Supplementary information A Ctnnb1 enhancer regulates neocortical neurogenesis by controlling the abundance of intermediate progenitors Junbao Wang^{1,#}, Andi Wang^{1,#}, Kuan Tian¹, Xiaojiao Hua¹, Bo Zhang¹, Yue Zheng¹, Xiangfei Kong¹, Wei Li¹, Lichao Xu¹, Juan Wang², Zhiqiang Li¹, Ying Liu^{1,*}, Yan Zhou^{1,*}

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11 Supplementary Figure S1. *neCtnnb1* is a putative enhancer upstream of *Ctnnb1*.

a-c Schematic representation of the upstream region of mouse *Ctnnb1* gene and the 12 13 location of putative enhancer *neCtnnb1* (orange shading). Enrichment of indicated 14 signals in developing forebrains (**a**), midbrains (**b**) and hindbrains (**c**) were shown. Data were obtained from ENCODE. d Enrichment of H3K27ac ChIP-seq signals in 15 16 indicated tissues of E15.5 embryos. Data were obtained from ENCODE. e-f The Hi-C 17 data (e) and virtual 4C (f) of *in-vitro* differentiated NPCs revealing the interaction 18 between *neCtnnb1* and *pCtnnb1*. **g** The Hi-C data of E14.5 cortical neurons were 19 obtained from the 3D genome browser. Boundaries of TADs and locations of *neCtnnb1* 20 and *Ctnnb1* gene (red bars) are indicated below. **g**' Regions magnified from (**g**). Boxed 21 area indicating the interaction between *neCtnnb1* and *pCtnnb1*. **h** Virtual 4C of E14.5 22 cortical neurons revealing the interaction between *neCtnnb1* and *pCtnnb1*. 23



Supplementary Figure S2. *neCtnnb1* is predominantly active in developing
 neocortex.

a-e X-Gal staining (blue) of whole embryos (**a-e**), sagittal whole-body sections (**b'-d'**), 27 brains (a"-e") and sagittal/coronal brain sections (a"'-e"') of neCtnnb1-LacZ-iCre 28 reporter mice. Due to the influence of integration sites and copy numbers on 29 expression, the reporter activity in a specific tissue was only considered reliable when 30 it was found in at least two or more independent individual embryos. **f** E15.5 sagittal 31 brains sections of *neCtnnb1-LacZ-iCre* mice were sequentially stained with LacZ/β-32 Gal (blue) for *neCtnnb1* activity and TBR2 (brown), with boxed Ncx regions magnified 33 on right panels. **g** Quantifications of normalized signal density of β -Gal and TBR2 34 signals in (f). h Immunofluorescence of NEUROD2 (gray), TBR2 (green), and β -Gal 35 36 (red) on coronal sections of E15.5 neCtnnb1-LacZ-iCre Ncx. Scale bars, 1mm (a-e, **b**'-**d**', **a**''-**e**''' and **f**), 100 µm (magnified views in **a**'''-**e**''' and **f**), 50 µm (**h**). 37 38



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40 Supplementary Figure S3. Knockout of *neCtnnb1* compromised *Ctnnb1*'s

41 reporter activity in developing neocortices.

a Representative images of adult (8 weeks) WT and *neCtnnb1*^{KO} mice. **b** Dorsal views 42 of adult WT and *neCtnnb1*^{KO} mouse brains. **c** Quantifications of adult WT and 43 *neCtnnb1*^{KO} mice in body weight, neocortex area and length. n = 5 for WT brains and 44 n = 4 for *neCtnnb1*^{KO} brains. Each point represents an individual brain. **d** X-Gal 45 staining (blue) on E15.5 coronal sections of WT BAT (left) and *neCtnnb1*^{KO} BAT (right) 46 Ncx, with boxed regions (R1s and R2s) magnified on the bottom. e-h Quantification of 47 normalized signal density of LacZ in two boxed regions of (d). n = 2 for WT BAT brains 48 49 and n = 2 for *neCtnnb1*^{KO} BAT brains. Each point represents an individual brain. **i** X-Gal staining (blue) in P8 WT BAT (left) and *neCtnnb1*^{KO} BAT (right) whole mount 50 brains. j Quantification of normalized signal density of LacZ in boxed regions of (i). n 51

