:-15126381 chr3:-101568667 chr14:-64490031 chr12:-114404285 chr16:-7102016 chr12:-109879952 chr7:-80374531 chr2:-497215507 chr15:-43712987 chr14:-447309640
	chr3:115341781	64	TGCATAGTTAATAATTGTGGAGG	245 (16 are in genes)	TGAGTGGGTAATAATTGTGGTG TTTAAAGTTAATAATTGTGTAG TTTATAGTCAAAAATTGTGGTAG TTTCATTGTAATAATTGTGAAAG TTTCATTTTATATAGTGTGGGG TGCAAAAGTTTATAATTCTGTGAG TGCCCAAGTAATAATTGGGGTAG TGTAAGTAAATTAATGTGGAAG TCCTTAGTTAATACTGTAGTGG TGCATAATTTCATCATTTTGGCAG TGCCATAGTAAAAGTCTGGGAG TGCATATTATAAAGTATAGGGG TGCATAATTAAAAATTGAAGTAG TGCAAAAGTTAATACCTTTGGAGG TGCAGAGTTAATAACGTCGAGG TGCATAGTTAATAAGTATTGG	0.8 0.7 0.4 0.3 0.3 0.2 0.2 0.2 0.1 0.1 0.1 0 0 0 0 0	4MMs [3:4-6:8] 4MMs [2:3-5:20] 4MMs [2:3-9:12] 4MMs [2:6-9:20] 4MMs [2:7-10:15] 4MMs [5:10-17:20] 4MMs [4:5-9:18] 4MMs [3:5-9:16] 4MMs [2:4-15:19] 4MMs [7:10-13:17] 3MMs [12:16-17] 4MMs [7:15-17:19] 4MMs [7:12-18:19] 4MMs [5:14-15:17] 4MMs [5:15-16:19] 4MMs [11:16-19:20]	NM_033112 NM_002156 NM_182536 NM_0020919 NM_0020919 NM_153348 NM_0030132 NM_138571 NM_007007 NM_207410 NM_000216 NM_032663 NM_031935 NM_053276 NR_027906 NM_032581	chr6:-42994990 chr2:-198351291 chr2:-69177259 chrX:-30748573 chr14:-7541940 chr12:-11736009 chr7:-107850023 chr6:-12630301 chr12:-69665698 chr6:-55216353 chrX:-8498795 chr12:-108059553 chr1:-185970652 chr2:-37028384 chr6:-168226140 chr7:-22983282
	chr3:115341818	54	AGATATGACTTATATTGTATAGG	396 (22 are in genes)	TGATAAGCACTATATTGTAATAG TGATTGAGTTAAATGTTATTGG AGAAATGAAGTATATTATATAAG ATAGATGATTATATTGTTTCAG AGAAATGCCTTCTATTTTATAGG TGATTTGAATATAATGTATAGG GGAGTACCTATGATGTGTAG AGGTATGAGTTATATTATAGAG ATATATGATATATATAGTATAGG AGATATTCCTTACATTGTGTGGG AGTTCTGACCTATTTGTATTAG ATATAAGACTTATAATTATATAAG AAATATTACTTATAATGTTTCAG AAATATTACTTATAATGTTTCAG AAATATTACTTATAATGTTTCAG AGACAACACTTATTTGTATAAG AGATAAGAGTTAAATTTTATAGG AGATATTTCTTATATAGTATGG AGATTTTCACTTATCTTCTATAG AGATATTACTTAATTTGTACAAAG AGATATGGCTTATATTACTTAAG AGATATTACTTATGATGAATTAG	0.4 0.4 0.3 0.3 0.3 0.2 0.2 0.3 0.2 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0	4MMs [1:6-10:20] 4MMs [1:5-9:13] 4MMs [4:9-10:17] 4MMs [2:4-9:19] 4MMs [4:8-12:17] 4MMs [1:5-9:15] 4MMs [1:4-13:19] 4MMs [3:9-17:20] 4MMs [2:9-10:16] 4MMs [7:8-13:19] 4MMs [3:5-11:14] 4MMs [2:6-15:17] 4MMs [2:7-15:19] 4MMs [2:7-15:19] 4MMs [2:7-15:19] 4MMs [4:6-7:14] 4MMs [8:9-13:17] 4MMs [7:8-16:20] 4MMs [5:7-14:17] 4MMs [7:11-14:20] 4MMs [8-17-18:19] 4MMs [7:14-16:18]	NM_018442 NR_033698 NR_015342 NM_006581 NM_015879 NM_032172 NM_000496 NM_0000049 NM_00277196 NM_0120200 NM_014612 NM_016224 NR_015424 NM_00160315 NM_025190 NM_00303748 NM_024677 NM_006212 NM_0014618 NM_198681 NM_003183 NM_00007965	chr1:-167973083 chr8:-42940214 chr9:-79400364 chr6:-96562066 chr18:-55031576 chr7:-46190255 chr5:-32230405 chr16:-46836257 chr8:-133858979 chr15:-31294361 chr9:-96289551 chr6:-158364190 chr2:-89104853 chr2:-97915841 chr2:-98123539 chr12:-40115790 chr4:-40763400 chr1:-207250341 chr22:-28692421 chrX:-106064190 chr2:-9663338 chr3:-100432614
