

Generation and analysis of mouse models of aberrant β -catenin function

A thesis submitted in partial fulfilment for the degree of Doctor of Philosophy
to the University of London

by

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Declaration

I, Pedro Manuel Ródenas Cuadrado, confirm that the work presented in this thesis is my original research work. Where contributions of others are involved, this has been clearly indicated in the thesis.

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Abstract

The key component of the Wnt/ β -catenin pathway is β -catenin, a 780 amino acid protein which was originally identified as a component of E-cadherin junctions, where it links E-cadherin with α -catenin and consequently to the actin cytoskeleton. In the absence of Wnt signalling, cytoplasmic β -catenin is phosphorylated and subsequently degraded by ubiquitinylation. Activation of Wnt signalling stabilises cytoplasmic β -catenin, which translocates into the nucleus where it binds to nuclear transcription factors TCF/LEF and regulates the expression of over thirty genes, including cell cycle activating genes.

The Wnt/ β -catenin pathway is essential for nervous system development and it is aberrantly active in common malignant tumours of the central nervous system, such as glioblastoma in adults and medulloblastoma in children.

We have generated a mouse model expressing a Cre-recombinase-inducible form of degradation-resistant (oncogenic) β -catenin. We generated compound mutant mice to activate the Wnt/ β -catenin pathway in specific brain regions and during several developmental time points. Compound mutant transgenic mice expressed dominant active β -catenin *in vivo*, but did not show developmental abnormalities or brain tumours even in combination with inactivated p53 alleles. Similarly, neural stem cells expressing dominant active β -catenin did not show a growth advantage or altered self-renewal. We attributed these results to low level expression of dominant active β -catenin.

In addition, we later acquired mice that carry an inducible deletion of the exon 3 of β -catenin (containing the phosphorylation site). Expression of this form of β -catenin did not increase neural stem cell growth and self-renewal. However, *in vivo* expression results in brain malformation and lethality depending on the cells in which β -catenin was activated, however, recombination in adult stem cells *in vivo* did not result in brain tumours.

Table of contents

Declaration	2
Acknowledgements	3
Abstract	5
Table of contents	6
Index of figures and tables	10
List of abbreviations and acronyms	13
1 Introduction	19
1.1 Brain tumours	20
1.1.1 Medulloblastomas	21
1.1.2 CNS Primary neuroectodermal tumours (PNETs)	23
1.1.3 Turcot's syndrome	23
1.2 Stem cells & cancer stem cells	24
1.3 Wnt Signalling	29
1.3.1 Wnt synthesis and secretion.....	31
1.3.2 Receptors	36
1.3.3 Extracellular Antagonists of the Wnt pathway	39
1.3.4 The Wnt/PCP or Wnt/JNK pathway	42
1.3.5 The Wnt/Ca ²⁺ pathway	44
1.3.6 The canonical Wnt/ β -catenin pathway	46
1.4 Mouse models.....	76
1.4.1 Conventional loss-of-function/knockout Models	76
1.4.2 Mouse models of conditional gene inactivation (Cre-loxP system)	82
1.4.3 Conditional Models for studying the Wnt/ β -catenin pathway in CNS tumours.....	85
2 Materials and methods	87
2.1 Mice	87
2.1.1 Genotyping.....	87
2.1.2 Embryonic LacZ expression.....	87
2.1.3 BrdU injection of mice	87
2.1.4 Adenovirus-Cre intraventricular injection	87
2.2 Tissue harvesting and preparation	88
2.2.1 Brain and peripheral organ harvesting	88

2.2.2	β-galactosidase staining assay	88
2.3	Generation of the pcall2-ΔGSK-β-catenin-IRES-GFP vector.....	89
2.3.1	Restriction enzyme digestion and ligation.....	89
2.3.2	Bacterial transformation and purification	89
2.3.3	ES cells electroporation	90
2.3.4	ES cell selection for LacZ	90
2.3.5	Southern blot analysis.....	91
2.4	Cell culture	92
2.4.1	Transfection of N2a cells.....	92
2.4.2	SVZ dissection and growth of neural stem cells	92
2.4.3	Infection of cultures with Adenovirus	94
2.4.4	WST-1 assay	95
2.4.5	Hoechst proliferation assay	95
2.4.6	NS size	96
2.4.7	Limited dilution assay	96
2.4.8	Differentiation of neural stem cells	96
2.4.9	Immunostaining of differentiated neurospheres	96
2.5	Immunohistochemistry (Paraffin Histology).....	97
2.6	Protein extraction and Western blot	98
2.7	Techniques involving nucleic acids	101
2.7.1	Extraction of DNA from tails or ear biopsies	101
2.7.2	Polymerase Chain Reaction	101
2.7.3	Agarose Gel Electrophoresis.....	103
3	Generation and expression analysis of ΔGSK-β-catenin transgenic mice	104
3.1	Background	104
3.1.1	Aims	105
3.1.2	Methods.....	105
3.2	Results.....	106
3.2.1	Generation of the pcall2-ΔGSK-β-catenin-IRES-GFP vector	106
3.2.2	N2a cells transfected with pcall2-ΔGSK-β-catenin-IRES-GFP vector express ΔGSK-β-catenin following Cre-mediated recombination.....	107
3.2.3	Selection of embryonic stem cells transfected with the pcall2-ΔGSK-β-catenin-IRES-GFP vector for blastocyst injection	108

3.2.4	GSK- β -catenin mice express LacZ in the brain and other organs	110
3.2.5	Nestin-Cre; Δ GSK- β -catenin mice do not show embryonic lethality.....	113
3.2.6	Recombination in Nestin-Cre; Δ GSK- β -catenin mouse brains.....	115
3.2.7	Nestin-Cre; Δ GSK- β -catenin mice express Δ GSK- β -catenin in the brain	118
3.2.8	GSK- β -catenin expression does not alter brain architecture or cellular morphology 121	
3.3	Discussion.....	124
3.4	Summary	126
4	<i>In vitro</i> analysis of ΔGSK-β-catenin expression	127
4.1	Background	127
4.1.1	Aims	128
4.1.2	Methods.....	128
4.2	Results.....	129
4.2.1	<i>In vitro</i> expression of Δ GSK- β -catenin does not influence neuronal stem cell biology 130	
4.2.2	Additional deletion of p53 does not affect brain morphology and does not promote neoplastic transformation	135
4.2.3	Additional deletion of p53 or Rb in neural stem cells does not have a consistent effect on proliferation.....	140
4.2.4	<i>In vivo</i> recombination in the SVZ niche of Δ GSK- β -catenin ^{A/-} ; p53 ^{flox/flox} mice does not cause CNS neoplasia	144
4.3	Discussion.....	145
4.4	Summary	149
5	Analysis of β-catenin^{Δex3} expression in the CNS.....	150
5.1.1	Background	150
5.1.2	Aims	151
5.1.3	Methods.....	151
5.2	Results.....	153
5.2.1	Adeno-Cre treated β -catenin ^{lox(ex3)/wt} NSCs do not show an enhanced growth potential.....	153
5.2.2	Expression of β -catenin ^{lox(ex3)/wt} does not increase differentiation.....	160
5.2.3	Nuclear wild type β -catenin is more abundant than nuclear β -catenin ^{Δex3} in Adeno- Cre treated cells	164
5.2.4	En2-Cre; β -catenin ^{lox(ex3)/wt} mice show developmental abnormalities.....	166

5.2.5	β -catenin ^{lox(ex3)/wt} mice develop SVZ hyperplasia, but no neoplasia following Adeno-Cre injection	169
5.3	Discussion.....	171
5.4	Summary	178
6	Conclusion and future work	179
6.1	Summary	179
6.2	Future work.....	180
6.3	Synergism between Wnt/ β -catenin, p53, PTEN and Rb pathways in CNS tumours.....	180
6.3.1	TP53, PTEN and RB in gliomas	180
6.3.2	TP53, PTEN and RB in medulloblastomas	181
6.3.3	Tumour suppressor genes on chromosome 6	183
7	References.....	185

Index of figures and tables

Figure 1.1 Models for tumour development	25
Figure 1.2 Neurogenesis at the sub-ventricular zone of adult mice	27
Figure 1.3 A possible model for Wg synthesis and secretion	35
Figure 1.4 Domains of the receptors of the Wnt signalling pathway (not to scale)	38
Figure 1.5 Mechanism for Wnt protein antagonism.....	41
Figure 1.6 Schematic representation of the Wnt/PCP pathway in <i>Drosophila</i>	43
Figure 1.7 Wnt/Calcium pathway	45
Figure 1.8 Schematic representation of the Wnt/ β -catenin pathway signalling cascade	47
Figure 1.9 Schematic representation of Wnt/ β -catenin pathway intracellular members (not to scale)	51
Figure 1.10 Wnt/ β -catenin pathway OFF state	54
Figure 1.11 Wnt/ β -catenin pathway ON state.....	58
Figure 1.12 Activation of the cell cycle by cyclin D1	61
Figure 1.13 Generation of knockout mice	77
Figure 1.14 Cre-recombinase recombination events	83
Figure 2.1 Dissection of the SVZ part 1	93
Figure 3.1 pcall2- Δ GSK- β -catenin-IRES-GFP vector	106
Figure 3.2 Cre-mediated recombination of pcall2- Δ GSK- β -catenin-IRES-GFP results in expression of Δ GSK- β -catenin and EGFP in N2a cells.....	107
Figure 3.3 Transfected ES cell clones were selected according to their EcoR I band pattern	109
Figure 3.4 Δ GSK- β -catenin transgenic mice express LacZ in the brain.....	111
Figure 3.5 LacZ expression in somatic organs of Δ GSK- β -catenin transgenic mice.....	112
Figure 3.6 The Δ GSK- β -catenin construct is expressed in the CNS during development	114
Figure 3.7 Nestin-Cre recombination of Δ GSK- β -catenin mouse brains (sagittal sections).....	116
Figure 3.8 Nestin-Cre recombination of Δ GSK- β -catenin mouse brains (coronal sections)	117
Figure 3.9 Nestin-Cre recombination activates the expression of Δ GSK- β -catenin	119
Figure 3.10 No abnormalities were detected in the cerebellum of Nestin-Cre; Δ GSK- β -catenin mice	121
Figure 3.11 No abnormalities in the hippocampus of Nestin-Cre; Δ GSK- β -catenin brains	122
Figure 3.12 No abnormalities in the cortex and thalamus of Nestin-Cre; Δ GSK- β -catenin brains.	123

Figure 4.1 Adeno-Cre infected NSCs express Δ GSK- β -catenin, but do not show increased cyclin D1 levels	130
Figure 4.2 Adeno-Cre infected NSCs do not show increased proliferation potential.....	131
Figure 4.3 Adeno-Cre infected NSCs are not bigger than controls.....	132
Figure 4.4 Adeno-Cre infected NSCs do not show increased self-renewal potential.....	133
Figure 4.5 No obvious difference in the differentiation of Δ GSK- β -catenin ^{A/-} NSCs.....	134
Figure 4.6 There are no abnormalities in the cerebellum of Nestin-Cre; Δ GSK- β -catenin; p53 ^{-/-} brains	136
Figure 4.7 There are no abnormalities in the hippocampus of Nestin-Cre; Δ GSK- β -catenin; p53 ^{loxP/loxP} brains.....	137
Figure 4.8 There are no abnormalities in the cortex and thalamus of Nestin-Cre; Δ GSK- β -catenin; p53 ^{loxP/loxP} brains.....	138
Figure 4.9 No significant difference in brain weight between Δ GSK- β -catenin ^{A/-} ; p53 ^{loxP/loxP} and Nestin-Cre; Δ GSK- β -catenin ^{A/-} ; p53 ^{loxP/loxP} mice	139
Figure 4.10 Adeno-Cre-infected Δ GSK- β -catenin ^{A/A} ; Rb ^{loxP/loxP} and Δ GSK- β -catenin ^{A/A} ; p53 ^{loxP/loxP} NSCs show a slightly enhanced proliferation potential	141
Figure 4.11 Adeno-Cre-infected Δ GSK- β -catenin ^{A/A} ; Rb ^{loxP/loxP} and Δ GSK- β -catenin ^{A/A} ; p53 ^{loxP/loxP} neurospheres are smaller than controls.....	142
Figure 4.12 Adeno-Cre-infected Δ GSK- β -catenin ^{A/A} ; p53 ^{loxP/loxP} NSCs show higher self-renewal, but Δ GSK- β -catenin ^{A/A} ; Rb ^{loxP/loxP} NSCs do not.....	143
Figure 4.13 SVZ recombined Δ GSK- β -catenin ^{A/-} ; p53 ^{flox/flox} mice do not develop abnormal cell proliferations.....	144
Figure 5.1 Adeno-Cre infected β -catenin ^{lox(ex3)/wt} NSCs express β -catenin ^{Δex3} , but do not have increased cyclin D1 levels	154
Figure 5.2 The optimal starting cell number for the WST-1 proliferation assay is 3.5 x 10 ³ cells/ml	155
Figure 5.3 No difference in the proliferation of β -catenin ^{Δex3} expressing NSCs (WST-1 proliferation assay)	156
Figure 5.4 No difference in the proliferation of β -catenin ^{Δex3} expressing NSCs (Hoechst proliferation assay)	157
Figure 5.5 No difference in the size of neurospheres from β -catenin ^{Δex3} expressing NSCs.....	158
Figure 5.6 There is no difference in self-renewal between Adeno-Cre and Adeno-GFP treated NSCs	159

Figure 5.7 β -catenin ^{lox(ex3)/wt} NSCs express MAP2, O4 and GFAP.....	161
Figure 5.8 β -catenin ^{lox(ex3)/wt} NSCs express Nestin, β -catenin and GFAP	162
Figure 5.9 No difference in differentiation between Adeno-Cre and Adeno-GFP treated β -catenin ^{lox(ex3)/wt} NSCs.....	163
Figure 5.10 β -catenin ^{Δex3} protein is not detected in the nucleus of Adeno-Cre recombined NSCs	165
Figure 5.11 The cerebella of En2-Cre; β -catenin ^{Δex3/wt} mice show signs of severe hypoplasia (coronal).....	167
Figure 5.12 The cerebella of En2-Cre; β -catenin ^{lox(ex3)/wt} mice show signs of severe hypoplasia (sagittal)	168
Figure 5.13 β -catenin ^{lox(ex3)/wt} mice develop SVZ enlargements after Adeno-Cre intra cranial (i.c.) injections.....	170
Figure 5.14 Patterning of the midbrain/hindbrain region	175
Figure 5.15 Granule neurone development in mice	177

Table 1.1 Gene nomenclature of key Wnt pathway proteins, antagonists and receptors.....	30
Table 1.2 Nomenclature for genes involved in the Wnt/ β -catenin pathway	48
Table 1.3 Mutations of the Wnt/ β -catenin pathway in selected human cancers	67
Table 1.4 Hypermethylation of Wnt antagonists in selected human cancers.....	71
Table 1.5 De-regulation of the Wnt/ β -catenin pathway in CNS tumours	72
Table 1.6 Phenotypes of Wnt protein ‘conventional’ knockout mice	79
Table 1.7 Phenotypes of Fzd and Lrp ‘conventional’ knockout mice	80
Table 1.8 Phenotypes of Wnt/ β -catenin downstream component ‘conventional’ knockout mice .	81
Table 5.1 Selected literature regarding β -catenin ^{Δex3} transgenic mice.....	152
Table 6.1 Selection of tumour suppressor genes located on the human chromosome 6.....	183

List of abbreviations and acronyms

aa	amino acid
ACC	Acinal cell carcinoma
ADP	Adenosine diphosphate ribose
AIM1	Absent in melanoma 1
APAF-1	Apoptotic protease-activating factor 1
APC	Adenomatous poliposis coli
APS	Ammonium Persulfate
ARF	ADP rybosylation factor
AVL	Avian leukosis virus
Bax	Bcl-2 associated X protein
BCA	Bicinchoninic acid
Bcl-2	B-cell lymphoma 2
BMP	Bone morphogenic protein
bp	base pair
BrdU	5-Bromo-2-deoxyuridine
BSA	Bovine serum albumin
β -TrCP	β -transducin repeats-containing protein
Ca^{2+}	Calcium
CAK	Cyclin activating kinase
CaMK	Calmodulin-dependent kinase
cAMP	cyclin Adenosine monophosphate
CBP	cAMP-binding protein
CCNC	Cyclin C
Cdc42	Cell division cycle 42
CDK	Cyclin-dependent kinase
CDKN1A	Cyclin-dependent kinase inhibitor 1A
cDNA	complementary DNA
Ck1 α	Casein kinase 1 α
cm	centimetre
CNS	Central nervous system
CRC	Colorectal cancer
CRD	Cysteine rich domain
Cre	Causes recombination
Cre-ER	Cre-Oestrogen receptor binding-domain
CSC	Cancer stem cells
CtBP	C-terminal binding protein
Daam1	Dishevelled associated activator of morphogenesis 1
DAG	Diacylglycerol
Dally	Division abnormally delayed
DNA	Deoxyribonucleic acid
DEP	Dvl-egl10-Pleckstrin
Dgo	Diego

DIX	Dishevelled-Axin
Dkk	Dickkopf
DLG	Discs-large protein
DlgA	<i>Drosophila</i> disc large tumour suppressor
Dly	Dally-like
DMEM	Dulbecco's modified Eagle's medium
DMSO	Dimethyl sulfoxide
dNTP	deoxyribonucleotide triphosphate
Drl	Derailed
Dsh/Dvl	Dishevelled
DTT	Dithiothreitol
E2F	E2 transcription factor
EB1	End-binding protein 1
ECM	Extracellular cell matrix
EDTA	Ethylenediaminetetraacetic acid
EF3	Elongation factor 3
EGF	Epidermal growth factor
EGL	External granule layer
En1/2	Engrailed 1/2
ER	Endoplasmic reticulum
ER	Oestrogen receptor
ErB4	Oestrogen receptor β 4
ES	Embryonic stem
FAP	Familial Adenomatous polyposis
FCS	Foetal calf serum
FGF β	Fibroblast growth factor β
Fmi	Flamingo
Fz	Frizzled
g	gram
<i>g</i>	gravitational force
GAG	Glycosaminoglycan
GBM	Glioblastoma
GBP	Gsk3 β binding protein
Gbx2	Gastrulation brain homeobox 2
GCN5	General control nonderepressible 5
GFAP	Glial fibrillary acidic protein
GFP	Green fluorescent protein
GPI	Glycosylphosphatidylinositol
GPCR	G-protein coupled receptor
Gsk3 β	Glycogen synthase kinase 3 β
H&E	Haematoxylin and Eosin
H3/4	Histone 3/4
HAT	Histone acetyltransferase
HCC	Hepatocellular carcinoma

HDAC	Histone deacetylase
HEAT	Huntingtin-EF3-PP2A-TOR1
HEK	Human embryonal kidney
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
HLH-LZ	Helix-loop-helix leucine zipper
HMG	High mobility group
HMT	Histone methyltransferase
HNPCC	Hereditary non-polyposis colorectal carcinoma
HRP	Horseradish peroxidase
HSPG	Heparin sulfate proteoglycans
IGL	Internal granule layer
IO	Isthmic organizer
IP3	Inositol 1,4,5-triphosphate
IPTG	isopropyl β -D-1-thiogalactopyranoside
IQ	Intelligence quotient
IRES	Internal ribosome entry site
JNK	Jun kinase
kb	Kilo base
kDa	Kilo Dalton
Krm	Kremen
L	Litre
LATS1	Large tumour suppressor 1
LB	Luria-Bertani
LDL	Low-density lipoprotein
LDLR	LDL receptor
LEF	Lymphoid enhancer factor
loxP	Locus of crossover (x) in P1
LPP	Lipoprotein
LRP	LDLR-related protein
M	Molar
MAP2	Microtubule associated protein-2
MAPK	Mitogen activated protein kinase
MAPKKK	Mitogen activated protein kinase kinase kinase
Mcl-1	Myeloid cell leukaemia-1
MCR	Mutational cluster region
MDCK	Madin Darby canine kidney
μ g	microgram
mg	milligram
min	minute
μ L	microlitre
mL	millilitre
MLH1/2	MutL homolog 1/2
mM	millimolar
mm	millimetre

µm	micrometer
µM	micromolar
MMP-7	Matrix metalloproteinase-7
MOI	Multiplicity of infection
MOMP	Mitochondrial outer membrane permeabilisation
mRNA	messenger RNA
Nck2	NCK adaptor protein 2
NeuN	Neuronal nuclei
NF200	Neurofilament 200
NFAT	Nuclear factor of activated T cells
NFκB	kappa-light-chain-enhancer of activated B cells
ng	nanogram
NLK	Nemo-like kinase
NLS	Nuclear localisation signal
nm	nanometre
NOL7A	Nucleolar protein 7
NOS	not otherwise specified
NS	Neurosperehere
NSC	Neuronal stem cell
OD	Optical density
Otx2	Orthodenticle homeobox 2
P/S	Penicillin/Streptomycin
pA	polyAdenosine
PBS	Phosphate buffered saline
PCNA	Proliferating cell nuclear antigen
PCP	Planar cell polarity
PCR	Polymerase chain reaction
PDZ	PSD95-DlgA-Zo1
PI	Phosphatidylinositol
PI3K	Phosphatidylinositol-3-kinase
PIP2	Phosphatidylinositol (4,5) biphosphate
Pk	Prickle
PKC	Protein kinase C
PLAGL1	Pleiomorphic Adenoma gene-like 1
PLC	Phospholipase C
pM	picomolar
PMS2	Postmeiotic segregation increased 2
PNET	Primary neuroectodermal tumour
porc	Porcupine
PP2A	Protein phosphatase 2A
PrP	Prion protein
PSD95	Post synaptic density protein 95
PTCH	Patched
PTEN	Phosphatase and tensin homolog

PTPRK	Protein tyrosine phosphatase receptor K
Rac	Ras-related C3 botulinum toxin substrate
Rb	Retinoblastoma
RGS	Regulator of G protein signalling
Rho	Rhodopsin
RhoA	Ras homolog gene A
RIPA	Radio-immunoprecipitation assay
RMS	Rostral migratory stream
RNA	Ribonucleic acid
Rok	Rho kinase
rpm	revolution per minute
rRNA	ribosomal RNA
RT	Room temperature
RTK	Receptor tyrosine kinase
S37A	Serine37Alanine
SAMP	Serine-Alanine-Methionine-Proline
SASH1	SAM and SH3 domain containing 1
SCF	Skp1-Cullin1-F box protein
SCID	Severe combined immuno-defficiency
SCZ	Sub-callosal zone
SDS	Sodium dodecyl sulphate
sFRP	secreted frizzled related protein
SGZ	Sub-granular zone
shh	sonic hedgehog
SL-IC	SCID leukaemia-initiating cell
sPNET	supratentorial PNET
SPT	Solid-pseudopapillary tumour
Stbm	Strabismus
SVZ	Sub-ventricular zone
Syp	Synaptophysin
TAE	Tris base-acetic acid-EDTA
TBP	TATA-binding protein
TBST	Tris-buffered saline Tween-20
TCF	T-cell factor
TE	Tris-EDTA
TEAD1	TEA domain 1
TEMED	Tetramethylethylenediamine
TGFβ	Tumour necrosis factor β
TIP	TATA-interactive protein
TLE-1	Transducin-like enhancer of split-1
tRNA	transfer RNA
TRRAP	Transformation/transcription domain-associated protein
U	units
V	volt

Vps	Vacuolar sorting protein
Wg	Wingless
WHO	World health organisation
WIF	Wnt inhibitory factor
Wls	Wntless
Wnt	Wg/int
Wts	Warts
WTX	Wilms tumour gene on the chromosome X
YAP1	Yes-associated protein 1
Yki	Yorkie
Zo-1	Zonula occludens-1 protein

1 Introduction

Brain tumours are associated with poor prognosis and a high mortality rate. The current approach to treating these tumours is a combination of surgical resection, radiotherapy and chemotherapy depending on the specific type of tumour. Evidence suggests that a population of cells with stem-like properties exist within tumours, called 'cancer stem cells' (CSCs) (Al Hajj *et al.*, 2003; Bonnet and Dick, 1997; Singh *et al.*, 2004). As these cells are rare, a small residual population may survive treatment; continue dividing and regenerate the tumour mass. Studies have demonstrated that these cells are resistant to chemotherapy and often have aberrant DNA repair mechanisms making them also resistant to radiotherapy (Bao *et al.*, 2006; Woodward *et al.*, 2007). Therefore, it is imperative to carefully analyse the molecular and genetic mechanisms underlying the transformation of these cells in order to develop more specific and targeted treatments. Stem cells and 'cancer stem cells' share many common pathways, one of which is the Wnt/ β -catenin pathway, important in differentiation, development and tumourigenesis (Haeghele *et al.*, 2003; Koch *et al.*, 1999; Nusse and Varmus, 1982; Thomas and Capecchi, 1990). In this pathway, β -catenin, a nuclear protein, has a key role (Siegfried *et al.*, 1994).

To study the role of the Wnt/ β -catenin pathway in tumourigenesis of the central nervous system (CNS) we developed a mouse model that inducibly expresses an oncogenic form of β -catenin. More specifically, the well-established Cre-loxP system was used to induce expression in the CNS or in adult neural stem cells to determine the oncogenic potential of activating this pathway.

1.1 Brain tumours

A tumour is an abnormal mass of tissue, which proliferates due to increased cell division and/or resistance to apoptosis. These properties, especially resistance to apoptosis, significantly increase the rate by which tumour cells accumulate random mutations. Some of these mutations confer improved growth/survival characteristics to tumour cells, which can result in a more aggressive phenotype (Sidransky *et al.*, 1992). Brain tumours can be either primary (arising from brain tissue) or secondary (arising from other organs and spreading to the brain by metastasis or direct invasion). Brain tumours are classified according to the patterns or features they express. The World Health Organisation (WHO) classification of tumours of the CNS (2007) provides morphological and immunohistochemical criteria by which to classify brain tumours and predict their biological behaviour. This WHO classification also grades tumours according to their malignancy in a scale from I to IV.

WHO grade I brain tumours are generally tumours with low proliferation, can be cured by surgical resection and have a low risk of recurrence. Grade II tumours also proliferate slowly, but they often recur after surgical resection, sometimes transforming to higher-grade tumours. Patients with WHO grade II tumours typically survive for more than five years following clinical diagnosis. In contrast, patients with WHO grade III tumours tend to survive for two to three years post-diagnosis. WHO grade IV tumours are the most malignant type and are rapidly fatal if left untreated. The prognosis of patients with WHO grade IV tumours is greatly determined by the availability of effective treatment regimens.

1.1.1 Medulloblastomas

Medulloblastomas (WHO grade IV) are the most common malignant brain tumours in childhood, affecting 1 in 200,000 children younger than fifteen years old (Central Brain Tumor Registry of the United States, 1995). Medulloblastomas are largely made up of poorly differentiated cells (Ellison, 2002). There have been significant advances in the treatment of childhood medulloblastomas; in the last five years 60-70 % of patients, compared to 30 % previously, survive for five years (Central Brain Tumor Registry of the United States, 2005). However, most patients suffer from severe long-term cognitive problems (Copeland *et al.*, 1999; Mulhern *et al.*, 1998; Mulhern *et al.*, 1999; Mulhern *et al.*, 2001; Palmer *et al.*, 2001; Palmer *et al.*, 2003; Ris *et al.*, 2001). The most common method for assessing these neuro-cognitive problems has been the Intelligence Quotient (IQ) test. Longitudinal and cross-sectional studies on patients receiving treatment for medulloblastomas have consistently shown a significant correlation of IQ deficiency with tumour resection, radiation dose and age of treatment (Mulhern *et al.*, 1999; Palmer *et al.*, 2001; Palmer *et al.*, 2003; Ris *et al.*, 2001). Deficits in memory and attention have also been observed (Copeland *et al.*, 1999; Mulhern *et al.*, 1998; Mulhern *et al.*, 2001). Histopathologically, medulloblastomas can be sub-divided into classic medulloblastoma, desmoplastic/nodular medulloblastoma, medulloblastoma with extensive nodularity, anaplastic medulloblastoma and large cell medulloblastoma. These sub-divisions correlate with prognosis and are therefore clinically relevant. Large cell and anaplastic medulloblastomas have significantly poorer prognosis, while medulloblastomas with nodular features tend to have a favourable outcome (Brown *et al.*, 2000; Eberhart *et al.*, 2002a; Giangaspero *et al.*, 1992; Giangaspero *et al.*, 2006; Lamont *et al.*, 2004; McManamy *et al.*, 2003; Rutkowski *et al.*, 2005; Sure *et al.*, 1995).

The most common genetic event in medulloblastoma is isochromosomy of 17q. This entails loss of 17p and gain of a second copy of 17q, and occurs in up to 40 % of medulloblastoma cases (Bigner *et al.*, 1988; Griffin *et al.*, 1988). Other common chromosomal losses include 10q (21 %), 8p (15-22 %), 16q (16-17 %) and 11q (11-16 %) (Eberhart *et al.*, 2002b; Rickert and Paulus, 2004).

1.1.1.1 De-regulation of developmental signalling pathways in medulloblastomas

The over-activation of developmentally important pathways such as Sonic Hedgehog, Notch and Wnt is common in medulloblastoma (Fan *et al.*, 2004; Lasser *et al.*, 1994; Pomeroy *et al.*, 2002). The Sonic Hedgehog (Shh) pathway is activated in a subset of medulloblastomas and the most common event is inactivation of Patched (PTCH) (8 % of medulloblastomas), which results in constitutive activation of the pathway (Pietsch *et al.*, 1997; Raffel *et al.*, 1997; Vorechovsky *et al.*, 1997; Wolter *et al.*, 1997; Zurawel *et al.*, 2000). Shh is an important mitogen for cerebellar granule cell progenitors, which are thought to be the cells of origin for the majority of medulloblastomas (Wechsler-Reya and Scott, 1999). Activation of the Shh pathway is associated with desmoplastic/nodular medulloblastomas (Pomeroy *et al.*, 2002; Schofield *et al.*, 1995; Thompson *et al.*, 2006).

Adenomatous polyposis coli (APC) protein is a key negative regulator of the Wnt pathway originally identified as a mutant form in familial Adenomatous polyposis (FAP), an inherited colon cancer syndrome (Grodin *et al.*, 1991; Joslyn *et al.*, 1991; Kinzler *et al.*, 1991). FAP patients have an increased susceptibility for other types of cancer, one of which is medulloblastoma. Subsequently, mutations of components of the Wnt pathway have been found in approximately 20 % of sporadic medulloblastomas (**Table 1.5**). However, pathway activation has been identified in as many as 25 % of medulloblastomas (Eberhart *et al.*, 2000; Ellison *et al.*, 2005; Yokota *et al.*, 2002). Interestingly, although Wnt/ β -catenin pathway activation is normally associated with enhanced proliferation and tumour aggressiveness, pathway activation in medulloblastomas appears to be a marker of favourable prognosis (Bondi *et al.*, 2004; Clifford *et al.*, 2006; Ellison *et al.*, 2005; Kotsinas *et al.*, 2002; Nhieu *et al.*, 1999; Zechner *et al.*, 2003). Studies have shown that 92 % of patients with nucleo-positive β -catenin medulloblastomas have an overall survival of five years in contrast to 65 % percent of patients with non-nuclear (i.e. cytoplasm or membrane-bound) β -catenin medulloblastomas (Clifford *et al.*, 2006; Ellison *et al.*, 2005). This prolonged survival may be due to the presence of fewer genetic mutations in medulloblastomas with an aberrant Wnt/ β -catenin pathway (when compared to other medulloblastomas) (Clifford *et al.*, 2006). Genomic alteration analysis of three β -catenin nucleo-positive medulloblastomas using array-comparative genomic hybridization techniques found that these tumours possessed few chromosomal mutations other than the loss of a copy of chromosome 6 (chromosome 6 monosomy) (Clifford *et al.*, 2006). In contrast, sixteen β -catenin nucleo-negative medulloblastomas harboured widespread chromosomal abnormalities (Clifford *et al.*, 2006).

1.1.2 CNS Primary neuroectodermal tumours (PNETs)

Another type of CNS tumours, in which aberrant activation of the Wnt/ β -catenin pathway has been identified, is the primitive neuroectodermal tumours of the CNS (CNS PNETs). These are a group of heterogeneous embryonal tumours, which predominantly arise in children (Central Brain Tumor Registry of the United States, 2006). 'CNS PNET, not otherwise specified' (CNS PNET, NOS), also termed supratentorial PNET (sPNET), is a WHO grade IV tumour composed of undifferentiated or poorly differentiated neuroepithelial cells arising from within the brain. The incidence of these tumours is difficult to determine due to their rarity and unclear classification. The percentage of cells undergoing proliferation in sPNET is generally high, reaching up to 85 % within a high-power field of view. Although medulloblastomas are also called infratentorial PNETs, they do not share genetic similarity with sPNETs (Pomeroy *et al.*, 2002). SPNETs are scarce, making it hard to determine the way in which these tumours arise. Wnt/ β -catenin pathway activation has been observed in these tumours, but its role remains unclear (Koch *et al.*, 2001; Rogers *et al.*, 2009).

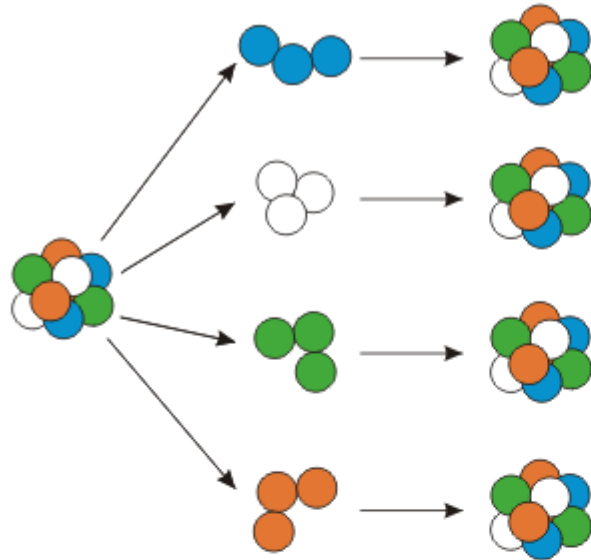
1.1.3 Turcot's syndrome

Turcot's syndrome is a rare hereditary disease and presents with CNS tumours and colorectal polyps or colorectal cancer (Hamilton *et al.*, 1995; Lasser *et al.*, 1994; Mori *et al.*, 1994; TURCOT *et al.*, 1959). According to the underlying genetic cause, Turcot's syndrome can be divided into two types (Hamilton *et al.*, 1995). Type I involves glioblastomas or astrocytomas along with hereditary non-polyposis colorectal carcinoma (HNPCC) and germline mutations in the DNA mismatch repair genes, postmeiotic segregation increased 2 (PMS2), mutL homolog 1 (MLH1) and/or MSH2 (Hamilton *et al.*, 1995). Type II is characterised by medulloblastomas and FAP, as a result of APC truncation mutations in the germline (Hamilton *et al.*, 1995; Lasser *et al.*, 1994; Mori *et al.*, 1994).

1.2 Stem cells & cancer stem cells

There are two hypotheses that explain how tumours arise and develop: the stochastic model and the hierarchical model [reviewed in (Dick, 2009)] (**Figure 1.1**). The stochastic model predicts that all the cells in a tumour are heterogeneous, but can promote tumour progression due to intrinsic or extrinsic variables [reviewed in (Dick, 2009)]. The hierarchical model predicts that only a small subset of cells in a tumour is capable of re-generating the bulk of the tumour, with the rest of the cells being more differentiated [reviewed in (Dick, 2009)]. The hierarchical model corroborates with the cancer stem cell (CSC) hypothesis, which postulates that tumours are initiated and maintained by a population of cells with similar properties to adult stem cells; termed CSCs (Al Hajj *et al.*, 2003; Bonnet and Dick, 1997). The first of these cells to be described was the severe combined immunodeficiency (SCID) leukaemia-initiating cell (SL-IC) in 1997 (Bonnet and Dick, 1997). Similarly, CSCs have been identified in breast and colon cancer and it is widely thought that the same may be true for most, if not all, cancers (Al Hajj *et al.*, 2003; O'Brien *et al.*, 2007; Ricci-Vitiani *et al.*, 2007). Recently, a third model containing elements of both the hierarchical and stochastic models has been suggested [reviewed in (Greaves, 2010)]. This model proposes that CSCs in a tumour may be heterogeneous, with sub-clones becoming more or less dominant than others due to stochastic and seemingly random variations.

A. Stochastic Model



B. Hierarchical Model

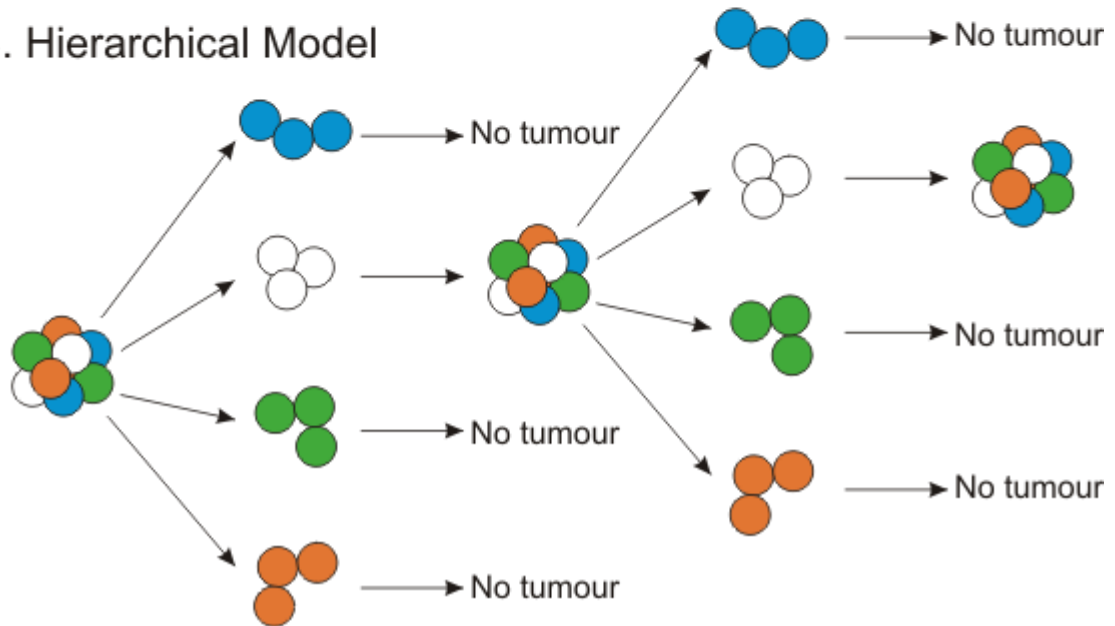


Figure 1.1 Models for tumour development¹

(A) Stochastic model for tumour development. This model predicts that all cells types in a tumour have the potential to be tumourigenic. (B) The hierarchical model predicts that only specific cells in a tumour have the capacity to drive tumour progression and re-generate the bulk of the tumour after treatment. The other cell populations in the tumour are made up of more differentiated cells.

¹ Adapted by permission from Macmillan Publishers Ltd: Nature Biotechnology, John E. Dick, Looking ahead in cancer stem cell research, **27**, pp. 44-46, copyright (2009).

Stem cells are defined by two key properties: their ability to differentiate into multiple cell types of the organ they are derived from (multipotency), and their ability to divide symmetrically or asymmetrically to maintain the stem cell pool (self-renewal).

For many years, the adult brain was thought to be capable of proliferation (Altman and Das, 1965; Dacey and Wallace, 1974; MESSIER *et al.*, 1958; Reynolds and Weiss, 1992). Since then, this has been convincingly demonstrated in rats, mice, humans and many other species (Eriksson *et al.*, 1998; Gould *et al.*, 1998; Kirschenbaum *et al.*, 1994; Kukekov *et al.*, 1999; Lois and Alvarez-Buylla, 1993; Luskin, 1993).

To date, four distinct stem cell niches have been identified in the murine brain. These include (i) the sub-ventricular zone (SVZ) of the lateral ventricle, (ii) the sub-granular zone (SGZ) in the dentate gyrus of the hippocampus, (iii) the sub-callosal zone (SCZ) located between the hippocampus and the corpus callosum, and (iv) a reservoir between the internal granule layer (IGL) and the white matter of the cerebellum (Doetsch *et al.*, 1999; Lee *et al.*, 2005; Seri *et al.*, 2001; Seri *et al.*, 2006). The largest of these areas is the SVZ (**Figure 1.2**). Alvarez-Buylla and colleagues identified a subset of cells within this area, which possess characteristics of both stem cells and astrocytes (Doetsch *et al.*, 1999). These were termed B-type cells and were shown to regenerate the whole SVZ cell population following *in vitro* ablation (Doetsch *et al.*, 1999). B-type cells are capable of slow division and differentiation into transiently amplifying C-type cells, which can rapidly proliferate and differentiate to give rise to large numbers of young neuroblasts (type A cells) (Doetsch *et al.*, 1999). Type A cells are restricted to a neuronal fate and migrate along the rostral migratory stream (RMS) until they reach the olfactory bulb where they differentiate into interneurons (Doetsch and Alvarez-Buylla, 1996; Lois *et al.*, 1996; Lois and Alvarez-Buylla, 1994).