52 = 2 for WT_BAT brains and n = 3 for *neCtnnb1*^{KO}_BAT brains. Each point represents 53 an individual brain. Quantification data are shown as mean \pm SEM. Statistical 54 significance was determined using an unpaired two-tailed Student's *t*-test (**c**, **f** and **h**) 55 **P* < 0.05, ***P* < 0.01, and ****P* < 0.001. ns, not significant. Scale bars, 1 cm (**a** and **i**), 56 500 µm (**b** and **d**), 50 µm (magnified views in **d**).



59 Supplementary Figure S4. neCtnnb1 regulates neocortical neurogenesis and IP

60 divisions.

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a-b Immunofluorescence (**a**) and quantification (**b**, top) of BrdU+ (green) and TBR2+ 61 (red) cells on boxed area of coronal sections (**b**) of E16.5 WT and *neCtnnb1*^{KO} Ncx. 62 Pregnant mice were injected with BrdU 30 min before sacrifice. n = 3 for WT brains 63 and n = 6 for *neCtnnb1*^{KO} brains. Each point represents an individual brain. c 64 Immunofluorescence of SATB2+ (red) and EGFP+ (green) cells on E18.5 coronal 65 sections of WT and *neCtnnb1^{KO}* Ncx. Neocortex were electroporated with EGPF-66 expressing constructs at E14.5. **d** Schematic diagram illustrating the strategy of *in* 67 *utero* electroporation (IUE) of WT and *neCtnnb1*^{KO} embryos. **e-f** Neocortices shown in 68 69 (c) were divided into 10 bins of equal height and fixed width, and EGFP+ (green) cells in each bin were counted and quantified. n = 3 for WT brains and n = 3 for neCtnnb1^{KO} 70 brains. Each point represents an individual brain. g Nissl-staining on E16.5 coronal 71 72 sections of Ctrl and WNT-iGOF Ncx. h Comparison of neocortical thickness of E16.5 73 Ctrl and WNT-iGOF mice. n = 13 for Ctrl brains and n = 10 for WNT-iGOF brains. Each 74 point represents an individual brain. i Comparison of cortical plate thickness of E16.5

Ctrl and WNT-iGOF mice. n = 10 for Ctrl brains and n = 7 for WNT-iGOF brains. Each 75 point represents an individual brain. j Comparison of dorsal ventricle surface length of 76 77 E16.5 Ctrl and WNT-iGOF mice. n = 10 for Ctrl brains and n = 7 for WNT-iGOF brains. Each point represents an individual brain. k-n Immunofluorescence (k) and 78 79 quantification (I-n) of TBR2+ (red) and BrdU+ (green) cells on boxed area of coronal 80 sections (I) of E16.5 Ctrl and WNT-iGOF Ncx. Pregnant mice were injected with BrdU 30 min before sacrifice. Each point represents an individual brain. Quantification data 81 are shown as mean ± SEM. Statistical significance was determined using unpaired 82 83 two-tailed Student's *t*-test (**b**, **h**, **i**, **j**, **l**, **m** and **n**); two-way ANOVA followed by Sidak's multiple comparisons test (**e** and **f**). **P* < 0.05, ***P* < 0.01, ****P* < 0.001, and *****P* < 84 0.0001. ns, not significant. Scale bars, 500 µm (g), 100 µm (a, c, k and magnified 85 86 views in **g**), 50 μ m (magnified views in **a** and **k**). 87



89 Supplementary Figure S5. Effects of selected trans-acting factors on

90 expressions of *Ctnnb1*.