	chr5:115910803	94	GGCGGAGAACTACGCGGTGTGG	44 (8 are in genes)	CACGGAAAATCTACGCGGTGGAG GGCAGATGAACACTCGGGGCGAG GGGGAGAGACCCAGCGGGGCGAG GGCCGACAAAACGACGGCGCGGG GGCGGAGCAGCTCCGGGTTGGG GGGAGGAGAACTCCGAGGAGCAG GGCGGAGAAACAGGTGGTGGAG GGCGGAGAAACTGCGGCCAGCAG	0.9 0.3 0.2 0.2 0.1 0 0 0	4MMs [1:2-7:10] 4MMs [4:7-8:19] 4MMs [3:10-12:19] 4MMs [4:7-12:19] 4MMs [8:10-13:18] 4MMs [3:13-16:19] 3MMs [12:14-16] 4MMs [13:17-18:19]	NM_199141 NM_002886 NR_026961 NM_177457 NM_00142376 NM_015284 NM_021819 NM_006469	chr19:-11022919 chr3:-152880965 chr21:-45230559 chr8:-143859255 chr17:-42989115 chr1:-43905617 chr15:-75115068 chr1:-185288312
	chr5:115910724	92	TGGCCCCACCGCGCTAGCGGG	71 (11 are in genes)	TGGCCCGCGCGCGCGGAGGTGG TGGCCCGCGCGCGGCTCGGGGG TGGCCCGCGCGCGCTAGGGGG GGGCCCGCACCGCGGCCAGCGGG TGGCCACACTGGGCGCAAGTTGG TGGCCCGCTGGGCGCTAAGAG TCTGCCACCGCGCGCGGAGG TGGCTCCACGCGCCCTCGGCGG TGGCCCGCCCGCTGCTAGGAGG TGGCCCGACAGGCGACTGGGGG TGGGCCCGCGCGCCACGCGGGG	0.7 0.5 0.4 0.3 0.2 0.1 0.1 0.1 0.1 0 0 0	3MMs [6:8-17] 3MMs [8:10-18] 3MMs [8:11-15] 4MMs [1:10-11:17] 4MMs [6:10-12:17] 4MMs [8:9-12:19] 4MMs [2:3-17:18] 4MMs [5:10-13:18] 4MMs [7:8-13:14] 4MMs [10:12-15:18] 4MMs [4:15-17:18]	NM_00303720 NM_00102692 NM_002013 NM_198478 NR_036573 NR_037652 NM_002209 NM_018847 NM_004996 NM_139317 NM_017723	chr9:-112403040 chr5:-16179488 chr14:-45603712 chr19:-45655730 chr7:-148991673 chr15:-80216144 chr16:-30485560 chr8:-21335193 chr16:-16177129 chr20:-61869450 chr9:-140175318
	chr5:115910905	94	CGTAGAGCGTCCATCGCTCTGG	22 (6 are in genes)	CTTGACGCGTGCATCGCTCAAG CGGAGCGCGCGCTCGCTCCAG CGTGAACGTGCAGCGCTTCCAG CGTAAAGCCTCCATCCCTTTTGG TGTAAGCGGCCATGCCTTCCAG CGGAGAGCGCTTCCCTGCCGG	0.8 0.3 0.1 0.1 0.1 0	4MMs [2:4-5:11] 4MMs [3:10-11:13] 4MMs [4:7-11:14] 4MMs [5:9-16:20] 4MMs [1:10-15:16] 4MMs [3:13-16:19]	NM_001012 NM_00007196 NM_174873 NM_052847 NM_014339 NM_0025234	chr1:-45244239 chr15:-88799681 chr12:-133197056 chr19:-25147141 chr22:-17585552 chr9:-130533686
	chr5:115911046	80	AATAAAATAGACGTAGTGACGG	236 (10 are in genes)	CTTAAAAATACAGCTAGTGTAA AAGAAAATAGAAAGTAGTGAGG AATTAATAAGACTTACTGCTGG AATCAAACTAGACTTAGTTCAGG AAAAAAATATACTTAGTGGAAG AACTAAAAATAGACTGGAGCAAG AATAAACACAGAGTGGTCTCGG AATAAAGATAGACTTAGTATGAG AATAAAAAATCACTAAGGACAAG AATAAAAAATAGACAACTACCAG	0.4 0.3 0.2 0.1 0.1 0.1 0 0 0 0 0	4MMs [1:2-11:20] 4MMs [3:8-13:20] 3MMs [4:14-17] 4MMs [4:8-14:19] 4MMs [3:11-14:20] 4MMs [3:4-16:18] 4MMs [7:9-13:16] 4MMs [14:19-20] 4MMs [11:14-17:18] 4MMs [14:15-17:19]	NM_00197223 NM_002845 NM_005212 NR_046535 NM_015978 NM_0019638 NR_036636 NR_002174 NM_016218 NM_00000313	chr5:-58271761 chr18:-8069698 chr4:-71113557 chr13:-94806346 chr1:-75010140 chr1:-157483718 chr12:-112337879 chr6:-25081265 chr5:-74895501 chr17:-10617170