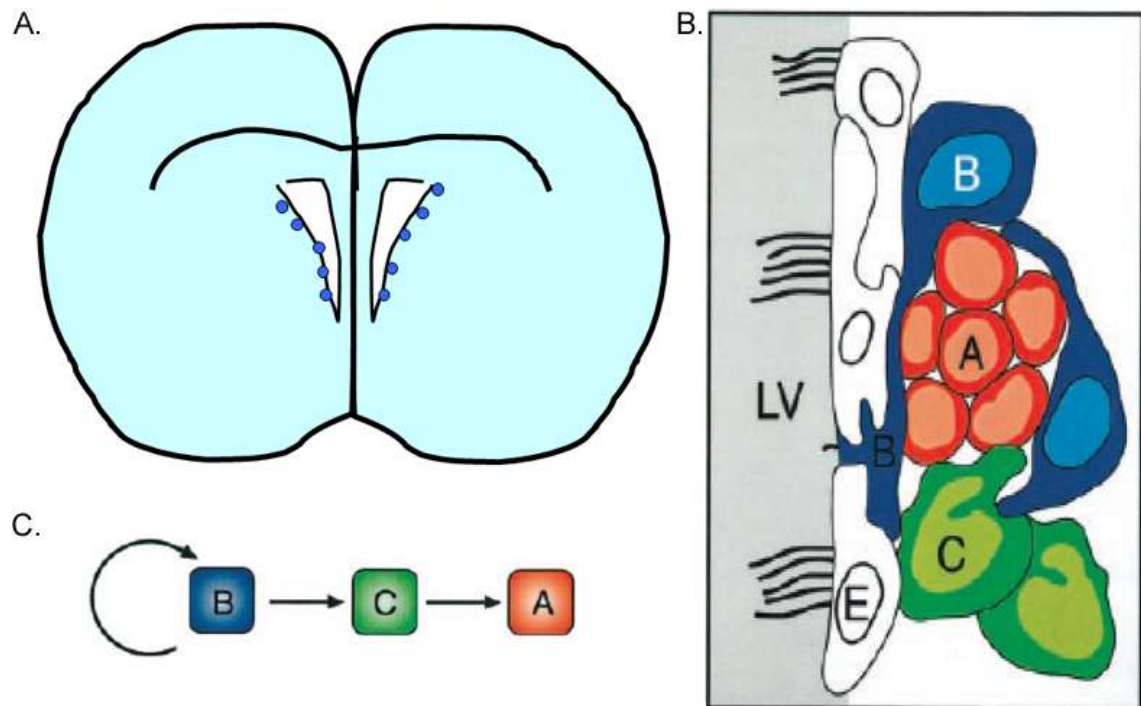


Figure 1.2 Neurogenesis at the sub-ventricular zone of adult mice²

(A) Diagram of a coronal section of a mouse brain. Neural stem cells (dark blue dots) are located in the sub-ventricular zone (SVZ) in the lateral wall of the lateral ventricle. These cells migrate out of the SVZ as they undergo differentiation. (B) Schematic diagram of cellular organisation of the SVZ at the lateral ventricle (LV), which comprises ependymal cells (E), type A neuroblasts (A), astrocytic putative stem cells (B), and transiently amplifying stem cells (C). (C) Type B cells undergo asymmetric division to generate a sister Type B cell and a Type C cell. Type C cells divide rapidly and differentiate to give rise to Type A neuroblasts, which migrate to the olfactory bulb to integrate as interneurons.

² Adapted by permission of Expert Reviews Ltd: Samantha J. Richardson *et al.*, Hormones and adult neurogenesis in mammals, Expert reviews of Endocrinology & Metabolism, 2, pp. 261-276, copyright (2007).

Neuronal stem cell (NSC) properties can be investigated *in vitro* by growing them under non-adherent conditions in medium rich in mitogens such as epidermal growth factor (EGF) and fibroblast growth factor β (FGF β) (Doetsch *et al.*, 1999; Doetsch *et al.*, 2002; Gritti *et al.*, 1996; Gritti *et al.*, 1999). Under these conditions most differentiated cells undergo apoptosis, while NSCs grow in response to the growth factors. An interesting property of *in vitro* cultured stem cells is their ability to grow as spherical conglomerates, termed 'neurospheres' (NS). NSCs can be serially passaged and cultured under these conditions confirming their ability to self-renew (Gritti *et al.*, 1996). Upon removal of growth factors NSCs differentiate into neurones, astrocytes or oligodendrocytes (Gritti *et al.*, 1996; Gritti *et al.*, 1999). Cells with stem-like characteristics were discovered in glioblastoma multiforme and medulloblastoma after use of such mitogen-enriched medium (Hemmati *et al.*, 2003; Ignatova *et al.*, 2002). The study by Ignatova and colleagues showed that these cells form spheres and that they could be serially passaged and differentiated along neuronal and glial lineages (astrocytes, oligodendrocytes) (Ignatova *et al.*, 2002). Furthermore, Hemmati *et al.*, 2003 were able to show that transplantation of glioblastoma cells, grown *in vitro*, into nude mice reproduced the original tumour (Hemmati *et al.*, 2003). Similarly, neurosphere growing cells from these tumours can be isolated and re-grafted to recapitulate glioblastoma, thus showing the *in vivo* self-renewal potential of these CSCs (Galli *et al.*, 2004) .

The growth similarities between intrinsic NSCs and CSCs are a good indication that parallel growth, survival and proliferation pathways are active in both types of cells. An important pathway in stem cells proliferation and differentiation is the Wnt signalling pathway, which is the focus of this thesis.

1.3 Wnt Signalling

Correct development requires precise coordination between evolutionary conserved signalling pathways [reviewed in (Chopra and Levine, 2009; Raible, 2006)]. One of these pathways is the Wnt signalling pathway, which has been shown to play a critical role in embryonic patterning/cell polarity, differentiation (Funayama *et al.*, 1995; Huelsken *et al.*, 2000; Lie *et al.*, 2005) and is de-regulated in tumours (**Table 1.3** and **Table 1.5**). There are currently 19 Wnt proteins described in mammals (www.stanford.edu/~rnusse/Wntwindow.html). Loss of function of Wnt genes has been shown to cause severe developmental abnormalities (**Table 1.6**). There are at least three pathways attributed to Wnt proteins; the Wnt/planar cell polarity (PCP) pathway (also known as the Wnt/JNK pathway in vertebrates), the Wnt/Calcium (Ca^{2+}) pathway and the canonical Wnt/ β -catenin pathway. The focus of this thesis is on the canonical pathway, mainly because of its de-regulation in human cancers (**Table 1.3** and **Table 1.5**). The Wnt/PCP and the Wnt/ Ca^{2+} pathway will also be briefly described.

Table 1.1 Gene nomenclature of key Wnt pathway proteins, antagonists and receptors

Values in parentheses are the number of known homologues

Species	Function in Wnt pathway	Nomenclature (gene)		
		Human	Mouse	<i>Drosophila</i>
Wnt	Ligand	WNT (19)	Int/Wnt (19)	Wg, DWnt (7)
Porc	Palmitoylation	PORC (4)	Porc (4)	porc
Wls	Wnt secretion	WLS	Wls	wls
Dkk	Wnt antagonist	DKK (4)	Dkk	-
sFRP	Wnt antagonist	SFRP1, 2, 4, 5, FRZB	Sfrp1, 2, 4, 5, FrzB	-
Fz	Receptor	FZD (10), SMO	Fzd (10), smo	Fz, dfz (5)
LRP	Co-receptor	LRP (2)	Lrp (11)	arrow
Ryk	Co-receptor	RYK	Ryk	Derailed
Ror	Co-receptor	ROR (2)	Ror (2)	Ror
Knypek	Co-receptor	GPC4, GPC6	Gpc4, Gpc6	dlp
Krm	Co-receptor	KREMEN (2)	Kremen (2)	-

1.3.1 Wnt synthesis and secretion

1.3.1.1 Wnt Synthesis

Wnt proteins are excreted as lipid-modified glycoproteins, which contain 23 cysteine residues, an N-terminal signal sequence and some possible N-glycosylation sites (Kurayoshi *et al.*, 2007; van Ooyen *et al.*, 1985). The highly conserved spacing of the cysteine residues suggests that intra-molecular disulphide bridges may be important for correct Wnt protein folding. Although not evident from the primary sequence, Wnt proteins are lipid modified by palmitoylation at two residues (Takada *et al.*, 2006; Willert *et al.*, 2003). The first modification discovered was in Cysteine77 on Wnt3A (Willert *et al.*, 2003). This residue, and by extrapolation the palmitate group, is conserved in all Wnt proteins. Mutation at this residue greatly impairs the signalling activity of Wnt proteins (Willert *et al.*, 2003). Recently, a second lipid modification was identified at Serine209 on Wnt3A (Takada *et al.*, 2006). This palmitoylation event is essential for proper intracellular trafficking of Wnt proteins as mutations have been demonstrated to lead to the accumulation of Wnt in the endoplasmic reticulum (ER) (Takada *et al.*, 2006). The acyltransferase porcupine (porc) has been suggested to catalyse palmitoylation at this residue, as loss of function of this protein mimics the Serine209 phenotype (Takada *et al.*, 2006). Porc encodes an ER multi-pass transmembrane protein from the O-acyltransferase superfamily (Hofmann, 2000; Kadowaki *et al.*, 1996). However, it is unclear if it also catalyses Cysteine77 palmitoylation, since any possible phenotype is probably masked by loss of the lipid modification at Serine209.

1.3.1.2 Wnt Secretion

Recent studies have identified factors involved in Wnt protein secretion (Bartscherer *et al.*, 2006; Coudreuse *et al.*, 2006). These factors consist of the retromer complex and the multi-pass transmembrane protein Wntless (WLS). Three independent laboratories have identified a protein called Wntless (Wls), which is required for secretion of Wnt proteins, *in vivo* and *in vitro* (Banziger *et al.*, 2006; Bartscherer *et al.*, 2006; Goodman *et al.*, 2006). Wls is a multi-pass transmembrane protein conserved in *C. elegans* and mammals, which directly interacts with Wnt proteins (Banziger *et al.*, 2006; Bartscherer *et al.*, 2006; Goodman *et al.*, 2006). It has been localised at the plasma membrane, the Golgi and endosomes (Bartscherer *et al.*, 2006; Belenkaya *et al.*, 2008; Port *et al.*, 2008). Whereas the molecular function of Wls remains to be elucidated, it has been proposed to help localisation and secretion of Wnt proteins (Yang *et al.*, 2008). Studies using a Wls-green fluorescent protein (GFP) fusion protein have shown that Wls is enriched in the apical membrane of polarised *Drosophila* follicle cells and largely absent at the basolateral membrane (Bartscherer *et al.*, 2006). Wingless (Wg), the *Drosophila* Wnt protein, accumulates at the apical side of polarised cells, but is retained in the ER in the absence of Wls (Marois *et al.*, 2006; Port *et al.*, 2008). This supports the idea that Wls might work as a cargo receptor assisting Wg/Wnt to reach the apical membrane, from where it is released (**Figure 1.3**).

In 2006, the retromer was shown to be able to regulate Wnt proteins (Coudreuse *et al.*, 2006; Prasad and Clark, 2006). The retromer is a complex of evolutionary conserved proteins from the Vps family. In yeast, the retromer complex is made up of Vacuolar sorting protein (Vps) 5, Vps17, Vps26, Vps29 and Vps35 and orthologs exist in *C. Elegans*, *Drosophila* and mammals [reviewed in (Seaman, 2005)]. These proteins function to selectively retrieve cargo receptors to the Golgi to rescue them from endosome-mediated degradation (Arighi *et al.*, 2004; Seaman, 2004). A key example of this is the recovery of mannose-6-phosphate in mammals (Arighi *et al.*, 2004). In the absence of retromer, Wnt protein secretion is abrogated (Coudreuse *et al.*, 2006). This phenotype closely resembles loss of Wls, suggesting that the retromer might act by recycling Wls back to the Golgi (Belenkaya *et al.*, 2008; Franch-Marro *et al.*, 2008; Port *et al.*, 2008). This hypothesis is strengthened by assays showing co-immunoprecipitation of Vps35 and Wls and antibody-uptake assays showing recycling of Wls (Belenkaya *et al.*, 2008; Franch-Marro *et al.*, 2008).

1.3.1.3 Extra-cellular transport

Extra-cellular detection of Wg in wing imaginal discs reveals two types of signalling: a steep and narrow gradient at the apical side termed short-range signalling and a broad Wg gradient across the basolateral surface, termed long-range signalling (Panakova *et al.*, 2005; Strigini and Cohen, 2000). The latter type is capable of up-regulating genes up to twenty to thirty cells away from the secreting cells (Zecca *et al.*, 1996). The way this is achieved is currently unclear as Wnt proteins are hydrophobic and possibly membrane-bound through lipid modifications (Takada *et al.*, 2006; Willert *et al.*, 2003). Currently, there are two hypotheses to explain how long-range signalling may occur. First, studies have indicated that palmitoylation may allow Wnt proteins to interact with each other to form multimeric complexes (Takada *et al.*, 2006; Willert *et al.*, 2003). Palmitoylation has been implicated in the extracellular movement of Hedgehog, another lipid-modified secreted morphogen (Chen *et al.*, 2004). In this manner Wnt proteins could overcome their inherent hydrophobicity and potentiate their signalling capacity. Second, recent studies in *Drosophila* have suggested that Wnt proteins may be secreted bound to lipoproteins (LPPs), which could act as vehicles facilitating long-range signalling (Panakova *et al.*, 2005). LPPs are spherical bodies consisting of a lipid monolayer, apolipoproteins and cholesterol, which contain triacylglycerides in their core [reviewed in (Brown and Goldstein, 1986)]. Once they bind to low density lipoprotein (LDL) receptors on receptor cells, they are endocytosed and their cargo is used by the cell [reviewed in (Brown and Goldstein, 1986)]. In *Drosophila*, Wg has been found to be associated with LPPs in the extracellular space and loss of lipophorin (the *Drosophila* LPP) reduces the range of Wg signalling (Panakova *et al.*, 2005). Both Wg and lipophorin localise to endosomes (Chen *et al.*, 2004). As such, it is possible that they become loaded into lipophorin and subsequently secreted at the basolateral membrane (Chen *et al.*, 2004).

Accumulating evidence suggests that glycosaminoglycan (GAG)-modified proteins might facilitate the extracellular movement of Wnt proteins (Baeg *et al.*, 2001; Lin and Perrimon, 1999; Nakato *et al.*, 1995; Perrimon *et al.*, 1996; Tsuda *et al.*, 1999). In *Drosophila*, mutations in two enzymes involved in the synthesis of heparin sulphate proteoglycans (HSPGs), namely sugarless (encodes a UDP-glucose dehydrogenase) and sulfateless (encodes a heparin sulphate N-deacetylase/N-sulfotransferase), result in aberrant Wg signalling (Binari *et al.*, 1997; Hacker *et al.*, 1997; Haerry and Gehring, 1997; Lin and Perrimon, 1999). HSPGs are extracellular cell membrane and cell surface proteins with attached heparin sulphate GAGs [reviewed in (Bernfield *et al.*, 1999)]. Various genetic screens have shown that two HSPGs, Dally (division abnormally delayed) and Dally-like (Dly) appear to be required for Wnt signalling (Baeg *et al.*, 2001; Tsuda *et al.*, 1999). This became

apparent when a study using dsRNA to knock-down the expression of these proteins recapitulated the phenotype seen when *Wg* is lost (Baeg *et al.*, 2001; Tsuda *et al.*, 1999). Dally and Dly belong to the glypican family of cell surface HSPGs, and are linked to the plasma membrane *via* a glycosylphosphatidylinositol (GPI) anchor (Tsuda *et al.*, 1999). The exact method by which these receptors mediate Wnt protein signalling is not understood. It has been hypothesised that they may interact with secreted Wnt proteins to sequester them at the membrane and promote binding to Wnt receptors (Cadigan *et al.*, 1998). Alternatively, interaction between Wnt proteins and Dally and Dly may be required for endocytosis and recycling of Wnt proteins. Finally, it may be that GPI-linked Dally and Dly stabilise Wnt proteins as they are transported in LPPs. Experimental evidence for this later hypothesis came from GFP studies in LPPs of *Drosophila* wing imaginal disc cells, which were found to express GPI-linked GFP (Greco *et al.*, 2001).

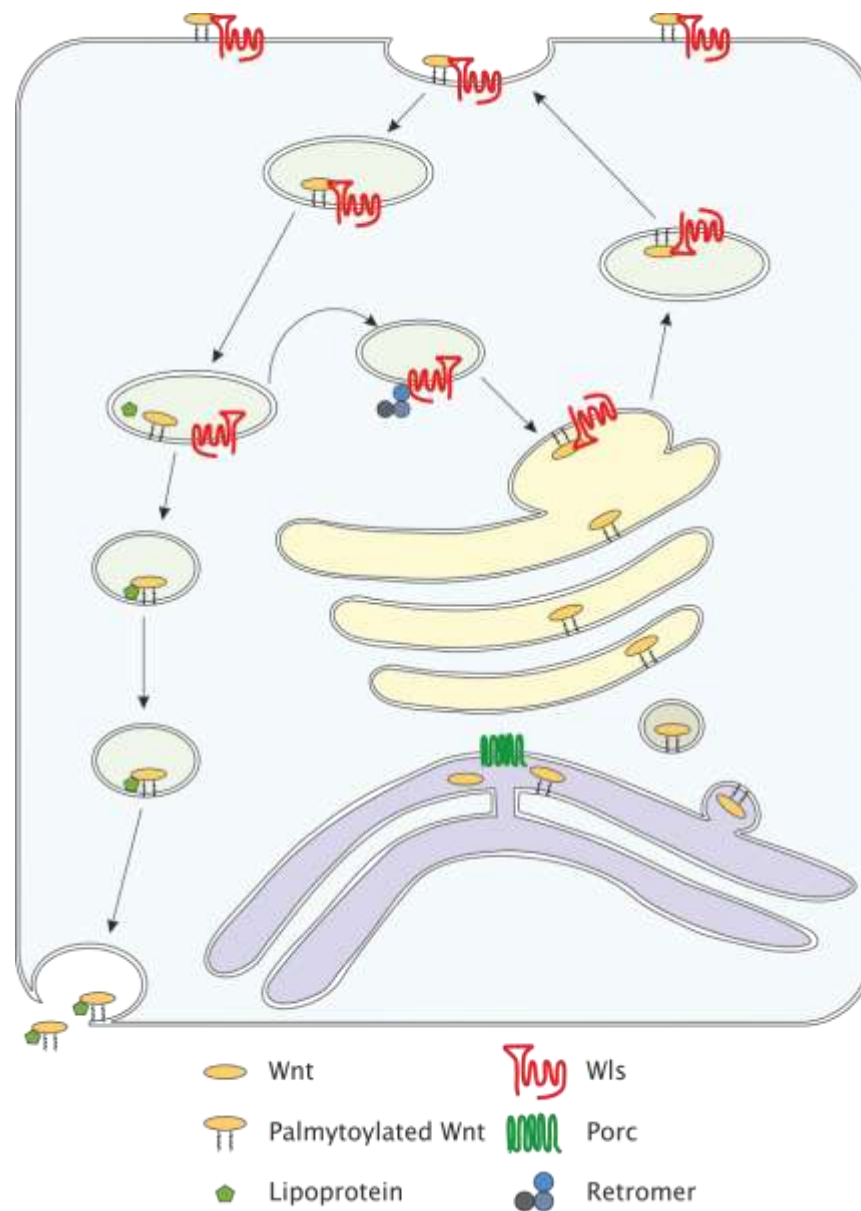


Figure 1.3 A possible model for Wg synthesis and secretion³

Wingless (Wg) is palmytoylated by Porcupine (Porc) in the endoplasmic reticulum. Subsequently, Wg is transported through the Golgi apparatus and secreted to the apical side in a complex with Wntless (Wls). At the apical side, Wg can mediate short range signalling. For basolateral secretion, Wg is endocytosed alongside Wls. In the endosome, Wls dissociates from Wg and is recycled to the Golgi apparatus by the retromer complex. Wg complexes with lipoproteins and is secreted at the basolateral side, where it can mediate long-range signalling.

³ Adapted by permission of Macmillan Publishers Ltd: EMBO Reports, Kerstin Bartscherer & Michael Boutros, Regulation of Wnt protein secretion and its role in gradient formation, 9, pp. 977-982, copyright (2008).

1.3.2 Receptors

There are two main types of receptors required for Wnt protein signal transduction: Frizzled receptors (Fz) and LDL receptor (LDLR)-related receptor proteins (LRPs) (Wehrli *et al.*, 2000; Yang-Snyder *et al.*, 1996). Fz are seven-pass transmembrane receptors, which are a common component of all three Wnt pathways. All Fz proteins share a highly glycosylated N-terminus containing ten invariantly spaced cysteines which is called the cysteine-rich domain (CRD) (Wang *et al.*, 1996). Additionally, Fz proteins contain a conserved seven-pass transmembrane domain and an intracellular domain with little homology between family members (Wang *et al.*, 1996) (**Figure 1.4**). Wnt proteins interact with Fz receptors *via* their CRD domain (He *et al.*, 1997; Yang-Snyder *et al.*, 1996). This interaction has been successfully characterised in *Drosophila* where Wg binds to *Drosophila* Fz1 (DFz1) and DFz2 with an affinity coefficient of 10^{-8} M and 10^{-9} M respectively (Bhanot *et al.*, 1996; Rulifson *et al.*, 2000). The precise mechanism by which Wnt protein signals are transduced is not known, but evidence suggests that heterotrimeric G proteins are involved (Liu *et al.*, 2001; Slusarski *et al.*, 1997a). This leads to the activation of either of the known Wnt signalling pathways (Wnt/PCP, Wnt/Ca²⁺, Wnt/ β -catenin). This is an inherently complicated process, not only because of the large diversity of Wnts (19 in mammals) and Fzs (10 in humans and mice), but also because of difficulties encountered in attempts to purify Wnt proteins (Willert *et al.*, 2003). Furthermore, some Wnt proteins can induce distinct Wnt pathways by interacting with different Wnt receptors. For example, Wnt5a can induce the Wnt/ β -catenin pathway when it interacts with Fz5 or Fz4 (He *et al.*, 1997; Mikels and Nusse, 2006). On the contrary, when the same protein interacts with Ror2, an alternative Wnt receptor, it is capable of inducing the Wnt/PCP pathway (Mikels and Nusse, 2006). Therefore, the action of Wnt proteins depends on the various Wnt protein receptors expressed by cells or tissues.

Whilst Wnt/Fz interaction is sufficient for inducing non-canonical Wnt pathways, activation of the Wnt/ β -catenin pathway also requires the involvement of LRP5 and LRP6 (Semenov *et al.*, 2001; Wehrli *et al.*, 2000). In *Drosophila*, the co-receptor is named Arrow (Wehrli *et al.*, 2000) and in vertebrates two LRP proteins have been identified; LRP5 and LRP6 (Pinson *et al.*, 2000; Tamai *et al.*, 2000). *Drosophila* mutants lacking Arrow reproduced Wg loss whereas LRP6 knockout mice resembled Wnt protein knockout defects (e.g. mid and hindbrain defects, ventralization of limbs etc.) (Pinson *et al.*, 2000). Furthermore, truncated LRP5/6 lacking the extracellular domain, but still anchored to membrane, were shown to constitutively activate the canonical pathway (Brennan *et al.*, 2004; Mao *et al.*, 2001a; Mao *et al.*, 2001b). Whilst the precise method of signal transduction is not known, it is thought that trimerisation of Wnt, Fz and LRP may be required (Schweizer and Varmus, 2003).

In addition to Fz and LRP two more types of potential transducers of Wnt signalling have been discovered. The first of these is Ror2, a single-pass transmembrane protein of the receptor tyrosine kinase (RTK) (Oishi *et al.*, 2003). This receptor interacts with Wnt5a to activate the Wnt/JNK pathway (Mikels and Nusse, 2006; Oishi *et al.*, 2003). Ror2 deficient mice exhibit skeletal, genital and cardiovascular abnormalities that have been attributed to aberrant convergent extension during gastrulation, a process mediated by the Wnt/JNK pathway in vertebrates (Oishi *et al.*, 2003). The second type of receptor is Ryk and its *Drosophila* (Derailed, Drl) and *C. Elegans* (Lin-18) homologues (Hovens *et al.*, 1992; Inoue *et al.*, 2004; Yoshikawa *et al.*, 2003). Studies in human embryonic kidney cells (HEK293) have shown that Ryk induces the Wnt/ β -catenin pathway as a co-receptor with Fz and Wnt proteins (Lu *et al.*, 2004). Functionally, Ryk appears to be required for neurite outgrowth, induced by Wnt3a and Wnt1, and for corticospinal tract axon repulsion, induced by Wnt1 and Wnt5a (Liu *et al.*, 2005; Lu *et al.*, 2004). Interestingly, Ryk contains an extracellular domain similar to the secreted Wnt inhibitor factor-1 (WIF), which is thought to mediate Ryk/Wnt interaction (Patthy, 2000).

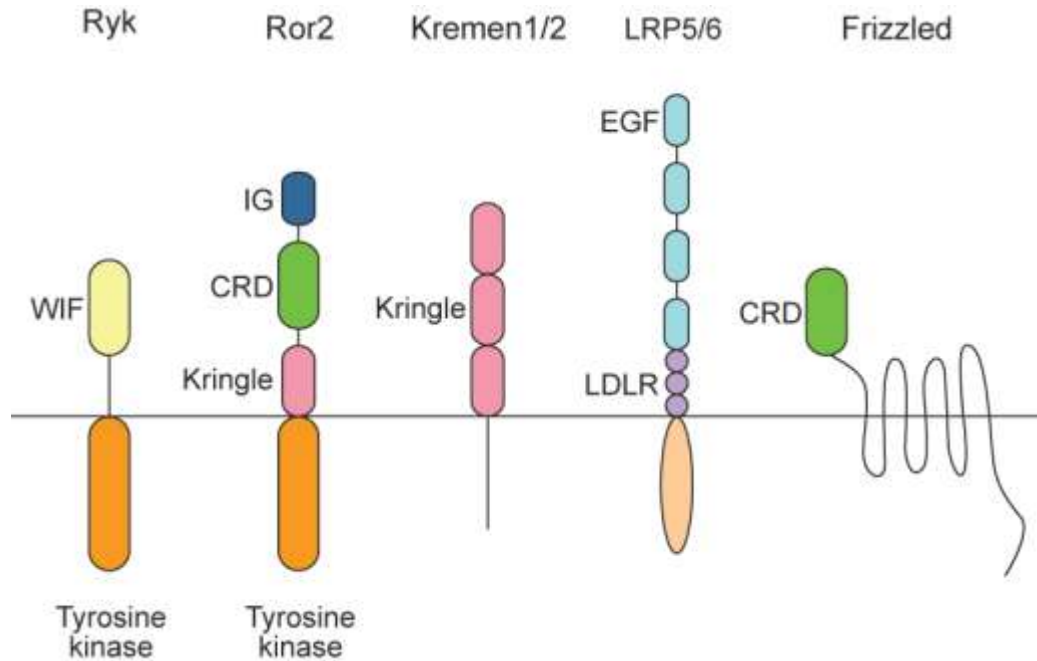


Figure 1.4 Domains of the receptors of the Wnt signalling pathway (not to scale)

Ryk contains an intracellular tyrosine kinase and an extracellular Wnt inhibitory factor (WIF) domain. Ror2 contains an intracellular tyrosine kinase and an extracellular Kringles domain, cysteine-rich domain (CRD) and an immunoglobulin (IG) domain. Kremen1/2 contains three extracellular kringles domains. LRP5/6 contains three low-density lipoprotein receptor (LDLR) domains and four epidermal growth factor-like (EGF) domains. Frizzled contains an extracellular CRD domain.

1.3.3 Extracellular Antagonists of the Wnt pathway

Binding of Wnt proteins to receptors is modulated by endogenously-secreted antagonists (Bafico *et al.*, 1999; Glinka *et al.*, 1998) (**Figure 1.5**). These antagonists can be divided into two functional classes: secreted frizzled related proteins (sFRPs) and Dickkopf (DKK) proteins (Bafico *et al.*, 1999; Semenov *et al.*, 2001). Members of the sFRP group include the sFRP family, WIF-1 and Cerberus. There are currently eight known sFRP family members, namely sFRP1 to 5, Sizzled, Sizzled2 and Crescent. These can be further sub-divided based on sequence homology: sFRP1, sFRP2 and sFRP5 form one group, and sFRP3 and sFRP4 form the second group. sFRP1 to 5 have not been identified in invertebrates, and Sizzled, Sizzled2 and Crescent, which make up the final subgroup, have not been identified in mammals. Structurally, sFRPs show homology with the Fz CRD domain at the N-terminus and with Netrin, an axonal guidance protein, at the C-terminus (Banyai and Patthy, 1999; Melkonyan *et al.*, 1997). The antagonistic effect of sFRPs is thought to arise from the interaction of their CRD-like domain with Wnt proteins (Lin *et al.*, 1997). However, sFRP1 has also been found to interact with Fz (Bafico *et al.*, 1999). Thus, sFRPs might modulate Wnt signalling by physically interacting with Wnt proteins or by preventing Wnt proteins from binding to Fz.

However, sFRPs do not always act as antagonists (Melkonyan *et al.*, 1997; Uren *et al.*, 2000). *In vitro* experiments with Madin Darby canine kidney (MDCK) cells demonstrated that sFRP1 could potentiate Wg signalling at low concentrations (Uren *et al.*, 2000). This potentiation was observed with truncated sFRP1 lacking the CRD domain, suggesting that the Netrin-like domain (NTR) may serve as a high affinity binding site for Wg (Uren *et al.*, 2000). An alternative hypothesis is that at high concentrations sFRP1 could interact with Frizzled, preventing Frizzled/Wg interaction. Indeed, sFRP1 was found to interact with human Fz6 (Bafico *et al.*, 1999). The obvious caveat with these assays is that they involve *Drosophila* Wg rather than mammalian Wnt. Although there is a high degree of conservation between Wg and Wnt proteins, it is possible that they interact differently with sFRPs. Similarly to sFRP1, sFRP2 can also function both as an antagonist and as an agonist (Ladher *et al.*, 2000; Melkonyan *et al.*, 1997). Injection of sFRP2 into *Xenopus* embryos blocks the dorsalising activity of Wnt-8 (Ladher *et al.*, 2000). However, sFRP2 has been shown to block the antagonistic activity of sFRP1 when co-expressed in the metanephric kidney (Yoshino *et al.*, 2001).

Although sFRPs have been postulated to be tumour suppressor genes, no genetic mutations have been discovered to date. Nonetheless, sFRP1 is found to be downregulated in cervical, kidney, breast and ovary carcinoma (Ko *et al.*, 2002; Ugolini *et al.*, 2001; Zhou *et al.*,

1998). Furthermore, chromosome 8p21, where sFRP1 is located, is frequently lost in human cancers (Wright *et al.*, 1998). Lastly, sFRP promoters have been shown to be commonly hypermethylated in human cancers (**Table 1.4** and **Table 1.5**).

The other group of antagonists, the Dickkopf (DKK) family, comprises five members: DKK1, DKK2, DKK3, DKK4, and a DKK3 related protein called Soggy. The most extensively studied member of this family is DKK1. Studies with Dkk1 knockout mice and experiments using injection of Dkk1 messenger RNA (mRNA) into *Xenopus* embryos have demonstrated a lack of anterior head structures, highlighting the importance of Dkk1 in head formation (Glinka *et al.*, 1998). In a similar fashion to sFRP2 and sFRP3, DKK1 can also block *Xenopus* Wnt-8 effects (XWnt8) (Glinka *et al.*, 1998). Unlike sFRPs, DKK1 does not inhibit activation of the Wnt signalling pathway by binding to Wnt proteins; it binds to LRP5/6 instead (Bafico *et al.*, 2001; Semenov *et al.*, 2001). DKK1 mediates the internalisation of LRP5/6 by forming a ternary complex with the single-pass transmembrane protein Kremen1 (Krm1) and Krm2 (Mao *et al.*, 2002). As mentioned in **section 1.3.2**, LRP5 and LRP6 are solely required for the activation of the canonical Wnt/ β -catenin pathway. This is exemplified by the inability of DKK1 and degradation-resistant LRP6 to inhibit the Wnt/PCP pathway (Semenov *et al.*, 2001). Moreover, there is also evidence to suggest that DKK1 may be able to activate the Wnt/PCP pathway (Caneparo *et al.*, 2007).

Whereas DKK4 functions in the same manner as DKK1, DKK3 and Soggy have no effect on the Wnt signaling pathway (Krupnik *et al.*, 1999; Mao and Niehrs, 2003). DKK2 appears to have both antagonistic and agonistic effects on Wnt signaling. DKK2 can bind to LRP6 and Krm2 to antagonise Wnt1 and XWnt8 binding (Brott and Sokol, 2002; Mao *et al.*, 2002; Wu *et al.*, 2000). However, ectopic expression of DKK2 in *Xenopus* embryos has shown that it synergises with LRP6 to potentiate axis duplication, an effect of Wnt/ β -catenin pathway activation (Brott and Sokol, 2002). This synergism was shown to be prevented by co-expression of Krm2, and therefore suggests that the relative levels of LRP5/6 and Krm2 dictate whether DKK2 functions as an agonist or antagonist (Mao and Niehrs, 2003).

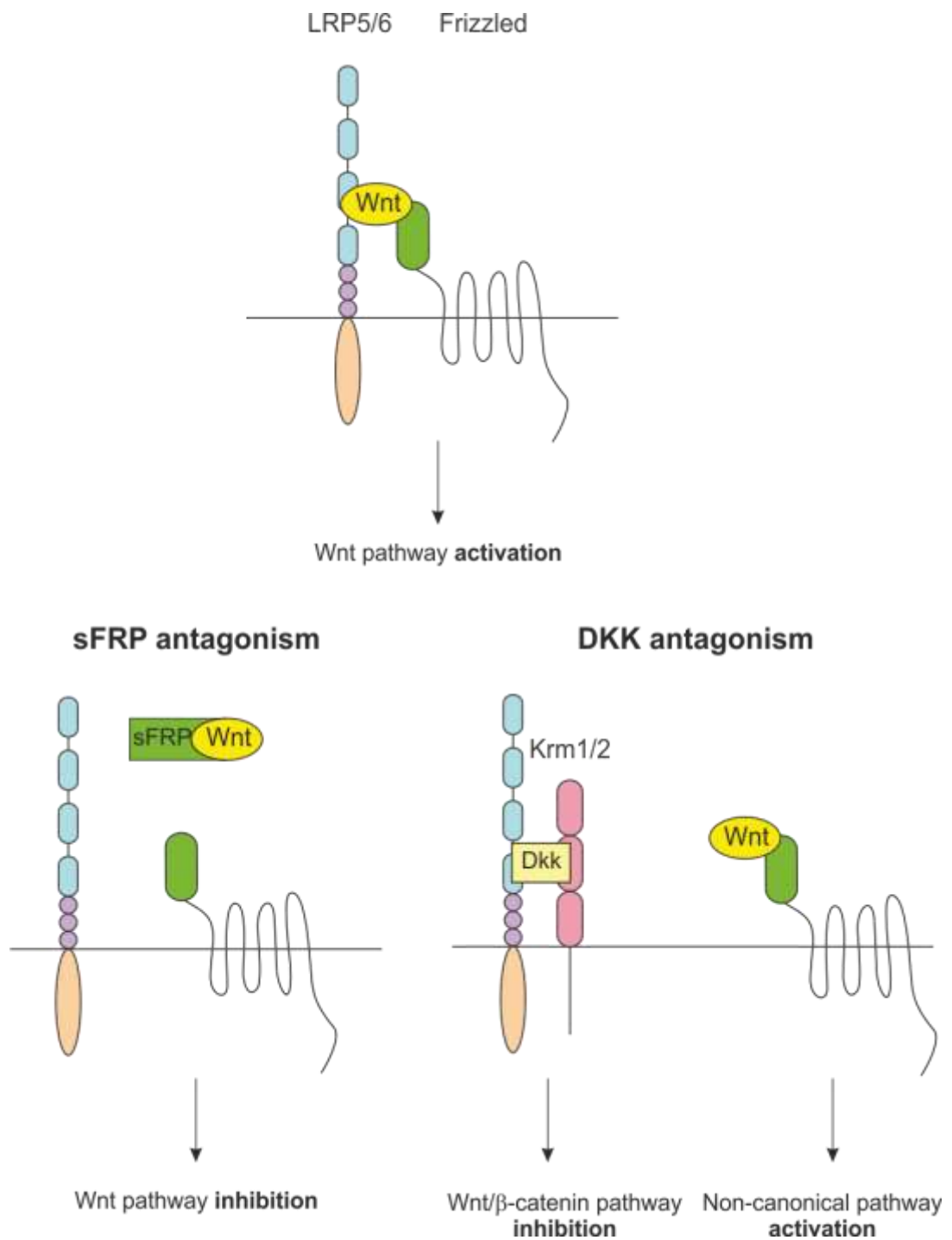


Figure 1.5 Mechanism for Wnt protein antagonism

Wnt proteins interact with Frizzled and Frizzled/LRP to activate the Wnt pathway. Secreted frizzled related proteins (sFRPs) inhibit the Wnt pathway by sequestering Wnt proteins. On the other hand Dickkopf (DKK) proteins specifically inhibit the Wnt/ β -catenin pathway by promoting the internalisation of LRP5/6.

1.3.4 The Wnt/PCP or Wnt/JNK pathway

Cells in tissues are highly coordinated both in terms of their arrangement and function. A key feature of this coordination is polarisation. The most common form of polarisation is the apical/basal polarisation of epithelial cells [reviewed in (Simons and Fuller, 1985)]. Nevertheless, polarisation has also been found to be essential for wing hair and eye photoreceptor orientation in *Drosophila*, mitotic spindle orientation in invertebrates, hair orientation, neural tube closure, convergent extension in mammals and ciliogenesis (De Calisto *et al.*, 2005; Gubb and Garcia-Bellido, 1982; Park *et al.*, 2006; Veeman *et al.*, 2003; Zheng *et al.*, 1995). This polarisation is controlled by the Wnt/Planar cell polarity (PCP) pathway in *Drosophila*, which in vertebrates is called the Wnt/JNK pathway (**Figure 1.6**).

PCP was first recognised in *Oncopeltus fasciatus* and studies in *Drosophila* helped to elucidate many of the components of the pathway (Lawrence, 1966). The two most studied PCP events in *Drosophila* are wing hair orientation and the polarity of photoreceptors in ommatidia (the units that make up the compound eyes). In the wing, planar cell polarity is dependent on the arrangement of six proteins, Fz, Dishevelled (Dsh), Flamingo (Fmi), Diego (Dgo), Strabismus (Stbm) and Prickle (Pk) (Chae *et al.*, 1999; Klingensmith *et al.*, 1994; Taylor *et al.*, 1998; Vinson *et al.*, 1989). These localise proximally or distally in the cells to coordinate actin microfilaments (Chae *et al.*, 1999; Klingensmith *et al.*, 1994; Taylor *et al.*, 1998; Vinson *et al.*, 1989). In vertebrates, activation is achieved by Wnt11 or Wnt5A binding to Fz receptor (Heisenberg *et al.*, 2000; Moon *et al.*, 1993). The intracellular domain of Fz interacts with Dsh to activate the Rhodopsin (Rho) GTPases ras homolog gene A (RhoA), ras-related C3 botulinum toxin substrate (Rac) and cell division cycle 42 (Cdc42) (Fukukawa *et al.*, 2009; Tanegashima *et al.*, 2008). These GTPases regulate the activity of Rho kinase (Rok), which activates the mitogen activated protein kinase (MAPK) cascade culminating in the activation of Jun kinase (JNK) (Fukukawa *et al.*, 2009; Winter *et al.*, 2001). JNK in turn phosphorylates c-Jun, which activates gene transcription (Pulverer *et al.*, 1991; Smeal *et al.*, 1991). The process by which c-Jun promotes cell polarity is not yet fully understood.

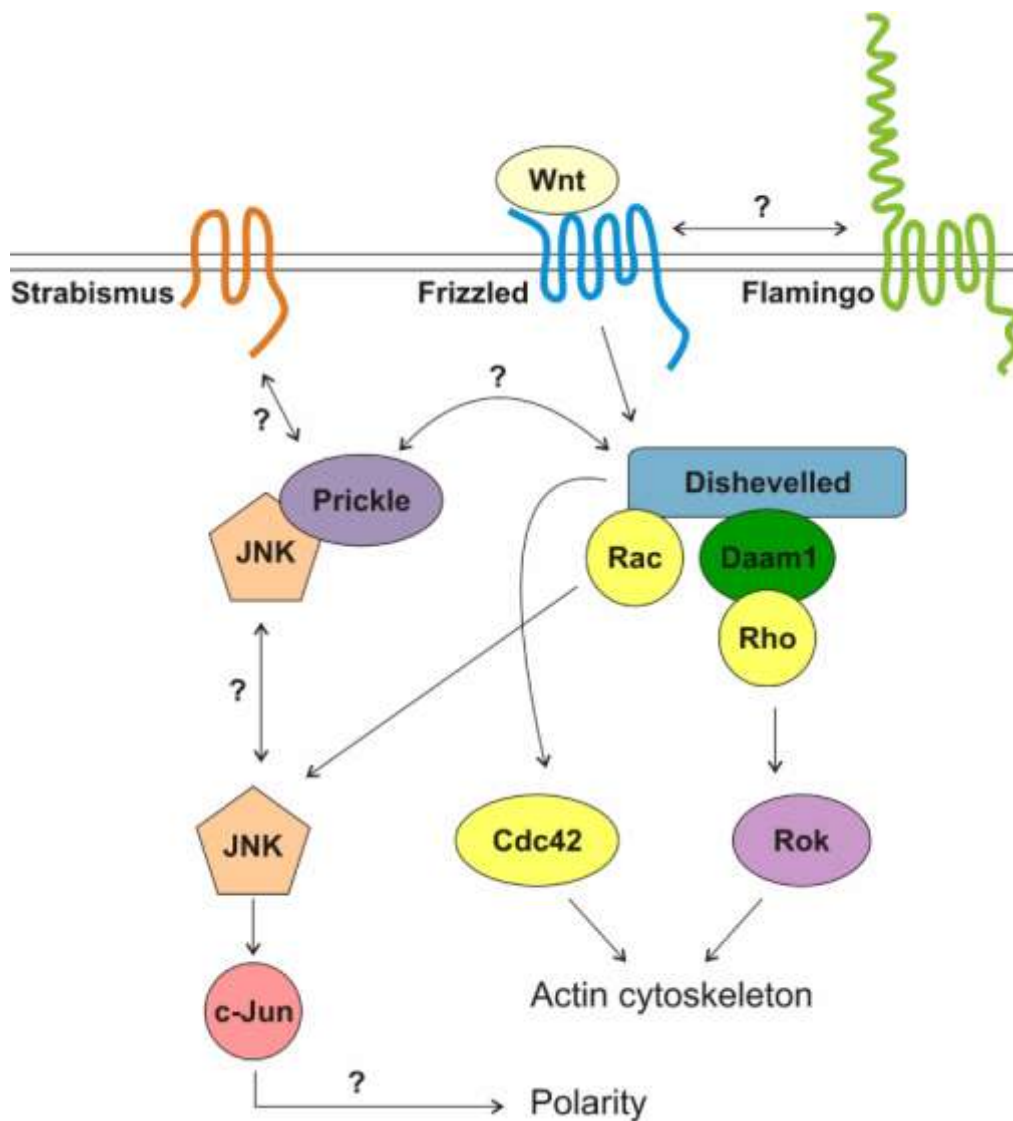


Figure 1.6 Schematic representation of the Wnt/PCP pathway in *Drosophila*⁴

Induction of the Wnt/Planar cell polarity pathway (Wnt/PCP) activates dishevelled (Dsh in *Drosophila*). Dsh in turn mediates the activation of ras-related C3 botulinum toxin substrate (Rac), cell division cycle 42 (Cdc42) and Rhodopsin (Rho). Cdc42 and Rho kinase mediate actin cytoskeleton remodelling. On the other hand, Rac promotes the activation of Jun Kinase (JNK). JNK phosphorylates c-jun and activates it. Activated c-jun promotes the expression of genes required for cell polarity. Prickle, Strabismus and Flamingo localise to the proximal or distal side of the cell, where they help organise PCP. However, the precise mechanism remains to be elucidated.