91 a Representative images showing in situ hybridization (ISH) of Foxp1, Neurod2, 92 *Neurog2*, *Tbr2*, *Satb2*, *Smad3* and *Sox2* on sagittal sections of E15.5 mouse embryos. 93 Data were extracted from the Allan Brain Atlas. **b-c** Expression patterns of *Eomes* (**b**) 94 and Ash2l (c) during mouse neocortical neurogenesis. Visualized single-cell RNA-seq 95 data were extracted from Humous.org (http://www.humous.org/). d-g RNA levels of Sox2 (d), Satb2 (e), NeuroD2 (f), Yy1 (g) and Ctnnb1 in Neuro-2a transfected with 96 97 indicated vectors for two days. Each point represents an independent experiment. hk RNA levels of Sox2 (h), Satb2 (i), NeuroD2 (j), Yy1 (k) and Ctnnb1 in WT and 98 *neCtnnb1*^{KO} neocortical NPCs transfected with indicated vectors for two days. NPCs 99 were derived from E12.5 Ncx. n = 3 for WT brains and n = 3 for *neCtnnb1*^{KO} brains. 100 Each point represents NPCs derived from an individual brain. Quantification data are 101 shown as mean ± SEM. Statistical significance was determined using two-way ANOVA 102 followed by Sidak's multiple comparisons test. (**d-k**). *P < 0.05, **P < 0.01, ***P < 0.01103 0.001, and *****P* < 0.0001. ns, not significant. 104



107 Supplementary Figure S6. Sequence conservation of *neCtnnb1*.

a UCSC genome browser track depicts conservation of *neCtnnb1* among vertebrates.

- **b** Multiple sequence alignment of the core conserved region of *neCtnnb1* among
- $\,$ selected vertebrates. Data were extracted from the UCSC genome browser.



112 Supplementary Figure S7. *neCTNNB1* interacts with *pCTNNB1* in developing

113 human brains.

a Schematic representation of ATAC-seq data upstream of human CTNNB1 gene and 114 the location of the putative enhancer *neCTNNB1* (blue shading). **b** The Hi-C data of 115 adult dorsolateral prefrontal Ncx were obtained from the 3D genome browser. The 116 117 boundaries of TADs and locations of neCTNNB1 and CTNNB1 are indicated below. b' Regions magnified from (b). *neCTNNB1* interacts with *pCTNNB1* in adult dorsolateral 118 prefrontal Ncx. c Virtual 4C of adult dorsolateral prefrontal Ncx revealing interactions 119 between *neCTNNB1* and *pCTNNB1*. PFC, dorsal lateral prefrontal cortex; Motor, 120 121 motor cortex; S1, primary somatosensory cortex; Temporal, temporal cortex; Parietal, parietal cortex, V1, primary visual cortex; MGE, LGE, CGE, medial, lateral, and caudal 122 ganglionic eminences. 123