MOUSE sgRNAs

Gene	Promoter location chromosome:GRCm38:3:55241764:55539668:1	sgRNAs score	sgRNA Sequence (5' to 3')	Total no. of offtarget sites (mm9)	off-target sites in exons (mm9)	score	mismatches	UCSC gene	locus
Dcl1		91	GGCAAGTCTCTCTAGCGACTGGG	53 (7 are in genes)	AGCAAGTCTCTCTGGGACTTAG GTGAAGTCTCTCTAGCGACTCAG GGCAAGTATGTCAGGGACTGAG GGCATGTCTCTTTAGGAAGTGGG CGCAAGTCTCTCTGGGACTGGG GGCAAGTCTTTTAGGCACTTGG GGCAAGTCTCTCAATGGGCTTAG GTTGAAAGTGACCTCAATACCAG TAGGAAGGCTACTTCAATACCAG GAGGAAGGAGACCTGAAGACAAG	0.5 0.1 0 0 0 0 0 1.1 0.5 0.1	3MMs [1:8-14] 4MMs [2:3-13:14] 4MMs [8:9-13:16] 4MMs [5:12-16:17] 4MMs [1:8-14:15] 4MMs [9:12-16:17] 4MMs [13:15-16:18] 3MMs [2:7-9] 4MMs [1:3-10:13] 4MMs [3:9-15:18]	NM_012275 NM_004656 NM_139072 NM_181719 NM_017671 NM_178822 NR_047467 NM_001818 NM_032358 NM_014663	chr2:-113816645 chr3:-52414991 chr2:-230271921 chr1:-20072874 chr20:-6090993 chr3:-151161162 chr10:-92806676 chr10:-5258816 chr12:-539790 chr1:-44133666
		91	GATGAAGGGGACCTCAATCTGG	47 (3 are in genes)	GTCTTGAGCGGCAATCCTAACAG GGCATGAGGGGCAATCCTACTGG CTTTTGGCGGCAATCCTACGAG GTTTGGGGGCAATCCTGAAAG GTTTGGAGGCAATCCTAACTGG GTTTGGAGTGCAATGATACAAG	0.9 0.2 0.2 0.1 0.1 0.1	3MMs [3:9-20] 4MMs [2:3-4:14] 4MMs [1:7-8:14] 4MMs [7:11-19:20] 4MMs [10:11-17:18] 4MMs [9:10-16:17]	NM_153774 NM_007955 NM_175556 NM_206935 NM_207533 NM_027724	chr1:-137300808 chr1:-137010643 chr4:-154365474 chr5:-77436483 chr15:-95455038 chr13:-38128622
		97	CGCGAATGACGAGTGGAACGTGG	10 (1 is in gene)	GCGAGTGGCGGGTGAACCCGAG	0.1	4MMs [6:9-12:20]	NM_020493	chr17:-46692840
		91	GTTTGGAGGGCAATCCTACTGG	67 (7 are in genes)	GTCTTGAGCGGCAATCCTAACAG GGCATGAGGGGCAATCCTACTGG CTTTTGGCGGCAATCCTACGAG GTTTGGGGGCAATCCTGAAAG GTTTGGAGGCAATCCTAACTGG GTTTGGAGTGCAATGATACAAG	0.9 0.2 0.2 0.1 0.1 0.1	3MMs [3:9-20] 4MMs [2:3-4:14] 4MMs [1:7-8:14] 4MMs [7:11-19:20] 4MMs [10:11-17:18] 4MMs [9:10-16:17]	NM_153774 NM_007955 NM_175556 NM_206935 NM_207533 NM_027724	chr1:-137300808 chr1:-137010643 chr4:-154365474 chr5:-77436483 chr15:-95455038 chr13:-38128622

Gap43

GRCm38:16:42247842:42341251:-1

67 GGCAGTTAGCAGCAACTGTAAGG 203 (15 are in genes)

GTTTTGGGGGACACGAGGAG 0
GGCAGTTAATGCAACTGGAGGG 0.5
GTCAGTTTGCAGCAACTGTGAG 0.4
GGCATGTGCAAACTGTGAGAG 0.4
GGCCATTAGGACCACTGTAAAG 0.4
GACATTTTGCAGCAACTCTAAGG 0.3
GGAAAGTTGCAGAACTGTTGAG 0.3
GGCAAGTAGAAGCAGCTGTAGGG 0.2
GCCACTTAGAAGCTACTGTAAGG 0.2
GGCAGTGAACAGCAAGTGTACAG 0.2
GCCAATTTAGCAGCAACTCTCAAG 0.1
GGCAGTGAAGAGTAGCTGTAGAG 0.1
TGCAGTTTGCAGCGCTGTGACAG 0.1
GGTAGATAGCAGCAATGAAGAG 0.1
GGCAGTTACCATAAATGTAAGG 0

4MMs [14:15:18:19] NM_153125 chr2:-26264906
3MMs [9:10:19] NM_021411 chr11:-115018195
4MMs [2:6:8:20] NM_008087 chr7:-59152876
4MMs [5:6:8:12] NM_172879 chr6:-3545284
4MMs [4:5:10:15] NM_009891 chr6:-137811454
4MMs [2:5:8:18] NM_009576 chr9:-91283726
4MMs [3:8:13:20] NM_029570 chr3:-35725955
4MMs [5:6:10:15] NM_010305 chr5:-17779237
4MMs [2:5:10:14] NM_00168297 chr10:-11017752
3MMs [7:9:16] NM_00165201 chr17:-25388871
4MMs [2:5:18:20] NM_1706589 chr10:-69342594
4MMs [7:10:13:19] NM_153054 chr8:-71562681
4MMs [1:8:14:15] NM_00104910 chr10:-58639639
4MMs [3:6:16:19] NM_011159 chr16:-15769835
4MMs [9:12:13:16] NM_181577 chr11:-28285825