⁴ Adapted from Seminars in Cell and Developmental Biology, 20, Roszko *et al.*, Regulation of convergence and extension movements during vertebrate gastrulation by the Wnt/PCP pathway, pp. 986, 997, copyright (2009), with permission from Elsevier.

1.3.5 The Wnt/Ca²⁺ pathway

The latest pathway to be linked to Wnt proteins is the Wnt/Ca²⁺ pathway (**Figure 1.7**). Wnt proteins were first linked to calcium signalling ten years ago, following the injection of *Xenopus* Wnt5A and/or rat Fz2 mRNA into early Zebrafish embryos, which resulted in intracellular Ca²⁺ release in a manner dependent on G-protein coupled receptors (GPCRs) and the phosphatidylinositol (PI) cycle (Ma and Wang, 2006; Slusarski *et al.*, 1997a; Slusarski *et al.*, 1997b). Furthermore, the expression of Pk, Wnt4, Wnt5 and Wnt11 has also been shown to stimulate Ca²⁺ release in Zebrafish embryos (Veeman *et al.*, 2003; Westfall *et al.*, 2003). One of the main classes of receptors that activate the PI cycle are G-protein coupled receptors (GPCRs) (Ma and Wang, 2006; Slusarski *et al.*, 1997a; Slusarski *et al.*, 1997b). These receptors activate PI-specific phospholipase C (PLC) that cleaves membrane-bound phosphatidylinositol (4,5) biphosphate (PIP₂) into membrane-bound diacylglycerol (DAG) and cytoplasmic inositol 1,4,5-triphosphate (IP₃) [reviewed in (Berridge *et al.*, 2000)]. IP₃ subsequently binds to Ca²⁺ channels in the ER, thereby triggering the rapid release of Ca²⁺ into the cytoplasm [reviewed in (Berridge *et al.*, 2000)]. Intracellular Ca²⁺ ions are rapidly taken up by proteins, which either act as Ca²⁺ buffers or require Ca²⁺ for activation. Two notable enzymes activated by Ca²⁺ ions are calmodulin and protein kinase C (PKC) (Haiech *et al.*, 1981; Oancea and Meyer, 1998; Sakai *et al.*, 1997). Calmodulin activates protein kinases like Ca²⁺/calmodulin-dependent kinases (CaMK), phosphatases, ion transporters and cytoskeletal proteins (Hoeflich and Ikura, 2002). A vital phosphatase activated in this manner is calcineurin, which activates the transcription factor nuclear factor of activated T cells (NFAT) (Ruff and Leach, 1995). Wnt-induced release of intracellular Ca²⁺ has since been shown to activate PKC, Calmodulin/CaMKII, and Calcineurin/NFAT, suggesting that Wnt proteins can activate the PI cycle (Kuhl *et al.*, 2000; Saneyoshi *et al.*, 2002; Sheldahl *et al.*, 1999). Interestingly, the Wnt/Ca²⁺ pathway has been linked with Nemo-like kinase (NLK) activation, which can antagonise the Wnt/ β -catenin pathway (Ishitani *et al.*, 2003). Finally, the Wnt/Ca²⁺ pathway has also been shown to be important for the patterning of embryos, regulation of the Wnt/ β -catenin pathway and tumourigenesis (Weeraratna *et al.*, 2002).

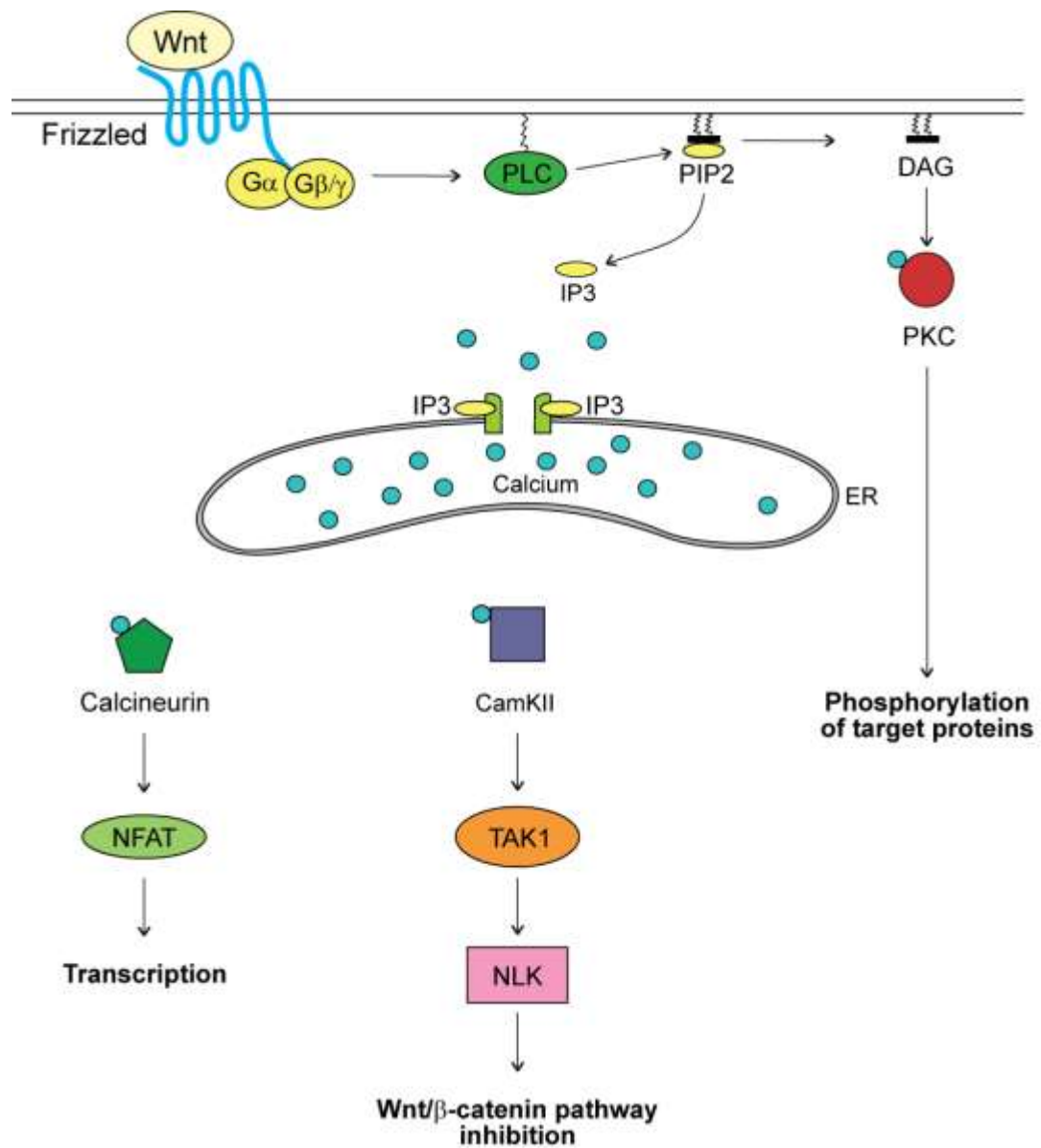


Figure 1.7 Wnt/Calcium pathway

Activation of the Wnt/Calcium pathway promotes the activation of phospholipase C, which cleaves membrane-bound phosphatidylinositol (4,5) biphosphate (PIP2) into membrane-bound diacylglycerol (DAG) and cytoplasmic inositol 1,4,5-triphosphate (IP3). IP3 binds to Calcium channels in the endoplasmic reticulum (ER), which promotes the release of Calcium ions into the cytoplasm. Three proteins activated by calcium ions are Calcineurin, Ca²⁺/calmodulin-dependent kinases (CamKII) and Protein kinase C (PCK). PCK additionally can be activated by DAG. Calcineurin promotes transcription, whilst PCK promotes the phosphorylation of target genes. CamKII phosphorylates and activates TGFβ activated kinase 1 (TAK1). TAK1 in turn phosphorylates nemo-like kinase (NLK), which translocates into the nucleus and inhibits β-catenin-dependent gene transcription.

1.3.6 The canonical Wnt/ β -catenin pathway

As the name implies, the key component of the Wnt/ β -catenin pathway is β -catenin. β -catenin is a 780 amino acid (aa) protein, which was originally identified as a component of E-cadherin junctions, where it links E-cadherin with α -catenin and consequently to the actin cytoskeleton (Aberle *et al.*, 1996; Redies and Takeichi, 1996; Takeichi, 1991). However, β -catenin was subsequently shown to be a component of the Wnt signalling pathway (Funayama *et al.*, 1995). As shown in **Figure 1.8**, in the absence of Wnt proteins (OFF state), cytoplasmic β -catenin is efficiently degraded *via* phosphorylation-dependent ubiquitinylation (Hart *et al.*, 1999; Marikawa and Elinson, 1998). However, in the presence of Wnt proteins (ON state) this phosphorylation, and thus degradation, is abolished (Liu *et al.*, 2002). Stable cytoplasmic β -catenin translocates into the nucleus and interacts with T-cell factor/Lymphoid enhancer factor (TCF/LEF) to promote the expression of over thirty genes; including oncogenes such as the cell cycle regulator cyclin D1, the transcriptional factor c-myc and the extracellular cell matrix (ECM)-degrading enzyme matrilysin (Crawford *et al.*, 1999; He *et al.*, 1998; Shtutman *et al.*, 1999).

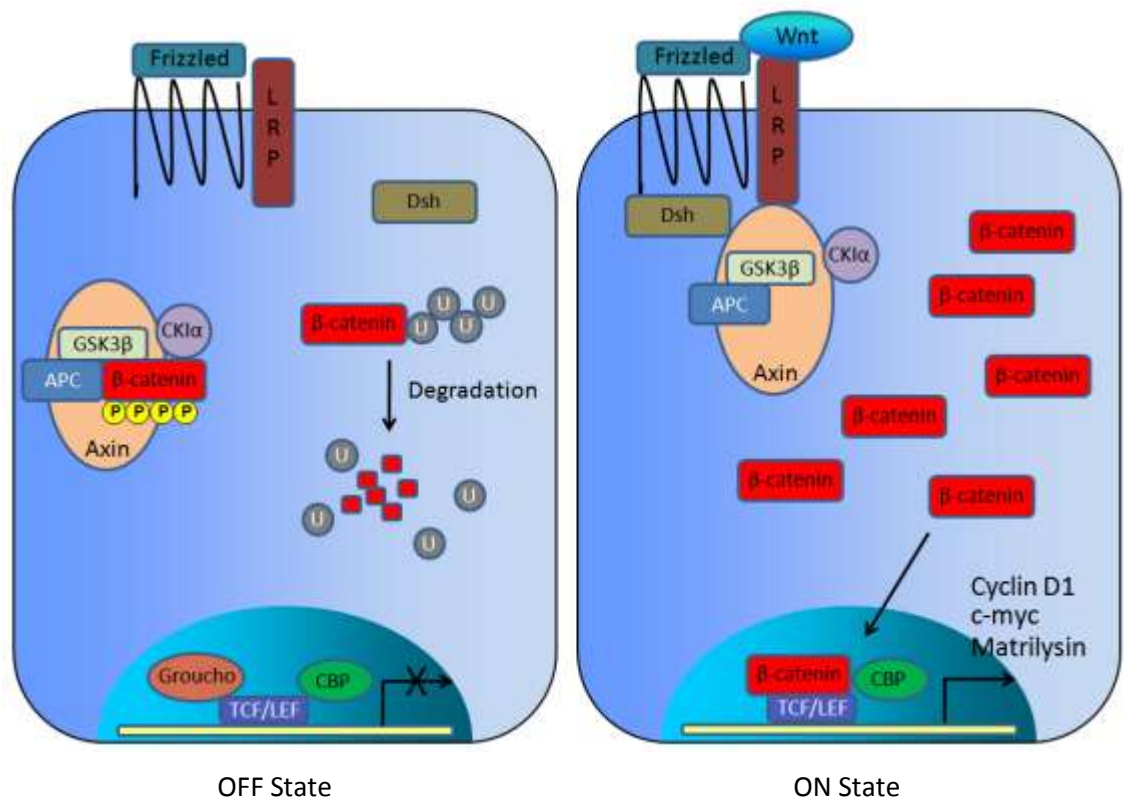


Figure 1.8 Schematic representation of the Wnt/β-catenin pathway signalling cascade

In the absence of Wnt proteins, cytoplasmic β-catenin is phosphorylated by CK1α and GSK3β and targeted for degradation by ubiquitination. The interaction of Wnt proteins with Frizzled/LRP stabilises β-catenin by disrupting the 'destruction complex' (Dvl, Axin, APC, CK1α and GSK3β). Stable cytoplasmic β-catenin translocates into the nucleus and activates gene expression by interacting with TCF/LEF.

Table 1.2 Nomenclature for genes involved in the Wnt/ β -catenin pathway

Numbers in parentheses represent the number of known homologues

Species	Function in Wnt pathway	Nomenclature (gene)		
		Human	Mouse	<i>Drosophila</i>
Ck1 ϵ	Dvl phosphorylation	CK1 ϵ	Ck1 ϵ	dco
Dvl	Disrupts the 'destruction complex'	DVL (3)	Dvl (3)	dsh
Axin	Scaffold	AXIN (2)	Axin (2)	daxin
Gsk3 β	Phosphorylation	GSK3B	Gsk3 β	sgg
Ck1 α	Phosphorylation	CK1 α	Ck1 α	ck1 α
Apc	Scaffold	APC, APC2/ APCL	Apc (2)	dapc, E-apc
β -catenin	Transcriptional factor	CTNNB1	Ctnnb1	armadillo
β -TrCP	Ubiquitination	β -TrcP (2)	β -TrcP (2)	slimb
GBP	GSK3 β antagonist	FRAT (2)	Frat (2)	-
TCF/LEF	Transcription factor	TCF, LEF (4)	Tcf/Lef (4)	pangolin
Groucho	Transcription repressor	TLE1, 2, 3, 4, 6	Tle1, 2, 3, 4, 6	groucho
CtBP	Transcription repressor	CTBP (2)	Ctbp (2)	CtBP
CBP	Transcription repressor/activator	CREBBP	Crebbp	CBP
Legless	Transcription factor	BCL9	Bcl9	legless
Pygopus	Transcription factor	PYGO (2)	Pygo (2)	pygopus
TBP	Transcription factor	TBP	Tbp	tbp
TIP48	Transcription factor	RUVBL2/TIP48	Ruvbl2/Tip48	rept
TIP49	Transcription factor	RUVBL1/TIP49	Ruvbl1/Tip49	pont

1.3.6.1 OFF state: Absence of Wnt signals

In the absence of Wnt proteins, β -catenin is phosphorylated and targeted for degradation by a complex of proteins designated the 'destruction complex'; APC, Axin, Glycogen synthase kinase 3 β (Gsk3 β), Casein kinase I α (Ck1 α) and Protein phosphatase 2A (PP2A) (**Figure 1.9**).

1.3.6.1.1 APC

APC is a 2843 amino-acid, 312 kDa multifunctional protein that was originally discovered as a truncated mutant in FAP (**section 1.1**). The role of APC in the Wnt/ β -catenin pathway is to stabilise the 'destruction complex' to promote β -catenin phosphorylation (Behrens *et al.*, 1998; Rubinfeld *et al.*, 1993; Su *et al.*, 1993b). APC has also been implicated in cell adhesion, cytoskeletal integrity, DNA repair/apoptosis and cell migration in a Wnt-independent manner (Balusu *et al.*, 2007; Barth *et al.*, 1997; Mahmoud *et al.*, 1997; Munemitsu *et al.*, 1994). Additionally, APC has been shown to interact with End-binding protein 1 (EB1), which regulates microtubule assembly and Discs-large protein (DLG), a tumour suppressor protein that regulates cell cycle progression from G0/G1 to S phase (Ishidate *et al.*, 2000; Nakamura *et al.*, 2001b). Structurally, APC contains several heptad domains that mediate homodimerisation, followed by seven armadillo repeats (Kinzler *et al.*, 1991; Su *et al.*, 1993a). The central part of the protein contains three 15 aa and seven 20 aa repeats shown to mediate β -catenin binding (Rubinfeld *et al.*, 1997a; Su *et al.*, 1993b). Interspersed within the 20 aa repeats are three Serine-Alanine-Methionine-Proline (SAMP) repeats, which have been demonstrated to be vital in Axin binding (Behrens *et al.*, 1998). At the C-terminus, APC contains a basic domain for microtubule interaction, an EB1 binding domain and a DLG binding domain (Matsumine *et al.*, 1996; Munemitsu *et al.*, 1994; Su *et al.*, 1995). APC expression is high during development; it is expressed in adult epithelial cells, especially in the brain (Midgley *et al.*, 1997; van Es *et al.*, 1999). Its homologue APC2 was identified in 1998 and it was found to be highly expressed in the brain (Nakagawa *et al.*, 1998; van Es *et al.*, 1999). APC2 is smaller than APC and does not contain the 15 aa repeats, but retains the 20 aa and two SAMP repeat motifs (van Es *et al.*, 1999). This suggests that it may down-regulate β -catenin (van Es *et al.*, 1999). However, this redundant role may not fully compensate for APC loss during tumourigenesis since C-terminal APC truncation mutations are sufficient to induce polyposis in the intestine (Andreu *et al.*, 2005; Fodde *et al.*, 1994; Oshima *et al.*, 1995). Recent studies have shown that APC can regulate β -catenin-mediated gene transcription at the nucleus (Hamada and Bienz, 2004; Sierra *et al.*, 2006). APC bound to β -transducin repeats-containing protein (β -TrCP) and to transcription repressors [C-terminal binding protein (CtBP), transducin-like enhancer of split-1(TLE-

1) and histone deacetylase 1 (HDAC1)] could interact with β -catenin at the MYC gene and facilitate its repression (Hamada and Bienz, 2004; Sierra *et al.*, 2006). Intriguingly, C-terminal truncated APC mutants commonly seen in human cancers are missing this CtBP binding domain and may account for some of the tumourigenic potential of these mutants (Hamada and Bienz, 2004; Sierra *et al.*, 2006).

1.3.6.1.2 **Axin**

Axin is the product of the *Fused* gene, which was originally identified as an inhibitor of the Wnt/ β -catenin pathway due to its ability to inhibit axis duplication in *Xenopus* (Zeng *et al.*, 1997). The Axin gene is conserved in mammals, *Drosophila* and *Xenopus* and although the protein it lacks enzymatic activity, it has been found to play a vital role in organising the 'destruction complex' (Hart *et al.*, 1998; Hedgepeth *et al.*, 1999; Ikeda *et al.*, 1998; Zeng *et al.*, 1997). It binds GSK3 β and β -catenin in its centre, physically facilitating their interaction (Behrens *et al.*, 1998; Ikeda *et al.*, 1998). Additionally, Axin contains an N-terminal regulator of G protein signalling (RGS) domain (that binds to APC) and a C-terminal DIX (acronym of Dishevelled-Axin) domain important for binding to Dishevelled and for Axin oligomerisation (Hsu *et al.*, 1999; Kishida *et al.*, 1998; Kishida *et al.*, 1999). These domains are critical, and loss of the DIX domain has been shown to severely disrupt β -catenin down-regulation (Kawahara *et al.*, 2000; Sakanaka and Williams, 1999). Regardless, Axin mutations are relatively rare in human cancers and have been mainly identified in hepatocellular carcinomas and medulloblastomas (**Table 1.5**). Similar to APC, Axin has also been found to interact with many Wnt-independent partners (Cowan and Henkemeyer, 2001; Zhang *et al.*, 1999). These include MAPK kinase kinase 1 (MAPKKK1) and MAPKKK4 and Smad3 [a member of the tumour growth factor β (TGF- β) pathway] (Furuhashi *et al.*, 2001; Luo *et al.*, 2003; Zhang *et al.*, 1999). Additionally, it can interact with NCK adaptor protein 2 (Nck2), an enzyme which modulates Ephrin B1 involved in axon growth (Cowan and Henkemeyer, 2001). These pathways have been implicated in cell proliferation, differentiation and apoptosis, suggesting that Axin may be a vital scaffold protein for regulating these processes (Furuhashi *et al.*, 2001; Luo *et al.*, 2003; Zhang *et al.*, 1999). A homologue of Axin, named Axin2, was identified by its interaction with GSK3 β using a yeast two-hybrid screen (Yamamoto *et al.*, 1998). Axin2 shares 44 % identity with Axin and can also promote β -catenin degradation (Behrens *et al.*, 1998; Yamamoto *et al.*, 1998). Interestingly, Axin2 is up-regulated by β -catenin, suggesting that it may serve as a feedback loop to modulate the duration and intensity of the active Wnt/ β -catenin pathway (Jho *et al.*, 2002; Lustig *et al.*, 2002; Yan *et al.*, 2001).

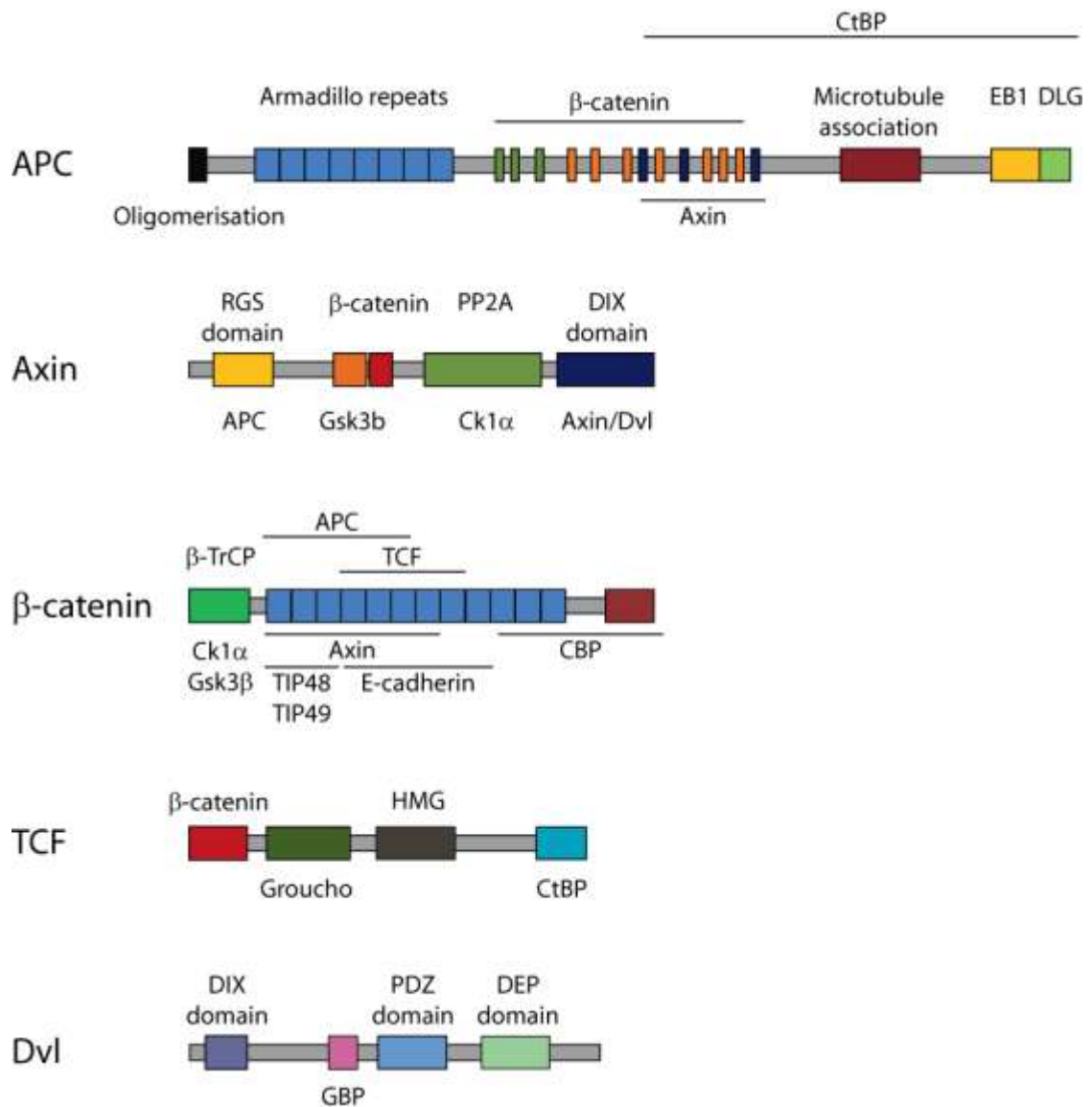


Figure 1.9 Schematic representation of Wnt/β-catenin pathway intracellular members (not to scale)

APC contains an oligomerisation domain, eight armadillo repeats, three 15 amino acid (aa) and seven 20 aa repeats that mediate β-catenin binding, three SAMP repeats important for binding to Axin, a microtubule association domain, an End-binding protein 1 (EB1) binding domain and a Discs-large protein (DLG) binding domain. Axin contains an RGS domain for binding to APC and a C-terminal DIX domain important for binding to Dishevelled and for Axin oligomerisation. Axin binds to β-catenin and Gsk3β at the centre. The N-terminus of β-catenin is phosphorylated by Gsk3β and Ck1α. Phosphorylation allows β-TrCP to bind to β-catenin and promote its degradation. Additionally, β-catenin contains twelve armadillo repeats. These repeats mediate the interaction of β-catenin with APC, TCF, E-cadherin, TIP48/49 and CBP among other binding partners. TCF interacts with β-catenin and Groucho at the N-terminus, a central HMG domain for binding to DNA and a CtBP binding domain at the C-terminus. Finally, Dvl contains a DIX domain, which mediates binding with Axin, a GBP binding domain and a PDZ and DEP domain, which are important for binding to proteins involved in the Wnt/PCP and Wnt/Ca²⁺ pathway.

1.3.6.1.3 **The destruction complex kinases: Gsk3 β and Ck1 α**

β -catenin degradation is dependent on the phosphorylation of four key serine/threonine residues at its C-terminus domain (Aberle *et al.*, 1997; Morin *et al.*, 1997; Yost *et al.*, 1996) (**Figure 1.10**). The two kinases responsible for this are Ck1 α and Gsk3 β (Amit *et al.*, 2002; Yost *et al.*, 1996). Both of these enzymes are unable to bind to β -catenin directly and require Axin and APC for interaction (Behrens *et al.*, 1998; Ikeda *et al.*, 1998; Rubinfeld *et al.*, 1996). The Ck1 family of protein kinases is highly conserved across species and regulates many critical processes such as Wnt signalling, nuclear import (Fish *et al.*, 1995; Vielhaber *et al.*, 2000). Ck1 α interacts with Axin and enhances β -catenin degradation by phosphorylating it at Serine45, priming it for subsequent phosphorylation by Gsk3 β (Amit *et al.*, 2002; Zhang *et al.*, 2002). Gsk3 β is an essential protein kinase that is involved in many cellular processes [reviewed in (Forde and Dale, 2007)]. It was originally identified by its ability to regulate glycogen synthase (Embi *et al.*, 1980). Subsequently, it has been implicated in microtubule dynamics, transcription factor regulation and many other cellular events (Lovestone *et al.*, 1996; Sears *et al.*, 2000)[reviewed in (Forde and Dale, 2007)]. In the Wnt/ β -catenin pathway, its main role is to sequentially phosphorylate β -catenin at Threonine41, Serine37 and Serine33, following priming (Liu *et al.*, 2002). Gsk3 β also phosphorylates Axin and APC, thereby increasing their stability and affinity for β -catenin (Hart *et al.*, 1998; Yamamoto *et al.*, 1999b). Phosphorylated Serine33/37 forms a docking site for β -TrCP1/2, a component of the SCF (acronym of Skp1-Cullin1-F-box protein) E3 ubiquitin ligase, which recognises Aspartic acid-Serine (phosphorylated)-Glycine-X-X-Serine (phosphorylated) [DS(p)GXXS(p)] motifs (Alkalay *et al.*, 1995; Fuchs *et al.*, 1999; Winston *et al.*, 1999). Phosphorylation at both residues is absolutely required and disruption of this motif inhibits the degradation of β -catenin (Miyoshi *et al.*, 1998a; Morin *et al.*, 1997). The SCF E3 ubiquitin ligase interacts with an E2 enzyme and sequentially transfers ubiquitin from E2 to the bound protein, in this case β -catenin [reviewed in (Krek, 1998)]. Polyubiquitinated β -catenin is then degraded by the 26S proteasome (Fuchs *et al.*, 1999; Hart *et al.*, 1999; Winston *et al.*, 1999).

Paradoxically, CK1 α and GSK3 β appear to perform opposite functions at the cell membrane. There, they have been shown to phosphorylate Proline-Proline-Proline-Serine-Proline (PPPSP) motifs in the intracellular domain of LRP6 (Brennan *et al.*, 2004). LRP5 contains three of these motifs and interaction with GSK3 β promotes its binding to Axin (Mao *et al.*, 2001b). The outcome of this interaction remains to be fully determined. However, a study in *Drosophila* using Arrow (homolog of LRP5/6), suggests that it may result in Axin degradation (Tolwinski *et al.*, 2003). As mentioned previously, LRP5/6 truncated mutants lacking the extracellular domain can constitutively activate the Wnt/ β -catenin pathway (Brennan *et al.*, 2004; Mao *et al.*, 2001a; Mao *et al.*, 2001b). Interestingly, LRP5 mutants-containing the intracellular and transmembrane domain were shown to activate the pathway more than mutants containing only the intracellular domain, indicating that membrane localisation of Axin may be important for activation (Mao *et al.*, 2001b). Recently, a role for caveolin in β -catenin stabilisation was also reported (Yamamoto *et al.*, 2006). In this study, Wnt3a protein promoted the internalisation of LRP6 by its interaction with caveolin in the human embryonic kidney cell line HEK293 (Yamamoto *et al.*, 2006). Furthermore, immunoprecipitation analysis of LRP6/GSK3 β /Axin/ β -catenin showed that caveolin inhibits the binding of β -catenin to Axin (Yamamoto *et al.*, 2006). Even though the exact method by which caveolin acts remains to be elucidated, it is possible that it accounts for the importance of membrane localisation of Axin in activation of the Wnt/ β -catenin pathway. In conclusion, it appears that CK1 α and GSK3 β promote the degradation of β -catenin in the absence of Wnt, but promote its stability during Wnt/ β -catenin signalling by promoting the interaction between LRP5/6 and Axin.

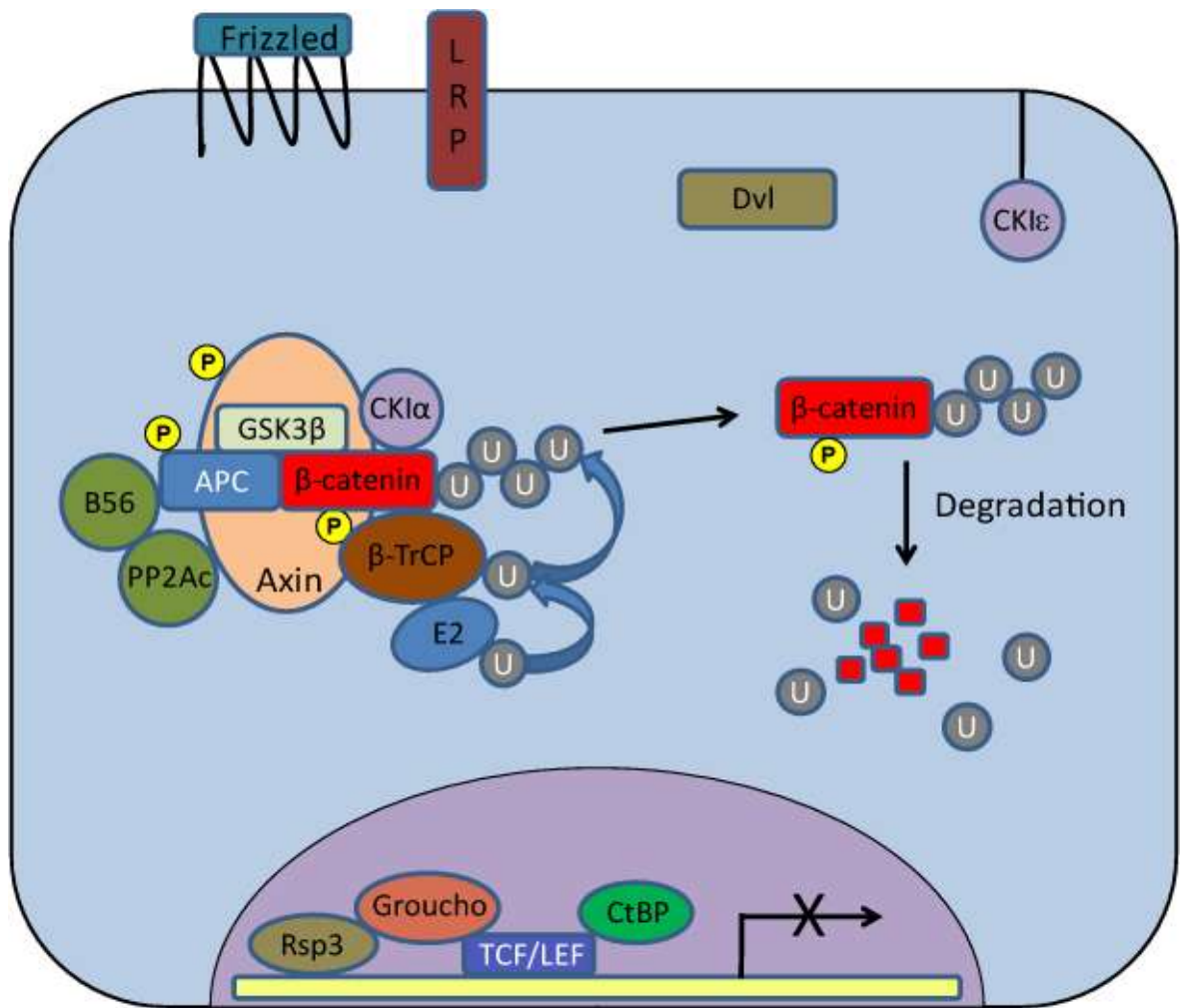


Figure 1.10 Wnt/β-catenin pathway OFF state

In the absence of Wnt proteins, an efficient complex made up of Axin, Gsk3β, APC, Ck1α and PP2A promotes the hyperphosphorylation of β-catenin. Phosphorylated β-catenin is recognised by β-TrCP, which targets it for ubiquitination and degradation by the 26S proteasome. In the absence of nuclear β-catenin, Wnt responsive genes are inhibited by Groucho, histone deacetylases (HDAC) and C-terminal binding protein (CBP).

1.3.6.2 ON state: Presence of Wnt signals

Activation of the Wnt/ β -catenin pathway recruits Dishevelled (Dvl in vertebrates) to the cell membrane, where it is hyperphosphorylated by membrane-bound Ck1 ϵ and thereby activated (Hino *et al.*, 2003; Kishida *et al.*, 2001; Peters *et al.*, 1999) (**Figure 1.11**). Dvl contains an N-terminal DIX domain, a central PDZ domain (acronym of post synaptic density protein [PSD95], *Drosophila* disc large tumor suppressor [DlgA], zonula occludens-1 protein [zo-1]) and a C-terminal DEP domain (acronym of Dishevelled, egl-10 and Pleckstrin). Hyperphosphorylated Dvl interacts with Axin *via* its DIX and PDZ domain (Kishida *et al.*, 1999; Li *et al.*, 1999). This interaction inhibits Gsk3 β -mediated phosphorylation of β -catenin (Kishida *et al.*, 1999). The mechanism of inhibition is not fully understood, but it may involve conformation changes in axin leading to a decreased affinity between Gsk3 β and β -catenin. Alternatively, Dvl has been shown to bind Gsk3 β binding protein (GBP) *via* its PDZ domain and recruit it to the 'destruction complex' (Li *et al.*, 1999). GBP can therefore interact with the C-terminus of GSK3 β and inactivate it (Li *et al.*, 1999).

Once Gsk3 β is inactivated, β -catenin is no longer phosphorylated and cannot be recognised by β -TrCP (Yost *et al.*, 1996). Nevertheless, β -catenin still needs to dissociate from Axin and APC before it can translocate into the nucleus. As abovementioned, GSK3 β phosphorylates Axin and APC to enhance their affinity to β -catenin (Hart *et al.*, 1998; Yamamoto *et al.*, 1999b). Therefore, they need to be de-phosphorylated. This is mediated by PP2A, one of the four major serine/threonine phosphatases (Cohen, 1989). PP2A is a heterotrimeric protein comprised of a catalytic subunit (C), a regulatory subunit (A), and one of variable regulatory subunits (B), which modulate its activity (Cohen, 1989). Axin directly interacts with PP2A C, and its inhibition (by okadaic acid) has been shown to prevent the de-phosphorylation of Axin and APC (Hsu *et al.*, 1999; Ikeda *et al.*, 2000a; Willert *et al.*, 1999). Interestingly B56, a regulatory subunit of PP2A, binds to APC and its over-expression promotes β -catenin down-regulation, probably by inhibiting PP2A C (Seeling *et al.*, 1999). On the other hand, the process by which Wnt proteins mediate a change from inactive to active PP2A remains to be elucidated.

1.3.6.3 Nuclear translocation of β -catenin and gene transactivation

β -catenin lacks any obvious nuclear localisation signal (NLS) and two different mechanisms for its translocation into the nucleus have been proposed. Microinjection or expression of TCF in *Xenopus* embryos promotes translocation of β -catenin indicating that they may translocate as a complex (Behrens *et al.*, 1996; Huber *et al.*, 1996; Molenaar *et al.*, 1996). However, deletion of the β -catenin TCF binding site did not prevent β -catenin translocation, suggesting a TCF independent mechanism (Orsulic and Peifer, 1996; Prieve and Waterman, 1999). This was further substantiated *in vitro*, where β -catenin was able to enter the nucleus independent of importins, a family of proteins involved in recognising proteins with NLS (Fagotto *et al.*, 1998; Yokoya *et al.*, 1999). Interestingly, the central armadillo repeats appear to be required for translocation (Funayama *et al.*, 1995). These repeats can also be found in importin- α and are structurally related to the importin- β HEAT repeats (acronym for Huntingtin, elongation factor 3 [EF3], PP2A, and TOR1) which bind to the nuclear pore complex (Gorlich *et al.*, 1995; Kutay *et al.*, 1997; Malik *et al.*, 1997). Once in the nucleus, β -catenin is either anchored to DNA by interacting with TCF/LEF or exported from the nucleus by interacting with nuclear Axin or APC (Cong and Varmus, 2004; Rosin-Arbesfeld *et al.*, 2000).

There are at least four mammalian TCF/LEF members; LEF1, TCF1, TCF2 and TCF4 (Korinek *et al.*, 1997; Travis *et al.*, 1991; van de Wetering *et al.*, 1991; Waterman *et al.*, 1991). They bind to the minor groove of DNA *via* a high motility group (HMG) box and induce a sharp bend (Giese *et al.*, 1992). However, they do not possess any transactivation activity (Giese *et al.*, 1992; Molenaar *et al.*, 1996). This activity is provided by the N- and C-terminus transactivation domains of β -catenin (Hecht *et al.*, 1999; Hsu *et al.*, 1998; van de Wetering *et al.*, 1997). In the absence of Wnt proteins, Groucho and CtBP interacts with TCF/LEF and represses gene expression by in/directly modifying chromatin structure (Brannon *et al.*, 1999; Cavallo *et al.*, 1998; Roose *et al.*, 1998). Groucho inhibits expression by recruiting HDAC2, which condenses chromatin by deacetylating histones (Chen *et al.*, 1999). On the other hand, the CtBP complex contains both HDAC and histone methyltransferase (HMT) activities which deacetylate and methylate histones to condense the structure of chromatin (Shi *et al.*, 2003). A further level of repression is observed in *Drosophila*, where cyclic Adenosine monophosphate (cAMP) response element binding protein (CBP) interacts with TCF/LEF and acetylates it at the β -catenin-binding domain weakening its interaction for the armadillo repeats (Waltzer and Bienz, 1998). Interaction of β -catenin with TCF/LEF displaces Groucho and CtBP from TCF/LEF and recruits transcriptional coactivators (Chen *et al.*, 1999).

Interestingly, the vertebrate CBP is recruited in this way and acetylates β -catenin to promote its transactivation activity (Hecht *et al.*, 2000; Takemaru and Moon, 2000). Furthermore, it binds to the TATA-binding protein (TBP), TATA-interactive protein 48 (TIP48) and TIP49, which are proposed to form a bridge between β -catenin and RNA polymerase II (Bauer *et al.*, 1998; Hecht *et al.*, 1999). In summary, binding of β -catenin to TCF/LEF promotes the organisation of an efficient complex that activates the expression of canonical Wnt pathway target genes.