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125	Table S1. Summar	v of data used in this studv.
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Source name	Organism	Age	Library strategy	Antibody	Serial number
Prefrontal cortex	Homo sapiens	14gw	ATAC-seq	/	GSE149268
Prefrontal cortex	Homo sapiens	17gw	ATAC-seq	/	GSE149268
Prefrontal cortex	Homo sapiens	18gw	ATAC-seq	/	GSE149268
Prefrontal cortex	Homo sapiens	19gw	ATAC-seq	/	GSE149268
Motor cortex	Homo sapiens	14gw	ATAC-seq	/	GSE149268
Motor cortex	Homo sapiens	17gw	ATAC-seq	/	GSE149268
Motor cortex	Homo sapiens	19gw	ATAC-seq	/	GSE149268
Somatosensory cortex	Homo sapiens	14gw	ATAC-seq	/	GSE149268
Somatosensory cortex	Homo sapiens	17gw	ATAC-seq	/	GSE149268
Somatosensory cortex	Homo sapiens	19gw	ATAC-seq	/	GSE149268
Temporal cortex	Homo sapiens	19gw	ATAC-seq	/	GSE149268
Parietal cortex	Homo sapiens	19gw	ATAC-seq	/	GSE149268
Visual cortex	Homo sapiens	14gw	ATAC-seq	/	GSE149268
Visual cortex	Homo sapiens	17gw	ATAC-seq	/	GSE149268
Visual cortex	Homo sapiens	19gw	ATAC-seq	/	GSE149268
Medial ganglionic eminence	Homo sapiens	14gw	ATAC-seq	/	GSE149268
Medial ganglionic eminence	Homo sapiens	18gw	ATAC-seq	/	GSE149268
Medial ganglionic eminence	Homo sapiens	19gw	ATAC-seq	/	GSE149268
Lateral ganglionic eminence	Homo sapiens	14gw	ATAC-seq	/	GSE149268
Lateral ganglionic eminence	Homo sapiens	18gw	ATAC-seq	/	GSE149268
Lateral ganglionic eminence	Homo sapiens	19gw	ATAC-seq	/	GSE149268
Caudal ganglionic eminence	Homo sapiens	14gw	ATAC-seq	/	GSE149268
Caudal ganglionic eminence	Homo sapiens	17gw	ATAC-seq	/	GSE149268
Caudal ganglionic eminence	Homo sapiens	18gw	ATAC-seq	/	GSE149268
Caudal ganglionic eminence	Homo sapiens	19gw	ATAC-seq	/	GSE149268
Prefrontal cortex	Homo sapiens	15gw	ChIP-seq	H3K27ac	GSE149268
Prefrontal cortex	Homo sapiens	17gw	ChIP-seq	H3K27ac	GSE149268
Prefrontal cortex	Homo sapiens	18gw	ChIP-seq	H3K27ac	GSE149268
Prefrontal cortex	Homo sapiens	15gw	ChIP-seq	H3K4me1	GSE149268
Forebrain	Mus musculus	E11.5	ChIP-seq	H3K27ac	ENCSR275KPI
Forebrain	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR691NQH
Forebrain	Mus musculus	P0	ChIP-seq	H3K27ac	ENCSR094TTT
Forebrain	Mus musculus	E11.5	DNase-seq	1	ENCSR014SFF
Forebrain	Mus musculus	E14.5	DNase-seq	1	ENCSR337EDG
Forebrain	Mus musculus	P0	DNase-seq	1	ENCSR791AJY
Forebrain	Mus musculus	E11.5	ChIP-seq	H3K4me1	ENCSR975QSF
Forebrain	Mus musculus	E15.5	ChIP-seq	H3K4me1	ENCSR875KRK
Forebrain	Mus musculus	P0	ChIP-seq	H3K4me1	ENCSR465PLB