38 AAGAGGAGGAAGGGACGAGAGGG 501 (39 are in genes)

AAGAGATGGAAGGGACGAGAAAG 2.2
GGGCGGAGGAAGGGACGAGGGAG 0.7
GATAGGAGGTAGGGACGAGAGAG 0.6
CAGACGTGGAAGGACGAGAGGG 0.5
AAGACGAGTTGGGGACGAGATAG 0.4
AAGACGAGTTGGGGACGAGATAG 0.4
AGAAAGGGGAAGGACGAGAGAG 0.4
CAGAAAGGAAGGGACGAGAGGG 0.4
AGAAAGGAGGATGCGACGAGAGAG 0.3
AAGGGGAGGGGGGACGAGAGGG 0.3
AAGAGAGGTTGGGACGAGATGG 0.3
TACAGGATGAAGGGAAGGAGAGAG 0.3
GTGAGAGGGAAGGGAGGAGACAG 0.3
GATAGGAAGAGGGGAAGGAGAGGG 0.3
CTGAGGAGGGGGGAAGGAGACAG 0.3
AAGCGTGTGAAGGACGAGATGG 0.2
AAGGTGAAGAGGACGAGAGAGAG 0.2
ATAAGGAGCAAGGGACGAGGAGAG 0.2
ACGAAGGAGGAAGGTCGAGTGTAG 0.2
TAGAGGAGTATGACGACGATGG 0.2
ACATGAGAAAGGGATGAGATGG 0.2
GGGAGGAGGAGGGGAGGAGAGGG 0.2
AGGAGGAGGAGGAGACGAGGGCAG 0.1
AAGAGGCAGAAAGGACGAGAGAG 0.1
AAGAGGAGGAGGGGAGGAGAGAG 0.1
AAGAGGAGGAGGGGAGGAGAGAG 0.1
GAGAGGAGGAGGGGAGGAGAGAG 0.1
AAGAGGAGGAGGGGAGGAGAGAG 0.1
AAGGAGGAGGAAGGACGTTGGCAG 0.1
AAGAGGAGCAAGGGATGAGGAGAG 0.1
CAGATGAGGAAGGGACCTGAGGG 0.1
ACGAGGAAGAGGGGAAGGAGCTGG 0.1
AAGAGGAGGAAGGAGGAGCAGAG 0.1
AAGAGTGGGAAGGACGAGAGGG 0.1
CAGAGCTGGAAGGAGGAGAGAGAG 0.1
TAGTGGAGGAAGGAGGAGAGAGAG 0.1
AAGGGGAGGAGGAGGAGGAGAGAG 0.1
CAGATGAGGAAGGAGGAGAGAGAG 0.1

2MMs [6:7] NM_007920 chr14:-79960522
4MMs [1:2:4:20] NM_023587 chr16:-35022475
4MMs [1:3:10:17] NR_033577 chr15:-77450885
4MMs [1:5:7:12] NM_01146380 chr6:-142734457
4MMs [5:9:10:11] NM_00100596 chr4:-42039230
4MMs [5:9:10:11] NM_00109348 chr4:-42339327
4MMs [5:9:10:11] NM_00100596 chr4:-42679198
4MMs [2:3:7:17] NM_178697 chr5:-13073894
4MMs [1:5:6:17] NM_00111143 chr3:-107021484
4MMs [2:3:11:13] NM_00148176 chr12:-78039496
4MMs [4:10:11:17] NM_010902 chr2:-75542808
4MMs [5:10:11:17] NR_046048 chr9:-47608999
4MMs [1:3:8:16] NM_021557 chr12:-480292732
4MMs [1:2:3:16] NM_009033 chr19:-4785282
4MMs [1:3:8:16] NM_00114179 chrX:-133527464
4MMs [1:2:10:16] NM_00170433 chr6:-146941991
4MMs [5:7:9:17] NM_010498 chrX:-67613300
4MMs [4:5:8:14] NM_00195025 chr1:-134213012
4MMs [2:3:9:18] NM_172945 chr11:-77284783
4MMs [2:5:15:20] NM_172339 chr2:-262252531
4MMs [1:9:12:17] NM_00165899 chr5:-11055845
4MMs [3:5:9:16] NM_026422 chr2:-35997190
4MMs [1:2:11:16] NM_00146307 chr4:-140953825
4MMs [2:11:13:20] NM_00108193 chr10:-120369007
4MMs [7:8:13:17] NM_138944 chr8:-80958559
4MMs [3:9:10:16] NM_146283 chr13:-21629528
4MMs [3:9:10:16] NM_177767 chr6:-96591501
4MMs [1:10:11:16] NM_021505 chr3:-123241770
4MMs [8:9:10:16] NM_011602 chr4:-43553320
4MMs [4:5:18:20] NM_028096 chr1:-37686626
3MMs [9:16:20] NM_00108132 chr2:-59770700
4MMs [1:5:17:18] NM_027248 chr14:-52628846
4MMs [2:8:16:20] NM_008876 chr11:-70368769
4MMs [5:9:13:19] NM_029741 chr7:-52605626
4MMs [7:7:12:17] NM_133674 chr6:-43233363
4MMs [1:6:7:16] NM_00102322 chr1:-121903510
4MMs [1:4:12:14] NM_00102825 chr1:-22369585
3MMs [4:16:18] NM_008192 chr11:-69032480
4MMs [1:5:13:16] NM_020002 chr14:-56243031

chr16:-42341184

50 AATTCTGAGAAAGGGACCCAGGG 430 (19 are in genes)

GCTTCAGAGAAAGGGACCCACGG 1.5
AGCTCTGAGAAAGGGAAACCAAG 1.2
TATTATGAAGAGGGACCCATGG 0.8
ATCTGGGAGAAAGGGACCCACAG 0.8
CATCTTTGAGAAAGGGACCCGTAG 0.7
AAAGCAGAGAGAGGGACCCAGGG 0.6
AAATAAGAGAAAGGGACCCGTGG 0.4
GTTTCTGACAAAGGGAAACCAAG 0.4
CATTGTGAGATAGGGACCAAGAG 0.3
GCTTCTGAGAAAGGAACCAAGAG 0.2
AAATCTGACAATGGGACCTACAG 0.2
AAGTCTGAGGAAGGGGAAGCAGAG 0.1
AATCTGAGAGAGAGGGACCCGTGG 0.1
AATCTGAAAGAGGGACCTCAAG 0.1
AATGCTGGGAAAAAGACCCAAAG 0.1
CATTTCTAGAAATGGGCCCATAG 0.1
AATTCTGACAATAGTACCCCAAGG 0
GATTCTGAGAAAGAGAGCAAGAG 0
AATCTGAGAAAGAGTCCCGTGG 0