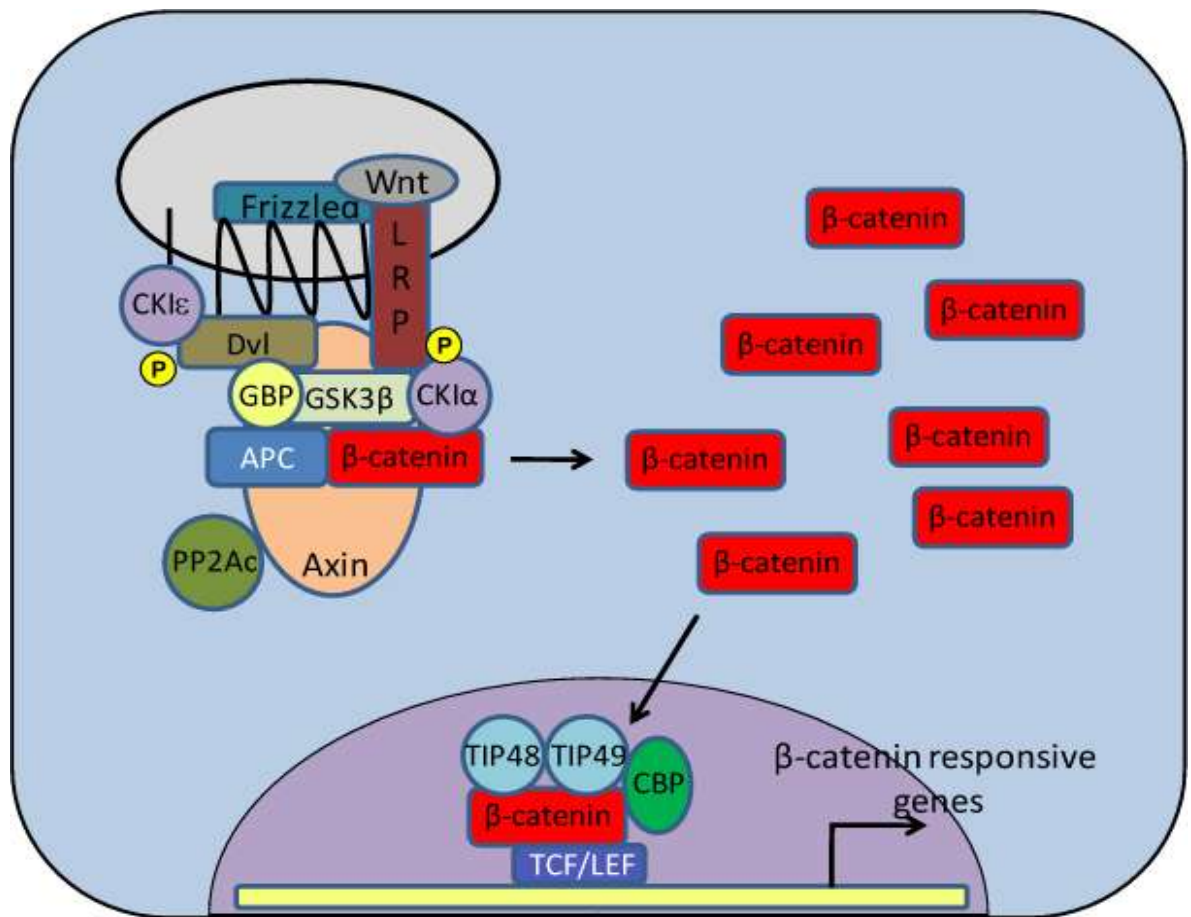


Figure 1.11 Wnt/ β -catenin pathway ON state

In the presence of Wnt proteins, Gsk3 β and Ck1 α phosphorylate the intracellular domain of LRP5/6 at PPPSP motifs. Phosphorylated LRP5/6 binds to Axin and disrupts the 'destruction complex'. Additionally, dishevelled (Dvl) becomes hyperphosphorylated by casein kinases. Phosphorylated Dvl promotes Gsk3 β inactivation by binding to Gsk3 β binding protein (GBP). PP2A dephosphorylates Axin and APC to decrease their affinity for β -catenin. These three events de-stabilise the 'destruction complex', thereby inhibiting β -catenin degradation. Stable β -catenin translocates into the nucleus where it promotes transcription by displacing the transcriptional repressors Groucho and C-terminal binding protein (CtBP) and binding to the transcriptional activator cAMP response element binding protein (CBP). Additionally, β -catenin binds to TIP48 and TIP49, which are thought to form a bridge β -catenin and RNA polymerase II.

1.3.6.4 Wnt/ β -catenin target genes

More than 30 genes are regulated by β -catenin. Among these, cyclin D1, c-myc and matrilysin stand out for their oncogenic potential (Crawford *et al.*, 1999; He *et al.*, 1998; Mann *et al.*, 1999; Shtutman *et al.*, 1999; Tetsu and McCormick, 1999). Cyclin D1 is a critical regulator of the cell cycle and is frequently activated in human cancers [reviewed in (Baldin *et al.*, 1993; Donnellan and Chetty, 1998)]. This activation can occur by chromosomal translocation of the cyclin D1 gene, gene amplification and deregulation of the Ras or Wnt/ β -catenin pathways [reviewed in (Donnellan and Chetty, 1998)]. Cyclin D1 is expressed during early to mid G1 phase and is involved in promoting cell cycle progression (Baldin *et al.*, 1993) (**Figure 1.12**). It functions as a regulatory subunit for cyclin-dependent-kinase 4 (CDK4) and CDK6 holoenzyme complex (Matsushime *et al.*, 1992; Meyerson and Harlow, 1994). One of the main targets of cyclin D1/CDK4 is the retinoblastoma (Rb) protein (Ewen *et al.*, 1993; Kato *et al.*, 1993; Matsushime *et al.*, 1992). Hypophosphorylated Rb suppresses cell cycle progression by sequestering E2 transcription factor proteins (E2F), an important family of transcription factors implicated in cell cycle progression (Ross *et al.*, 2001; Wu *et al.*, 2001a). Cyclin D1/CDK4 partially phosphorylates Rb, but it does not disrupt its interaction with E2F (Lundberg and Weinberg, 1998). Additionally, cyclin D1 and CDK4 have been shown to promote the expression of the transcriptional factor Sp1 (Tapias *et al.*, 2008). Mutation of Sp1 binding sequences in the cyclin E promoter prevents full expression of the gene (Kim *et al.*, 2006). These results suggest that Cyclin D1/CDK4-mediated expression of Sp1 may promote cyclin E expression. Cyclin E/CDK2 complexes fully phosphorylate Rb, disrupting its interaction with E2F (Lundberg and Weinberg, 1998). This prompts the cell to progress to S phase (Muller *et al.*, 2001). Overexpression of cyclin D1 *in vitro* shortens the G1 phase but requires co-operation with other proto-oncogenes to promote cell transformation (Jiang *et al.*, 1993; Musgrove *et al.*, 1994; Zhou *et al.*, 1995). Cyclin D1 can transform rat kidney cells and rat embryo fibroblasts in conjunction with Ras and can co-operate with c-myc to induce B cell lymphomas in transgenic mice (Lovec *et al.*, 1994a; Lovec *et al.*, 1994b). Interestingly, studies in human cancers have shown that cyclin D1 overexpression can promote carcinogenesis independently of CDKs (Lamb *et al.*, 2003; Oyama *et al.*, 1998; Zukerberg *et al.*, 1996). To ascertain the significance of this activity, a comprehensive analysis of deregulated genes in breast cancer was undertaken (Lamb *et al.*, 2003). This study showed that in breast cancer, overexpression of cyclin D1 did not correlate with Rb disruption and cell cycle deregulation. In oestrogen sensitive tissues, cyclin D1 has been shown to regulate growth by activating the oestrogen receptor (ER) (Neuman *et al.*, 1997; Zwijsen *et al.*, 1997). Cyclin D1 can bind to ER and promote ER-mediated transcription in the absence of

oestrogen ligand (Neuman *et al.*, 1997; Zwijsen *et al.*, 1997). This may underlie the oncogenic role of cyclin D1 in ER-positive breast cancer. Cyclin D1 can therefore promote tumourigenesis by shortening cell cycle progression or by CDK-independent gene transcription.

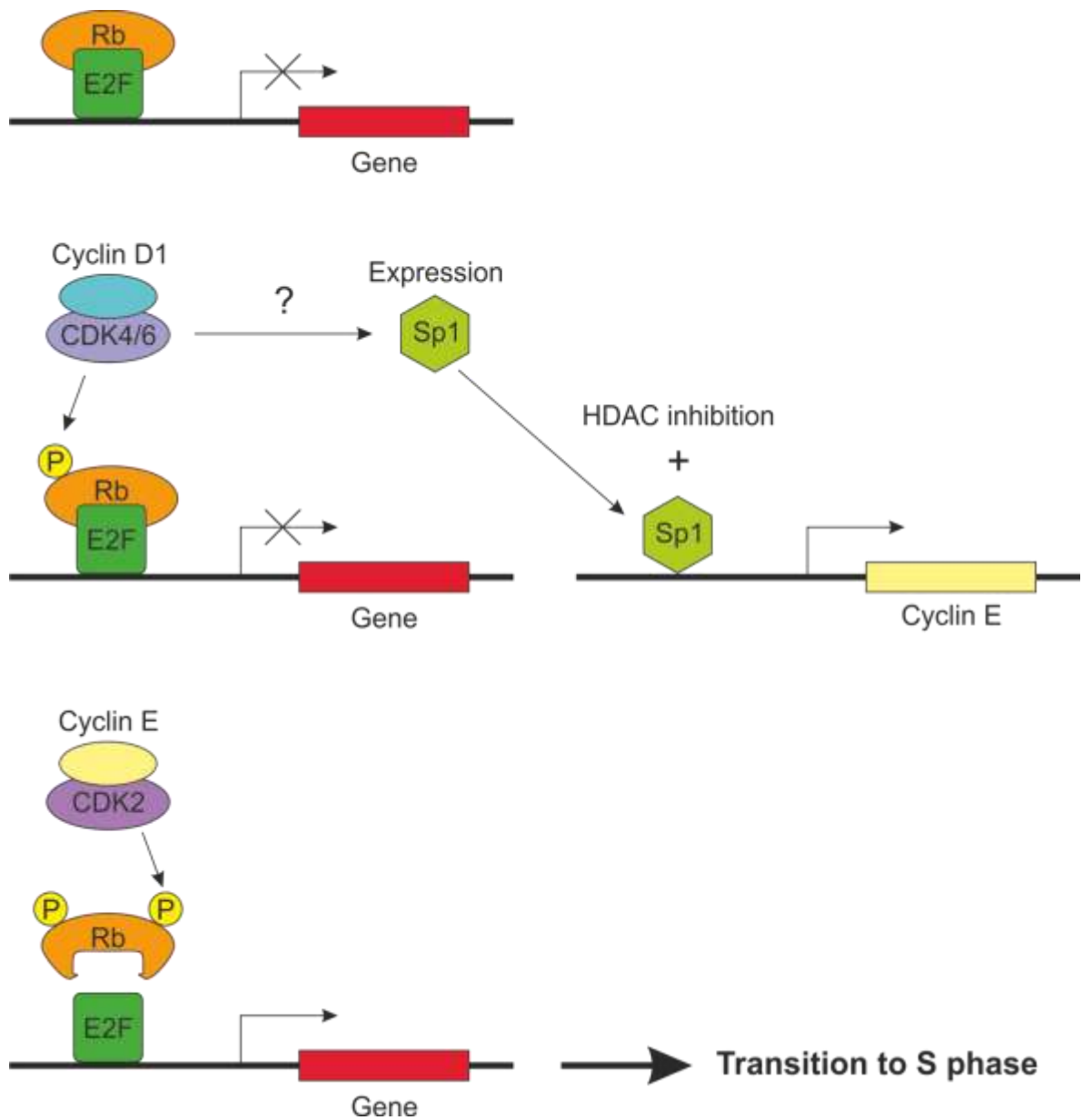


Figure 1.12 Activation of the cell cycle by cyclin D1

At G₀, the Retinoblastoma protein (Rb) binds to E2 transcription factors (E2F) and prevents their transcription activity. At mid-G₁ phase cyclin D1 binds to cyclin dependent kinases 4 or 6 (CDK4/6) and phosphorylates Rb. This phosphorylation event induces a conformation change in Rb, but it does not disrupt Rb-E2F interaction. Cyclin D1-CDK4/6 promote the expression of the transcription factor Sp1 by an unknown mechanism. Inhibition of histone deacetylases promotes the expression of cyclin E. Expression of cyclin E depends on Sp1. Cyclin E interacts with CDK2 and phosphorylates Rb in a site exposed by the conformation change induced by cyclin D1-CDK4/6 phosphorylation. Phosphorylation at this site disrupts the interaction between Rb and E2F. Subsequently, E2F mediates the expression of genes required for G₁ to S phase transition.

C-myc is a member of the MYC family of helix-loop-helix leucine zipper (HLH-LZ) transcriptional factors (Kato *et al.*, 1990; Murre *et al.*, 1989). It dimerizes with Max to bind specific DNA sequences, such as the E-box sequences (CACGTC) to promote target gene expression (Blackwood and Eisenman, 1991; Prendergast and Ziff, 1991). C-myc/Max dimers promote gene transcription by modulating chromatin condensation (McMahon *et al.*, 2000). This process is dependent on recruited factors like TIP48/49/60, General control nonderepressible 5 (GCN5) and transformation/transcription domain-associated protein (TRRAP) (Bellosta *et al.*, 2005; Bouchard *et al.*, 2001; McMahon *et al.*, 1998; McMahon *et al.*, 2000). TRRAP is a protein that interacts with c-myc during chromatin binding and is believed to bridge c-myc to histone acetyltransferases (HATs) (McMahon *et al.*, 1998). TIP60 and GCN5 are HATs, which interact with c-myc to acetylate histone 3 (H3) and H4 to relax chromatin condensation and promote gene transcription (Allard *et al.*, 1999; McMahon *et al.*, 2000; Xu *et al.*, 1998). C-myc promotes proliferation and aberrant expression is associated with aggressive, poorly differentiated tumours (Fults *et al.*, 2002; Lamont *et al.*, 2004). C-myc induces G1→S phase transition by several mechanisms. C-myc promotes the activity of cyclin E/CDK2 (Berns *et al.*, 1997; Steiner *et al.*, 1995). It also directly promotes the expression of cyclin D2 and CDK4 (Bouchard *et al.*, 1999; Hermeking *et al.*, 2000). Furthermore, c-myc promotes the degradation of p27, and inhibitor of cyclin E/CDK4 (O'Hagan *et al.*, 2000). Inhibitor-free cyclin/CDK complexes are subsequently activated by cyclin activating kinase (CAK) and promote cell cycle progression by hyperphosphorylating Rb (Kato *et al.*, 1993; Russo *et al.*, 1996). C-myc also induces proliferation by up-regulating RNA polymerase III, an enzyme involved in generating transfer RNA (tRNA) and 5S ribosomal RNA (rRNA), which is required for protein synthesis during cell growth (Gomez-Roman *et al.*, 2003). Whilst being a potent inducer of cell proliferation, c-myc can also induce apoptosis. This can be achieved in several ways. In certain cell lines, c-myc has been shown to increase the expression of B-cell lymphoma 2 (Bcl-2) associated X protein (Bax), an inducer of mitochondrial outer membrane permeabilisation (MOMP) (Juin *et al.*, 2002; Mitchell *et al.*, 2000). This releases cytochrome c from mitochondria, which associates with apoptotic protease-activating factor 1 (APAF-1) to induce activation of Caspase-9 and promote apoptosis (Acehan *et al.*, 2002). C-myc can also down-regulate members of the anti-apoptotic Bcl-2 protein family (Eischen *et al.*, 2001; MacLean *et al.*, 2003). Finally, c-myc can promote apoptosis by inhibiting nuclear factor kappa-light-chain-enhancer of activated B cells (NFκB) and indirect activation of p53 *via* Adenosine diphosphate ribose (ADP) ribosylation factors (ARFs) (Klefstrom *et al.*, 1997; You *et al.*, 2002; Zindy *et al.*, 1998). The decision between proliferation and apoptosis is

likely to be dependent on the cell type, the presence or absence of additional mutations and the presence of mitogenic signal and nutrients.

Matrix metalloproteinase-7 (MMP-7, also known as matrilysin) is an enzyme that belongs to a family of zinc dependent endopeptidases which cleave ECM components [reviewed in (Roy *et al.*, 2009)]. Matrilysin recognises many components of the ECM including elastin, type IV collagen, fibronectin, vitronectin, aggrecan and proteoglycans (Miyazaki *et al.*, 1990; Wilson and Matrisian, 1996; Woessner, Jr. and Taplin, 1988). Tumour metastasis is dependent on ECM degradation so MMPs are commonly up-regulated in malignant tumours [reviewed in (Roy *et al.*, 2009)]. Matrilysin is no exception and its over-expression has been identified in oesophageal, colon, pancreatic, liver and stomach invasive tumours among others (Aihara *et al.*, 2005; Jones *et al.*, 2004; Yamamoto *et al.*, 1997; Yamamoto *et al.*, 1999a; Yamamoto *et al.*, 2001; Yamamoto *et al.*, 2003). Apart from degrading ECM components, matrilysin has also been shown to promote tumourigenesis by indirectly inhibiting E-cadherin junctions, activating the Oestrogen receptor β 4 (ErB4) receptor and inhibiting apoptosis (Noe *et al.*, 2001; Yu *et al.*, 2002).

1.3.6.5 Wnt/ β -catenin pathway mutations in human cancers

The Wnt/ β -catenin pathway is de-regulated in many types of cancer (**Table 1.3** and **Table 1.5**). The most commonly mutated proteins in the Wnt/ β -catenin pathway in tumours are β -catenin, APC and Axin1 (**Table 1.3** and **Table 1.5**). Activating β -catenin mutations occur mostly at exon 3, which corresponds to the CK1 α /GSK3 β phosphorylation site (Wright *et al.*, 1999). Mutations in this region tend to be missense mutations either adjacent to (Asparagine32, Glycine34) or on codons (Serine33, Serine37, Threonine41, Serine45) which are phosphorylation sites of β -catenin (Garcia-Rostan *et al.*, 2001). These mutations interfere with β -catenin phosphorylation resulting in protein stabilisation (Miyoshi *et al.*, 1998a). In contrast, most mutations in APC are either nonsense mutations (C-terminal truncation) or frameshift mutations [reviewed in (Beroud and Soussi, 1996)]. Around 68-77 % of somatic mutations fall on a region called the mutation cluster region (MCR) which corresponds to 8 % of the gene (codons 1286-1513) (Nishisho *et al.*, 1991). Whilst APC truncation products generally retain the β -catenin binding domain, they lose the Axin-binding domain, highlighting the importance of Axin-APC interaction in β -catenin down-regulation [reviewed in (Beroud and Soussi, 1996)]. Interestingly, complete deletion of both APC alleles has not been observed in human cancers. The N-terminal part of the APC protein contains proline-free blocks with heptad repeats of hydrophobic residues (Joslyn *et al.*, 1993; Su *et al.*, 1993b). This pattern is characteristic of coiled coils and has been shown to mediate APC homodimerisation *in vitro* (Joslyn *et al.*, 1993; Su *et al.*, 1993a). Dimerisation suggests that truncated APC may negatively affect full length APC. Indeed, expression of truncated APC in enterocytes increases β -catenin activity and extends proliferation (Mahmoud *et al.*, 1997). Furthermore, the ability of wild-type APC in controlling β -catenin transcription is strongly attenuated when a mutant APC truncated at codon 1309 is present (Dihlmann *et al.*, 1999). Colorectal cancers (CRCs) with truncated APC retaining one or two β -catenin binding sites seem to have an increased selective advantage (Albuquerque *et al.*, 2002; Smits *et al.*, 2000). These APC species can partially regulate β -catenin mediated transcription (Dihlmann *et al.*, 1999; Munemitsu *et al.*, 1995; Rubinfeld *et al.*, 1997a). Therefore N-terminal APC seems to promote tumourigenesis by retaining optimal control over β -catenin. This has been named the 'just-right' hypothesis.

AXIN1 plays a central role in the 'destruction complex' by interacting with all of its members (Amit *et al.*, 2002; Behrens *et al.*, 1998; Ikeda *et al.*, 1998). However, AXIN1 mutations are unexpectedly rare in cancer and are mostly restricted to CRC, medulloblastoma and hepatocellular carcinoma (HCC) (**Table 1.3** and **Table 1.5**). By far the most common types of mutations in AXIN1 are missense mutations (Satoh *et al.*, 2000; Taniguchi *et al.*, 2002; Wu *et al.*,

2001b). These are predominantly found in the APC-GSK3 β binding domains, which are hypothesised to disrupt the 'destruction complex' (Satoh *et al.*, 2000; Taniguchi *et al.*, 2002; Wu *et al.*, 2001b). Indeed, Leucine396Methionine mutation in the GSK3 β binding domain has been shown to disrupt Axin-GSK3 β interaction (Webster *et al.*, 2000). Interestingly, in medulloblastoma, AXIN1 deletions are much more frequent than missense mutations (Dahmen *et al.*, 2001; Yokota *et al.*, 2002). These can occur at the C-terminus, ablating the APC-GSK3 β - β -catenin binding domains or at the N-terminus, deleting the DIX domain essential for AXIN1 oligomerisation and down-regulation of β -catenin (Dahmen *et al.*, 2001; Yokota *et al.*, 2002). Mutations in β -catenin, APC and AXIN1 promote β -catenin stabilisation and are mostly mutually exclusive; e.g. a tumour with an APC mutation will be likely to be wild-type for β -catenin or AXIN1 (Sparks *et al.*, 1998; Yokota *et al.*, 2002).

By contrast, GSK3 β mutations have not been found in human cancers to date. GSK3 β is involved in glycogen metabolism, transcription, translation, cytoskeletal regulation, differentiation, proliferation and apoptosis so inactivating mutations are likely to be detrimental for survival [reviewed in (Forde and Dale, 2007)]. Instead, tumours seem to control GSK3 β through phosphorylation. Phosphorylation at Ser9 inhibits GSK3 β whereas phosphorylation at Tyr216 fully activates the enzyme (Hughes *et al.*, 1993; Sutherland *et al.*, 1993). GSK3 β negatively regulates many oncogenic proteins and cell cycle regulators so it was predicted to act as a tumour suppressor (de Groot *et al.*, 1993; Nikolakaki *et al.*, 1993). Indeed, in a mouse model for skin carcinogenesis phosphorylation and Ser9 is increased whilst phosphorylation at Tyr216 is decreased (Leis *et al.*, 2002). Furthermore, a recent study found that pGSK3 β (Ser9) was strongly expressed in squamous cell carcinomas and basal cell carcinomas (Ding *et al.*, 2007b; Ma *et al.*, 2007). This also appears to be the case for mammary tumours (Farago *et al.*, 2005). Expression of inactive degradation-resistant GSK3 β in mammary glands promotes tumourigenesis (Farago *et al.*, 2005). Interestingly, this transformation was accompanied by cytoplasmic/nuclear accumulation of β -catenin and cyclin D1, suggesting that tumourigenesis was mediated by the activation of the Wnt/ β -catenin pathway (Farago *et al.*, 2005). Mutagenesis studies with primary breast tumours have shown that β -catenin and APC mutations are rare events (**Table 1.3** and **Table 1.5**). However, nuclear accumulation of β -catenin and cyclin D1 are frequent and are associated with poorer prognosis (**Table 1.3**). Studies in breast cancer cell lines show that expression GSK3 β or constitutively active GSK3 β (Serine9Alanine mutant) can induce cell cycle arrest or apoptosis (Ding *et al.*, 2007b; Wang *et al.*, 2006). This implicates GSK3 β as a tumour suppressor in breast tumourigenesis. In contrast, GSK3 β protein appears to play an oncogenic role in human ovarian,

colon and pancreatic carcinomas, suggesting an oncogenic role (Cao *et al.*, 2006; Ougolkov *et al.*, 2006). Pharmacological inhibition of GSK3 β suppresses proliferation of ovarian cancer cells *in vitro* and prevents tumour formation after injection of these cells into nude mice (Cao *et al.*, 2006). Similarly, inhibition of GSK3 β decreases survival and proliferation of colon and pancreatic cancer cells (Ougolkov *et al.*, 2005; Ougolkov *et al.*, 2006; Shakoori *et al.*, 2005; Shakoori *et al.*, 2007). An oncogenic role of GSK3 β in hepatocellular, prostate, lymphocytic leukaemia and medullary thyroid cancer cells have also been suggested (Erdal *et al.*, 2005; Kunnimalaiyaan *et al.*, 2007; Liao *et al.*, 2003; Mazor *et al.*, 2004; Ougolkov *et al.*, 2007). However, these effects may not be related to activation of the Wnt/ β -catenin pathway. For example, GSK3 β -induced suppression of mammary tumours has been suggested to be mediated by myeloid cell leukaemia-1 (Mcl-1) (Ding *et al.*, 2007a; Ding *et al.*, 2007b). Mcl-1 is an anti-apoptotic member of the Bcl-2 family, which is related to high grade breast cancer and poor survival (Ding *et al.*, 2007b). Inactivation of GSK3 β promotes accumulation of Mcl-1 which has been linked with increased mammary tumour chemoresistance (Ding *et al.*, 2007a; Ding *et al.*, 2007b).

Table 1.3 Mutations of the Wnt/ β -catenin pathway in selected human cancers

Cancer type	Gene	Mutation frequency	Comments	References
Primary Breast Cancer	β -catenin	0/177	Mutations in components of the Wnt/ β -catenin pathway are rare but nuclear β -catenin and nuclear cyclin D1 are associated with poor prognosis	(Jonsson <i>et al.</i> , 2000; Lin <i>et al.</i> , 2000)
	APC	4/271		(Jonsson <i>et al.</i> , 2000; Sorlie <i>et al.</i> , 1998)
	Nuclear β -catenin	74/123		(Lin <i>et al.</i> , 2000)
	Nuclear cyclin D1	49/123		
Breast Fibromatosis	β -catenin	15/33	Breast fibromatosis are rare non-metastasing tumours	(Abraham <i>et al.</i> , 2002b)
	APC	11/33		
	Nuclear β -catenin	27/33		
Desmoid tumours	β -catenin	39/85	Desmoid tumours are a locally invasive soft tissue tumour composed of spindle cells	(Miyoshi <i>et al.</i> , 1998b; Saito <i>et al.</i> , 2001; Saito <i>et al.</i> , 2002; Tejpar <i>et al.</i> , 1999)
	APC	12/48		(Alman <i>et al.</i> , 1997; Tejpar <i>et al.</i> , 1999)
	Nuclear β -catenin	19/38		(Saito <i>et al.</i> , 2001)
Colorectal carcinoma	APC	128/164	The 27 samples tested for β -catenin mutations corresponded to APC wild-type tumours.	(Jen <i>et al.</i> , 1994; Powell <i>et al.</i> , 1993; Samowitz <i>et al.</i> , 2007)
	β -catenin	13/27		(Sparks <i>et al.</i> , 1998)
Gastric carcinoma	β -catenin	26/161	Reduced expression of β -catenin is associated with metastasis and larger tumours. Of the 90 tumours with nuclear β -catenin only 19 possessed mutations in β -catenin	(Clements <i>et al.</i> , 2002; Kim <i>et al.</i> , 2009; Woo <i>et al.</i> , 2001; Yoon <i>et al.</i> , 2008)
	Nuclear β -catenin	90/311		(Clements <i>et al.</i> , 2002)
Gastric Adenoma without associated Adenocarcinoma	β -catenin	0/96	Gastric Adenomas are rare gastric polyps that often progress to Gastric Carcinoma	(Abraham <i>et al.</i> , 2003; Lee <i>et al.</i> , 2002)
Gastric intestinal-type Adenocarcinoma	β -catenin	7/26	40 of the 41 tumours with nuclear β -catenin were early gastric cancer suggesting that de-regulation of the Wnt/ β -catenin pathway may play a role in tumorigenesis	(Park <i>et al.</i> , 1999)
	Nuclear β -catenin	41/154		(Miyazawa <i>et al.</i> , 2000; Song <i>et al.</i> , 2004)
	APC	67/96		(Park <i>et al.</i> , 1999) (Miyazawa <i>et al.</i> , 2000; Song <i>et al.</i> , 2004)

Cancer type	Gene	Mutation frequency	Comments	References
Hepatocellular carcinoma	β -catenin	91/223	Hepatocellular carcinoma is one of the most common types of cancers worldwide and has poor prognosis	(De La <i>et al.</i> , 1998; Legoix <i>et al.</i> , 1999; Miyoshi <i>et al.</i> , 1998a; Nhieu <i>et al.</i> , 1999; Satoh <i>et al.</i> , 2000; Taniguchi <i>et al.</i> , 2002; Wong <i>et al.</i> , 2001)
	AXIN1	15/179		(Satoh <i>et al.</i> , 2000; Taniguchi <i>et al.</i> , 2002)
	AXIN2	2/73		(Taniguchi <i>et al.</i> , 2002)
Hepatoblastoma	β -catenin	125/223	Hepatoblastoma is a malignant childhood neoplasm and represents the most common malignant liver tumour in childhood	(Blaker <i>et al.</i> , 1999; Jeng <i>et al.</i> , 2000; Koch <i>et al.</i> , 1999; Park <i>et al.</i> , 2001; Takayasu <i>et al.</i> , 2001; Taniguchi <i>et al.</i> , 2002; Udatsu <i>et al.</i> , 2001; Wei <i>et al.</i> , 2000)
	APC	0/68		(Takayasu <i>et al.</i> , 2001)
	APC	9/13		(Oda <i>et al.</i> , 1996)
	AXIN1	2/27		(Taniguchi <i>et al.</i> , 2002)
Lung Adenocarcinoma	β -catenin	3/137	Patients with low β -catenin expression have significantly poorer prognosis	(Nozawa <i>et al.</i> , 2006; Shigemitsu <i>et al.</i> , 2001; Sunaga <i>et al.</i> , 2001)
Solid-pseudopapillary tumours (SPTs)	β -catenin	18/20	SPTs account for around 1 % of pancreatic cancers have a low malignant potential. These tumours mostly arise in young women	(Abraham <i>et al.</i> , 2002a)
	Nuclear β -catenin	19/20		(Abraham <i>et al.</i> , 2002a)
Wilms Tumour	β -catenin	39/286	Wilms tumour is a paediatric kidney cancer that affects 1 in 100,000 children	(Koesters <i>et al.</i> , 1999; Kusafuka <i>et al.</i> , 2002; Maiti <i>et al.</i> , 2000; Zirn <i>et al.</i> , 2006)
	WTX	15/51	Wilms tumour gene on the chromosome X (WTX) is a protein that has been recently linked with promoting β -catenin degradation	(Rivera <i>et al.</i> , 2007) Rivera <i>et al.</i> 2007 Science, Major <i>et al.</i> , 2007 Science

Cancer type	Gene	Mutation frequency	Comments	References
Prostate cancer	β -catenin	14/264	-	(Chesire <i>et al.</i> , 2000; Gerstein <i>et al.</i> , 2002; Voeller <i>et al.</i> , 1998)
	APC	2/22		(Gerstein <i>et al.</i> , 2002)
	β -TrCP	2/22		(Gerstein <i>et al.</i> , 2002)
Uterine endometrial	β -catenin	33/182	Nuclear β -catenin generally corresponds to type I endometrial tumours, which have a improved prognosis	(Ashihara <i>et al.</i> , 2002; Fukuchi <i>et al.</i> , 1998; Ikeda <i>et al.</i> , 2000b; Mirabelli-Primdahl <i>et al.</i> , 1999; Moreno-Bueno <i>et al.</i> , 2001b; Nei <i>et al.</i> , 1999)
	Nuclear β -catenin	74/319		(Machin <i>et al.</i> , 2002; Ng <i>et al.</i> , 2005; Scholten <i>et al.</i> , 2003)
Ovarian Carcinoma (endometrial type)	β -catenin	47/153	Common ovarian cancer	(Moreno-Bueno <i>et al.</i> , 2001b; Palacios and Gamallo, 1998; Wright <i>et al.</i> , 1999; Wu <i>et al.</i> , 2001b)
	APC	1/47		(Wu <i>et al.</i> , 2001b)
	AXIN1	2/47		(Wu <i>et al.</i> , 2001b)
	AXIN2	1/47		(Wu <i>et al.</i> , 2001b)
Malignant melanoma	β -catenin	11/221	The Wnt/ β -catenin pathway plays an important role in melanocyte development. However nuclear β -catenin is associated with improved prognosis. De-regulation of the Wnt/ β -catenin pathway is hypothesised to be important for the early stages of melanoma development, but not for later stages	(Omholt <i>et al.</i> , 2001; Pollock and Hayward, 2002; Reifenberger <i>et al.</i> , 2002; Rimm <i>et al.</i> , 1999; Rubinfeld <i>et al.</i> , 1997b)
	APC	3/63		(Reifenberger <i>et al.</i> , 2002; Rubinfeld <i>et al.</i> , 1997b)
	Nuclear β -catenin	28/111		(Chien <i>et al.</i> , 2009; Omholt <i>et al.</i> , 2001; Rimm <i>et al.</i> , 1999)
Pilomatrixoma	β -catenin	36/57	Pilomatrixoma is a common skin tumour arising from the hair follicles	(Chan <i>et al.</i> , 1999; Kajino <i>et al.</i> , 2001; Moreno-Bueno <i>et al.</i> , 2001a; Xia <i>et al.</i> , 2006)
Thyroid carcinoma	β -catenin	26/57	Nuclear β -catenin or mutations are associated with poor prognosis in these tumours	(Garcia-Rostan <i>et al.</i> , 2001)

Cytoplasmic and nuclear β -catenin accumulation is associated with activation of the Wnt/ β -catenin pathway and is commonly used as a diagnostic marker in cancer (Eberhart *et al.*, 2000; Terris *et al.*, 1999). Interestingly, nuclear β -catenin is observed more frequently than mutations, suggesting the presence of undiscovered mutations and alternative mechanisms for Wnt/ β -catenin pathway activation. For example, the Wilms tumour gene on the chromosome X (WTX) is a recently discovered gene that is mutated in Wilms tumour, a paediatric cancer of the kidney (Rivera *et al.*, 2007). WTX protein has been suggested to form a complex with β -catenin, AXIN1, β -TrCP, and APC and promote β -catenin ubiquitination and degradation (Major *et al.*, 2007). Alternative tumour mechanisms of activating the Wnt/ β -catenin pathway include promoter hypermethylation of Wnt protein antagonists, Wnt protein up-regulation and down-regulation of E-cadherin. Promoter hypermethylation of SFRP and DKK silences their expression and is a common event in tumourigenesis (**Table 1.4**). Up-regulation of Wnt5a mRNA occurs in gastric, colorectal and uterine cancer and the Wnt2 proto-oncogene is up-regulated in breast, uterine, colorectal and kidney cancer (Katoh, 2001; Saitoh *et al.*, 2002; Taki *et al.*, 2003). β -catenin associates with E-cadherin to mediate epithelial cell-cell adhesion (Rimm *et al.*, 1995). Down-regulation of E-cadherin in the absence of Wnt/ β -catenin pathway mutations does not promote tumourigenesis (Caca *et al.*, 1999; van de Wetering *et al.*, 2001), but down-regulation in the presence of APC mutations has been reported in colorectal tumours and exacerbates pathway activation (Gottardi *et al.*, 2001; Kuphal and Behrens, 2006).

Table 1.4 Hypermethylation of Wnt antagonists in selected human cancers

Cancer type	Gene involved	Mutation Frequency	Comments	References
Hepatocellular carcinoma	SFRP1	9/19	Hypermethylation is also detected in liver cirrhosis. This suggests that hypermethylation could be an early event in liver carcinogenesis	(Takagi <i>et al.</i> , 2008)
	SFRP2	12/19		
	SFRP5	8/19		
Acute myeloid leukaemia	SFRP1	29/100	No activating mutations in the Wnt/ β -catenin identified have been identified in acute myeloid leukaemia to date	(Jost <i>et al.</i> , 2008)
	SFRP2	19/100		
	SFRP4	0/100		
	SFRP5	9/100		
Pancreatic cancer	SFRP1	42/60	Hypermethylation and subsequent loss of expression of sFRPs appears to be an early event in the pathogenesis of pancreatic cancer	(Bu <i>et al.</i> , 2008)
	SFRP2	29/60		
	SFRP4	36/60		
	SFRP5	46/60		
Oral squamous Cell carcinoma	SFRP1	7/17	No mutations have been identified in β -catenin or APC in these tumours to date. These hypermethylation events were found in cell lines grown from tumours	(Sogabe <i>et al.</i> , 2008)
	SFRP2	16/17		
	SFRP5	14/17		
Breast cancer	SFRP1	31/78	Methylation of SFRP5 is associated with reduced survival	(Suzuki <i>et al.</i> , 2008; Veeck <i>et al.</i> , 2008)
	SFRP2	60/78		
	DKK1	15/78		
	SFRP5	123/168		
Gastric cancer	SFRP1	42/46	-	(Nojima <i>et al.</i> , 2007)
	SFRP2	44/46		
	SFRP5	30/46		

As mentioned in **section 1.1** aberrant activation of the Wnt/ β -catenin pathway has been implicated in CNS tumours, including medulloblastomas, CNS PNET, NOS and glioblastomas (**Table 1.5**). However not much is known about the role the Wnt/ β -catenin pathway plays in these tumours. In order to address these issues transgenic mouse models are necessary to study the role of β -catenin in CNS tumourigenesis.

Table 1.5 De-regulation of the Wnt/ β -catenin pathway in CNS tumours

Tumour	Abnormality	Mutation frequency	Description	References
Diffuse astrocytoma WHO grade II	β -catenin mutations	0/16	-	(Gotze <i>et al.</i> , 2009)
	APC allelic imbalance	1/5	-	(Nikuseva-Martic <i>et al.</i> , 2007)
	Increased levels of Dvl3 mRNA	-	Dvl3 de-stabilises of the 'destruction complex'	(Sareddy <i>et al.</i> , 2009b)
	Increased levels of β -catenin mRNA and protein	-	Higher expression of these targets correlates with increased malignancy	
	Increased expression of TCF4, LEF1, c-myc, cyclin D1	-		
	NKD2 promoter hypermethylation	1/16	Promoter hypermethylation correlates with decreased expression of the target genes (6/16 tumours possessed Wnt antagonist promoter hypermethylation)	(Gotze <i>et al.</i> , 2009)
	SFRP1 promoter hypermethylation	1/16		
	SFRP2 promoter hypermethylation	2/16		
	SFRP4 promoter hypermethylation	1/16		
	SFRP5 promoter hypermethylation	1/16		
Anaplastic astrocytoma WHO grade III	β -catenin mutations	1/19	-	(Gotze <i>et al.</i> , 2009; Nikuseva-Martic <i>et al.</i> , 2007)
	Increased levels of Dvl3 mRNA	-	Dvl3 de-stabilises of the 'destruction complex'	(Sareddy <i>et al.</i> , 2009b)
	Increased levels of β -catenin mRNA and protein	-	Higher expression of these targets correlates with increased malignancy	
	Increased expression of TCF4, LEF1, c-myc and cyclin D1	-		
	Patients with Turcot's syndrome type 2	4/24	-	(Attard <i>et al.</i> , 2007)
	DKK1 promoter hypermethylation	1/14	Promoter hypermethylation correlates with decreased expression of the target gene	(Gotze <i>et al.</i> , 2009)
	SFRP1 promoter hypermethylation	2/14		

Tumour	Abnormality	Mutation frequency	Description	References
	SFRP4 promoter hypermethylation	1/14	(4/16 tumours possessed Wnt antagonist promoter hypermethylation)	
	SFRP5 promoter hypermethylation	1/14		
Glioblastoma (GBM) WHO grade IV	APC loss of heterozygosity or allelic imbalances	6/18	-	(Nikuseva-Martic <i>et al.</i> , 2007)
	β -catenin mutations	1/58	-	(Gotze <i>et al.</i> , 2009; Nikuseva-Martic <i>et al.</i> , 2007)
	Glioblastoma cell lines (T98G, GO-G-CCM, U373 and C6) overexpress β -catenin protein	-	Inhibition of Wnt signalling in these cell lines decreases proliferation	(Sareddy <i>et al.</i> , 2009b)
	Increased levels of β -catenin mRNA and protein	-	Higher expression of these targets correlates with increased malignancy	
	Increased expression of TCF4, LEF1, c-myc, cyclin D1	-		
Primary GBM	NKD2 promoter hypermethylation	13/20	Promoter hypermethylation correlates with decreased expression of the target gene (23/30 tumours possessed Wnt antagonist promoter hypermethylation)	(Gotze <i>et al.</i> , 2009)
	SFRP1 promoter hypermethylation	16/30		
	SFRP2 promoter hypermethylation	13/30		
	SFRP4 promoter hypermethylation	2/30		
	SFRP5 promoter hypermethylation	1/30		
Secondary GBM	NKD2 promoter hypermethylation	2/10	Promoter hypermethylation correlates with decreased expression of the target gene (7/10 tumours possessed Wnt antagonist promoter hypermethylation)	(Gotze <i>et al.</i> , 2009)
	DKK1 promoter hypermethylation	5/10		
	DKK3 promoter hypermethylation	2/10		
	SFRP1 promoter hypermethylation	1/10		
	SFRP2 promoter hypermethylation	2/10		
	SFRP5 promoter hypermethylation	2/10		

Tumour	Abnormality	Mutation frequency	Description	References
CNS PNET, NOS WHO grade IV	β-catenin mutations	2/30	-	(Koch <i>et al.</i> , 2001; Rogers <i>et al.</i> , 2009)
	APC mutations	0/24	-	
	Nuclear β-catenin	10/28	-	(Rogers <i>et al.</i> , 2009)
	Nuclear Cyclin D1	12/28	8 of the 12 tumours positive for cyclin D1 were also positive for nuclear β-catenin. However, no correlation was found between proliferation and cyclin D1 overexpression	
Medulloblastoma WHO grade IV	β-catenin mutations	16/253	-	(Huang <i>et al.</i> , 2000; Koch <i>et al.</i> , 2001; Rogers <i>et al.</i> , 2009; Yokota <i>et al.</i> , 2002; Zurawel <i>et al.</i> , 1998)
	APC mutations	4/162	-	(Dahmen <i>et al.</i> , 2001; Huang <i>et al.</i> , 2000; Rogers <i>et al.</i> , 2009)
	Axin1 mutations	9/109	-	(Dahmen <i>et al.</i> , 2001; Yokota <i>et al.</i> , 2002)
	Nuclear β-catenin	51/220	-	(Eberhart <i>et al.</i> , 2000; Ellison <i>et al.</i> , 2005; Rogers <i>et al.</i> , 2009; Yokota <i>et al.</i> , 2002)
	Nuclear Cyclin D1	12/28	There was no significant correlation between nuclear β-catenin and cyclin D1 overexpression. Additionally, no correlation was found between proliferation and cyclin D1 overexpression	(Rogers <i>et al.</i> , 2009)
	Patients with Turcot's syndrome type 2	17/26	Turcot's syndrome arises from APC germline mutations	(Attard <i>et al.</i> , 2007)
Ependymoma	Patients with Turcot's syndrome type 2	3/28	Turcot's syndrome arises from APC germline mutations	(Attard <i>et al.</i> , 2007)
	β-catenin mutations	0/77	-	(Onilude <i>et al.</i> , 2006)
	APC mutations	0/77	-	
Germinoma	β-catenin mutations	1/1	-	(Nikuseva-Martic <i>et al.</i> , 2007)

Tumour	Abnormality	Mutation frequency	Description	References
Meningioma WHO grade II	APC loss of heterozygosity	4/16	-	(Nikuseva-Martic <i>et al.</i> , 2007)
	β-catenin mutations	2/16	-	
	miRNA-200a downregulation	10/14	miRNA-200a downregulation results in downregulation of E-cadherin and upregulation of β-catenin	(Saydam <i>et al.</i> , 2009)
Neurinoma	APC loss of heterozygosity	1/6	-	(Nikuseva-Martic <i>et al.</i> , 2007)
Oligoastrocytoma	APC loss of heterozygosity	1/1	-	(Nikuseva-Martic <i>et al.</i> , 2007)

1.4 Mouse models

1.4.1 Conventional loss-of-function/knockout Models

Mice are widely used to model human diseases due to their genetic similarity and genetic techniques available. One of the greatest breakthroughs in disease modelling was the cellular targeting of genes to introduce mutations (Folger *et al.*, 1985). This was achieved by 'homologous recombination', which involves the recombination between two homologous DNA sequences (Folger *et al.*, 1982).