Forebrain	Mus musculus	E11.5	ChIP-seq	H3K4me3	ENCSR739DVM
Forebrain	Mus musculus	E15.5	ChIP-seq	H3K4me3	ENCSR022KDE
Forebrain	Mus musculus	P0	ChIP-seq	H3K4me3	ENCSR258YWW
Forebrain	Mus musculus	E11.5	ChIP-seq	H3K36me3	ENCSR066LZB
Forebrain	Mus musculus	E15.5	ChIP-seq	H3K36me3	ENCSR437SFX
Forebrain	Mus musculus	P0	ChIP-seq	H3K36me3	ENCSR069TDC
Midbrain	Mus musculus	E11.5	ChIP-seq	H3K27ac	ENCSR088UKA
Midbrain	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR428GHF
Midbrain	Mus musculus	P0	ChIP-seq	H3K27ac	ENCSR672ZXY
Midbrain	Mus musculus	E11.5	DNase-seq	/	ENCSR292QBA
Midbrain	Mus musculus	E14.5	DNase-seq	/	ENCSR367FCW
Midbrain	Mus musculus	P0	DNase-seq	/	ENCSR767AJS
Midbrain	Mus musculus	E11.5	ChIP-seq	H3K4me1	ENCSR450ITF
Midbrain	Mus musculus	E15.5	ChIP-seq	H3K4me1	ENCSR449EUZ
Midbrain	Mus musculus	P0	ChIP-seq	H3K4me1	ENCSR391WSS
Midbrain	Mus musculus	E11.5	ChIP-seq	H3K4me3	ENCSR283RFW
Midbrain	Mus musculus	E15.5	ChIP-seq	H3K4me3	ENCSR486MHP
Midbrain	Mus musculus	P0	ChIP-seq	H3K4me3	ENCSR427ZJU
Midbrain	Mus musculus	E11.5	ChIP-seq	H3K36me3	NCSR535NVF
Midbrain	Mus musculus	E15.5	ChIP-seq	H3K36me3	ENCSR487RAU
Midbrain	Mus musculus	P0	ChIP-seq	H3K36me3	ENCSR951UWY
Hindbrain	Mus musculus	E11.5	ChIP-seq	H3K27ac	ENCSR129LAP
Hindbrain	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR066XFL
Hindbrain	Mus musculus	P0	ChIP-seq	H3K27ac	ENCSR332JYZ
Hindbrain	Mus musculus	E11.5	DNase-seq	/	ENCSR358ESL
Hindbrain	Mus musculus	E14.5	DNase-seq	/	ENCSR179PIH
Hindbrain	Mus musculus	P0	DNase-seq	/	ENCSR469VGZ
Hindbrain	Mus musculus	E11.5	ChIP-seq	H3K4me1	ENCSR695FPP
Hindbrain	Mus musculus	E15.5	ChIP-seq	H3K4me1	ENCSR921ILW
Hindbrain	Mus musculus	P0	ChIP-seq	H3K4me1	ENCSR617VBE
Hindbrain	Mus musculus	E11.5	ChIP-seq	H3K4me3	ENCSR928CYU
Hindbrain	Mus musculus	E15.5	ChIP-seq	H3K4me3	ENCSR335TVR
Hindbrain	Mus musculus	P0	ChIP-seq	H3K4me3	ENCSR472YGQ
Hindbrain	Mus musculus	E11.5	ChIP-seq	H3K36me3	ENCSR175QZX
Hindbrain	Mus musculus	E15.5	ChIP-seq	H3K36me3	ENCSR809NWL
Hindbrain	Mus musculus	P0	ChIP-seq	H3K36me3	ENCSR458PAO
Forebrain	Mus musculus	E12.5	ChIP-seq	P300	GSE88789
Facial prominence	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR382DRK
Heart	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR574VME
Intestine	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR599GVS

Kidney	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR711SVB
Limb	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR988BRP
Liver	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR479LFP
Lung	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR895BMP
Neural tube	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR241BSK
Stomach	Mus musculus	E15.5	ChIP-seq	H3K27ac	ENCSR929SEW
Cortical plate	Mus musculus	8 weeks	ChIP-seq	H3K27ac	ENCSR000CDD
Cortex	Mus musculus	E14.5	ChIP-seq	TBR2	GSE63621
Cortex	Mus musculus	E14.5	ChIP-seq	NEUROD2	GSE67539
Cortex	Mus musculus	E14.5	ChIP-seq	NEUROG2	GSE63621
Embryonic neural stem cells	Mus musculus	E14.5	ChIP-seq	FOXP1	GSE101632
Cortex	Mus musculus	E15	ChIP-seq	SATB2	GSE68910
Cortex	Mus musculus	E12.5	ChIP-seq	SMAD3	GSE36673
ES-derived NPCs	Mus musculus	/	ChIP-seq	SOX2	GSE35496
ES-derived NPCs	Mus musculus	/	ChIP-seq	YY1	GSE25197
AtT-20 cells	Mus musculus	/	ChIP-seq	ASH2	GSE87180
Embryonic Stem Cells	Mus musculus	E14	ChIP-seq	GFP	GSE52071
B cells	Mus musculus	6-14 weeks	ChIP-seq	ASH2	GSE20852
in vitro differentiated NPC	Mus musculus	/	Hi-C	/	GSE96107
Neuron	Mus musculus	E14.5	Hi-C	/	GSE96107
H1 Neuronal Progenitor cells	Homo sapiens	/	Hi-C	/	GSE52457
H1 embryonic stem cells	Homo sapiens	/	Hi-C	/	GSE52457
H1 Mesendoderm cells	Homo sapiens	/	Hi-C	/	GSE52457
H1 Trophectoderm cells	Homo sapiens	/	Hi-C	/	GSE52457
H1 Mesenchymal stem cells	Homo sapiens	/	Hi-C	/	GSE52457
Dorsolateral Prefrontal Cortex	Homo sapiens	Adult	Hi-C	1	GSE87112