3MMs [1:2:6] NM_027292 chr17:-48590231
3MMs [2:3:17] NM_007687 chr19:-5492831
4MMs [1:5:9:10] NM_026886 chr5:-116925274
4MMs [2:3:5:6] NM_010626 chr7:-86844986
4MMs [1:4:5:20] NM_025360 chr8:-89594203
4MMs [3:4:6:11] NM_011201 chr2:-1570426
4MMs [4:5:6:20] NM_009154 chr15:-3231428
4MMs [1:2:9:17] NM_00177571 chr10:-41289604
4MMs [1:5:11:19] NM_145394 chr3:-121162875
4MMs [1:2:15:17] NM_010382 chr17:-34451964
4MMs [3:9:12:19] NM_025655 chr11:-76723724
4MMs [3:10:17:18] NM_030035 chr16:-36919767
4MMs [4:11:17:19] NM_010427 chr5:-1609893
4MMs [3:9:11:18] NM_00194200 chr14:-62223790
4MMs [4:8:13:14] NM_021380 chr1:-132804998
4MMs [1:7:13:16] NM_178703 chr6:-114252681
4MMs [9:12:13:15] NM_00103546 chr9:-80156942
4MMs [1:14:17:19] NM_153145 chr11:-109933195
4MMs [3:14:16:20] NM_178759 chr11:-46629293

chr16:-42341007

38 GCTATGGGTTGGGGGTAGAAAGG 500 (42 are in genes)

CTGAGGTTGGGGGTAGAAAGG 1.4
AGAAAGGGGTGGGGGTAGAAAGG 1.3
GCTTTGGGAGGGGTAGGAGAG 0.9
GGTTTGGGCTGGGGGTAGAAAGG 0.7
GCTGGGAGTGGGGGTAGGAGAGG 0.7
GATATGGGTTGGGGGTAGGAGAG 0.4
GCTATGGGTTAGGGGTGGAAGGG 0.3
GCTTTGGAGTTGTGTAAGATGG 0.3
GATATGGGTTGGGGGTAGCAAGG 0.3
TCTTGGGGGTGGGGGAGAAAGG 0.3
ACCGTGGGTTGGGGGAGAAAGGG 0.3
GCTGGGGGTGGGGGAGAGAGGG 0.3
GTTGGGGGTGGGGGAGAAAGG 0.3
GGGGTGGGTTGGGGGAGAAAGGG 0.3
GCTTGGGGGGGGGGGAGAAAGGG 0.2
GCTATGGGTTGGGGGTAGGTTGG 0.2
TCTCTGGGTTGGGGTTGCAAGG 0.2
GCTGTTGGGTTGGGTAGACGGG 0.2
GTCTTGGGTTGGGGGTGGGAGGG 0.2
GTTAGGGGTGGGGGTGGCAGAG 0.2
GTGATGGGTTGGGGGTGGGAGGG 0.2
GCAGTGGGTTGGGGGTGGGAGGG 0.2
GATGATGGGTTGGGGGTACAAAGG 0.2
GCTATGGAATGAGGGTAGAGAGG 0.2
GCACTGAGGTTGGGGGAGAAAGG 0.2
CCTGTTGGGTTGGGGGAGAGAGG 0.2
GCTATGGGTTGGGGGTGTAAGAG 0.1
GCTATGGGTTGGGGGTAGATGGG 0.1
ACTAGGGGTGGGGGAGCAAGGG 0.1
GGGATGGGTTGGGGGCAAGTAGGG 0.1
GCTCTGAGGTTGAGGGAAGAAAG 0.1
GGTATGGGTTGGGGGTGGGAGAG 0.1
GGTATGGGGGGGGGGCAGCACAG 0.1
GCTTTGGGTTGGGGGTGTTGTTGG 0.1
GCTCTGGGAGGAGTCAAGAGG 0.1
GCGATGTGTTGGGGGTGTAAGGG 0.1
GCTACGGGTTGGGGTGGGGAGGG 0.1
GCTATGGGGGTGGGGGTGGGAGAG 0.1
GCTATAGTTGGGGTAGSGTGGG 0.1
GCCATAGGGTAGGTGTAAGAAAGG 0.1
GATATGGGTTGGGGTTGAGAGGG 0.1
GCTCTGGGTTGGGGTTAAAAAG 0.1

4MMs [1:4:5:8] NM_029864 chr11:-117668477
4MMs [1:2:3:5] NM_016765 chr17:-35197006
3MMs [4:10:19] NM_008269 chr11:-96162656
4MMs [2:4:10:11] NM_175184 chr2:-33680573
4MMs [4:5:8:20] NM_016674 chr16:-26371409
3MMs [2:17:19] NM_00303294 chr3:-87585874
3MMs [9:11:17] NM_008063 chr9:-44207630
4MMs [4:8:11:13] NM_019995 chr3:-54502607
3MMs [2:15:19] NM_00125887 chr7:-112710791
4MMs [1:3:4:16] NM_173423 chr18:-46684585
4MMs [1:3:4:16] NM_00134969 chr11:-3831345
4MMs [2:4:5:16] NM_153137 chr1:-195023809
4MMs [2:4:5:16] NM_008453 chr5:-65221410
4MMs [2:3:4:16] NM_010927 chr11:-78734566
4MMs [4:5:10:16] NM_011467 chr6:-85084044
3MMs [9:19:20] NM_080470 chr15:-84943022
4MMs [1:4:17:19] NM_178379 chr11:-63869699
4MMs [4:6:12:20] NM_177129 chr1:-134425439
4MMs [2:4:17:18] NM_028043 chr1:-3953218
4MMs [2:5:17:19] NM_022428 chr8:-95198986
4MMs [2:3:17:19] NM_021042 chr6:-142621227
4MMs [3:4:17:19] NR_045283 chr15:-37351701
4MMs [2:4:6:18] NM_008065 chr16:-84835437
4MMs [8:9:12:20] NR_045332 chr9:-98649856
4MMs [3:4:7:16] NM_022886 chr9:-44706276
4MMs [1:4:16:20] NR_045873 chr11:-78837043
4MMs [4:4:17:18] NM_177352 chr9:-96051225
4MMs [5:6:15:20] NM_007494 chr2:-31365860
4MMs [1:5:16:19] NM_172487 chr6:-113451604
4MMs [2:3:16:19] NM_016753 chr3:-67267448
4MMs [4:7:12:16] NM_028940 chr4:-9208713
4MMs [2:17:19:20] NM_009697 chr7:-77498800
4MMs [2:10:16:19] NM_018813 chr12:-21318290
4MMs [4:17:19:20] NR_003568 chr13:-12710209
4MMs [4:10:14:17] NM_00198733 chr17:-34046903
4MMs [3:7:17:18] NM_00100363 chr5:-12331117
4MMs [5:17:19:20] NM_172887 chr5:-151293626
4MMs [10:12:17:18] NM_002714 chr9:-42776273
4MMs [6:9:12:19] NM_008667 chr1:-52523674
4MMs [3:6:11:14] NM_175644 chr12:-76513870
4MMs [2:15:17:20] NM_00190703 chr12:-110699597
4MMs [4:9:17:18] NM_019640 chr5:-111816965