Another breakthrough in disease modelling was the development of techniques that allowed embryonic stem (ES) cells to be cultured *in vitro* (Evans and Kaufman, 1981; Martin, 1981). These cells remain undifferentiated *in vitro*, but retain the ability to differentiate into all cell types, including germ cells, when returned to the environment of the early embryo (Bradley *et al.*, 1984). ES cells carrying genetic mutations can be generated using homologous recombination (Thomas and Capecchi, 1987). Subsequently, these cells can be injected into the inner cell mass of blastocysts, where they can differentiate and contribute to the development of the embryo (**Figure 1.13**) (Bradley *et al.*, 1984). To generate a stable transgenic mouse line, the mutant ES cells need to incorporate into the germline so the null mutations can be inherited (Bradley *et al.*, 1984). In this manner, mice carrying null mutations for specific genes could be generated (Koller and Smithies, 1989; Thomas and Capecchi, 1990). These mice were named knockout mice.

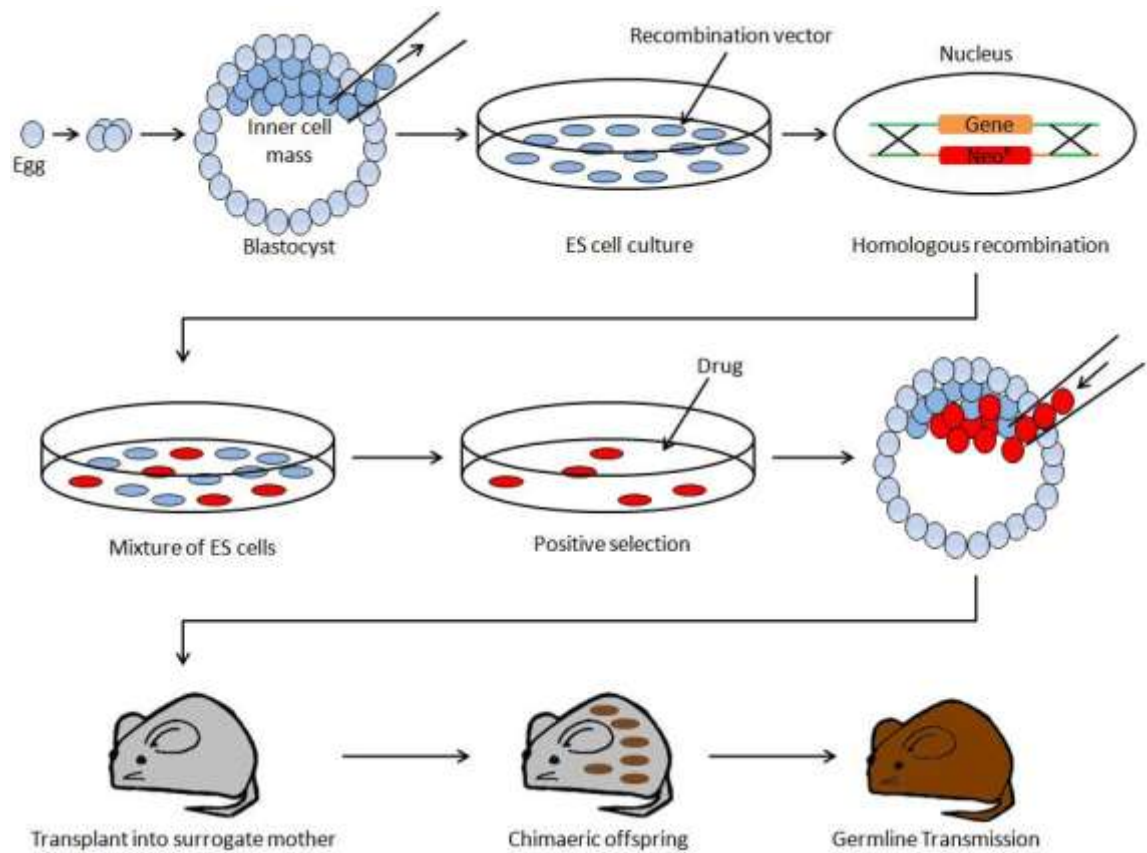


Figure 1.13 Generation of knockout mice

Embryonic stem cell cultures are established from inner cell mass cells. Once in culture, these cells are electroporated with vectors containing the null allele and a drug resistant gene. In the example above, the Neo^R gene confers resistance to neomycin. Electroporation results in a mixed culture containing recombined and non-recombined cells. The recombined cells are positively selected by administering neomycin. Only the recombined cells will survive the treatment. Recombined ES cells are subsequently injected into blastocysts, which are transplanted into a surrogate mother. The ES cells are derived from mice with agouti (brown) fur whilst the surrogate mother is non agouti. In the image above, the agouti patches are derived from the ES knockout cells. This allows for chimaeric mice to be identified. If the ES cells were incorporated into the germline, the null allele can be transmitted to the offspring of the chimaeric mice.

There are two major draw-backs to knockout mice. First, many genes are essential for embryonic development and ablation can result in embryonic lethality (Thomas and Capecchi, 1990). Hence, only the first vital function of a developmentally important gene can be studied. Second, if a gene knockout is not embryonic lethal, null expression occurs in all tissues of the body. This often results in complex phenotypes, which can complicate the interpretation. The Wnt pathway plays a very important role during development and 'conventional' knockout models of many its components result in embryonic lethality (**Table 1.6, Table 1.7** and **Table 1.8**).

Table 1.6 Phenotypes of Wnt protein ‘conventional’ knockout mice

Gene	Phenotype	References
Wnt1	Severe mid-hindbrain abnormalities	(Mcmahon and Bradley, 1990; Thomas and Capecchi, 1990)
Wnt2	Placental defects	(Monkley <i>et al.</i> , 1996)
Wnt3	Lack of Anterior-Posterior patterning, no primitive streak formed	(Liu <i>et al.</i> , 1999)
Wnt3a	Disruption of notochord, no tailbud or caudal somites	(Takada <i>et al.</i> , 1994)
	Paraxial mesoderm defects	(Yoshikawa <i>et al.</i> , 1997)
	Underproliferation of hippocampal progenitors	(Lee <i>et al.</i> , 2000)
	Abnormalities in left-right body symmetry	(Nakaya <i>et al.</i> , 2005)
	Truncation of rostral hindlimbs and absence of tail bud	(Greco <i>et al.</i> , 1996)
Wnt4	Failure to form Kidney tubules	(Stark <i>et al.</i> , 1994)
	Ectopic testosterone synthesis in female mice and absence of Mullerian duct	(Vainio <i>et al.</i> , 1999)
	Role in male gonad development	(Jeays-Ward <i>et al.</i> , 2004)
Wnt5a	Truncation of Anterior-Posterior axis	(Yamaguchi <i>et al.</i> , 1999)
	Abnormalities in distal lung morphogenesis	(Li <i>et al.</i> , 2002)
	Abnormal pituitary gland development	(Cha <i>et al.</i> , 2004)
	Required for pancreatic insulin-cell migration	(Kim <i>et al.</i> , 2005)
Wnt7a	Dorsal-Ventral defects, lack of posterior digits	(Parr and McMahon, 1995)
	Role in Anterior-Posterior patterning, defects in uterus and vagina	(Miller and Sassoon, 1998)
	Mullerian duct regression failure in males	(Parr and McMahon, 1998; Stevens <i>et al.</i> , 1991)
	Delayed synaptic maturation in cerebellum	(Hall <i>et al.</i> , 2000)
Wnt7b	Placental abnormalities	(Parr <i>et al.</i> , 2001)
	Defects in pulmonary vessels	(Shu <i>et al.</i> , 2002)
Wnt9a	Defects in skeletogenesis, loss of synovial chondroid metaplasia	(Spater <i>et al.</i> , 2006)
Wnt9b	Essential for caudal extension of Mullerian duct in females	(Carroll <i>et al.</i> , 2005)
Wnt10A	Unknown	-
Wnt10b	Excess lipid accumulation in regenerating muscle	(Vertino <i>et al.</i> , 2005)
Wnt11	Kidney hypoplasia from ureteric branching defects	(Majumdar <i>et al.</i> , 2003)

Table 1.7 Phenotypes of Fzd and Lrp ‘conventional’ knockout mice

Gene	Phenotype	References
Fzd3	Defects in axon tracts in the forebrain	(Wang <i>et al.</i> , 2002)
Fzd4	Progressive cerebellar, auditory and oesophageal dysfunction	(Wang <i>et al.</i> , 2001)
	Infertility due to impaired formation of corpora lutea	(Hsieh <i>et al.</i> , 2005)
Fzd5	Yolk sac and placental angiogenesis defects	(Ishikawa <i>et al.</i> , 2001)
Fzd6	Hair patterning defects	(Guo <i>et al.</i> , 2004)
Fzd9	Defects in B-cell development	(Ranheim <i>et al.</i> , 2005)
	Hippocampal and visuospatial learning defects	(Zhao <i>et al.</i> , 2005)
Fzd10	Unknown	-
Lrp5	Low bone mass as a result of decreased osteoblast proliferation, impaired vascular regression	(Kato <i>et al.</i> , 2002)
	Increased plasma cholesterol and decreased glucose-induced insulin secretion	(Fujino <i>et al.</i> , 2003)
Lrp6	Truncated Anterior-Posterior axis, neural tube closure, mid-hindbrain and dorsal-ventral patterning defects	(Pinson <i>et al.</i> , 2000)
	Small eyes and aberrant lenses	(Stump <i>et al.</i> , 2003)
	Reduced dentate granule neurone production, abnormalities of the radial glia scaffolding	(Zhou <i>et al.</i> , 2004b)
	Smaller and severely disorganized dorsal thalamus	(Zhou <i>et al.</i> , 2004a)

Table 1.8 Phenotypes of Wnt/ β -catenin downstream component 'conventional' knockout mice

Gene	Phenotype	References
Dvl1	Abnormal social interaction	(Lijam <i>et al.</i> , 1997; Long <i>et al.</i> , 2004)
Dvl2	Cardiovascular outflow tract defect, vertebral and rib malformations, neural tube closure defects	(Hamblet <i>et al.</i> , 2002)
Dvl3	Cardiac outflow tract abnormalities	(Etheridge <i>et al.</i> , 2008)
GBP1-2-3	No obvious defects in Wnt signal transduction	(van Amerongen <i>et al.</i> , 2005)
Axin1	No knockout generated. Fused mutant allele results in Anterior-Posterior duplication, neuroectodermal and cardiac abnormalities	(Zeng <i>et al.</i> , 1997)
Axin2	Malformation of skull due to increased osteoblast proliferation and differentiation	(Yu <i>et al.</i> , 2005)
Gsk3 β	Liver degeneration due to defects in NF κ B signalling	(Hoeflich <i>et al.</i> , 2000)
	Hypertrophic cardiomyopathy and cardiomyoblast hyperproliferation	(Kerkela <i>et al.</i> , 2008)
Apc1	Development of primitive ectoderm fails before gastrulation	(Moser <i>et al.</i> , 1995)
Apc2	Unknown	-
β -catenin	Failure in Anterior-Posterior formation	(Huelsenken <i>et al.</i> , 2000)
	Defects in the embryonic ectoderm cell layer	(Haegel <i>et al.</i> , 1995)
Lef1	Defects in pro-B-cell proliferation and survival	(Reya <i>et al.</i> , 2000)
	Defects in the formation of organs that require inductive tissue interaction	(van Genderen <i>et al.</i> , 1994)
	Varying degrees of hippocampal abnormalities	(Galceran <i>et al.</i> , 2000)
Tcf1	Defects in thymocyte proliferation and differentiation	(Schilham and Clevers, 1998; Verbeek <i>et al.</i> , 1995)
Tcf3	Failure in Anterior-Posterior axis formation	(Merrill <i>et al.</i> , 2004)
Tcf4	Depletion of epithelial stem cell compartments in the intestine	(Korinek <i>et al.</i> , 1998)

1.4.2 Mouse models of conditional gene inactivation (Cre-loxP system)

Conditional gene inactivation allows for inactivation of genes in a time- and/or tissue-specific manner (Gu *et al.*, 1993). This relies on enzymes that can recombine specific DNA sequences with high fidelity. The most common system for conditional gene inactivation is the Cre-loxP system. Cre-recombinase is a bacteriophage P1 enzyme that belongs to a large family of DNA recombinases (Sternberg and Hamilton, 1981). It recognises sequences called locus of crossover (x) in P1 (loxP), which consist of two 13bp inverted repeats separated by an 8bp asymmetric spacer (Hoess and Abremski, 1984; Sternberg and Hamilton, 1981). Cre-recombinase accomplishes recombination by binding to two loxP sites and mediating strand cleavage, exchange and ligation at the asymmetric spacer (Sadowski, 1995, Hoess 1985). In this manner, Cre-recombinase can mediate the excision or inversion of DNA flanked by loxP sites (**Figure 1.14**). Furthermore, it can also mediate the insertion of circular DNA molecules into linear molecules or the exchange of DNA between two linear molecules as long as each one contains a loxP site (**Figure 1.14**).

By flanking a gene with loxP sites its excision can be triggered in the presence of Cre-recombinase (Gu *et al.*, 1994). Therefore, by controlling Cre-recombinase expression it is possible to conditionally inactivate gene function (Gu *et al.*, 1994). The most common method for controlling Cre-recombinase is by generating mice that express the enzyme under the control of a specific promoter (Orban *et al.*, 1992). As a result, only the cells in which the promoter is active will express Cre-recombinase and be recombined (Orban *et al.*, 1992). The limitation of this approach is the need of multiple Cre-recombinase-expressing mice to study the effect of a gene in different cell populations.

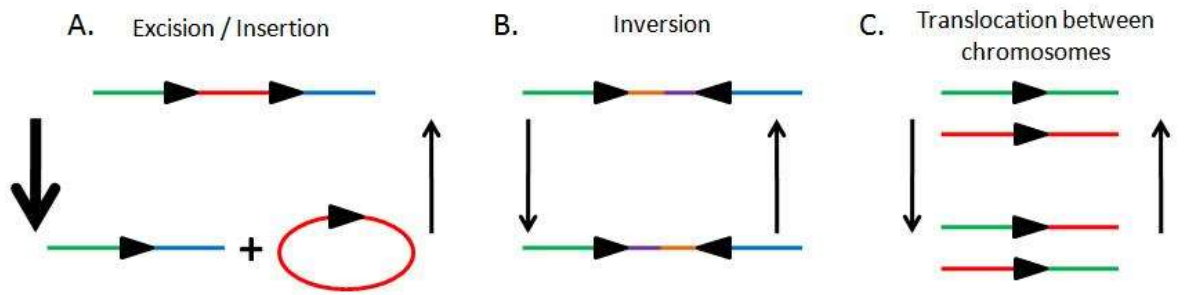


Figure 1.14 Cre-recombinase recombination events

Cre-recombinase can mediate excision/insertion (A) inversion (B) and translocation between chromosomes (C) depending of the location and the direction of the loxP sites. The arrows represent the direction of recombination and the thickness represents the likelihood of the recombination event taking place.

Cre-recombinase expression can also be controlled by inducible systems. An example of this is the Cre-Tamoxifen system (Metzger *et al.*, 1995). Tamoxifen is a synthetic drug which competes with oestrogen for binding to the oestrogen receptor (ER) (Wakeling *et al.*, 1984). In the Cre-Tamoxifen inducible system, transgenic mice, which express a Cre-Oestrogen receptor binding-domain fusion protein (Cre-ER), are used (Feil *et al.*, 1996). When tamoxifen binds to the oestrogen receptor it translocates from the cytosol into the nucleus (Dix and Jordan, 1980). Therefore, in the presence of Tamoxifen, the Cre-ER fusion protein is translocated into the nucleus where it can mediate loxP site recombination (Metzger *et al.*, 1995). This method is highly versatile as Tamoxifen can be administered to localised areas within tissues *via* postnatal injection (Andersson *et al.*, 2010). Alternatively, it can be delivered orally to pregnant mice for recombination during embryonic development (Andersson *et al.*, 2010).

Finally, Adenoviral vectors expressing Cre-recombinase can also be used to mediate loxP site recombination (Anton and Graham, 1995; Sakai *et al.*, 1995). In this system, all infected cells transiently express Cre-recombinase and are irreversibly recombined.

The nature of the scientific investigation determines which of the methods for Cre-mediated recombination is most appropriate. Cre-recombinase-expressing mouse lines are useful for studying gene inactivation in specific cell populations. On the other hand, inducible and Adenoviral systems are useful for studying the effect of null mutations in targeted areas.

1.4.3 Conditional Models for studying the Wnt/ β -catenin pathway in CNS tumours

De-regulation of the Wnt/ β -catenin pathway has been observed in CNS tumours (Table 1.5). However, the role of the Wnt/ β -catenin pathway in the development and maintenance of these tumours is poorly understood. To study this role, mouse models in which the pathway is constitutively active are necessary. The most common method used to achieve this is mutating the four phosphorylation residues of β -catenin. As discussed in section 1.3.6, phosphorylation at those residues is necessary for β -catenin degradation. Hence, abolishing their phosphorylation prevents β -catenin from being degraded, resulting in constitutive activation of the pathway.

Several β -catenin gain-of-function conditional mouse models have been generated. The first of these models expressed Serine37Alanine (S37A) β -catenin under the control of the prion protein (PrP) promoter (E11.5) (Kratz *et al.*, 2002). PrP is a GPI-anchored membrane protein predominantly expressed in neurones (Bailly *et al.*, 2004). Although a doubling in nuclear S37A β -catenin was observed in the cerebella of transgenic mice, no brain tumours were detected. In this model S37A β -catenin was expressed in neuronally committed cells. However, evidence suggests that stem/progenitor cells are the cell of origin of CNS tumours (Jacques *et al.*, 2010; Sanai *et al.*, 2005). Therefore, degradation-resistant β -catenin may need to be expressed in neural stem cells for tumourigenesis to take place. This possibility was explored by Holland's group (Fults *et al.*, 2002; Momota *et al.*, 2008). In the first study, transgenic mice were infected with an avian leukosis virus (ALV) expressing S37A β -catenin (ALV-S37A- β -catenin) (Fults *et al.*, 2002). Murine cells are not susceptible to AVL. However, the transgenic mice used in this study expressed TVA, the avian receptor for ALV, in Nestin-expressing cells (Nestin-TVA mice). This allowed for Nestin-expressing cells to be specifically infected with ALV-S37A- β -catenin. These mice did not develop tumours within eight weeks, the endpoint of the experiment. However, this is unsurprising since inactivation of two tumour suppressor genes in the SVZ results in the development of tumours after up to thirty weeks (Jacques *et al.*, 2010). Additionally, infection of Nestin-TVA mice with an avian leukosis virus (AVL) expressing the potent oncogene c-myc (ALV-c-myc) did not yield any tumours (Fults *et al.*, 2002). Hence, the lack of tumours may be explained by the lack of additional mutations and/or short follow-up of the experiment. In their second study, Holland's group addressed the issue of additional mutations by using mice expressing TVA under the control of the GFAP promoter (GFAP-TVA) on a p53^{-/-} genetic background (Momota *et al.*, 2008). GFAP-TVA; p53^{-/-} mice infected with ALV-c-myc, but not with ALV-S37A- β -catenin, formed tumours (Momota *et al.*, 2008). However, the endpoint of the experiment was at three months due to the development of lymphomas and sarcomas, a known phenotype of p53 knockout mice (Harvey

et al., 1993). Interestingly, combined infection with ALV-c-myc and ALV-S37A- β -catenin increased the phenotypic diversity and halved the tumour latency in GFAP-TVA; p53^{-/-} mice without increasing tumour incidence in comparison to ALV-c-myc infected mice (Momota *et al.*, 2008). These results suggest that constitutive activation of the Wnt/ β -catenin pathway does not promote tumourigenesis. Instead, it appears to influence tumour phenotype and behaviour. However, the possibility that degradation-resistant β -catenin may promote tumourigenesis in the long-term can not be ruled out.

In order to address these unresolved issues and investigate further, a conditional mouse model, which expresses a degradation-resistant form of β -catenin (Δ GSK- β -catenin) was generated (**Figure 3.1**). Δ GSK- β -catenin contains point mutations at the four phosphorylation sites required for β -catenin down-regulation (S33A, S37A, T41A and S45A). These mutations abolish GSK3 β and CK1 α mediated phosphorylation and therefore prevent Δ GSK- β -catenin from being degraded (**section 1.3.6**). Expression of Δ GSK- β -catenin in embryonic stem (ES) cells up-regulated the expression of the Wnt/ β -catenin downstream targets (Haegeler *et al.*, 2003). This phenotype was reproduced by the expression of a truncated form of APC (Haegeler *et al.*, 2003). These results confirmed that this Δ GSK- β -catenin construct can effectively activate the Wnt/ β -catenin pathway. Therefore, transgenic mice expressing this construct (**Figure 3.1**) were generated to study the Wnt/ β -catenin pathway in the CNS.

2 Materials and methods

2.1 Mice

All mice were housed and maintained under specific pathogen-free conditions in accordance with Institutional and UK Home Office guidelines (Project license 70/6603). They were kept on a 12 hour light-dark cycle and given food and water *ad libitum*. All procedures, including culling of the mice, were carried out in accordance with Home Office regulations.

2.1.1 Genotyping

Mice were assessed for the presence of transgenes by ear biopsies, which were used for DNA extraction and subsequent analysis by polymerase chain reaction (PCR) (**section 2.7**).

2.1.2 Embryonic LacZ expression

After timed matings, embryos were harvested at embryonic day 10.5, 12.5, or 16.5 and β -galactosidase-stained (**section 2.2.2**). They were then photographed using a Nikon Coolpix 995 camera mounted on a Zeiss Stemi SV11 microscope and paraffin-embedded.

2.1.3 BrdU injection of mice

5-Bromo-2-deoxyuridine (BrdU) (Sigma; 5 mg/ml or 10 mg/ml) was made in distilled water and dissolved using a sonicator (Fisherbrand FP11002). To label proliferating cells, mice were given intraperitoneal injections of BrdU at a concentration of 50 μ g per gram of body weight. As a base analogue of thymidine, BrdU substitutes for thymidine during DNA synthesis and incorporates into the newly synthesized DNA. Therefore, by BrdU administration, dividing (stem) cells are labelled. BrdU-positive cells can be detected on brain sections by immunohistochemical techniques.

2.1.4 Adenovirus-Cre intraventricular injection

Viral infection of SVZ cells was achieved by unilateral stereotaxic injections of 10^9 plaque-forming units of Adenovirus-Cre in phosphate buffered saline (PBS) into anaesthetized mice placed in a Narishige SR 6N stereotaxic frame. The injection in relation to bregma was anterior 0 mm; lateral 0.5 mm and ventral 2.5 mm. Injections (usually of 2-4 μ L volume) were administered with a Hamilton syringe 1701RN and a 26 gauge needle (Hamilton).

2.2 Tissue harvesting and preparation

2.2.1 Brain and peripheral organ harvesting

For histology (**section 2.5**) and β -galactosidase staining (**section 2.2.2**), the mice were killed by increasing concentration of CO₂ in order to retain the structural integrity of the entire brain. For primary cell cultures (**section 2.4**), mice were killed by cervical dislocation and their brains removed under sterile conditions, to minimise cell death.

For Western blotting (**section 2.6**) brains were sagittally cut with one hemisphere used for β -galactosidase staining (**section 2.2.2**). The other hemisphere was sub-divided into forebrain and cerebellum, which were further sub-divided into halves. The pieces were then submerged in isopentane (Sigma) and snap-frozen in liquid nitrogen. Excess isopentane was blotted out and the samples were stored at -80°C until use. Peripheral organs such as heart, kidney, lung, liver, spleen, and testis of mice were removed for β -galactosidase staining (**section 2.2.2**).

2.2.2 β -galactosidase staining assay

Brains were incubated in formalin (Pioneer Research) for 30 min at room temperature (RT), cut sagittally and then incubated for a further 30 min in formalin. They were then permeabilised (by shaking) in permeabilisation buffer, which consisted of β -gal staining solution (10 mM Phosphate buffer [pH: 7-7.2][Fisher Chemicals], 150 mM NaCl [Fisher Chemicals], 1 mM MgCl₂ [Sigma], 3.3 mM K₄Fe(CN)₆ x 3H₂O [Sigma], 3.3 mM K₃Fe(CN)₆ [Sigma]), 1 % MgCl₂ [w/v] [Sigma], 0.02 % Igepal (v/v) (Fluka BioChemika) and 0.01 % Sodium Deoxycholate (w/v) (Sigma). The brains were then incubated overnight at 37°C (shaking) in permeabilisation buffer and 1 % X-Gal (w/v) (Merck; dissolved in N,N-Dimethylformamide [Sigma]). X-Gal is cleaved by β -galactosidase, when the latter is expressed by the LacZ gene, yielding galactose and 5-bromo-4-chloro-3-hydroxyindole. The resulting compound is then oxidised into 5,5'-dibromo-4,4'-dichloro-indigo, an insoluble blue product. The brains were subsequently photographed using a Nikon Coolpix 995 camera mounted on a Zeiss Stemi SV11 microscope to record the staining pattern of β -galactosidase. Somatic organs were prepared in exactly the same way, but they were not sectioned. When staining for embryos, permeabilisation was not required.

2.3 Generation of the pcall2- Δ GSK- β -catenin-IRES-GFP vector

2.3.1 Restriction enzyme digestion and ligation

The pUHD10-3/ Δ GSK- β -catenin vector containing Δ GSK- β -catenin was a kind gift from Dr Nelson, Department of Molecular and Cellular Physiology, Stanford University School of Medicine, Stanford, California, United States of America (Barth *et al.*, 1999). A BamH I restriction enzyme site (GGATCC) was inserted upstream of Δ GSK- β -catenin cDNA sequence by doing a PCR with the pUHD10-3/ Δ GSK- β -catenin vector and primers TJ1 and TJ3 (**section 2.7.2**). The PCR product and pUHD10-3/ Δ GSK- β -catenin vector were digested with 0.5 U/ μ l Sac II and 0.5 U/ μ l Sph I (both from New England Biolabs), NE buffer 4 (New England Biolabs) for three hours at 37°C. The digests were run on a 2 % agarose gel (w/v) (Sigma) containing 75 ng/ml ethidium bromide (Sigma) for 30 min. The bands were briefly visualised under UV light, cut out of the gel and purified using the QIAquick gel purification kit (QIAGEN). The digested PCR product and the digested pUHD10-3/ Δ GSK- β -catenin vector were subsequently ligated with T4 DNA ligase (20 U/ml, New England Biolabs) in T4 DNA ligase buffer (New England Biolabs) overnight at 16°C.

The modified pUHD10-3/ Δ GSK- β -catenin vector was restriction enzyme digested with 0.5 U/ μ l BamH I (New England Biolabs), NE Buffer 2 (New England Biolabs) supplemented with 100 μ g/ml bovine serum albumin (BSA) (Sigma) and incubated at 37°C for three hours. The digest was run on gel and purified as mentioned above to obtain the Δ GSK- β -catenin cDNA. Subsequently, the pcall2-updated-IRES-GFP vector was digested with 0.5 U/ μ l Bgl II (New England Biolabs), NE Buffer 3 (New England Biolabs) at 37°C for three hours. The pcall2-updated-IRES-GFP digest was gel purified as mentioned above. Both BamH I and Bgl II leave the same overhang so the digested Δ GSK- β -catenin cDNA and pcall2-updated-IRES-GFP can be ligated together. For ligation, the DNA digests were incubated with 20 U/ml T4 DNA ligase (New England Biolabs) in T4 DNA ligase buffer (New England Biolabs) overnight at 16°C.

2.3.2 Bacterial transformation and purification

Prior to bacterial transformation, Luria Bertani (LB) agar plates containing neomycin were prepared. For this purpose, 37 g/L LB agar (Sigma) was made and autoclaved. Subsequently, Isopropyl β -D-1-thiogalactopyranoside (IPTG) (100 μ M final concentration) (Promega), Neomycin (100 μ g/ml final concentration) (Sigma) and X-gal (20 mg/ml final concentration) (Merck; dissolved in N,N-Dimethylformamide [Sigma]) were added. This mixture was poured into 10 cm tissue culture plates and allowed to cool and solidify.

For transformation, 2 μ l of ligation product was added to 90 μ l of thawed JM109 competent cells (Promega). This mixture was incubated on ice for 20 min. Following

incubation, the cells were heat-shocked by heating for 45 seconds at 42°C followed by incubation on ice for 5 min. 1 mL of LB broth (25 g/L, sterile) (Sigma) was added and the cells were incubated at 37°C for one hour (shaking). After incubation, cells were pelleted for 10 min at 3000 x *g* and re-suspended in 100 µl of LB broth. The cells were plated on an LB agar plate and incubated at 37°C overnight. The following day, single colonies were picked with a pipette tip and transferred to a 15 mL Falcon tube containing 2 mL of LB broth supplemented with neomycin 100 µg/ml (Sigma) and incubated at 37°C overnight (shaking). The cells were pelleted for 10 min at 3000 x *g*. The DNA from the pellet was harvested using the QIAprep spin miniprep kit (QIAGEN). Finally, the plasmid DNA was linearised by restriction enzyme digestion with 0.5 U/µl Sca I (New England Biolabs), NE Buffer 3 (New England Biolabs) incubated at 37°C for three hours and purified using the QIAquick PCR purification kit (QIAGEN).

2.3.3 ES cells electroporation

The ES cell medium (Dulbecco's modified Eagle's medium [DMEM] [Sigma], 20 % foetal calf serum (v/v) [FCS] [Invitrogen], 1 mM Na pyruvate [Sigma], 2 mM L-glutamine [Sigma], 0.1 mM non-essential amino acids [Sigma], 0.1 mM 2-mercaptoethanol [Sigma], 103 units/ml ESGRO murine LIF [Millipore], and 1.000U/ml Penicillin/Streptomycin [P/S] [Lonza]) of C57BL/6J ES cell cultures was changed two to three hours prior to electroporation. The C57BL/6J ES cells were harvested following a 5 min incubation with trypsin (Sigma). The trypsin was inactivated with surplus ES cell medium. The cells were subsequently centrifuged for 10 min at 300 x *g* and re-suspended in ES cell medium to a concentration of 1×10^7 cells/ml. 30 µg of the linearised plasmid (**section 2.3.2**) was added per 0.8 mL of re-suspended cells and aliquoted into electroporation cuvettes (Biorad). The cells were electroporated using a Biorad GenePulser at 230V, 500 µF. The time constant was set to 7.0. Following electroporation, the cuvettes were incubated at room temperature for 5 min and the cells were transferred to 10 cm plates with fresh ES cell medium.

2.3.4 ES cell selection for LacZ

Electroporated ES cells were treated with trypsin (Sigma) for 5 min. The trypsin was inactivated with surplus ES cell medium. The cells were counted and diluted to a concentration of 200 cells/ml. 200 µl/well of this mixture was plated on wells of a 96-well plate (around 1 cell/well final concentration). The plate was incubated at 37°C in an atmosphere of 5 % CO₂ and 95 % rH (relative humidity) for three days. Subsequently, the cells from each well were harvested individually. The cells were plated in duplicate into 96-well plates. One of the 96-well plates was used for β-galactosidase staining (**section 2.2.2**). The A7, B4, C11, E3, E6, E11, F9, G1 and H4 clones (the names correspond to the well position) were positive for β-galactosidase. The corresponding ES cell clones from the other 96-well plate were harvested

and used for southern blotting (**section 2.3.5**) and microinjection into blastocysts. The blastocysts were injected into pseudo-pregnant 129sv female mice.

2.3.5 Southern blot analysis

2.3.5.1 Gel electrophoresis and transfer

DNA was extracted from the B4, C11, E3, E6, E11, F9, G1 and H4 ES cell clones using the Dynabeads DNA DIRECT Kit (Invitrogen). Subsequently the DNA was digested with 0.5 U/ μ l EcoR I (New England Biolabs), EcoR I Buffer (New England Biolabs) incubated at 37°C for 19 hours. The digested DNA was separated on a 1 % agarose gel (w/v) (Sigma). The DNA on the gel was then depurinated by immersing it in 0.25 M HCl and gently rocking it for 10 min. Afterwards the gel was neutralised and alkaline denatured with three washes in 0.4M NaOH for 15 min each wash. Subsequently, the gel was submerged in 20x SSC buffer (3 M NaCl [Fisher Chemicals], 300 mM Na₃Citrate [Trisodium citrate], pH 7) for 5 min (shaking). The blotting set-up was as follows (from bottom to top):

1. 20x SCC buffer reservoir
2. Glass plate
3. 2x pieces of wick-blotting paper wetted with 20x SCC buffer cut to the width of the gel and length such that the wick is in contact with the bottom of the dish
4. Agarose gel
5. Plastic wrap to cover the entire gel
6. Hybond N+ nylon membrane (GE healthcare) wetted with distilled water cut to the size of the gel
7. 4x pieces of blotting paper cut to size of the gel (the first piece wetted with 20x SSC)
8. Glass plate
9. A weight to keep blot in place

The blot was transferred overnight. Subsequently the membrane was cross-linked by UV using the auto-crosslink program of a Stratalinker (Stratagene).

2.3.5.2 Probe synthesis, hybridisation and visualisation

The membrane was prehybridised in CG solution (0.5 M NaP [Sigma] pH7.2, 7 % sodium dodecyl sulphate [v/v] [SDS] [BioChemika], 1 % BSA [w/v] [Sigma] and 1 mM ethylenediaminetetraacetic acid [EDTA] [Fluka BioChemika] pH8.0) for four to six hours. Whilst the membrane was prehybridising, the Δ GSK- β -catenin probe was synthesised using the NEBlot kit (New England Biolabs). The probe was then added to the membrane and incubated at 65°C overnight. The following day, the membrane was washed three times with CG wash

solution (40 mM NaP [Sigma] pH7.2, 1 % SDS [v/v] [BioChemika] and 1 mM EDTA [Fluka BioChemika] pH8.0) at 65°C for 10 min/wash. The membrane was dried, placed in Saran Wrap and exposed overnight in a PhosphorImaging cassette.

2.4 Cell culture

2.4.1 Transfection of N2a cells

N2a cells were grown in DMEM supplemented with L-glutamine (BioWhittaker), 10 % FCS (v/v) (Invitrogen) and 1.000 U/ml P/S (Lonza). 3 µL of Fugene 6 reagent (Roche) was diluted in 95 µL of serum free media per transfection reaction. A total of 1 µg of plasmid DNA was added to each Fugene/Medium mixture. N2a cells were grown at a density of 4×10^5 cells/well in seven wells of two 6-well plates overnight. The following day the cells were transfected as follows (each combination corresponds to one well):

1. 0.5 µg pEGFP + 0.5 µg pBlue II Ks+ (vehicle)
2. 0.5 µg pCre + 0.5 µg pBlue II Ks+
3. 0.5 µg pcall2-ΔGSK-β-catenin-IRES-GFP #3 + 0.5 µg pBlue II Ks+
4. 0.5 µg pcall2-ΔGSK-β-catenin-IRES-GFP #18 + 0.5 µg pBlue II Ks+
5. 0.5 µg pCre + 0.5 µg pcall2-updated-IRES-GFP
6. 0.5 µg pcall2-updated-IRES-GFP + 0.5 µg pBlue II Ks+
7. 0.5 µg pCre + 0.5 µg pcall2-ΔGSK-β-catenin-IRES-GFP #3
8. 0.5 µg pCre + 0.5 µg pcall2-ΔGSK-β-catenin-IRES-GFP #18

48 hours post-transfection, the cells were washed with PBS and harvested. The cells were then centrifuged for five minutes at $300 \times g$ (4°C). Finally, the cell pellets were re-suspended in 100 µL of Radio-immunoprecipitation assay (RIPA) buffer (50 mM Tris pH7.4 [Sigma], 1 % Igepal [v/v] [Fluka BioChemika], 0.25 % Sodium Deoxycholate [w/v] [Sigma], 150 mM NaCl [Fisher Chemicals], 1 mM EGTA [Sigma]) containing protease inhibitor (1 tablet in 7 mL RIPA buffer)(Roche) and kept for Western blotting (**section 2.6**).

2.4.2 SVZ dissection and growth of neural stem cells

All surgical instruments were sterilised by heat or by immersing in 70 % ethanol. Mice were killed as previously mentioned (**section 2.2.1**). Brains were removed for NSC isolation; they were placed in a 10 cm dish containing ice-cold HIB buffer to preserve the tissue. Each brain was processed individually by transferring it into a sterile Petri dish and dissected under a Zeiss Stemi SV11 microscope as illustrated in **Figure 2.1**.

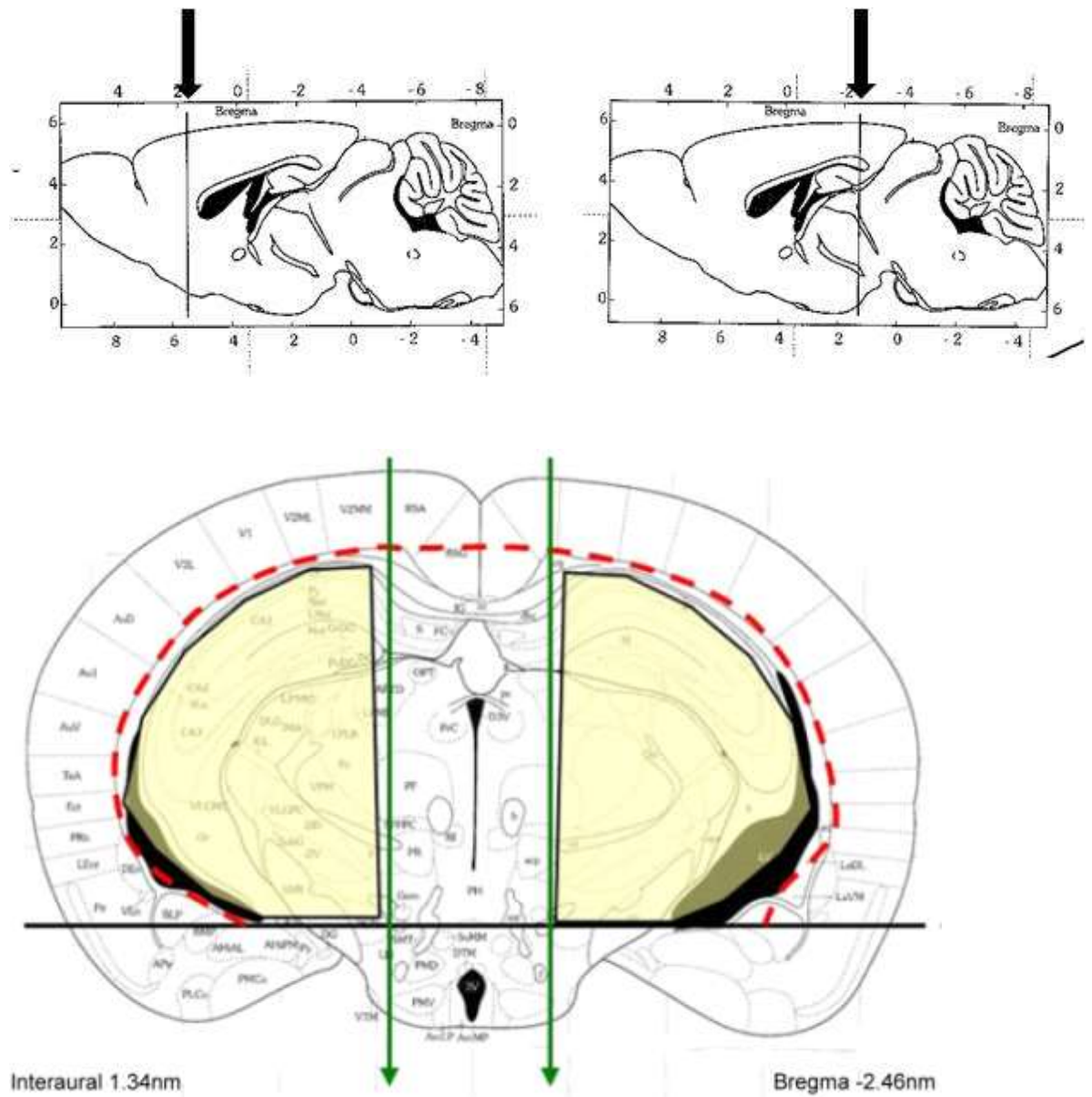


Figure 2.1 Dissection of the SVZ part 1

Top panel: The brain is cut along the arrows shown. The brain slice is placed with the rostral side facing down. **Bottom panel:** The brain slice is cut along the green, black and red lines and the tissue represented in yellow is used for subsequent steps in the protocol.

The dissected tissue was transferred into ice-cold HIB buffer whilst the other brains were dissected. Following dissection, the tissue was transferred onto a sterile Teflon disk and minced five times (in different positions) using a Tissue Chopper (Mcllwain) set to cut at 400 μm intervals. The tissue was then treated with Papain (Worthington, USA) and mechanically dissociated into a single cell suspension. The cells were pelleted by centrifugation at 300 x g for 5 min at RT. The pellet was reconstituted in a DNase-albumin-inhibitor mixture and spun in a discontinuous density dependent gradient over an albumin-inhibitor mixture at 70 x g for 6 min at RT. The purified cell pellet was re-suspended in NSC medium (DMEM/Ham's F12 [Sigma] supplemented with 1x B27 [Gibco], 1.000 U/ml P/S [Lonza], 20 ng/ml recombinant murine EGF [Peprotech] and 20 ng/ml recombinant human FGF β [Peprotech]). The cells were plated in wells of a 6-well plate for five days before replacing the medium. The cells then grew as free-floating aggregates called neurospheres (NS). For the first passage NS were incubated with Accumax (Chemicon) for 5 min at 37°C and mechanically dissociated. Following this, media was replaced every two to three days. Further passages were performed approximately every seven days depending on NS size. These passages were performed by incubation in Accumax (Chemicon) for 20 min at 37°C and by mechanical dissociation. All cultures were maintained at 37°C in an atmosphere of 5 % CO₂ and 95 % relative humidity.

2.4.3 Infection of cultures with Adenovirus

NS were collected in a 15 or a 50 mL tube and allowed to settle. All but 1 mL media was aspirated and a 50 μL aliquot was taken and incubated in 350 μL AccuMax (Chemicon) at 37°C for 20 min. Following incubation, the cells were mechanically dissociated to a single cell suspension and counted using a Haemocytometer. The number of cells in the remaining 1 ml of medium was calculated. The cells were divided equally among three 10 cm plates with 10 mL NS medium for each. One plate was for Adeno-Cre infection, one plate was for Adeno-GFP infection and the remaining plate was left untreated. For infection with Adeno-Cre and Adeno-GFP, five times more virus was added than cells in a 10 cm plate (both viral titres were $\sim 2.5 \times 10^9$ pfu/ml). The NS medium was changed 2 days after infection and the NS were passaged the following day. Infection efficiency was determined by visualising GFP immunofluorescence at 488 nm excitation wavelength using a Zeiss Axiovert 200 fluorescence microscope. Photographs were taken with a Nikon Coolpix 995 3 Megapixel digital camera.