	usea in this study.				
Primers	Sequence (5'-3')	Description			
sg1	gtgagaagcaagagctcact	used for CRISPRa			
sg2	ggaggcagctgtgggcctga	used for CRISPRa and FLAG-dCas9-ChIP to <i>neCtmph1</i>			
sal	cctagacagaacttaagcag				
sg1	agaagetaccatgataccaa				
	yyaayoiyocaiyaiyoaa				
sg1	ggcgcacgcgcagagcgact	used for FLAG-dCas9-ChIP to <i>pCtnnb1</i>			
sg1	atacagcatgagagcaccgt	used for screen functional region of			
sg2	gacactttcgtcgctgctcc				
sg3	ggggtctcctagacatgtag	used for screen functional region of neCtnnb1			
0.01	aaaaaaatataaaaataa	used for screen functional region of			
594	yyayycayciyiyyycciya	neCtnnb1			
295	apportatogottopostap	used for screen functional region of			
syb	gacacialagellaceeige	neCtnnb1			
cab	taactatattatoogoooga	used for screen functional region of			
sgo	เลลงเยเยแบเงงงงงอน	neCtnnb1			
og7	atataaaataaaatttaaaa	used for screen functional region of			
Sgr	aigicacalaggaillacgg	neCtnnb1			
608	actetacatgaagtgecgtg	used for screen functional region of			
	aciciacalyyayiyeeyiy	neCtnnb1			
9na	atagagactagcctactta	used for screen functional region of			
	giggggaelageeelgelig	neCtnnb1			
sq10	assaattastteensseet	used for screen functional region of			
3910	gaayyyiiaaliooyaacoi	neCtnnb1			
neCtnnb1_3C_1	cctgactgaagcaggcatcg	used for 3C			
neCtnnb1_3C_2	gcagggagttacccggtagaa	used for 3C			
neCtnnb1_3C_3	agactctttcttcctctcgtaggct	used for 3C			
neCtnnb1_3C_4	atgatcagtgagagcctgaaatgaa	used for 3C			
neCtnnb1_3C_5	actcatctctctctgcttcccaatat	used for 3C			
neCtnnb1_3C_6	tggcacttcaagtctcttccagg	used for 3C			
pCtnnb1_3C	gccactcctggtgttggagg	used for 3C			
Probe_Ctnnb1_F	cacgactagttcagctgcttgt	used for ISH			
Probe_ <i>Ctnnb1</i> _R	tccacacatgaacatctccttc	used for ISH			
neCtnnb1_ChIP_F	accgtcagagagttaacagc	used for ChIP-qPCR			
neCtnnb1_ChIP_R	actcccctctggtgggtact	used for ChIP-qPCR			
pCtnnb1_ChIP_F	ggcccgctctcgattccttt	used for ChIP-qPCR			
pCtnnb1_ChIP_R	actggcggggactactttcc	used for ChIP-qPCR			
Ctnnb1_Ex3_F	atggagccggacagaaaagc	used for ChIP-qPCR			