Sema6a

chr18:-47528597

93 TGGCGTCTCTCCGACCCGAGG 45 (8 are in genes)

TGGCGGCTCTCTCCGACCCGGAG 3.1
CAGCGGCTCTCTCCGACCCGAGGG 0.3
TGGCGTCTCCACGGGCCGAGG 0.2

2MMs [6:20] NM_008429 chr1:-174256637
4MMs [1:2:6:15] NM_030563 chr8:-48948776
3MMs [9:11:15] NM_020605 chr8:-124254601

chr18:~47528713	92	CAGGAGTAGTGCCGCACG GGG	53 (8 are in genes)	TGGGGGCGCTCGAGACCGGAAGG	0.2	4MMs [4:6:13:13]	NM_1777733	chr4:-135728775
				DGGCGTCTCTCCGCGCTGAAGG	0.2	3MMs [1:15:18]	NM_0272795	chr5:-42099324
				TGGCATCTCTCAGACCTGGAAG	0.1	4MMs [5:13:18:20]	NM_011941	chr2:-119848102
				CGGGCGCTCTCCACCCAAAGG	0	4MMs [1:6:14:19]	NM_027496	chr15:-31297336
				TGGCTCTCTCCACCCATTGG	0	4MMs [5:6:14:19]	NM_1777078	chr5:-113341910
chr18:~4752885	95	TCTCCTAGAGTCGCCCGCG TGG	44 (12 are in genes)	CATGTGCAGTGTGCCGCCGTGG	0.2	4MMs [3:5:7:18]	NM_146019	chr11:-69171334
				CTGGAGTAGTGCCGCTGAGG	0.1	4MMs [2:12:18:20]	NM_0102277	chr6:-14632840
				CAGCGCTTGTGTGCCACACTGG	0	4MMs [5:8:14:16]	NM_010491	chr6:-142251862
				CAGGAGAAGTGTGCAGCAGCTGG	0	4MMs [7:15:19:20]	NM_00123370	chr17:-15117236
				CAGGAGAAGTGTGCAGCAGCTGG	0	4MMs [7:15:19:20]	NM_00123372	chr17:-15148608
chr18:~47528787	61	CAGGGCTCAGTAATGCTGT CTGG	274 (26 are in genes)	CAGGAGAAGTGTGCAGCAGCTGG	0	4MMs [7:15:19:20]	NM_0038652	chr17:-15179983
				CAGGAGTAGTGTGAAGACCGGG	0	4MMs [14:15:17:20]	NM_001037298	chr8:-125010442
				CCTCCGGGAAGCCGCCGCCGGGG	0.3	4MMs [1:6:7:11]	NM_0072696	chr18:-35812234
				GCTCCAGAGTGGCGCGCGCGGG	0.2	4MMs [1:6:12:17]	NM_016974	chr7:-52962339
				TCTCCCAAGCCGCCCCCTCCGG	0.1	4MMs [6:10:11:19]	NM_1385589	chr7:-129210764
				TAACCTAGAGTCGCCCTTGCAGG	0.1	4MMs [2:3:17:18]	NM_027389	chr3:-88711270
				TCTCCTCTAGTCGGCGTCGCGGG	0.1	4MMs [7:8:14:17]	NM_027215	chr7:-31514486
				TCTCCTTGTACTTCCCGCTGG	0.1	4MMs [7:8:13:14]	NM_008604	chr3:-63165842
				TCTCCTCGAGCAGCCCCAGCAGG	0.1	4MMs [7:11:12:18]	NM_010856	chr14:-55575434
				TCTCCCAAGAGCTCTCCGCCAG	0	4MMs [6:11:13:16]	NM_146260	chr9:-110782556
				TCTCTAGAGTCCGCCAGCAGAG	0	4MMs [5:11:13:16]	NM_008041	chr2:-180510702
				TCAACCTAGAGTCAACCCACAGG	0	4MMs [3:13:14:19]	NM_138306	chr2:-91782897
				TCTCCTAGAGACTCTCCAGCCAG	0	4MMs [11:13:15:18]	NM_177809	chr13:-56544269
				TCTCCTAGTGTCACTCTGCCAG	0	4MMs [9:13:16:18]	NM_008131	chr1:-155756516
								CATGCCTCAGTAATGCTGTCTCAG
CAGCTGTCTATTATGCTGAGG	0	4MMs [6:10:13:17]	NM_139816					chr10:-10034040
CAACCTCTCAGGAATGCTCTCAAG	0.8	3MMs [3:4:5:11]	NM_0016984					chr3:-8980709
CAGTGTTCATGTAATGCAAGCTGG	0.7	3MMs [4:6:17]	NM_00169364					chrX:-68407403
CAAGGCTAGTACTGCTGTCGGG	0.5	4MMs [3:7:8:12]	NM_009190					chr1:-108676778
				CAGTGTGAGAGATGCTGTCAGG	0.4	4MMs [4:8:11:12]	NM_027258	chr11:-116199115
				CAGAGCTCATGCTGCTGCTCAAG	0.4	4MMs [4:10:11:12]	NM_130884	chr2:-130109681
				CTGGGCTCTGAGATGCTGTCAGG	0.2	4MMs [2:8:11:12]	NM_0016986	chr1:-177914509
				CAGGGGACAGAGTGTCTGCTGG	0.2	4MMs [1:7:11:19]	NM_172892	chr9:-35211919
				CAGGGCTCAGCACTGCTGGCTGG	0.2	4MMs [11:13:19]	NM_00169258	chr7:-107064636
				CAGGACTCAGGGATGCTGTGGGG	0.2	4MMs [5:11:12:20]	NM_177611	chr2:-24263264
				CAGGACTGAGTCTGCTGTGCCAG	0.1	4MMs [5:8:12:20]	NM_033324	chr16:-18258518
				CGGTGCTCAGGAAAGGCTGTCAAG	0.1	4MMs [2:4:11:14]	NM_00163721	chr4:-153396331
				CAGGGCTAAGTTCTGCTGTGGGG	0.1	4MMs [8:12:13:20]	NM_133351	chr7:-135071529
				CAGGCCTCAGGAATGCTCGAAGG	0.1	4MMs [5:11:19:20]	NM_146261	chrX:-133811782
				CAGGCTCAGAGTGTGCTGTCAAG	0	4MMs [7:8:12:20]	NM_026960	chr15:-15694725
				CAGGCTCAGCATTGCCGACAG	0	4MMs [11:13:17:19]	NM_0094277	chr15:-102070320
				CAGGGCTCTGGAACGCTGTGTGG	0	4MMs [9:11:14:20]	NR_045159	chr4:-139499454
				CAGGGCTCAGTGTCTCTGTGTGG	0	4MMs [12:13:15:20]	NM_145532	chr2:-127530847
				CAGGCCTCAGAAAAGCTTCTCGG	0	4MMs [5:11:14:18]	NR_029880	chr12:-110947179
				CAGGGGCCAGTAAAGCTGGGAGG	0	4MMs [7:14:19:20]	NM_009025	chr8:-13578554
				CAGGGCTCGGTAAGTACTCTCAGG	0	4MMs [9:13:15:18]	NM_00126360	chr11:-3190474
				CAGGGCTCAGTGTGAGAGCTGG	0	4MMs [12:16:17:19]	NM_026544	chr17:-12412007
				CAGGGCTCAGAAATGCTTTCAGG	0	4MMs [11:16:17:18]	NM_212445	chr9:-53198823
				CAGGGCTCAGTACTGTTTGTGG	0	4MMs [13:16:18:20]	NM_138652	chr14:-570506472
				CAGGGCTCAGTACGTGTGCTGG	0	4MMs [13:14:15:16]	NM_011708	chr6:-125504583