2.4.4 WST-1 assay

The WST-1 assay was used to measure the relative proliferation rates of cells *in vitro*. The assay principle is based on the conversion of the tetrazolium salt WST-1 into an orange coloured dye (formazan salt) by mitochondrial dehydrogenase enzymes. Over time, this reaction produces a colour change of the medium, which is directly proportional to the amount of mitochondrial dehydrogenase, and therefore cell number, in a given culture. This reaction product can be detected on a spectrophotometer (Tecan Sunrise microplate reader with XFluor 4 software) at detection wavelength of 440 nm, with a reference of 620 nm.

This analysis was performed in a 96-well plate. NS were dissociated with Accumax (**section 2.4.2**) and seeded at 6×10^4 cells/well in 10 wells containing 100 μL of neural stem cell media. The cells were left for 3 days before the addition of 10 μL WST-1 reagent per well and the optical density (OD) was recorded at 4, 6 and 8 hours. Alternatively, cells were plated in triplicate at either 6×10^4 cells/well or 3.5×10^3 cells/well (specified in text in the relevant results chapters). WST-1 reagent was added to one plate at day one post-passage and OD was measured at 4 hours. The other plates were treated at day two and three post-passage, respectively, and OD was measured as previously.

All samples were run in groups of 10 or 5 repeats (specified in text in the relevant results chapters) and corrected against control wells containing NSC media. Statistical analysis was performed using two-tailed t-test.

2.4.5 Hoechst proliferation assay

NS were dissociated with AccuMax (**section 2.4.2**) to a single cell suspension. Subsequently, cells were plated in quintuplicate for each treatment in wells of a 96-well plate at a cell density of 3.5×10^3 cells/well in 100 μL of NSC medium. 96-well plates were prepared in triplicates. At day one post-passage, 50 μL of 5 $\mu\text{g}/\mu\text{L}$ of Hoechst 33342 (Sigma) dissolved in dimethylsulfoxide (DMSO) was added to each well of one of the plates and incubated for 30 min at 37°C. The plate was centrifuged for 1 min at 1000 $\times g$. Subsequently, the medium was removed from the wells to remove as much unbound Hoechst as possible and replaced with 1X PBS. Fluorescence was detected using a spectrophotometer (Tecan Sunrise microplate reader with XFluor 4 software) with an excitation wavelength of 360 nm and an emission wavelength of 465 nm. This was repeated at day 3 and 5 post-plating or day 2 and 3 post-plating using the remaining 96-well plates (specified in text in the relevant results chapters). Statistical analysis was performed using a two-tailed t-test.

2.4.6 NS size

NS were dissociated with AccuMax (**section 2.4.2**) and plated on a 6 cm plate at a cell density of 0.5×10^6 cells/well. On the fourth day post-passage, the cells were media changed. The cultures were media changed every two days thereafter. On day ten post-passage, the diameter of the cells was measured using an Axiovert 135 microscope (Zeiss) and Openlab 5 software. An average diameter was calculated from ≥ 100 neurospheres (each diameter was measured twice). Statistical analysis was performed using a two-tailed t-test.

2.4.7 Limited dilution assay

100 μ L of NSC media was pipetted into each well of a 96-well plate. NS were dissociated with AccuMax (**section 2.4.2**) and 100 μ L of single cell suspension (5×10^3 cells/ml) was pipetted into each well of the row of wells of the plate. Using a 12-channel pipette, 100 μ L from the top row of wells was serially diluted with each row of wells. This results in a gradient of cell concentrations ranging from around 250 cells/well for the top row and 1 cells/well for the bottom row.

2.4.8 Differentiation of neural stem cells

NS differentiation was induced by plating NS on laminin (1 mg/ml) coated glass coverslips (13 mm) in DMEM/Ham's F12 (Sigma) with 1 % FCS (v/v) (Invitrogen), for two days. Cells were fixed in 4 % paraformaldehyde (w/v) for 30 min and processed for immunofluorescence (**section 2.4.9**).

2.4.9 Immunostaining of differentiated neurospheres

Coverslips were washed with PBS and permeabilised with 0.1 % TritonX-100 (v/v) (Sigma) diluted in PBS for 10 min. The cells were washed three times with PBS for 5 min each time and blocked with 0.1 % BSA (w/v) for 15 min. For anti-O4 immunostaining, coverslips were blocked in 5 % FCS (v/v) for 30 min. Following blocking, the cells were washed three times with PBS for 5 min/wash and incubated with primary antibody (1:500 rabbit polyclonal anti-GFAP [Dako], 1:500 mouse monoclonal anti- microtubule associated protein 2 [MAP2] [Chemicon], 1:200 mouse monoclonal anti-Nestin [BD Pharmingen], 1:500 mouse monoclonal anti- β -catenin [BD Pharmingen] and 1:400 mouse monoclonal anti-O4 [Chemicon]) for 1 hour at room temperature. The cells were washed three times with PBS for 5 min/wash and incubated with 1:1000 secondary antibody (goat anti-mouse IgG Alexa 546 [Molecular probes], goat anti-mouse IgM Alexa 546 [Molecular probes] for anti-O4 immunostaining and goat anti-rabbit Alexa 488 [Molecular probes] for anti-GFAP immunostaining) and 1:1000 Hoechst 33342 diluted in DMSO (250 ng/ml) to label the nuclei. The coverslips were washed once in PBS and once in distilled water. Excess water was removed and the coverslips were placed on glass

slides face down with DAKO fluorescent mounting medium (DAKO). The slides were kept in the dark at 4°C.

2.5 Immunohistochemistry (Paraffin Histology)

Brains were fixed in formalin, embedded in paraffin, cut into sections of 3 µm nominal thickness and stained with haematoxylin and eosin (H&E). On selected sections, immunostains were carried out according to the manufacturer's instructions: anti-GFAP (rabbit polyclonal, 1:1000 [DAKO]), anti-neuronal nuclei (NeuN; mouse monoclonal, 1:2000 [Chemicon]), anti-Nestin (mouse monoclonal IgG1, 1:100, [BD Pharmingen]), anti-synaptophysin (rabbit polyclonal, prediluted; [Zymed]), anti-BrdU (rat monoclonal, 1:100, [Abcam]); anti-GFP (rabbit polyclonal; 1:300, [Abcam]); anti-MAP2 (mouse monoclonal; 1:200, [Chemicon]).

Biotinylated secondary antibodies were used in conjunction with the primary antibodies, and visualisation was carried out using the horseradish peroxidase-conjugated streptavidin system with diaminobenzidine as a chromogen.

All immunostaining was carried out using the automated NEXES (Ventana Medical Systems; www.ventanamed.com), or Vision Biosystems (www.vision-bio.com) automated staining apparatus in accordance with the manufacturer's guidelines. Photographs were obtained on a ColorView II digital camera (www.soft-imaging.de) mounted on a ZEISS Axioplan microscope.

2.6 Protein extraction and Western blotting

2.6.1.1 Brain and NS homogenisation

The entire procedure is performed on ice. Brain pieces were homogenised using a glass mortar and pestle in RIPA buffer (50 mM Tris pH7.4 [Sigma], 1 % Igepal [v/v] [Fluka BioChemika], 0.25 % Sodium Deoxycholate [w/v] [Sigma], 150 mM NaCl [Fisher Chemicals], 1 mM EGTA [Sigma]) containing protease inhibitor (1 tablet in 7ml RIPA buffer) (Roche). The protein extracts were stored at -80°C.

NS from a 10 cm plate were allowed to settle, washed with PBS and re-suspended in 100 µl of RIPA buffer containing protease inhibitor. The protein extracts were stored at -80°C.

2.6.1.2 Nuclear fractionation

The procedure is performed on ice or at 4°C (where stated). NS were NS from a 10 cm plate were allowed to settle and re-suspended in 500 µl of buffer A (10 mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid [HEPES] [Sigma], 1.5 mM MgCl₂ [Fisher Chemicals], 10 mM KCl [Fisher Chemicals], 0.5 mM dithiothreitol (DTT) [Sigma], 0.05 % Igepal [v/v] [Fluka BioChemika] pH7.9) containing protease inhibitor (1 tablet in 7ml RIPA buffer [Roche]). Subsequently, the cells were centrifuged at 3000 rpm for 10 min (4°C). The supernatant was removed and the pellet, containing the nuclei was re-suspended in 374 µl of buffer B (5 mM HEPES [Sigma], 1.5 mM MgCl₂ [Fisher Chemicals], 0.2 mM EDTA [Fluka BioChemika], 0.5 mM DTT [Sigma], 26 % glycerol (v/v) [Sigma] pH 7.9) and 26 µl of 4.6 M NaCl (final conc. 300mM) (Fisher Chemicals) and incubated for 30 min. Finally, the solution was centrifuged at 24000 x *g* for 20 min (4°C). The supernatant contained the proteins and was stored at -80°C.

2.6.1.3 Determination of protein concentration.

BSA standards of 0.2 mg/ml to 1.2 mg/ml in 0.2mg/ml increments were prepared by diluting BSA (stock 2mg/ml) (Fisher chemicals) in RIPA buffer. The forebrain and cerebellum homogenates were diluted 20-fold and 10-fold respectively with RIPA/protease inhibitor. Bicinchoninic acid (BCA) protein assay reagent A and B (Fisher Chemicals) were mixed in a 50:1 ratio and 200 µL were pipetted into the wells of a 96-well plate. 10 µL of each sample were added in duplicate and the plate was incubated at 37°C for 30 min before analysis by a Tecan Sunrise microplate reader (with XFluor 4 software). Detection wavelength was 570 nm and reference 690 nm. Using the BSA standard, the protein concentration of the brain homogenates was calculated.

2.6.1.4 Polyacrylamide gel

0.75 mm polyacrylamide gels were made with 10 % separating gel (10 % Bis-acrylamide [v/v] [Promega], separating gel buffer [0.38 M Tris-base [Sigma], 1.4 mM SDS [BioChemika] pH8.8], 0.08 % ammonium persulfate [w/v] [APS] [Sigma], 0.2 % tetramethylethylenediamine [TEMED] [w/v] [Sigma]) and 5 % stacking gel (5 % Bis-acrylamide [v/v] [Promega], stacking gel buffer [0.13 M Tris-base {Sigma}, 3.5 mM SDS {BioChemika}, traces of Bromphenolblue [Sigma] pH6.8, 0.08 % APS [w/v] [Sigma], 0.2 % TEMED [v/v] [Sigma]) for the wells. Prior to loading, the protein samples were made up to 1mg/ml with 1x XT sample buffer (BioRad), 0.35 M DTT (Sigma) and distilled water. The samples were then boiled for 5' at 95°C. 10 µL corresponding to 10 µg of protein were loaded into each well. Two different protein markers were used, biotinylated protein ladder (Cell Signalling) and Precision Plus protein ladder (BioRad). Empty wells were loaded with 10 µL 1x XT sample buffer (BioRad) to ensure even running of the bands. The gel was then run at 200V for 30 min in 'running buffer' (250 mM Tris-base [Sigma], 1.92 M Glycine [Sigma], 1 % SDS [v/v] [BioChemika]). The stacking gel and any unused wells were then removed.

2.6.1.5 Immunoblotting

Immobilon-P membrane (Millipore) and gel bloating paper (Schleicher & Schuell) were cut to the size of the gel. The membrane was dipped in 100 % methanol for 15 seconds, washed in distilled water and equilibrated in cold transfer buffer (20 % methanol [v/v] [Fisher Chemicals], 25 mM Tris [Sigma], 0.2 M Glycine [Sigma]) for 5 min. The gel, four filter paper sheets and two foam pads were also equilibrated in cold transfer buffer for 15 min. The blot was assembled as follows; 1x foam pad, 2x filter paper, equilibrated gel, Immobilon-P membrane, 2x filter paper, 1x foam pad. A glass tube was used to gently roll air bubbles trapped in between the layers. The blot was placed in a cassette into the mini-trans blot cell (BioRad) filled with cold 'transfer buffer' for 1 hour at 100V. The membrane was air-dried to improve protein binding, dipped in 100 % methanol [Fisher Chemicals] for 10 seconds and air dried again. After drying, the blot was washed in tris-buffered saline tween-20 (TBST) (1 mM Tris-base pH7.8 [Sigma], 0.1 M NaCl (Fisher Chemicals), 0.05 % Tween-20 [v/v] [Fisher Scientific]) and blocked overnight in 5 % milk powder (w/v) (Marvel, Premier International Foods)/TBST at 4°C. After washing, the blot was incubated overnight with primary antibody (see below) in 1 % milk powder (w/v)/TBST at 4°C. Excess antibody was washed off with TBST and the blot was incubated for 1 hour with horseradish peroxidase (HRP)-conjugated secondary antibody (see below) in 1 % milk powder (w/v)/TBST. Excess antibody was washed off with TBST and the blot was incubated with SuperSignal WestPico Chemiluminescent

substrate (Fisher Chemicals) to enhance the HRP signal. The bands were visualised with an Image Station 440 (Kodak) with Kodak 1D v3.6 software.

Antibodies: anti- β -catenin (mouse monoclonal, 1:500, [BD transduction Laboratories]), anti-GFP (mouse monoclonal, 1:500, [Chemicon]), anti-KT-3 (rabbit polyclonal, 1:5000, [Abcam]), anti- β -actin (mouse monoclonal, 1:1000, [Sigma]), anti-mouse IgG-HRP (Sigma) and anti-rabbit IgG-HRP (Sigma).

2.7 Techniques involving nucleic acids

2.7.1 Extraction of DNA from tails or ear biopsies

The tails of mice were anaesthetised with ethyl chloride and up to 0.5 cm were biopsied into separate sterile Eppendorf tubes. Each tail was submerged in 0.5 mL of tail lysis buffer (50 mM Tris pH8 [Sigma], 100 mM EDTA pH8 [Fluka BioChemika], 100 mM NaCl [Fisher Chemicals], 1 % SDS [v/v] [BioChemika]) containing 3 μ L of Proteinase K (Roche) and digested for at least 2 hours at 55°C (shaking).

After complete digestion, the samples were spun for 10 min at \geq 16000 rpm using an Eppendorf centrifuge 5415D to settle debris at the bottom. The supernatant was transferred to Eppendorf tubes and 0.5 mL of Isopropanol (Fisher Chemicals) was added to precipitate the DNA. The samples were centrifuged for 1 min at \geq 16000 rpm. The supernatant was discarded and the DNA was air-dried for 5-10 min. Finally 200 μ L of tris-EDTA (TE) buffer (10 mM Tris pH7.5 [Sigma], 1 mM EDTA [Fluka BioChemika] pH7) was added and the samples were incubated for \geq 2 hours (shaking) at 37°C to dissolve the DNA. Samples were kept at 4°C thereafter until used for polymerase chain reaction (PCR) analysis.

DNA was also extracted from mouse embryos tails. In this case smaller amount of reagents were used and the 10' centrifugation step was omitted as no debris needed to be separated.

2.7.2 Polymerase Chain Reaction

GoTaq Flexi DNA polymerase kit (Promega) was used and kept on ice at all times. All PCR primers were obtained from MGW Biotech, dissolved in sterile water to a concentration of 100 pmol/ μ L.

A mastermix containing 5x Green GoTaq Flexi Buffer (1x final concentration), MgCl₂ (1.5 mM), GoTaq DNA polymerase (1U), deoxyribonucleotide triphosphates (dNTPs) (0.25 mM) (PCR nucleotide mix [Promega]), primers (0.5 pmol/ μ L) (MGW Biotech) was made. Per sample, 1 μ L of DNA was dissolved in 24 μ L of mastermix. The PCR was performed using an AB Applied Biosystems GeneAmp PCR System 9700. All PCRs had a common initial heating phase of 94°C for 2 min to activate the Taq polymerase and a final phase of 72°C for 7 min. Annealing temperatures varied with the primers (see below). The PCR products were stored at 4°C for 2 days or at -20°C until used.

LacZ/ JunD

Primers : JunD 1: 5' TCG CTC TTG GCA ACA GCG GCC GCC ACC AGG
3'
JunD 2: 5' GGC CGC TCA GCG CCT CCT CGC CAT AGA AGG
3'
LacZ -f: 5' CGT CAC ACT ACG TCT GAA CG 3'
LacZ -r: 5' CGA CCA GAT GAT CAC ACT CG 3'

Band size: LacZ: 500bp
JunD: 300bp (internal control)

PCR program: Denaturing 94°C 30''
Annealing 58°C 40'' 35 cycles
Extension 72°C 1'30''

eGFP/β-actin

Primers: eGFP-F: 5' CCT ACG GCG TGC AGT GCT TCA GC 3'
eGFP-R: 5' CGG CGA GCT GCA CGC TGC GTC CTC 3'
Actin-F: 5' GAT GAC GAT ATC GCT GCG CTG GTCG 3'
Actin-R: 5' GCC TGT GGT ACG ACC AGA GGC ATA CAG 3'

Band size: β-Actin: 1Kb (internal control)
eGFP: 300bp

PCR program: Denaturing 94°C 30''
Annealing 60°C 45'' 35 cycles
Extension 72°C 45''

Cre/p53

Primers Cre 1: 5' ACC AGC CAG CTA TCA ACT C 3'
Cre 2: 5' TAT ACG CGT GCT AGC GAA GAT CTC CAT CTT
CCA
GCA G 3'

p53 Int10 fwd: 5' AAG GGG TAT GAG GGA CAA GG 3'
p53 Int10 rev: 5' GAA GAC AGA AAA GGG GAG GG 3'

Band size: Cre: 300bp
p53 wt: 400bp (internal control)
p53 floxed: 600bp

PCR program: Denaturing 94°C 30''
Annealing 56°C 30'' 35 cycles
Extension 72°C 50''

Rb

Primers	Rb18:	5'	GGC GTG TGC CAT CAA TG	3'
	Rb19:	5'	AAC TCA AGG GAG ACC TG	3'
Band size:	Rb wt:	690bp		
	Rb floxed:	740bp		
PCR program:	Denaturing	94°C	30''	
	Annealing	58°C	40''	35 cycles
	Extension	72°C	1'	

β -catenin exon 3

Primers	β -cat ex3-F:	5'	GCT GCG TGG ACA ATG GCT AC	3'
	β -cat ex3-R:	5'	GCT TTT CTG TCC GGC TCC AT	3'
Band size:	Rb wt:	690bp		
	Rb floxed:	740bp		
PCR program:	Denaturing	94°C	30''	
	Annealing	58°C	40''	35 cycles
	Extension	72°C	1'	

2.7.3 Agarose Gel Electrophoresis

The PCR products were separated by agarose gel electrophoresis. 1.5-2 % Agarose (w/v) (Sigma) was dissolved in 1x Tris base-acetic acid-EDTA (TAE) buffer (Sigma). 1.5 μ L of 10 mg/ml ethidium bromide (Sigma) was added per 200 mL of Agarose gel. The gel was poured into a mould and allowed to solidify. It was then transferred to a running chamber and filled with enough 1x TAE buffer to completely submerge the gel. 10 μ L of PCR samples were pipetted into the wells. 6 μ L of 100 bp ladder (Promega) was loaded as a marker and the gel was run at 140V for 1 hour. The bands were visualised with a BioRad Gel Doc 1000 and QuantityOne software.

3 Generation and expression analysis of Δ GSK- β -catenin transgenic mice

3.1 Background

The Wnt/ β -catenin pathway plays an important role in development, stem cell maintenance and tumorigenesis (chapter 1). The central member of this pathway is β -catenin, a 780 aa protein, which was originally identified as a component of E-cadherin junctions (Takeichi, 1991). In the absence of Wnt proteins, cytoplasmic β -catenin is phosphorylated at key residues and is thereby targeted for degradation (Aberle *et al.*, 1997; Morin *et al.*, 1997; Yost *et al.*, 1996). However, in the presence of Wnt proteins this phosphorylation, and thus degradation, is abolished (Liu *et al.*, 2002). Under these circumstances, stable β -catenin can translocate into the nucleus where it interacts with transcription factors to promote the expression of genes involved in proliferation and differentiation (Orsulic and Peifer, 1996; Prieve and Waterman, 1999). Some of the genes that are up-regulated by β -catenin include the potent oncogenes c-myc, cyclin D1 and MMP-7 (Crawford *et al.*, 1999; He *et al.*, 1998; Shtutman *et al.*, 1999).

Mutations in components of the Wnt/ β -catenin pathway are common in human cancers (**Table 1.3** and **Table 1.5**). This pathway is aberrantly activated in central nervous system (CNS) tumours such as medulloblastomas, 'CNS PNET, NOS', Turcot's syndrome and glioblastomas (**Table 1.5**). Of these, the most extensively studied are medulloblastomas, the most common malignancy in children (Central Brain Tumor Registry of the United States, 1995; Stevens *et al.*, 1991). In medulloblastomas, nuclear β -catenin, a marker of pathway activation, has been observed in around 23 % of cases (Eberhart *et al.*, 2000; Ellison *et al.*, 2005; Rogers *et al.*, 2009; Yokota *et al.*, 2002). Interestingly, even though activation of the Wnt/ β -catenin pathway is generally associated with enhanced proliferation/aggressiveness, activation in medulloblastomas appears to be a marker of a favourable outcome (Bondi *et al.*, 2004; Clifford *et al.*, 2006; Ellison *et al.*, 2005; Kotsinas *et al.*, 2002; Nhieu *et al.*, 1999; Zechner *et al.*, 2003). However, patients suffer severe neuro-cognitive defects as a result of current treatment regimes (Copeland *et al.*, 1999; Mulhern *et al.*, 1998; Mulhern *et al.*, 1999; Mulhern *et al.*, 2001; Palmer *et al.*, 2001; Palmer *et al.*, 2003; Ris *et al.*, 2001). Therefore, it is important to develop more targeted therapies in order to improve the quality of life of these individuals. Nevertheless, not much is known about the role of the Wnt/ β -catenin pathway in medulloblastomas. A recent report suggests that the Wnt/ β -catenin pathway may promote

the progression of anaplastic astrocytomas (WHO grade II) to glioblastomas (WHO grade IV) (Sareddy *et al.*, 2009b).

To understand the role of the Wnt/ β -catenin pathway in tumours of the CNS, a transgenic mouse model was generated in which the Wnt/ β -catenin pathway is constitutively activated. This model relies on the conditional expression of Δ GSK- β -catenin (Barth *et al.*, 1999). Δ GSK- β -catenin is a form of β -catenin, which contains the point mutations Serine33Alanine, Serine37Alanine, Threonine41Alanine and Serine45Alanine. These mutations abolish Gsk3 β and Ck1 α mediated-phosphorylation of β -catenin and prevent this molecule from being degraded (**section 1.3.6.1.3**). As such, Δ GSK- β -catenin can up-regulate the expression of genes downstream of β -catenin in the absence of Wnt proteins (Barth *et al.*, 1999; Haegeler *et al.*, 2003).

3.1.1 Aims

The aim of this study was to generate a transgenic mouse model to investigate the role of the Wnt/ β -catenin pathway in CNS tumours.

3.1.2 Methods

Restriction digestion and ligation were used to generate the pcall2- Δ GSK- β -catenin-IRES-GFP vector (**section 2.3.1**). The vector was transfected into neuroblastoma (N2a) cells (**section 2.4.1**) and Western blotting was used to confirm recombination and expression of Δ GSK- β -catenin (**section 2.6**). ES cells were electroporated with the vector (**section 2.3.3**) and β -galactosidase staining was used to confirm integration and expression of the vector (**section 2.2.2**). Southern blot analysis was used to select ES cell clones with few copies of the pcall2- Δ GSK- β -catenin-IRES-GFP vector (**section 2.3.5**). Vector expression and recombination was assessed in mouse brains by β -galactosidase staining (**section 2.2.2**). Western blotting was performed to detect Δ GSK- β -catenin expression (**section 2.6**). Finally, mouse brains were immunohistochemically stained to visualise brain morphology (**section 2.5**).

3.2 Results

3.2.1 Generation of the pcall2- Δ GSK- β -catenin-IRES-GFP vector

The pUHD10-3/ Δ GSK- β -catenin vector containing Δ GSK- β -catenin was a kind gift from Dr Nelson (Barth *et al.*, 1999). In order to excise the intact Δ GSK- β -catenin cDNA from the pUHD10-3/ Δ GSK- β -catenin vector, a BamH I restriction site was inserted 5' to the start codon. Subsequent BamH I restriction enzyme digestion yielded a 2.49 kb fragment containing the full Δ GSK- β -catenin cDNA. This fragment was inserted into the Bgl II site of the pcall2-updated-IRES-GFP vector. Integration of the 2.49 kb fragment into the correct site was confirmed by sequencing (data not shown). This new vector was named pcall2- Δ GSK- β -catenin-IRES-GFP (Figure 3.1).

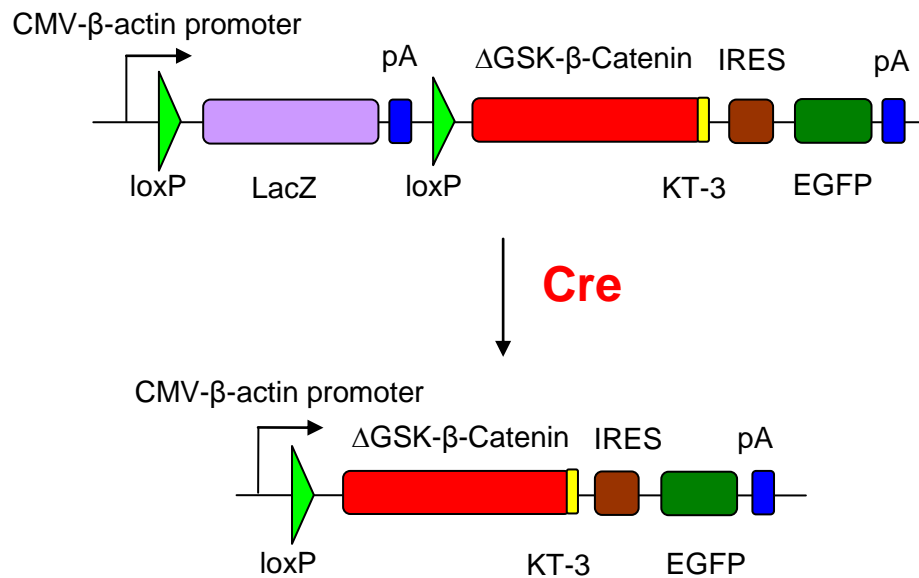


Figure 3.1 pcall2- Δ GSK- β -catenin-IRES-GFP vector

Transgenic mice, which express this construct, were generated. The construct uses the CMV- β -actin promoter which confers ubiquitous expression. In non recombined cells, β -galactosidase (LacZ) is expressed but not Δ GSK- β -catenin. Following Cre-recombinase administration, the loxP sites are recombined resulting in the excision of the LacZ stop cassette. Recombination induces the expression of Δ GSK- β -catenin.

3.2.2 N2a cells transfected with pcall2- Δ GSK- β -catenin-IRES-GFP vector express Δ GSK- β -catenin following Cre-mediated recombination

To confirm that expression of Δ GSK- β -catenin and EGFP occurs only after Cre-mediated recombination, the pcall2- Δ GSK- β -catenin-IRES-GFP vector was transiently transfected into neuroblastoma (N2a) cells in the presence, or absence, of a vector expressing Cre-recombinase. Immunoblotting of transfected cells with anti-GFP and anti- β -catenin antibodies showed expression of both Δ GSK- β -catenin and EGFP only when Cre-recombinase was present (Figure 3.2).

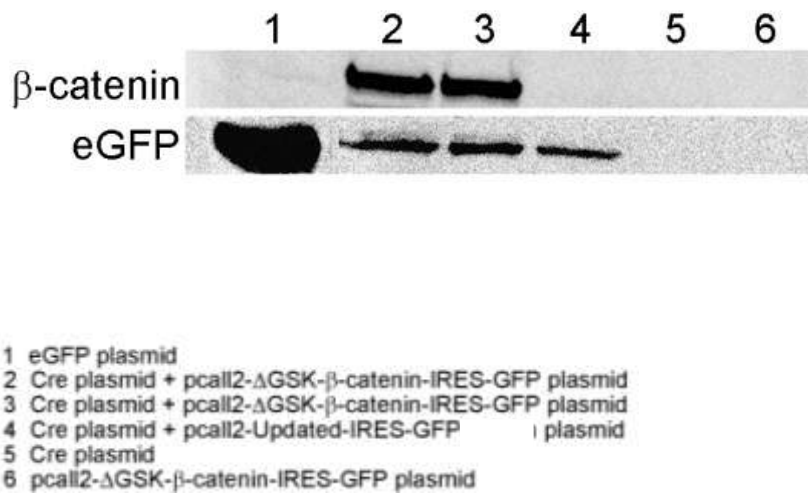


Figure 3.2 Cre-mediated recombination of pcall2- Δ GSK- β -catenin-IRES-GFP results in expression of Δ GSK- β -catenin and EGFP in N2a cells

Cell lysates from transfected neuroblastoma (N2a) cells were immunoblotted using anti- β -catenin and anti-GFP antibodies. 20 μ g of total protein were loaded per lane. Co-transfection of a Cre-expressing plasmid with the pcall2- Δ GSK- β -catenin-IRES-GFP plasmid resulted in the expression of Δ GSK- β -catenin and EGFP (lanes 2 and 3). *This experiment was performed by H. Naumann, UCL Institute of Neurology, and Thomas Jacques, UCL Institute of Child Health.*

3.2.3 Selection of embryonic stem cells transfected with the pcall2-ΔGSK-β-catenin-IRES-GFP vector for blastocyst injection

The pcall2-ΔGSK-β-catenin-IRES-GFP vector expresses LacZ in the absence of Cre-recombinase (**Figure 3.2**). LacZ encodes the bacterial enzyme β-galactosidase, which hydrolyzes β-galactosidase sugars. β-galactoside expressing cells can be detected by the addition of X-gal, which is a synthetic compound. In the presence of β-galactosidase, X-gal can be hydrolysed into galactose and 5-bromo-4-chloro-3-hydroxyindole (X), a blue insoluble compound.

To insert the pcall2-ΔGSK-β-catenin-IRES-GFP vector into the genome of embryonic stem (ES) cells, ES cells were electroporated with the vector and clones were plated into duplicate 96-well plates. ES cells from one plate were stained using X-gal to confirm the expression of the pcall2-ΔGSK-β-catenin-IRES-GFP vector. Nine clones (A7, B4, C11, E3, E6, E11, F9, G1 and H4) were positive for β-galactosidase expression (data not shown; *from Dr. Behrens, Cancer Research UK*). Transfected cells may contain more than one copy of the transfected vector. However, β-catenin mutations in tumours occur only in one allele, with only one copy of the mutant gene present (Morin *et al.*, 1997; Zurawel *et al.*, 1998). To model this scenario, the ES cell clones, which were positive for LacZ expression, were analysed for the insertion of pcall2-ΔGSK-β-catenin-IRES-GFP vector. DNA from each clone was harvested and then digested with the EcoR I restriction enzyme. Subsequently, the DNA fragments were separated by gel electrophoresis and analysed by southern blot hybridisation. A probe, which recognises the C-terminal domain of β-catenin cDNA was used to detect DNA fragments derived from the mutant transgene. Clones A7, C11, E11 and H4 were found to contain the smallest amounts of the transgene and were selected for injection into blastocysts (**Figure 3.3**). To this end, pseudopregnant foster mice were injected with A7, C11 or H4 ES cells, and produced chimaeric offspring. To test whether LacZ was expressed in the offspring of the chimaeric mice, a PCR was performed, which confirmed that the injected pcall2-ΔGSK-β-catenin-IRES-GFP vector had been inserted into the germline and could therefore be inherited. Three transgenic mouse lines were generated in this manner, which were named ΔGSK-β-catenin^A, ΔGSK-β-catenin^C and ΔGSK-β-catenin^H, corresponding with the ES cell clone from which they originate (A7, C11 and H4).

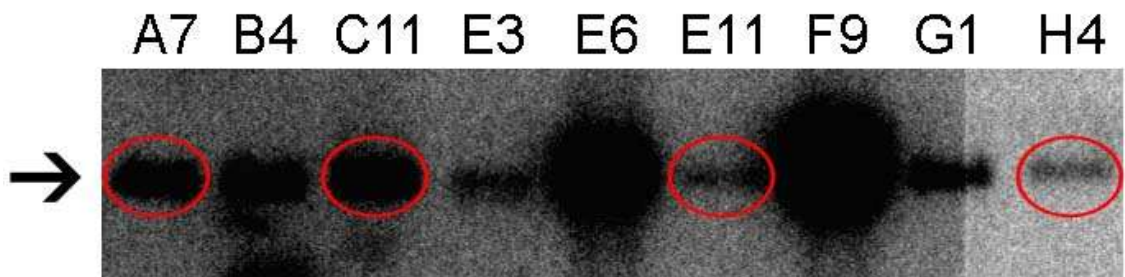


Figure 3.3 Transfected ES cell clones were selected according to their EcoR I band pattern

DNA from embryonic stem (ES) cell clones A7, B4, C11, E3, E6, E11, F9, G1 and H4 was digested with EcoR I restriction enzyme and analysed by Southern blot. The probe was generated to target the C-terminal domain of β -catenin cDNA. A7, C11, E11 and H4 were selected for injection into blastocysts. *This experiment was performed by Dr Thomas Jacques, in the laboratory of Dr. Behrens, Cancer Research UK.*

3.2.4 Δ GSK- β -catenin mice express LacZ in the brain and other organs

During electroporation, vectors are inserted randomly into the genome. Hence, the location of insertion influences the expression level and the expression pattern. To determine the expression pattern of the pcall2- Δ GSK- β -catenin-IRES-GFP insert in Δ GSK- β -catenin mice, brains and somatic organs were stained for β -galactosidase expression. Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} mice showed strong β -galactosidase expression in the brain, heart and testis (**Figure 3.4** and **Figure 3.5**). Additionally, Δ GSK- β -catenin^{C/-} mice showed weak β -galactosidase expression in the kidney and liver (**Figure 3.4** and **Figure 3.5**). In contrast, Δ GSK- β -catenin^{H/-} mice weakly expressed β -galactosidase in the brain (**Figure 3.4**). Δ GSK- β -catenin^{-/-} littermate control mice did not show any β -galactosidase staining in the organs tested (**Figure 3.4** and **Figure 3.5**).

During development, β -galactosidase expression was strong in Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} embryos and weak in Δ GSK- β -catenin^{H/-} embryos (**Figure 3.6**).

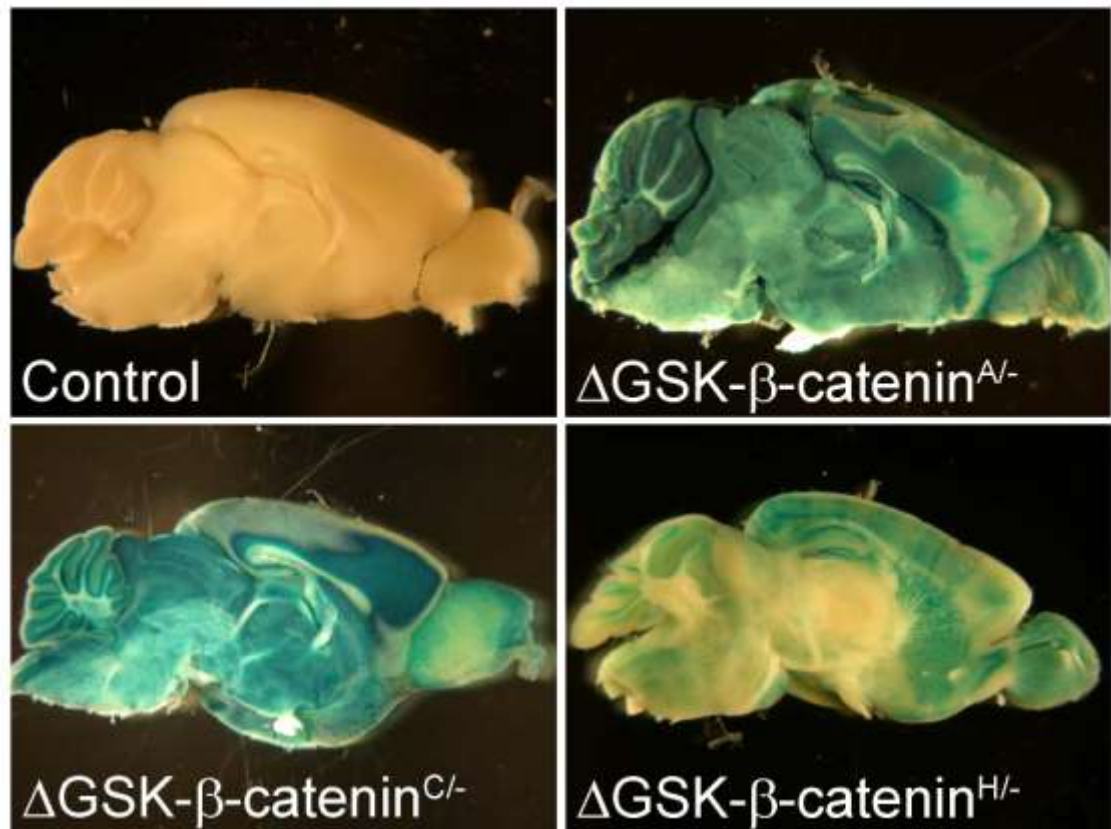


Figure 3.4 Δ GSK- β -catenin transgenic mice express LacZ in the brain

Brains from Δ GSK- β -catenin^{A/-}, Δ GSK- β -catenin^{C/-}, Δ GSK- β -catenin^{H/-} transgenic mice and Δ GSK- β -catenin^{-/-} littermate control mice were formalin-fixed and stained using the β -galactosidase staining assay. β -galactosidase metabolises X-gal into galactose and an insoluble blue indole compound (5-bromo-4-chloro-3-hydroxyindole). Δ GSK- β -catenin^{A/-} (top right panel) and Δ GSK- β -catenin^{C/-} (bottom left panel) transgenic mice expressed LacZ in all visible areas of the brain (blue staining) except for the corpus callosum and the white matter of the cerebellum. Furthermore, in these mice weak LacZ expression could be detected in the brain stem and olfactory bulb. By comparison, Δ GSK- β -catenin^{H/-} (bottom right panel) expressed LacZ (blue staining) weakly in the cortex, cerebellum, caudate putamen, hippocampus and olfactory bulb. There was no LacZ expression seen in Δ GSK- β -catenin^{-/-} littermate control mice (top left panel).

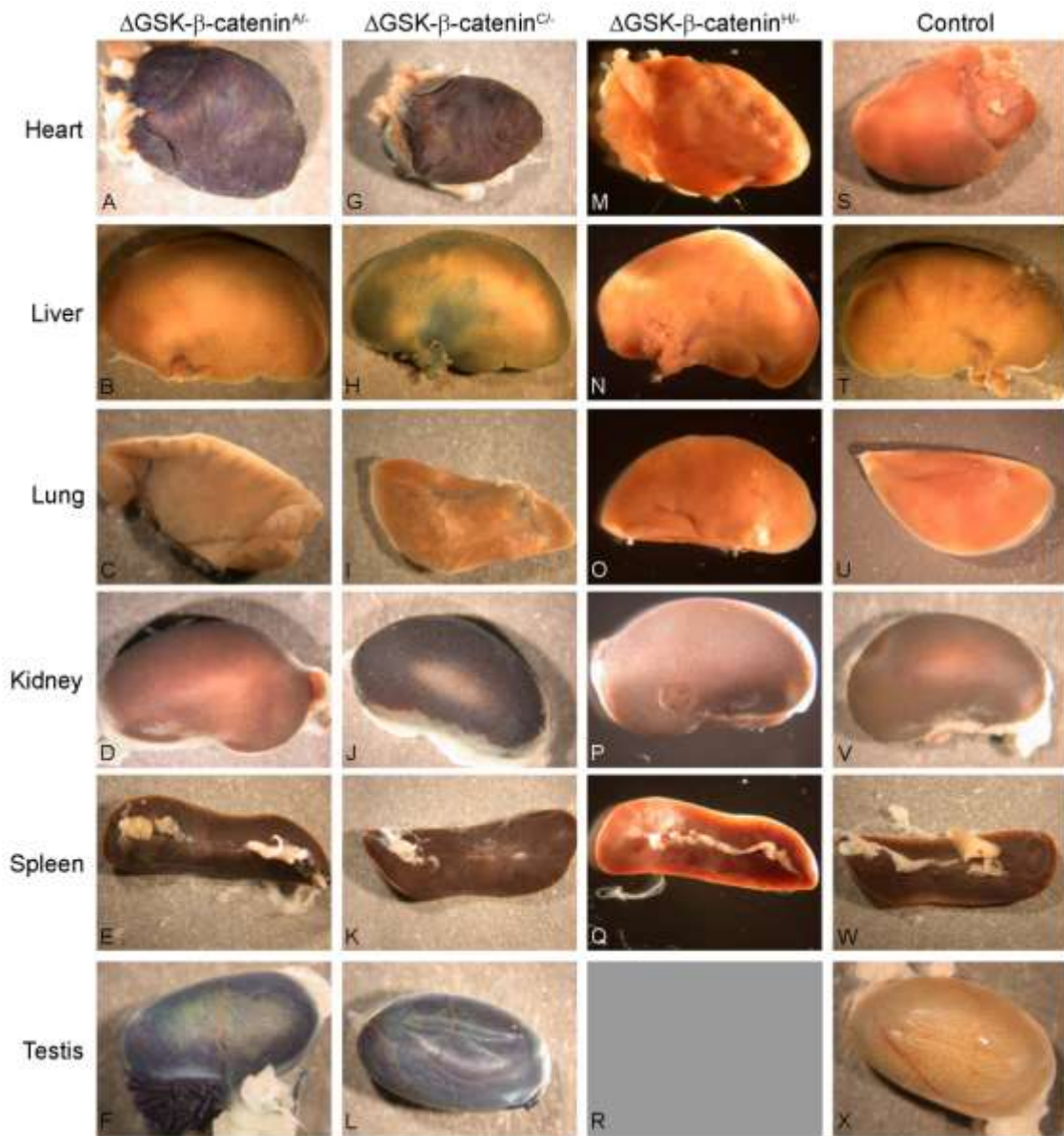


Figure 3.5 LacZ expression in somatic organs of Δ GSK- β -catenin transgenic mice

The heart, liver, lung, kidney, spleen and testis were dissected out from Δ GSK- β -catenin^{A/-} (A-F), Δ GSK- β -catenin^{C/-} (G-L), Δ GSK- β -catenin^{H/-} (M-R) and Δ GSK- β -catenin^{-/-} littermate control mice (S-X), were formalin-fixed and stained using the β -galactosidase staining assay. LacZ expression (blue staining) was seen in the heart, lung and testis of Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} transgenic mice. Δ GSK- β -catenin^{C/-} transgenic mice also showed LacZ expression in the liver and kidney. In contrast, Δ GSK- β -catenin^{H/-} transgenic mice showed no LacZ expression in any of the organs tested. There was no LacZ expression seen in Δ GSK- β -catenin^{-/-} littermate control mice. The Δ GSK- β -catenin^{H/-} transgenic mouse tested was female, hence no testes were tested.