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Ctnnb1_Ex3_R	cttgccactcagggaagga	used for ChIP-qPCR			
neCtnnb1_ctrl_F	ctgcttaagctctgcccagg	used for ChIP-qPCR			
neCtnnb1_ctrl_R	ttgacatcatggcagcttcc	used for ChIP-qPCR			
hDesert_F	gggagatggagaaaggtggaaggtt	used for ChIP-qPCR			
hDesert_R	cccaaggccataaaatatgagctggg	used for ChIP-qPCR			
pCTNNB1-ChIP-F	gagaggtgggatccaccatcc	used for ChIP-qPCR			
<i>pCTNNB1</i> -ChIP-R	tcgccgaccttgtggtctgtg	used for ChIP-qPCR			
neCtnnb1-ChIP-F	gcgggcttcttatccccatctg	used for ChIP-qPCR			
neCtnnb1-ChIP-R	tgatgtggcaccttcgggacc	used for ChIP-qPCR			
Ash2l_sh1	ccttaggctatgataagttta	used for knockdown Ash2l			
Ash2l_sh2	cctgtgtctgtgtgttccaaa	used for knockdown Ash2l			
ASH2L_sh1	gtgacttgttatcctactata	used for knockdown ASH2L			
ASH2L_sh2	cctgcttgtatgaacgggttt	used for knockdown ASH2L			
Ash2l_F	cctactttctccggaagcaag	used for RT-qPCR			
Ash2l_R	gacaatgttattgggccaagtc	used for RT-qPCR			
ASH2L_F	agaatggccgacagttggg	used for RT-qPCR			
ASH2L_R	ccttcaagtttgcttgcttcc	used for RT-qPCR			
Ctnnb1_F	atggagccggacagaaaagc	used for RT-qPCR			
Ctnnb1_R	cttgccactcagggaagga	used for RT-qPCR			
CTNNB1_F	aaagcggctgttagtcactgg	used for RT-qPCR			
CTNNB1_R	cgagtcattgcatactgtccat	used for RT-qPCR			
Satb2_F	gccgtgggaggtttgatgatt	used for RT-qPCR			
Satb2_R	accaagacgaactcagcgtg	used for RT-qPCR			
Neurod2_F	aagccagtgtctcttcgtgg	used for RT-qPCR			
Neurod2_R	gccttggtcatcttgcgttt	used for RT-qPCR			
Sox2_F	gcggagtggaaacttttgtcc	used for RT-qPCR			
Sox2_R	cgggaagcgtgtacttatcctt	used for RT-qPCR			
<i>Yy1_</i> F	cagtggttgaagagcagatcat	used for RT-qPCR			
<i>Yy1_</i> R	agggagtttcttgcctgtcat	used for RT-qPCR			
Gapdh_F	aggtcggtgtgaacggatttg	used for RT-qPCR			
Gapdh_R	tgtagaccatgtagttgaggtca	used for RT-qPCR			
Ctnnb1 ^{lox(ex3)} -F	ggtagtggtccctgcccttgacac	used for validation of <i>Ctnnb1</i> ^{lox(ex3)} mice			
Ctnnb1 ^{lox(ex3)} -AS5	acgtctggcaagttccgcgtcatcc	used for validation of <i>Ctnnb1</i> ^{lox(ex3)} mice			
Ctnnb1 ^{lox(ex3)} -P85	ctaagcttggctggacgtaaactc	used for validation of <i>Ctnnb1</i> ^{lox(ex3)} mice			
<i>Ctnnb1</i> ^{ко} -WT-F	ccctgcccctgcatatagcatttga	used for validation of <i>Ctnnb1</i> ^{KO} mice			
<i>Ctnnb1</i> ^{ко} -WT-R	ccccacctgtgatgctttgatgtct	used for validation of <i>Ctnnb1</i> ^{KO} mice			
Ctnnb1 ^{KO} -Mut-R	atgctgtgtgagtgaccctactcct	used for validation of <i>Ctnnb1</i> ^{KO} mice			
Lac7 F	atectetocatorateagote	used for validation of neCtnnb1-LacZ-iCre			
		and BAT-Gal mice			
Lac7 R	catagoctastication	used for validation of neCtnnb1-LacZ-iCre			
		and BAT-Gal mice			