Supplementary Table 6. Primer and oligonucleotide sequences.

Primers for cloning		
Primer Name	Forward or Reverse	Primer sequence (5'-3')
Cjk-SA1	Reverse	CAATTCCTATCAACTAGGAGCTG
Cjk-SA3	Reverse	ACGCGTCGACATGCTTCCTTCCTGGGTGCA
Cjk-SA4	Reverse	ATAGTTTAGCGGCCCTTAAAGAAGACGTCCTCTGCATTC
Cjk24	Forward	ACGCGTCGACATGATGGATCCATGTTTCAGTTG
Cjk25	Reverse	ATAGTTTAGCGGCCGCTTATCCAGCATGTTTATATGAAT

RT-qPCR (mouse)		
Primer Name	Forward (5'-3')	Reverse (5'-3')
<i>C11orf46</i>	GACCGAAAGTGGCTGTATG	ATATGGGTGACAGGGAGATAA
<i>Dclk1</i>	TCCACCGGAATTGAACCTCGG	GGGAGCGAACAGCTCTAGA
<i>Sema6a</i>	ACAGCCTGCCCTAAAGT	AGCTCCTCTTATATTCGAGCCC
<i>Plxna4</i>	ACAGGGCACATTATTGGGG	CACTTGGGGTTGTCTCATCT
<i>Nuak1</i>	CAGGCCGAGTGGTTGCTATAA	TGTTTGGGGATGACATGATCT
<i>Gap43</i>	TGGTGTCAAGCCGGAAGATAA	GCTGGTGCATCACCTTCT
<i>Hprt1</i>	TCAGTCAACGGGGACATAAA	GGGGCTGTACTGCTTAACCA

sgRNA protospacer sequences		
Region of Interest	Oligonucleotide Name	protospacer sequence (5'-3')
mouse <i>Dclk1</i>	mDclk1-A	AGTCGCTAGAAGGACTTGCC
	mDclk1-D	GTAGGATTGCCCTCAAAC
mouse <i>Sema6a</i>	mSema6a-A	TCGGGTCGGAGGAGACGCCAC
	mSema6a-D	GACAGCATTAAGGCCCTGC

ChIP-qPCR (mouse)		
Primer Name	Forward (5'-3')	Reverse (5'-3')
<i>Dclk1</i>	TTTGAGGGGCAATCCTACTG	GCCTTCATCAAAGGAGACCA
<i>Sema6a</i>	AGAGGGAGGCAGAGAGTGTG	GGCTGGGCTTCTCTAGAGT