3.2.5 Nestin-Cre; Δ GSK- β -catenin mice do not show embryonic lethality

Previous work by Chenn and Walsh has shown that expression of oncogenic β -catenin (Δ 90N- β -catenin) in neuronal progenitor cells results in a gross increase in brain size, which culminates in embryonic lethality (Chenn and Walsh, 2002). To confirm these results in our mouse model, the Δ GSK- β -catenin transgenic mice were crossed with Nestin-Cre transgenic mice. Nestin-Cre transgenic mice express Cre-recombinase under the control of the Nestin promoter, which is active in neural stem cells during development and in adulthood (Lendahl *et al.*, 1990; Reynolds and Weiss, 1992). However, Nestin is also expressed in the developing skeletal muscle (Sejersen and Lendahl, 1993). To overcome this, the Nestin-Cre transgenic mice used contained the Nestin second intron downstream of the promoter. These mice express Cre-recombinase specifically in neural stem cells and neural crest cells (Lothian and Lendahl, 1997). In contrast to Chenn and Walsh's findings, Nestin-Cre; Δ GSK- β -catenin transgenic mice were not embryonic lethal, despite strong β -galactosidase expression during development (**Figure 3.6**).

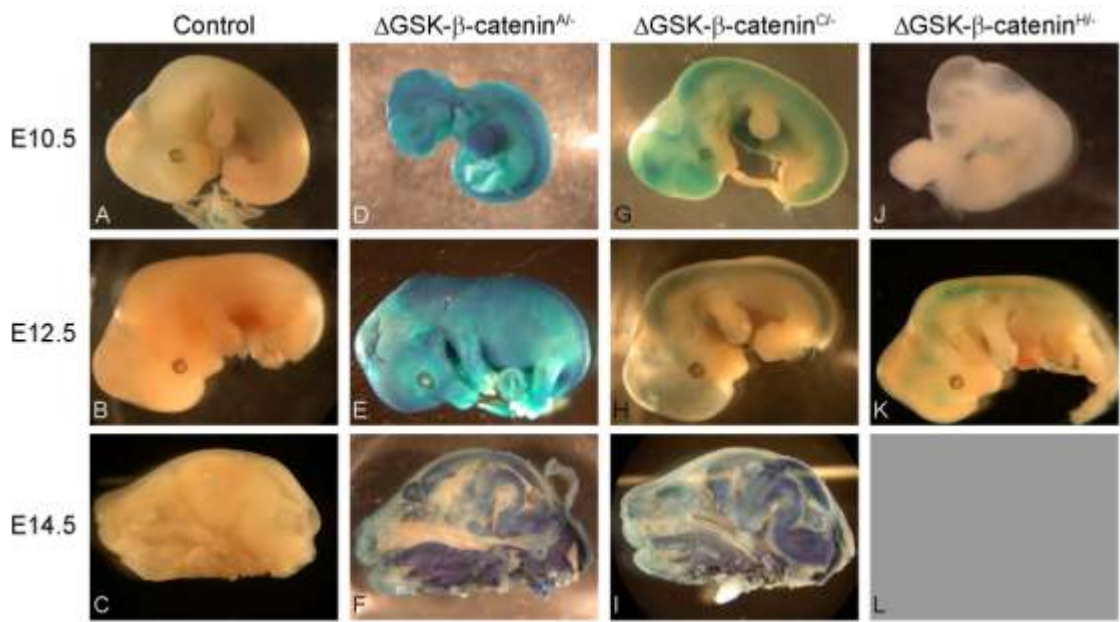


Figure 3.6 The Δ GSK- β -catenin construct is expressed in the CNS during development

Δ GSK- β -catenin^{-/-} littermate control (**A-C**), Δ GSK- β -catenin^{Al-} (**D-F**), Δ GSK- β -catenin^{Cl-} (**G-I**) and Δ GSK- β -catenin^{Hl-} (**J and K**) embryos from embryonic (E) days E10.5, E12.5 and E14.5 were formalin-fixed and stained using the β -galactosidase assay. Δ GSK- β -catenin^{Al-} embryos showed strong LacZ expression in the skin and the CNS during development. Similarly, Δ GSK- β -catenin^{Cl-} embryos expressed LacZ in the CNS. In contrast, Δ GSK- β -catenin^{Hl-} embryos only expressed LacZ weakly in the CNS. E14.5 embryos from the Δ GSK- β -catenin^{Hl-} mouse line were not tested as a result of the weak expression observed at E12.5. Δ GSK- β -catenin^{-/-} littermate control mice showed no LacZ expression at all time points tested.

3.2.6 Recombination in Nestin-Cre; Δ GSK- β -catenin mouse brains

To analyse which CNS regions in Nestin-Cre; Δ GSK- β -catenin mice were recombined, brains from Nestin-Cre; Δ GSK- β -catenin^{A/-}, Nestin-Cre; Δ GSK- β -catenin^{C/-} and Nestin-Cre; Δ GSK- β -catenin^{H/-} were stained for β -galactosidase expression. In the mouse model studied here, the LacZ gene, which encodes β -galactosidase, is flanked by loxP sites and is excised upon Cre-mediated recombination. Hence, cells that are recombined do not express β -galactosidase and therefore remain unstained. β -galactosidase staining of Nestin-Cre; Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{C/-} brains showed widespread recombination in comparison to controls (**Figure 3.7** and **Figure 3.8**). Recombination was marked in the thalamus, cerebellum, caudate putamen and SVZ (**Figure 3.7** and **Figure 3.8**). Additionally, the hippocampus, hypothalamus, cortex and brainstem were partially recombined (**Figure 3.7** and **Figure 3.8**). Nestin-Cre; Δ GSK- β -catenin^{H/-} brains showed extensive recombination (**Figure 3.7**).

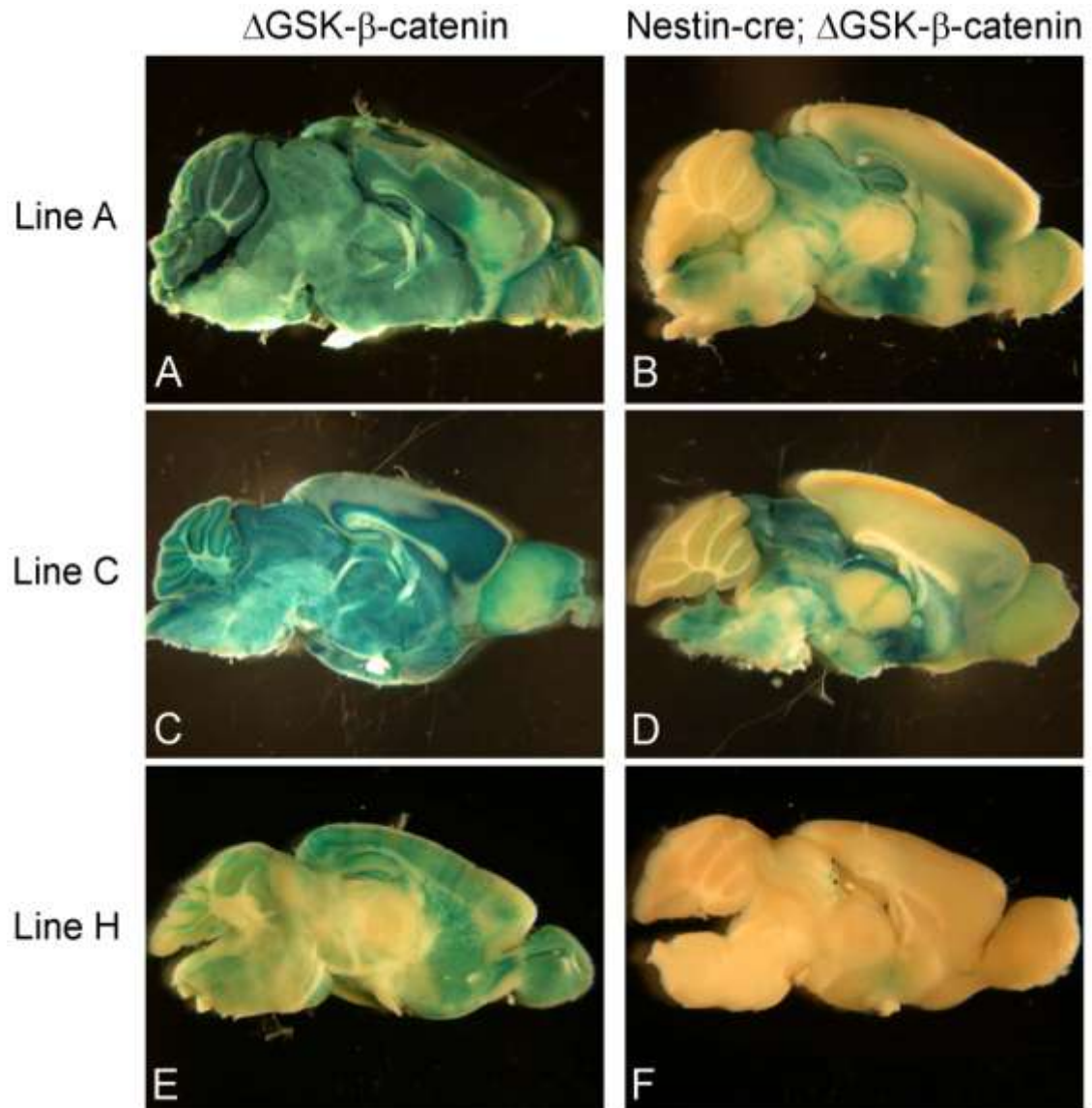


Figure 3.7 Nestin-Cre recombination of Δ GSK- β -catenin mouse brains (sagittal sections)

Following dissection, brains from Δ GSK- β -catenin and Nestin-Cre; Δ GSK- β -catenin transgenic mice were formalin-fixed, sectioned in the sagittal plane and stained using the β -galactosidase assay. Nestin-Cre; Δ GSK- β -catenin^{A/-} (B) showed extensive recombination in the cerebellum and thalamus, and partial recombination in the brainstem, cortex and olfactory bulb when compared to a Δ GSK- β -catenin^{A/-} control brains (A). Nestin-Cre; Δ GSK- β -catenin^{C/-} brains showed a very similar recombination pattern (D). Finally, Nestin-Cre; Δ GSK- β -catenin^{H/-} brains (F) were also extensively recombined, compared to control brains (E).

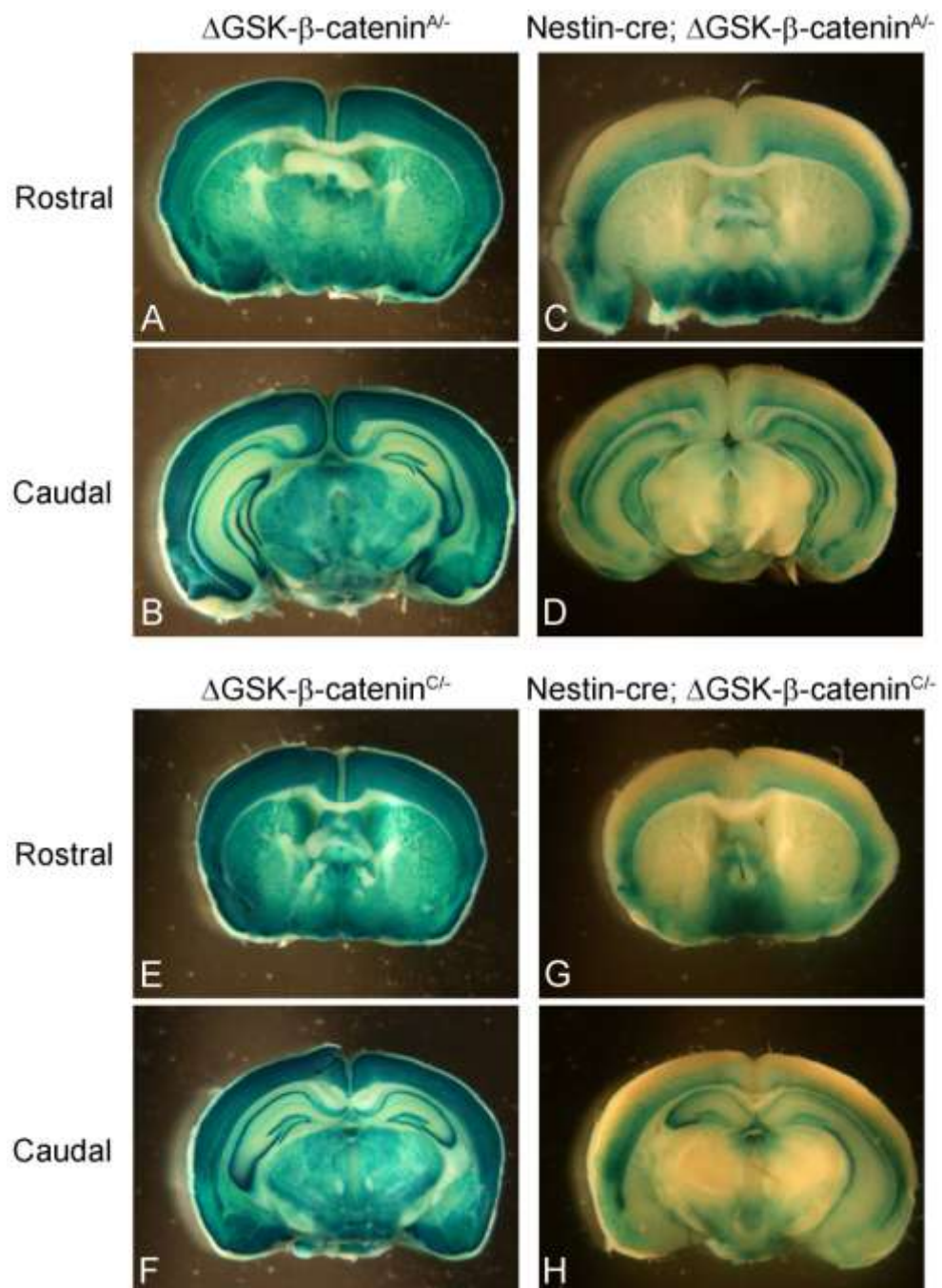
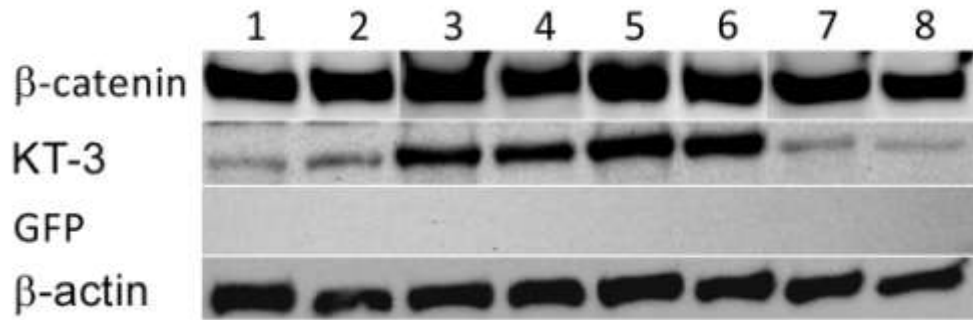


Figure 3.8 Nestin-Cre recombination of Δ GSK- β -catenin mouse brains (coronal sections)

Following dissection, brains from Δ GSK- β -catenin and Nestin-Cre; Δ GSK- β -catenin mice were formalin-fixed, sectioned coronally and stained using the β -galactosidase staining assay. Nestin-Cre; Δ GSK- β -catenin^{A/-} (**C and D**) showed complete recombination in the caudate putamen and the tissue surrounding the lateral ventricle, with partial recombination in the cortex and hippocampus in comparison to Δ GSK- β -catenin^{A/-} control brains (**A and B**). Nestin-Cre; Δ GSK- β -catenin^{C/-} brains (**G and H**) showed a similar recombination pattern compared to Δ GSK- β -catenin^{C/-} control brains (**E and F**).

3.2.7 Nestin-Cre; Δ GSK- β -catenin mice express Δ GSK- β -catenin in the brain

Nestin-Cre; Δ GSK- β -catenin brains were recombined but were not found to be enlarged. This could be attributed to a lack of Δ GSK- β -catenin protein expression post-recombination. To investigate this, forebrain and cerebella fractions of brains from Nestin-Cre; Δ GSK- β -catenin^{A/-}, Nestin-Cre; Δ GSK- β -catenin^{C/-} and Nestin-Cre; Δ GSK- β -catenin^{H/-} mice were homogenised and tested for β -catenin expression by Western blot analysis. Immunoblotting with an anti- β -catenin antibody showed that Nestin-Cre; Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{C/-} mouse brains expressed marginally higher levels of total β -catenin compared to control brains (**Figure 3.9**). However, in order to selectively visualise Δ GSK- β -catenin protein, brain homogenates were immunoblotted with an anti-KT-3 antibody. KT-3 is a thirteen amino acid tag at the C-terminus of Δ GSK- β -catenin. This demonstrated that Δ GSK- β -catenin protein could be detected in brain homogenates of Nestin-Cre; Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{C/-} mice (**Figure 3.9**). In contrast, very low levels of Δ GSK- β -catenin protein were detected in Nestin-Cre; Δ GSK- β -catenin^{H/-} brain homogenates in comparison to controls (**Figure 3.9**). Control brain homogenates from C57Bl/6J mice also showed a weak band of the same size as Δ GSK- β -catenin (**Figure 3.9**). This was one of several non-specific bands seen as a result of the cross-reaction of the anti-KT-3 antibody with other targets present in the homogenates. GFP protein was not detected after recombination (**Figure 3.9**).



- 1 Nestin-cre; Δ GSK- β -catenin^{H/+} forebrain
- 2 Nestin-cre; Δ GSK- β -catenin^{H/+} cerebellum
- 3 Nestin-cre; Δ GSK- β -catenin^{C/+} forebrain
- 4 Nestin-cre; Δ GSK- β -catenin^{C/+} cerebellum
- 5 Nestin-cre; Δ GSK- β -catenin^{A/+} forebrain
- 6 Nestin-cre; Δ GSK- β -catenin^{A/+} cerebellum
- 7 C57Bl/6 forebrain
- 8 C57Bl/6 cerebellum

Figure 3.9 Nestin-Cre recombination activates the expression of Δ GSK- β -catenin

Forebrain and cerebellar homogenates from Nestin-Cre; Δ GSK- β -catenin^{A/+}, Nestin-Cre; Δ GSK- β -catenin^{C/+} and Nestin-Cre; Δ GSK- β -catenin^{H/+} transgenic mice as well as C57Bl/6J control mice were immunoblotted for β -catenin (1:500), KT3 (1:5000), GFP (1:500) and β -actin (1:1000). 10 μ g of total protein was loaded per lane. Expression levels of total β -catenin were not significantly increased after recombination. Δ GSK- β -catenin is tagged with KT-3 at the C-terminus. Immunoblotting with anti-KT-3 antibody showed that Δ GSK- β -catenin protein could be detected in the forebrain and cerebellum of Nestin-Cre; Δ GSK- β -catenin^{A/+} (**lanes 5 and 6**), Nestin-Cre; Δ GSK- β -catenin^{C/+} (**lanes 3 and 4**) mice. Nestin-Cre; Δ GSK- β -catenin^{H/+} mice (**lanes 1 and 2**) expressed little or no Δ GSK- β -catenin. C57Bl/6J brains (**lanes 7 and 8**) showed a faint band with an equivalent size to Δ GSK- β -catenin protein. This was one of several unspecific bands seen as a result of the cross-reaction of the anti-KT-3 antibody with other targets. β -actin was used as an internal loading control .

3.2.8 Δ GSK- β -catenin expression does not alter brain architecture or cellular morphology

Expression of Δ GSK- β -catenin in Nestin-positive cells was not embryonic lethal as previously reported (Chenn and Walsh, 2002). However, it is possible that Δ GSK- β -catenin expression could exert a more a subtle effect on brain morphogenesis. To examine this possibility, brains from Nestin-Cre; Δ GSK- β -catenin^{A/-} mice were immunohistochemically stained for the neuronal markers NeuN, MAP2 and neurofilament 200 (NF200), the glial marker GFAP, and for β -catenin protein. Stronger β -catenin staining was detected in the hippocampus, cortex and thalamus, but not in the cerebellum of recombined mice in comparison to Δ GSK- β -catenin^{A/-} control brains (**Figure 3.10**, **Figure 3.11** and **Figure 3.12**). However, no morphological defects or tumours were detected in any region analysed (**Figure 3.10**, **Figure 3.11** and **Figure 3.12**). Of note, some morphological differences were observed in the cerebellum and hippocampus (**Figure 3.10** and **Figure 3.11**). However, these were attributed to variations in the depth of the brain sections rather than being caused by expression of Δ GSK- β -catenin.

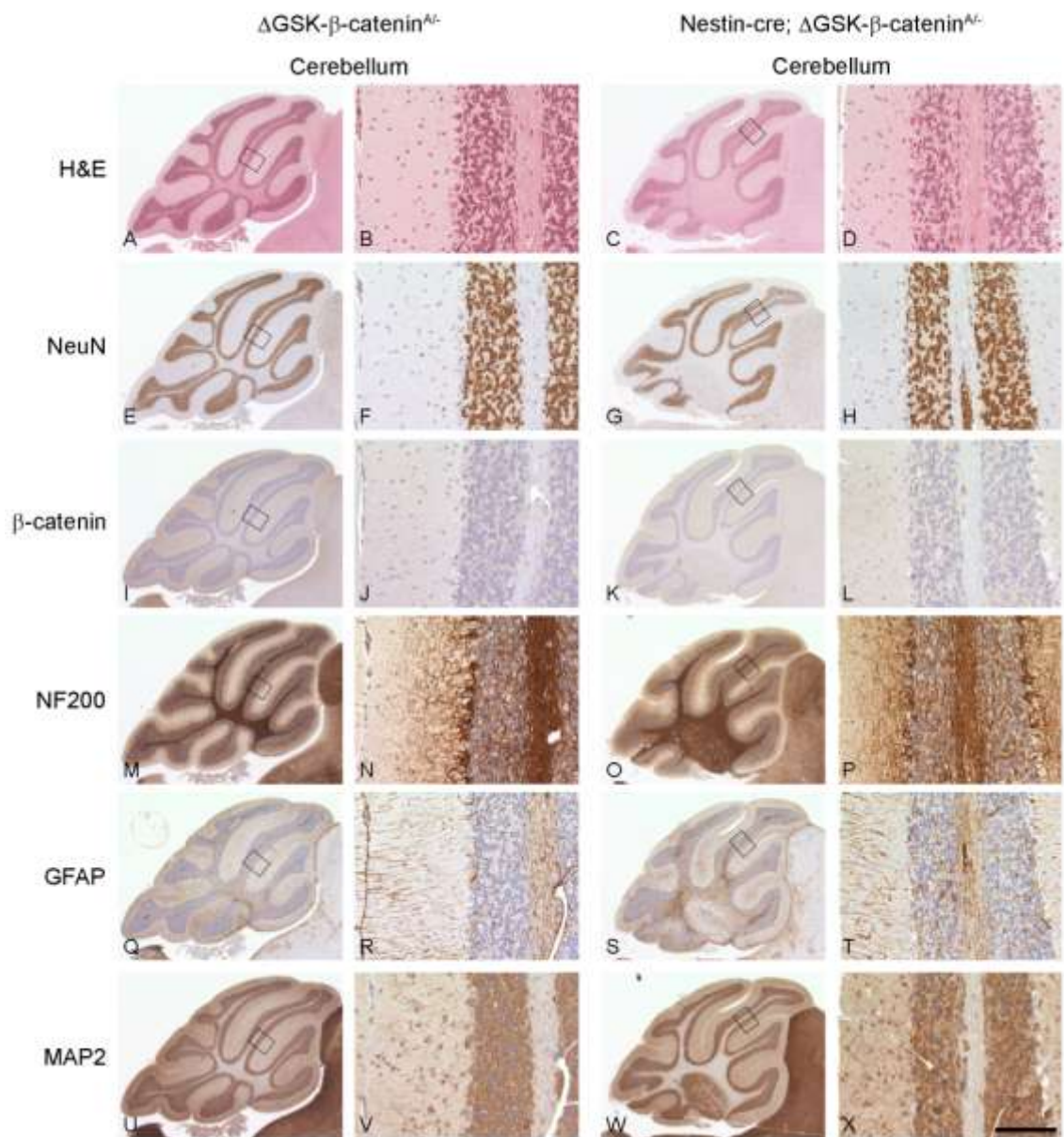


Figure 3.10 No abnormalities were detected in the cerebellum of Nestin-Cre; Δ GSK- β -catenin mice

Immunohistochemical studies of control Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{A/-} mice. Cerebella were stained with H&E (A-D), NeuN (E-H), β -catenin (I-L), NF200 (M-P), GFAP (Q-T) and MAP2 (U-X). The first and second columns correspond to low and high power magnification of a control Δ GSK- β -catenin^{A/-} cerebellum. The third and fourth columns correspond to low and high power magnification of a Nestin-Cre; Δ GSK- β -catenin^{A/-} cerebellum (note the slightly deeper (i.e. lateral) section of this brain compared to the control). High power magnification images correspond to the fifth and sixth lobule of the cerebellum (black box). β -catenin staining in Nestin-Cre; Δ GSK- β -catenin^{A/-} was not altered after recombination (K and L) compared to control (I and J). Furthermore, recombined brains showed no abnormalities in comparison to controls. The structural differences observed between Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{A/-} are explained by the lateral depth of the histological sections. The scale bar in X corresponds to 1300 μ m and 140 μ m for low power and high power magnification respectively.

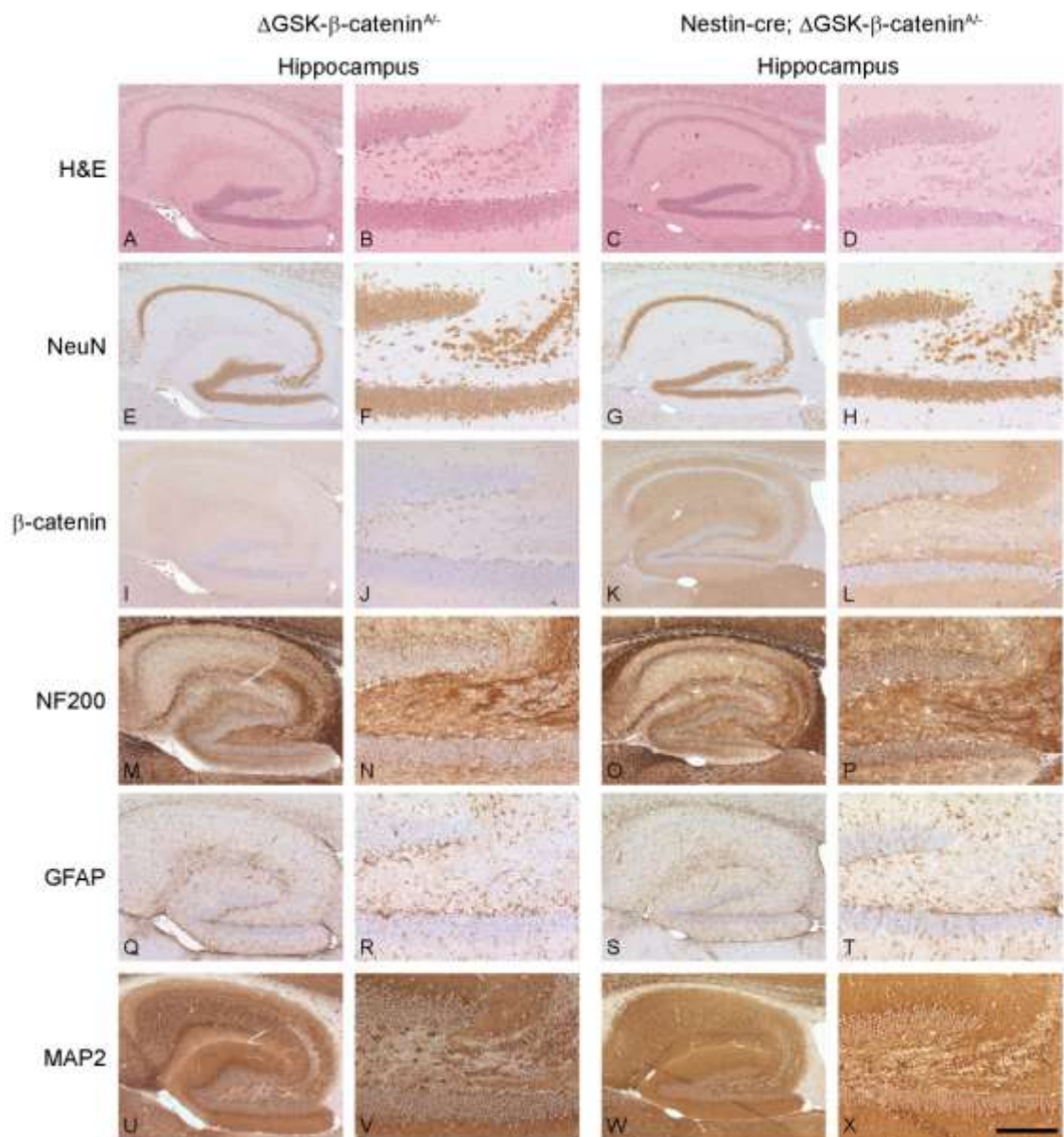


Figure 3.11 No abnormalities in the hippocampus of Nestin-Cre; Δ GSK- β -catenin brains

Immunohistochemical studies of control Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{A/-} mice. Hippocampi were stained with H&E (A-D), NeuN (E-H), β -catenin (I-L), NF200 (M-P), GFAP (Q-T) and MAP2 (U-X). The first and second columns correspond to low and high power magnification of a control Δ GSK- β -catenin^{A/-} hippocampus. The third and fourth columns correspond to low and high power magnification of a Nestin-Cre; Δ GSK- β -catenin^{A/-} hippocampus. β -catenin staining was stronger after recombination (K and L) compared to control (I and J), but no abnormalities were detected. The structural differences between Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{A/-} are explained by the lateral depth of the histological sections. The scale bar in X corresponds to 700 μ m and 220 μ m for low power and high power magnification respectively.

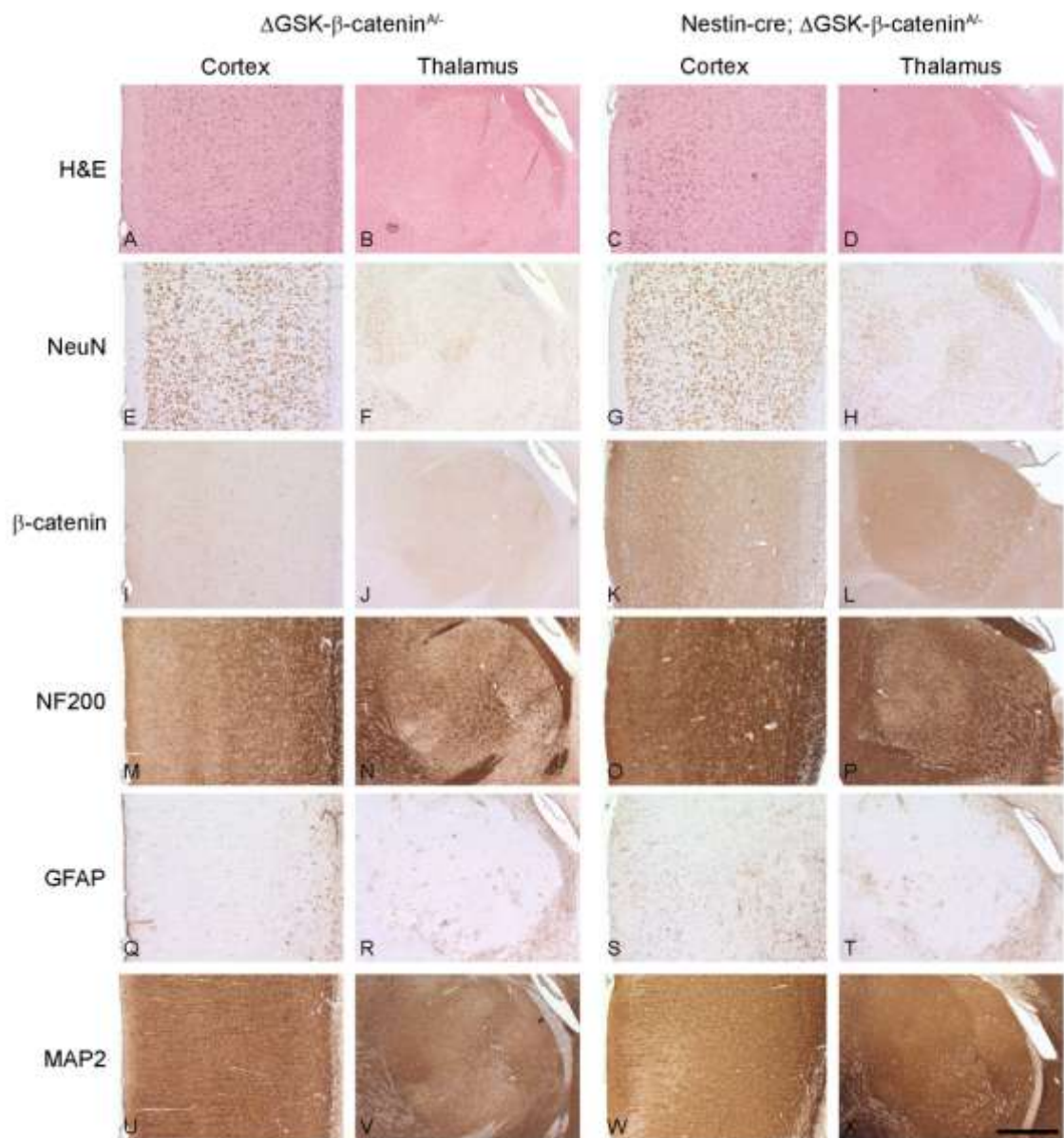


Figure 3.12 No abnormalities in the cortex and thalamus of Nestin-Cre; Δ GSK- β -catenin brains

Immunohistochemical studies of control Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{A/-} mice. Cortex and thalamus was stained with H&E (A-D), NeuN (E-H), β -catenin (I-L), NF200 (M-P), GFAP (Q-T) and MAP2 (U-X). The first and second columns correspond to control Δ GSK- β -catenin^{A/-} cortex and thalamus respectively. The third and fourth columns correspond to Nestin-Cre; Δ GSK- β -catenin^{A/-} cortex and thalamus respectively. β -catenin staining in Nestin-Cre; Δ GSK- β -catenin^{A/-} (K and L) was stronger after recombination compared to control (I and J), but no abnormalities were detected. The structural differences between Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{A/-} are explained by the lateral depth of the histological sections. The scale bar in X corresponds to 850 μ m and 450 μ m for low power and high power magnification respectively.

3.3 Discussion

The Wnt/ β -catenin pathway plays an important role in the development of the CNS and maintenance of neural stem cells (Thomas and Capecchi, 1990; Wexler *et al.*, 2009). Certain CNS tumours show aberrant activation of the Wnt/ β -catenin pathway (**Table 1.5**). For example, patients with APC germline mutations have an increased risk of developing medulloblastomas, astrocytomas and ependymomas (Attard *et al.*, 2007). Similarly, mutations of β -catenin, APC and Axin have been found in approximately 17 % of medulloblastomas (Dahmen *et al.*, 2001; Huang *et al.*, 2000; Koch *et al.*, 2001; Rogers *et al.*, 2009; Yokota *et al.*, 2002; Zurawel *et al.*, 1998). Furthermore, mutations have also been detected in CNS PNET, NOS and glioblastomas, albeit rarely (Gotze *et al.*, 2009; Koch *et al.*, 2001; Nikuseva-Martic *et al.*, 2007; Rogers *et al.*, 2009). On the other hand, the Wnt/ β -catenin pathway is commonly deregulated by other mechanisms, as shown by nuclear β -catenin immunoreactivity, a marker of pathway activity (Eberhart *et al.*, 2000; Terris *et al.*, 1999). Indeed, around 23 % of medulloblastomas and 35 % of CNS PNET, NOS cases have been shown to be positive for nuclear β -catenin, a much higher rate than detected pathway mutations (Eberhart *et al.*, 2000; Ellison *et al.*, 2005; Rogers *et al.*, 2009; Yokota *et al.*, 2002). Only about 1 % of glioblastomas harbour β -catenin mutations (Gotze *et al.*, 2009; Nikuseva-Martic *et al.*, 2007). However, a recent study has reported that promoter hypermethylation of Wnt inhibitors is common in primary and secondary glioblastomas (Gotze *et al.*, 2009). Furthermore, expression levels of β -catenin, TCF4, LEF1 and β -catenin downstream targets are increased in glioblastomas and lower grade astrocytic tumours (Sareddy *et al.*, 2009b). Interestingly, the expression levels of these targets correlate with malignancy, which suggests that the Wnt/ β -catenin pathway may play a role in glioma progression (Sareddy *et al.*, 2009a; Sareddy *et al.*, 2009b).

The role of the Wnt/ β -catenin pathway in tumours of the CNS is not completely understood. To study putative roles of this pathway in CNS tumours, transgenic mice, which conditionally express Δ GSK- β -catenin, were generated. Δ GSK- β -catenin has four point mutations at key phosphorylation residues, which renders the protein resistant to degradation (Barth *et al.*, 1999). As a result, Δ GSK- β -catenin can constitutively activate the Wnt/ β -catenin pathway (Barth *et al.*, 1999). This was also demonstrated in ES cells, where Δ GSK- β -catenin expression up-regulates the expression of Wnt/ β -catenin downstream target genes and inhibits neuronal differentiation (Haegeler *et al.*, 2003). This phenotype has been reproduced by expressing truncated APC (Haegeler *et al.*, 2003). Collectively, these studies provide strong evidence for the ability of Δ GSK- β -catenin to activate the Wnt/ β -catenin pathway.

The transgenic mice described in this chapter express the LacZ gene prior to recombination. This allowed for identification of cells expressing the pcall2- Δ GSK- β -catenin-IRES-GFP insert using the β -galactosidase staining assay. LacZ expression was widespread in the CNS during development and in adulthood (**Figure 3.4** and **Figure 3.6**). Expression could also be detected in somatic organs, especially in the testis and heart (**Figure 3.5**). In 2002, Chenn and Walsh reported that the expression of dominant active β -catenin (Δ 90N- β -catenin) in Nestin-expressing cells resulted in severe CNS abnormalities (Chenn and Walsh, 2002). This was attributed to an increase in the proportion of ventricular zone (VZ) neural precursors, which continued to divide instead of differentiating (Chenn and Walsh, 2002). To compare this result to our experimental models, Δ GSK- β -catenin mice were crossed with Nestin-Cre transgenic mice. In the Δ GSK- β -catenin mice, recombination can be detected by loss of LacZ expression (**Figure 3.1**). However, despite widespread recombination, Nestin-Cre; Δ GSK- β -catenin transgenic mice did not show any developmental abnormalities (**Figure 3.7** and **Figure 3.8**). Of relevance, recombination was observed in the tissue surrounding the lateral ventricle, where the SVZ is located, which is anatomically related to the developmental VZ (**Figure 3.8**). However, the SVZ was not enlarged in these mice. These results suggest that the Δ GSK- β -catenin protein may not be expressed after recombination. No difference in total β -catenin protein levels was detected between Δ GSK- β -catenin and Nestin-Cre; Δ GSK- β -catenin mouse brains (**Figure 3.9**). Of note, Δ GSK- β -catenin protein contains a C-terminal KT3 tag. Using an antibody raised against KT-3, Δ GSK- β -catenin protein was detected in brain homogenates from Nestin-Cre; Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{C/-} mice, but not in brain homogenates from control mice. A faint band could be detected in Δ GSK- β -catenin^{H/-} brain homogenates. However a similar band was also detected in C57Bl/6 homogenates. Therefore this faint band is likely to be non-specific binding of the antibody to other targets. In cancers with β -catenin mutations, 50 % of the expressed β -catenin is degradation-resistant. This raises the possibility that low-level expression of Δ GSK- β -catenin may not be sufficient to promote CNS abnormalities. However, in theory, degradation-resistant β -catenin should be able to constitutively activate the Wnt/ β -catenin pathway irrespective of expression levels. This suggests that Nestin-Cre; Δ GSK- β -catenin mice may have a more subtle phenotype than that observed in the Nestin- Δ 90N- β -catenin mice.

To assess this phenotype, brains from Nestin-Cre; Δ GSK- β -catenin mice were processed for immunohistological analysis. Brains were immunostained for the neuronal markers, NeuN, MAP2 and NF200, the glial marker GFAP, and β -catenin. No morphological differences were found between Nestin-Cre; Δ GSK- β -catenin and control Δ GSK- β -catenin mice (**Figure 3.10**, **Figure 3.11** and **Figure 3.12**). β -catenin staining was stronger in the hippocampus,

cortex and thalamus of Nestin-Cre; Δ GSK- β -catenin brains. These findings correlated with the loss of LacZ staining (**Figure 3.7** and **Figure 3.8**). However, no difference in β -catenin staining was detected in the cerebellum, despite extensive recombination (**Figure 3.7** and **Figure 3.10**). The β -catenin antibody detects both wild-type β -catenin and Δ GSK- β -catenin. Therefore, the small increase in total β -catenin levels observed by Western blotting may not be sufficient to be visualised histologically in the cerebellum (**Figure 3.9**).

3.4 Summary

Transgenic mice, which conditionally expressed degradation-resistant β -catenin were generated. However, despite extensive recombination in the CNS and expression of the mutant β -catenin no developmental abnormalities were detected. To investigate the lack of a phenotype, we then extended our studies to *in vitro* systems to detect potential subtle functional effects of Δ GSK- β -catenin in neural stem cells.

4 *In vitro* analysis of Δ GSK- β -catenin expression

4.1 Background

The hierarchical model for tumour development (**section 1.2**) postulates that only a subset of cells in a tumour is capable of re-generating the bulk of the tumour. This model is in keeping with the CSC hypothesis, which suggests that tumours are initiated and maintained by a population of cells with stem-like properties (Al Hajj *et al.*, 2003; Bonnet and Dick, 1997). These cells have been identified in many types of cancer (Al Hajj *et al.*, 2003; Bonnet and Dick, 1997; O'Brien *et al.*, 2007; Ricci-Vitiani *et al.*, 2007). Evidence suggests that stem cells may be the cell of origin of tumours and CSCs (**section 1.2**).

Developmental pathways are vital for stem cell maintenance and are often dysregulated in CSCs. Such pathways include the Shh, Notch, Bone morphogenic protein (BMP), TGF- β and the Wnt pathway. The Wnt/ β -catenin pathway plays a complex role in stem cells, regulating proliferation and differentiation (Chenn and Walsh, 2002; Hirabayashi *et al.*, 2004; Lie *et al.*, 2005; Wexler *et al.*, 2008; Wrobel *et al.*, 2007). For example, activation of the Wnt/ β -catenin pathway in crypt progenitor cells of the gut has been shown to promote their proliferation (Sansom *et al.*, 2004). Interestingly, constitutive activation of the Wnt/ β -catenin pathway in these progenitors promotes the development of Adenomas (Barker *et al.*, 2009).