	Primer	Sequence 5' - 3'	Species	Size
qRT-PCR	Primer bank ID			
Human primers: <i>C11orf46</i> (NM_152316)	22748692c1-forward	TGGAGTCCAGCTTCGTACTAC	human	140bp
	22748692c1-reverse	TGTTCCCGAAGAGTGCAATTC	human	
<i>SETDB1</i> (NM_001145415)	224177466c3-forward	TAAGACTTGGCACAAAGGCAC	human	104bp
	224177466c3-reverse	TCCCCGACAGTAGACTCTTTT	human	
<i>ATF7IP</i> (MCAF1) (NM_018179)	38261961c1-forward	AAGGCTCGAAAAACGATGAGAG	human	102bp
	38261961c1-revers	GCATTTAAACAGCTTGACATCAG	human	
<i>TRIM28</i> (KAP1) (NM_005762)	14971416c3-forward	CGGGATGGTGAACGTACTGTC	human	93bp
	14971416c3-reverse	GTCTCGGCAGGTGAGAGTATC	human	
<i>HPRT1</i> (NM_000194)	164518913c1-forward	CCTGGCGTCGTGATTAGTGAT	human	131bp
	164518913c1-reverse	AGACGTTCAAGTCTGTCATAA	human	
<i>beta-Actin</i> (NM_001101)	4501885a1-forward	CATGTACGTTGCTATCCAGGC	human	250bp
	4501885a1-reverse	CTCCTTAATGTCACGCACGAT	human	
Mouse primers: <i>C11orf46</i> (NM_173750)	68299772c3-forward	CAATGGAAGTGTGGACGTTGA	mouse	103bp
	68299772c3-reverse	TGGGTTGTAAACTGTAGTGACC	mouse	
<i>Hprt</i> (NM_013556)	7305155a1-forward	TCAGTCAACGGGGGACATAAA	mouse	142bp
	7305155a1-reverse	GGGGCTGTACTGCTTAACCAAG	mouse	
<i>beta Actin</i> (NM_007393)	6671509a1-forward	GGCTGTATTCCCTCCATCG	mouse	154 bp
	6671509a1-reverse	CCAGTTGGTAACAATGCCATGT	mouse	
<i>Ctnnd2</i>	112363089c1-forward	ATGGCTCTGAGACGGAAACC	mouse	112 bp
	112363089c1-reverse	CTGGCTACGATCTGGCGTTC	mouse	
<i>Dclk1</i>	26328245a1-forward	TCCACCGGAATTGAACCTCGG	mouse	65 bp
	26328245a1-reverse	GGGAGCGAACAGCTCTAGA	mouse	
<i>Enc1</i>	31560703a1-forward	CTGTTTCATAAGTCTCCTACGC	mouse	169
	31560703a1-reverse	CACCACTGAACATGGCTTCG	mouse	
<i>Map2</i>	Map2-forward	GGAAAGATGAAGGAAGGCACCAC	mouse	344
	Map2-reverse	GGCTGGTCTTGTATTGGGCTTCC	mouse	
<i>Nuak1</i>	52138543c3-forward	CAGGCCGAGTGGTTGCTATAA	mouse	
	52138543c3-reverse	TGGTTGAGGGATGACATGATCT	mouse	
<i>Plxna4</i>	28461143a1-forward	ACAGGGCACATTATTTGGGG	mouse	107
	28461143a1-reverse	CACTTGGGGTTGTCTCATCT	mouse	
<i>Ptn</i>	12857177a1-forward	CTCTGCACAATGCTGACTGTC	mouse	135
	12857177a1-reverse	ACAGCTTCTTACCTTGAGGCTT	mouse	
<i>Sema6a</i>	11093909a1-forward	ACAGCCTGCCCTAAAGT	mouse	100
	11093909a1-reverse	AGCTCCTCTTATATTCGAGCCC	mouse	
<i>shc3</i>	6677937a1-forward	GCCGGGAGTCACTTATGTG	mouse	112
	6677937a1-reverse	TTCCCTGGTAACCTGAGTTCTT	mouse	
<i>Slc8a3</i>	30851385a1-forward	GTGAACCGAAATGGATGGAACG	mouse	92
	30851385a1-reverse	TCACCCAATACTGGCTTTCCC	mouse	
<i>Syt1</i>	356640230c3-forward	GACAAAAGTCCACCGGAAACC	mouse	140
	356640230c3-reverse	CCAGTGTCTTGCCACCTAATTC	mouse	
<i>Cdk5r1</i>	6753384a1-forward	CTGTCCCTATCCCCAGCTAT	Human	133
	6753384a1-reverse	GGCAGCACCGAGATGATGG	Human	
<i>DCLK1</i>	4758128a2-forward	GCTGATTGACCCGAACCTG	Human	119
	4758128a2-reverse	AGCCACATACATAACTCTCTCT	Human	
<i>SEMA6A</i>	145553983c2-forward	ACATTGCTGCTAGGGACCAT	Human	167
	145553983c2-reverse	TCTGCATGTGTCTACATCGGC	Human	
<i>GAP43</i>	194248055c1-forward	GGCCGCAACCAAAATTCAGG	Human	107
	194248055c1-reverse	CGGCAGTAGTGGTGCCCTTC	Human	
<i>PLXNA4</i>	157738644c1-forward	GTCAATTTGCACATTCCGAGGA	Human	108
	157738644c1-reverse	GCTTGTAAATCCGATTGACGGC	Human	
<i>NUAK1</i>	48374438c3-forward	ATATACTGCTCGATGACAACTGC	Human	127
	48374438c3-reverse	CATAGAGTGGAGTCCCAACAAAC	Human	
<i>NDRG1</i>	207028746c1-forward	CTCCTGCAAGAGTTTGATGTCC	Human	
	207028746c1-reverse	TCATGCCGATGTCATGGTAGG	Human	