The Wnt/ β -catenin pathway plays an important role in NSC maintenance during development (Lee *et al.*, 2000; Thomas and Capecchi, 1990). For example, Wnt1 knockout mice show a marked decrease in the expansion of neural precursors during mid/hindbrain development (Mcmahon and Bradley, 1990; Thomas and Capecchi, 1990). Similarly, Wnt3a knockout mice show a reduced proliferation of precursor cells in the caudomedial cortical epithelium (Lee *et al.*, 2000). Conversely, increasing Wnt1 expression in turn increases proliferation and leads to the expansion of the developing mid/hindbrain (Castelo-Branco *et al.*, 2003; Panhuysen *et al.*, 2004).

The Wnt/ β -catenin pathway is also vital for adult NSCs. Several Wnt family members are expressed in the dentate gyrus, the stem cell niche of the hippocampus (Lie *et al.*, 2005; Shimogori *et al.*, 2004). Injection of a lentivirus expressing Wnt3 into the dentate gyrus of adult rats doubled the number of newly generated neurones (Lie *et al.*, 2005). In contrast, injection with a lentivirus expressing DKK1, a Wnt antagonist, into the same area, decreased the amount of new neurones by 13 % (Lie *et al.*, 2005). These results suggest that the Wnt/ β -catenin pathway is an important regulator of hippocampal progenitor proliferation and differentiation. However, the role of the Wnt/ β -catenin pathway in the sub-ventricular zone (SVZ) stem cell

niche is not completely understood. Interestingly, a report by Adachi *et al.* suggests that activation of this pathway in SVZ precursors promotes proliferation and inhibits differentiation (Adachi *et al.*, 2007).

4.1.1 Aims

The aims of this study were to determine the effect of Δ GSK- β -catenin expression in NSCs and to study the synergism between Wnt/ β -catenin pathway activation and p53 or Rb knockout in NSCs and brain tumourigenesis.

4.1.2 Methods

NSC cultures were derived from the sub-ventricular zone (SVZ) and hippocampus of adult Δ GSK- β -catenin^{A/-}, Δ GSK- β -catenin^{C/-}, Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} and Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} mice (**section 2.4.2**). NSCs were infected with Adeno-Cre to mediate recombination (**section 2.4.3**). Western blotting was used to detect levels of Δ GSK- β -catenin and cyclin D1 (**section 2.6**). NSC growth was assayed with the WST-1 assay (**section 2.4.4**), Hoechst assay (**section 2.4.5**) and neurosphere size assay (**section 2.4.6**). Self-renewal was determined with the limited dilution assay (**section 2.4.7**). Neurospheres were differentiated (**section 2.4.8**), and the multi-lineage potential of NSCs was assayed using immunocytochemistry (**section 2.4.9**). Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} were analysed histologically (**section 2.5**). Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice were injected intra-ventricularly with Adeno-Cre to assess the interaction between p53 and the Wnt/ β -catenin pathway, and ultimately to test a potentially tumourigenic effect (**section 2.1.4**).

4.2 Results

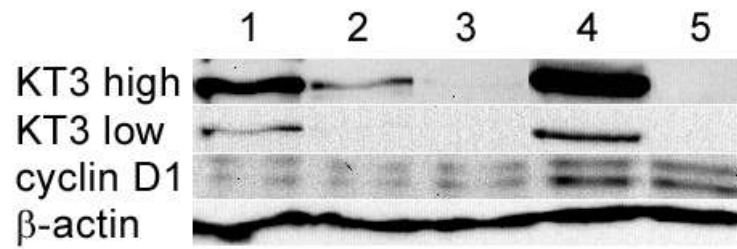
4.2.1 *In vitro* expression of Δ GSK- β -catenin does not influence neuronal stem cell biology

Nestin-Cre; Δ GSK- β -catenin mice did not develop tumours or gross abnormalities (**chapter 3**). Transgenic mice expressing Δ 90N β -catenin under the control of the Nestin promoter showed enlarged ventricles as a result of an increase in the pool of sub-ventricular zone (SVZ) progenitors (Chenn and Walsh, 2002). Chapter 3 shows that although the SVZ appears to be recombined in Nestin-Cre; Δ GSK- β -catenin mice, it is not enlarged (**Figure 3.8**). As previously discussed, absence of abnormalities may be explained by low expression of Δ GSK- β -catenin, but this could still result in a more subtle effect on NSCs. To test this hypothesis, NSCs from adult Δ GSK- β -catenin mice were cultured *in vitro*. Expression of Δ GSK- β -catenin was achieved by infecting the cells with an Adenovirus expressing Cre-recombinase (Adeno-Cre) (**Figure 4.1**). To control for the effect of the virus, a percentage of the cells was infected with Adenovirus expressing GFP (Adeno-GFP).

The WST-1 proliferation assay and neurosphere size assay were used to measure the growth of Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} expressing NSCs. Despite Δ GSK- β -catenin expression after recombination, there was no significant growth difference in Adeno-Cre recombined NSCs compared to controls (**Figure 4.2** and **Figure 4.3**).

The *Ccnd1* gene encodes the protein Cyclin D1, which is up-regulated during Wnt/ β -catenin signalling (Shtutman *et al.*, 1999; Tetsu and McCormick, 1999). Immunoblotting with anti-Cyclin D1 antibody did not show increased levels of Cyclin D1 in Adeno-Cre treated Δ GSK- β -catenin (**Figure 4.1**).

Similarly, no difference in self-renewal was observed using the limited dilution assay (**Figure 4.4**).



- 1 Nestin-cre; Δ GSK- β -catenin^{A/-} forebrain
- 2 Adeno-cre Δ GSK- β -catenin^{C/-} NSCs
- 3 Adeno-GFP Δ GSK- β -catenin^{C/-} NSCs
- 4 Adeno-cre Δ GSK- β -catenin^{A/-} NSCs
- 5 Adeno-GFP Δ GSK- β -catenin^{A/-} NSCs

Figure 4.1 Adeno-Cre infected NSCs express Δ GSK- β -catenin, but do not show increased cyclin D1 levels

Nestin-Cre; Δ GSK- β -catenin^{A/-} brain homogenates (**lane 1**), Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} NSCs (**lanes 2-5**) were immunoblotted using anti-KT-3 (1:5000), cyclin D1 (1:2000) and β -actin (1:1000) antibodies. 10 μ g of total protein was loaded per lane. 'KT-3 high' refers to long blot exposure and 'KT-3 low' refers to short blot exposure. Δ GSK- β -catenin protein is only expressed in Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} NSCs that have been infected with Adeno-Cre (**lanes 2 and 4 respectively**). Adeno-Cre-treated Δ GSK- β -catenin^{A/-} NSCs express markedly more Δ GSK- β -catenin than Adeno-Cre-treated Δ GSK- β -catenin^{C/-} NSCs. Cyclin D1 protein levels were unchanged (**lane 2 versus lane 3 and lane 4 versus lane 5**). Nestin-Cre; Δ GSK- β -catenin^{A/-} brain homogenates were used as positive controls. β -actin was used as an internal loading control.

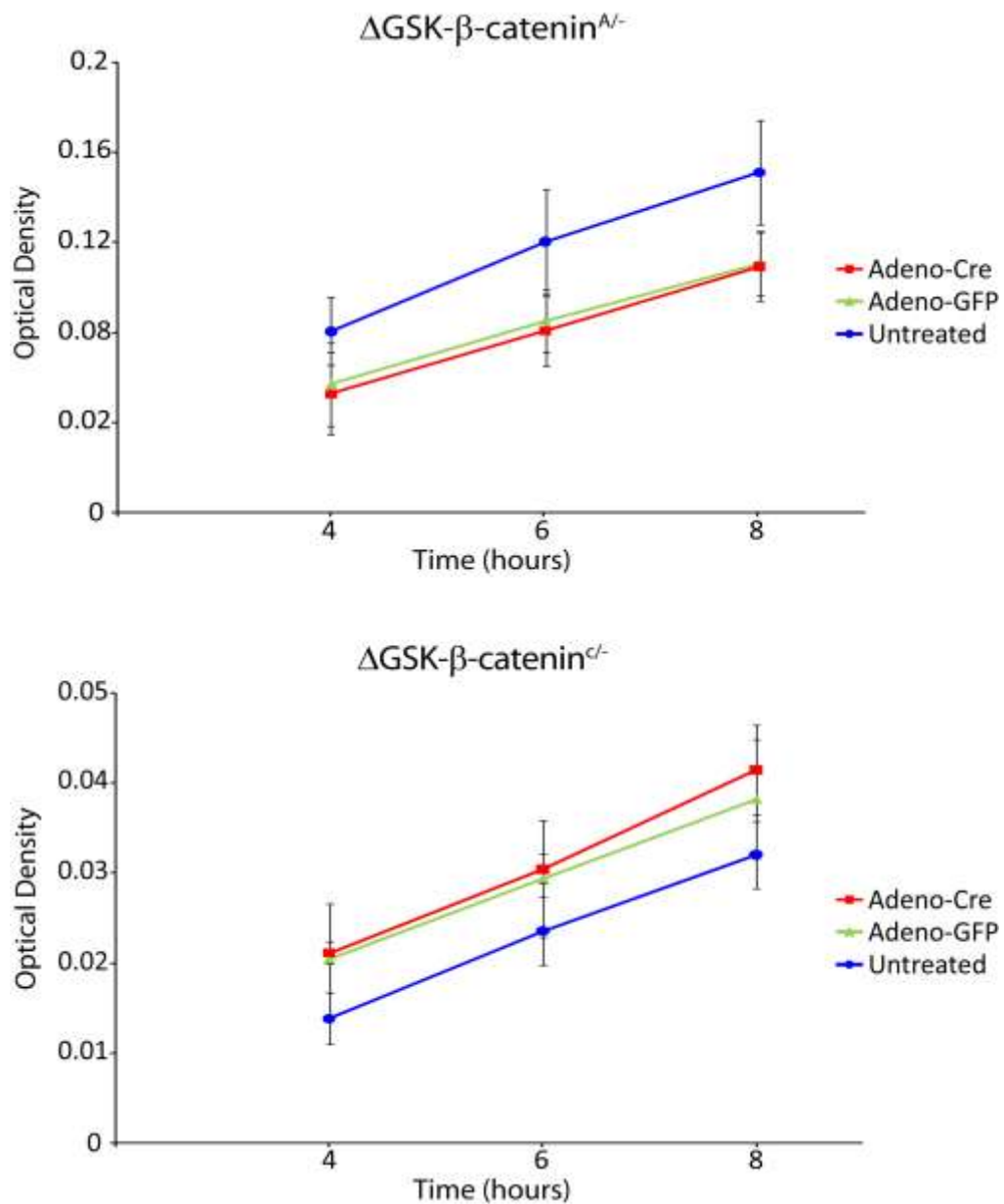


Figure 4.2 Adeno-Cre infected NSCs do not show increased proliferation potential

Neurospheres were passaged to a single cell suspension and plated at a concentration of 6×10^5 cells/ml. Three days following passage, the WST-1 reagent was added. The reagent is metabolised by mitochondria into a coloured formazan salt and the optical density (OD) measured at 440nm, which correlates with cell number. The OD was measured 4, 6 and 8 hours after WST-1 addition. The results are from three independent cultures for each line. Each experiment represents an average of ten wells. No significant difference was detected between any two treatment groups at any time point for Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} NSCs (two-tailed t-test). OD values were tested for normality and homoscedasticity (i.e. all random variables have the same variance).

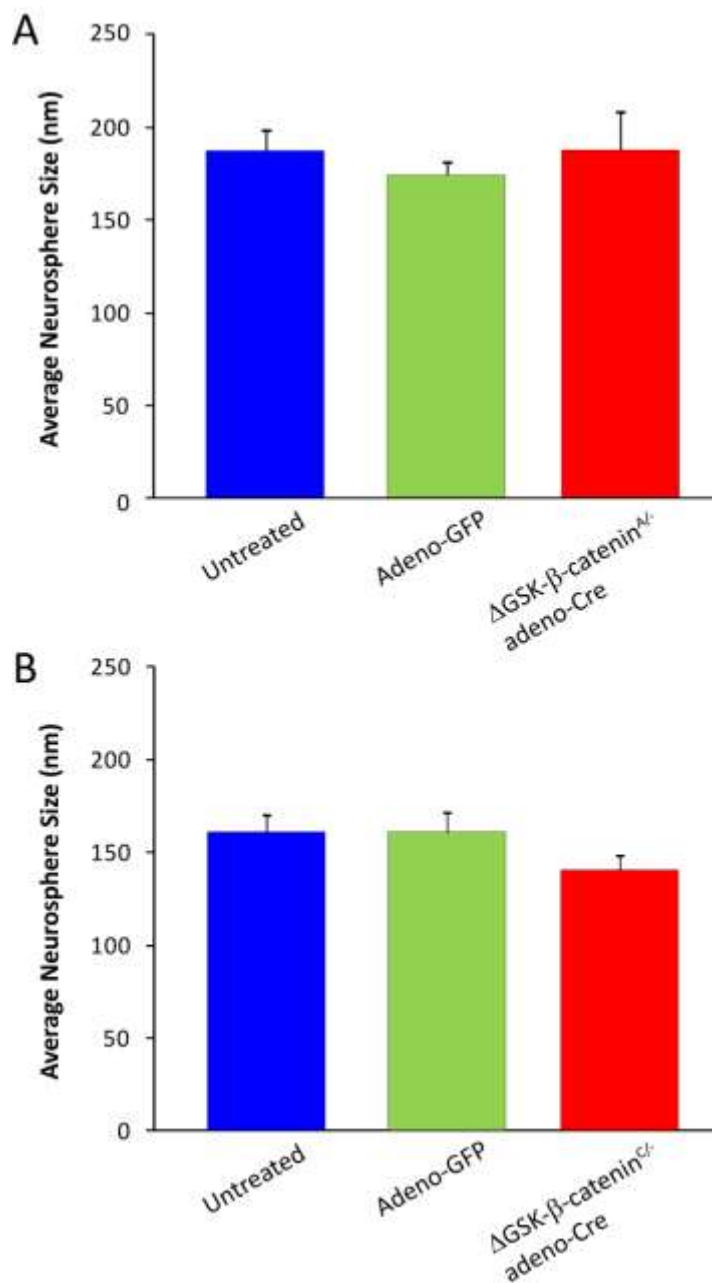


Figure 4.3 Adeno-Cre infected NSCs are not bigger than controls

Neurospheres were passaged to a single cell suspension and 0.5×10^6 cells were plated on a 6 cm plate. Ten days following passage, the diameter of the neurospheres was measured using an Axiovert 135 microscope (Zeiss) and the Openlab 5 software. An $n=3$ was calculated from three separate cultures for each cell line. Each experiment represents the average of 100 neurospheres. There was no significant difference in neurosphere diameter for Δ GSK- β -catenin $^{\Delta/-}$ (A) or Δ GSK- β -catenin $^{C/-}$ (B) NSCs. Neurosphere diameter measurements were checked for normality and homoscedasticity.

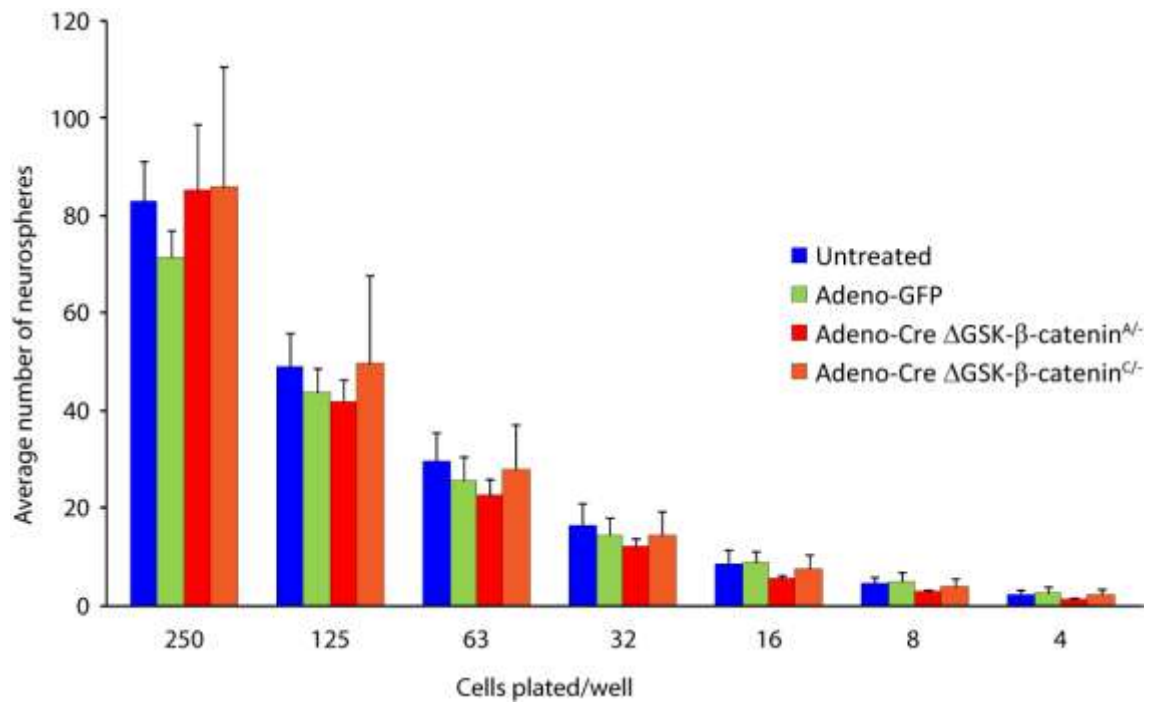


Figure 4.4 Adeno-Cre infected NSCs do not show increased self-renewal potential

Neurospheres were passaged to a single cell suspension. Around 500 cells were plated into each well of the top row of a 96-well plate. The cells were serially diluted for each remaining row of wells. Ten days following passage, the number of neurospheres was counted. An $n=3$ was calculated from three separate cultures for each line. Each single experiment represents the average of twelve wells. The untreated and Adeno-GFP-treated results from Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} were pooled for an $n=6$. There was no significant difference in the number of neurospheres for both Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} at any concentration. Neurosphere numbers were checked for normality and homoscedasticity.

One of the hallmarks of NSCs is their ability to differentiate into neurones, astrocytes and oligodendrocytes. To investigate the effect of Δ GSK- β -catenin in differentiation Δ GSK- β -catenin^{A/-} NSCs were differentiated *in vitro* and analysed by immunofluorescence. Neurones were detected using an antibody against MAP2, astrocytes with an antibody against GFAP and oligodendrocytes with an antibody against O4. Type B NSCs were detected by double staining with an anti-GFAP and anti-Nestin antibodies (Doetsch, *et al* 1999). No obvious difference was observed for any cell population (**Figure 4.5**). To detect β -catenin, differentiated cells were immunostated with an anti- β -catenin antibody. However, no increase in nuclear β -catenin was observed (data not shown). As a result, an anti-KT3 antibody was used to specifically detect Δ GSK- β -catenin, but the staining pattern of this antibody was unspecific (data not shown). As a result of this and of the negative results with Δ GSK- β -catenin mice thus far, the cells were not counted.

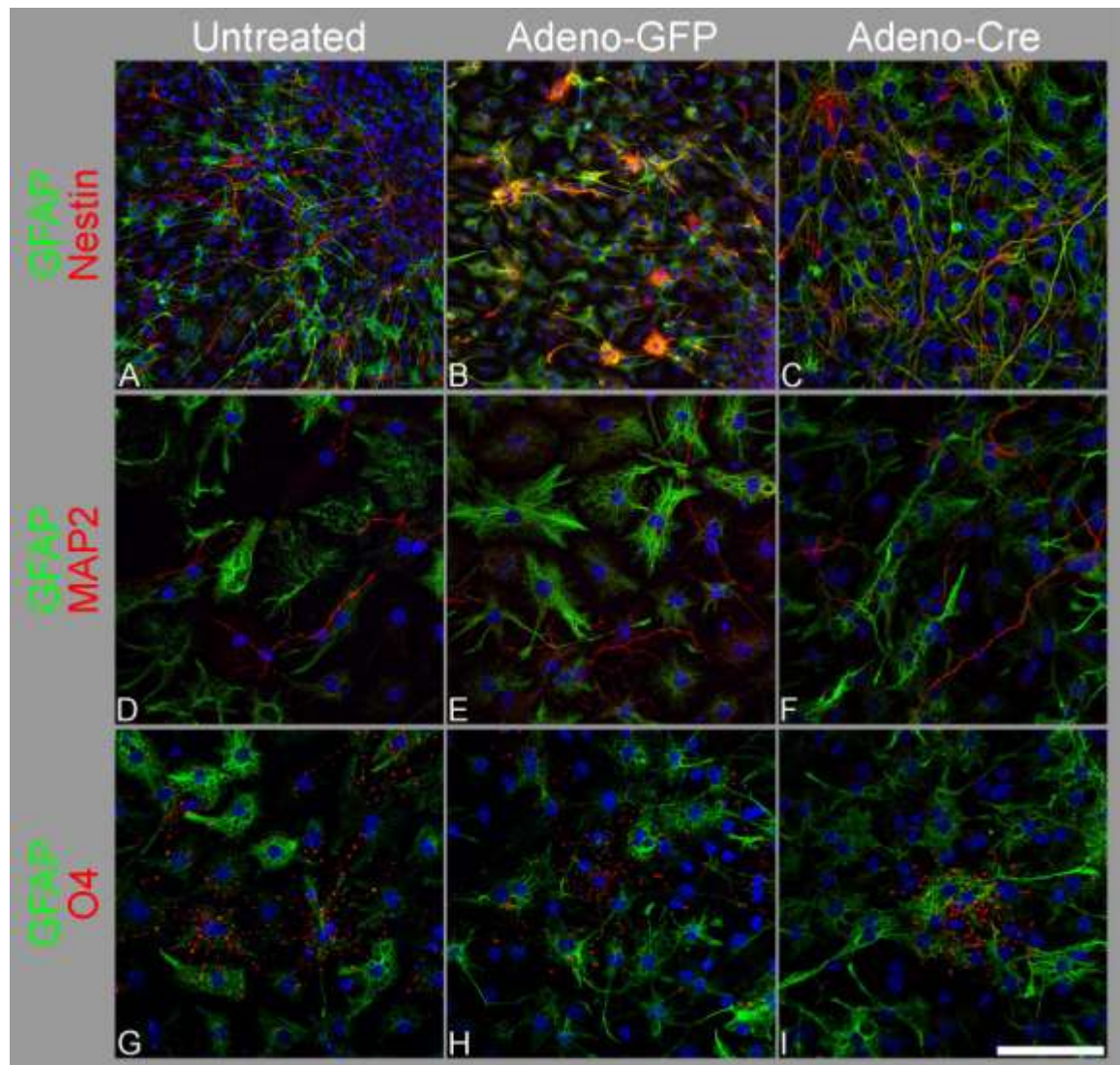


Figure 4.5 No obvious difference in the differentiation of Δ GSK- β -catenin^{A/-} NSCs

Adeno-Cre, Adeno-GFP treated and untreated Δ GSK- β -catenin^{A/-} neurospheres were plated on laminin-coated glass slides in DMEM/Ham-F12 media supplemented with 10 % FCS. Forty eight hours post-culture, cells were fixed with 4 % formaldehyde and immunostained with rabbit polyclonal anti-GFAP (1:500), mouse monoclonal anti-MAP2 (1:500) and mouse monoclonal anti-O4 (1:300). Hoechst 33342 (1:1000) was added to label the nuclei. The scale bar in **H** corresponds to 76 μ m (**A and B**) and 153 μ m (**C-I**). No obvious difference in the differentiation pattern was detected

4.2.2 Additional deletion of p53 does not affect brain morphology and does not promote neoplastic transformation

TP53, the gene encoding p53, is one of the most commonly mutated genes in human cancers (Hainaut and Hollstein, 2000). For example, TP53 is mutated in up to 25 % of primary and 65 % of secondary glioblastomas (Ohgaki *et al.*, 2004; Watanabe *et al.*, 1996; Watanabe *et al.*, 1997). However, p53 knockout in mice does not result in brain tumour development (Donehower *et al.*, 1992; Harvey *et al.*, 1993). In contrast, combination of p53 knockout with phosphatase and tensin homolog (PTEN) or Rb knockout in mice, promotes the development of PNETs and glial tumours corresponding to human oligoastrocytomas (Jacques *et al.*, 2010). Therefore, Nestin-Cre; Δ GSK- β -catenin mice were crossed with p53^{loxP/loxP} conditional mice to promote neoplastic transformation.

Brains from Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} and Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice were immunohistochemically stained for NeuN, MAP2 and NF200, GFAP and β -catenin but no malformations or brain tumours were detected (**Figure 4.6**, **Figure 4.7** and **Figure 4.8**). Increased GFAP staining was detected in Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice, but not in Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice or Nestin-Cre; Δ GSK- β -catenin mice. This suggests that p53 loss of function is associated with this phenotype. GFAP marks astrocytes and type B NSCs (Doetsch, *et al* 1999). However, type B NSCs are unlikely to be present in an adult cerebellum. This suggests that the increased GFAP staining corresponds with an increase in gliosis. Additionally, there was no difference in brain weight between Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} and Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice (**Figure 4.9**).

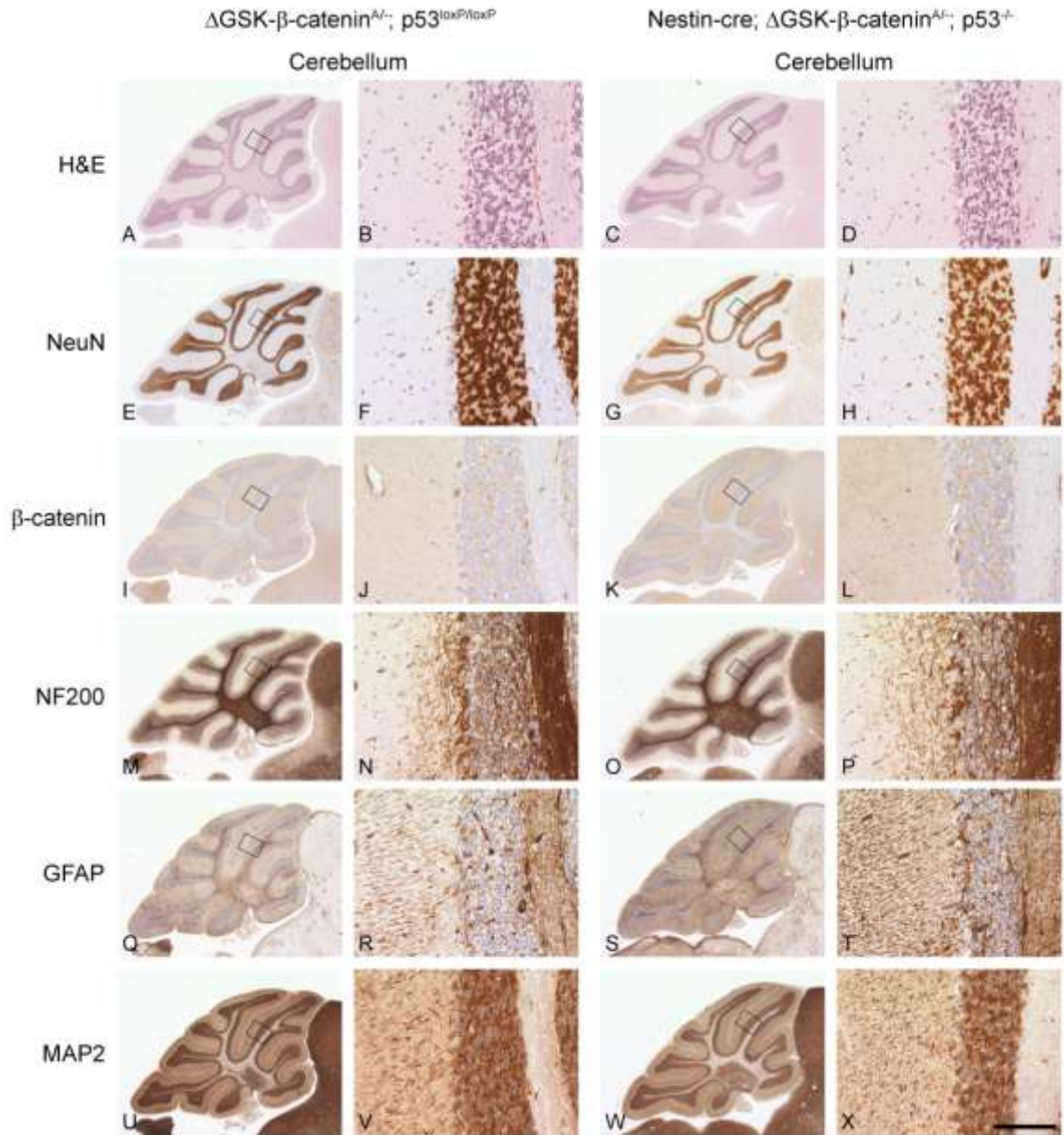


Figure 4.6 There are no abnormalities in the cerebellum of Nestin-Cre; Δ GSK- β -catenin; p53^{-/-} brains
 Cerebella from Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} and Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice were stained for H&E (A-D), NeuN (E-H), β -catenin (I-L), NF200 (M-P), GFAP (Q-T) and MAP2 (U-X). The first and second columns correspond to low and high power magnification of a Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} cerebellum. The third and fourth columns correspond to low and high power magnification of a Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{-/-} cerebellum. High power magnification images correspond to the fifth and sixth lobule of the cerebellum (black box). β -catenin staining was unchanged after recombination. Furthermore, recombined brains showed no abnormalities when compared to controls. Stronger gliosis was observed in Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} cerebella. The scale bar in X corresponds to 1300 μ m and 140 μ m for low power and high power magnifications respectively.

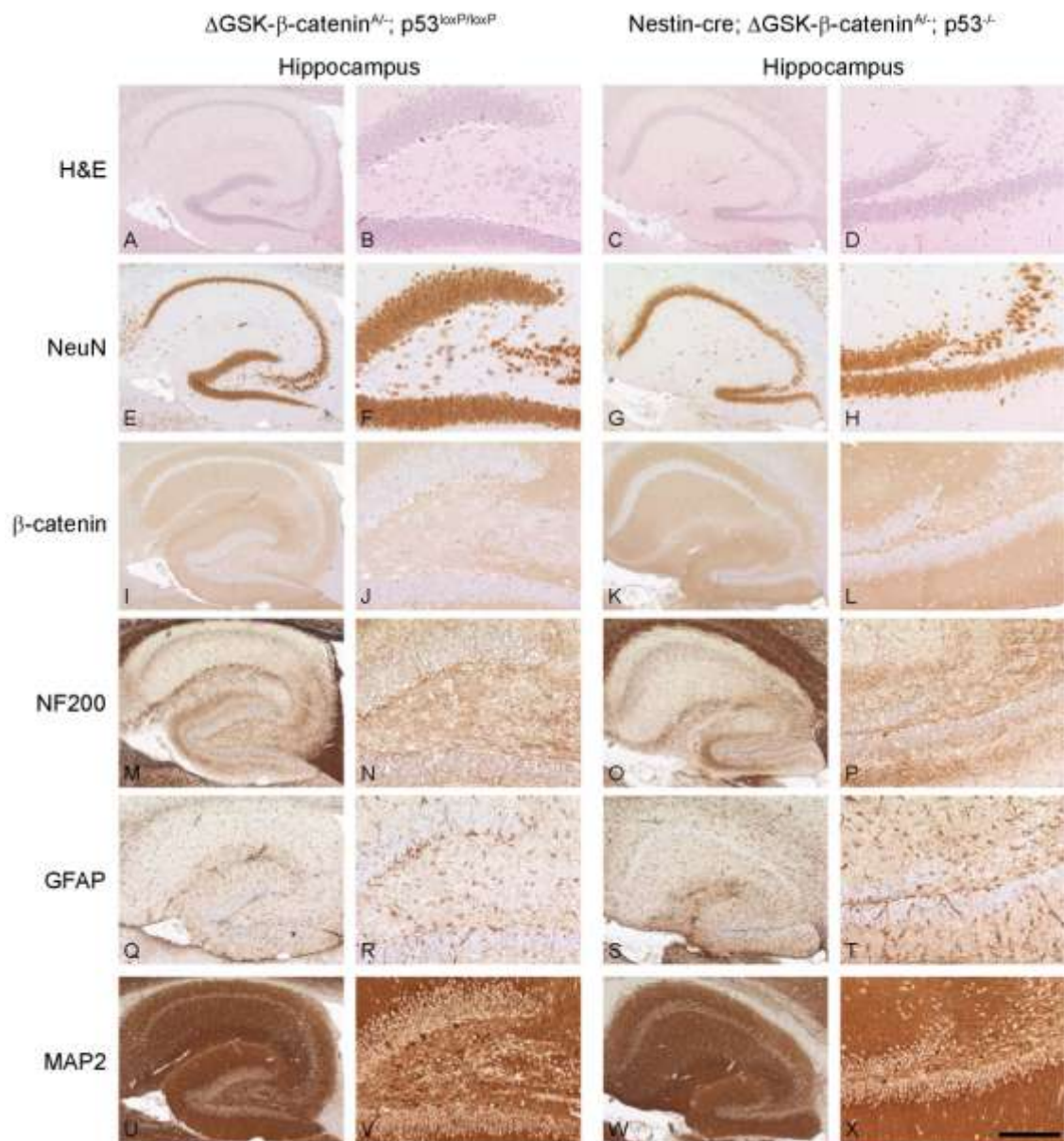


Figure 4.7 There are no abnormalities in the hippocampus of Nestin-Cre; Δ GSK- β -catenin; p53^{loxP/loxP} brains

Hippocampi from Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} and Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice were stained for H&E (A-D), NeuN (E-H), β -catenin (I-L), NF200 (M-P), GFAP (Q-T) and MAP2 (U-X). The first and second columns correspond to low and high power magnification of a Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} hippocampus. The third and fourth columns correspond to low and high power magnification of a Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{-/-} hippocampus. β -catenin staining was unchanged after recombination. Furthermore, recombined brains showed no abnormalities when compared to controls. Stronger gliosis was observed in Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} brains. The structural differences between the hippocampi of Δ GSK- β -catenin^{A/-} and Nestin-Cre; Δ GSK- β -catenin^{A/-} are explained by the lateral depth of the histological sections. The scale bar in X corresponds to 700 μ m and 220 μ m for low power and high power magnifications respectively.

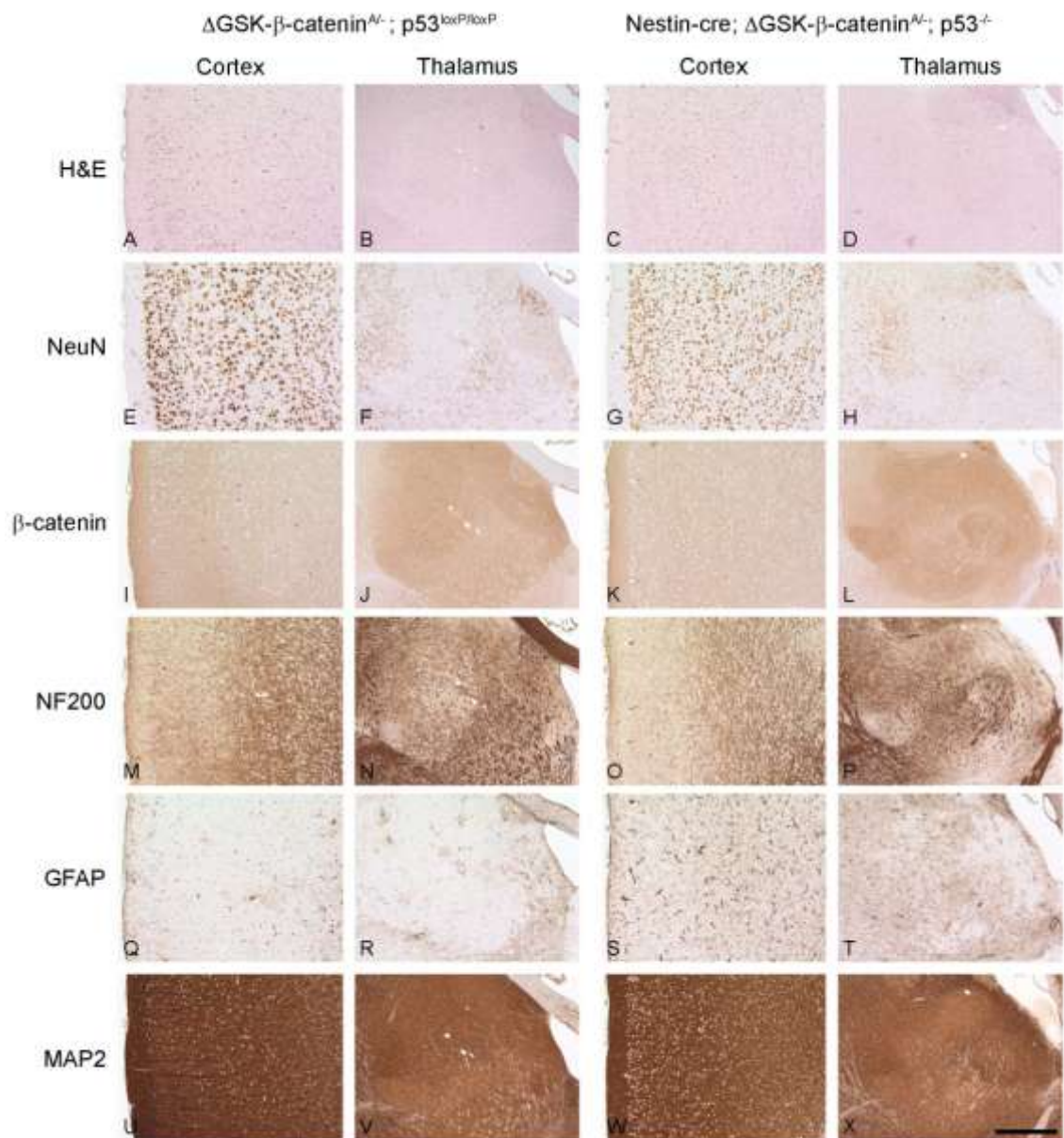


Figure 4.8 There are no abnormalities in the cortex and thalamus of Nestin-Cre; Δ GSK- β -catenin; p53^{loxP/loxP} brains

Cortices and thalami from Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} and Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice was stained for H&E (A-D), NeuN (E-H), β -catenin (I-L), NF200 (M-P), GFAP (Q-T) and MAP2 (U-X). The first and second columns correspond to the cortex and thalamus of a Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mouse. The third and fourth columns correspond to the cortex and thalamus of a Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{-/-} mouse. β -catenin staining was unchanged after recombination. Furthermore, recombined brains showed no abnormalities when compared to controls. Stronger gliosis was observed in Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} brains. The scale bar in X corresponds to 850 μ m and 450 μ m for low power and high power magnifications respectively.

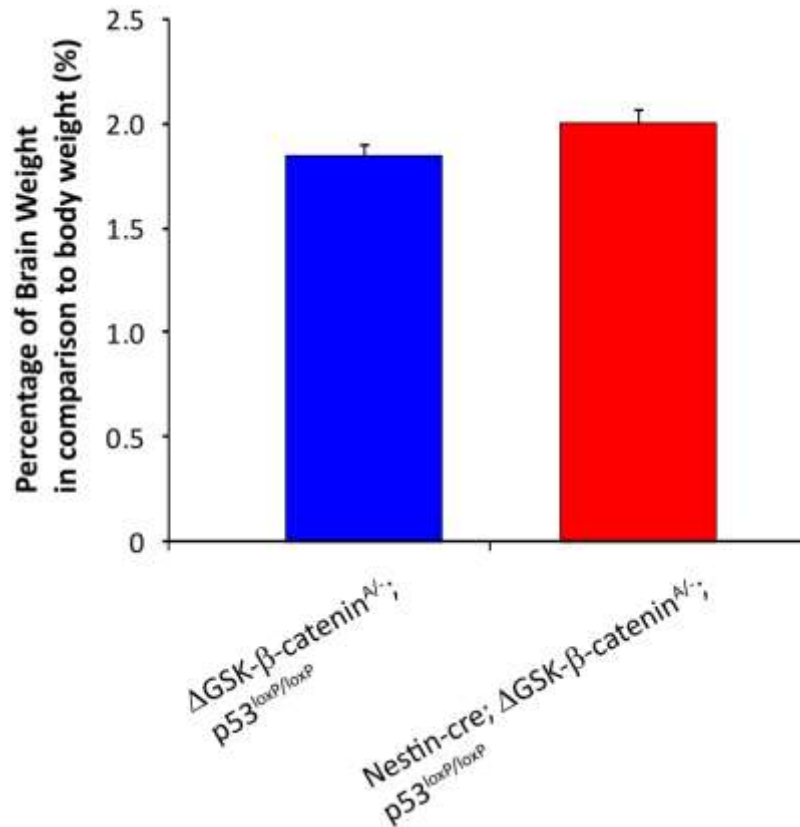


Figure 4.9 No significant difference in brain weight between Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} and Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice

Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} (n=14) and Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} (n=17) brains were weighed and the value converted to a percentage of body weight. There was no significant difference between Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} and Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice (p=0.06, two-tailed t-test).

4.2.3 Additional deletion of p53 or Rb in NSCs does not have a consistent effect on proliferation

As Δ GSK- β -catenin expression was predicted to be low, Δ GSK- β -catenin^{A/A} homozygous mice were generated to increase expression. These mice were then crossed with either p53^{loxP/loxP} or Rb^{loxP/loxP} conditional knockout mice to assess the synergistic effect, if any, of these mutations in NSCs. Subsequently, NSC cultures were derived and grown as previously discussed.

NSC growth was measured using the Hoechst proliferation assay. Hoechst 33342 is a cell-permeant nuclear counterstain that emits blue fluorescence when bound to dsDNA; fluorescence is proportional to the amount DNA, which is an indication of the number of cells in culture. Using this assay, the amount of fluorescence was measured at days 1, 3 and 6 post-plating. A modest increase in the proliferation of Adeno-Cre infected Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} and Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} NSCs (n=1) was detected (**Figure 4.10**).

Proliferation was also assessed using the neurosphere size assay. Adeno-Cre recombined Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} and Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} NSCs grew smaller in size than controls (n=1) (**Figure 4.11**).

The limited dilution assay was used to determine self-renewal and indicated that Adeno-Cre treated Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} cultures grew fewer neurospheres than Adeno-GFP treated controls (n=1) (**Figure 4.12**). Conversely, Adeno-Cre-infected Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} cultures produced more neurospheres than Adeno-GFP infected controls (n=1) (**Figure 4.12**). However, the number of neurospheres was similar between untreated cultures and Adeno-Cre treated cultures for both cell lines.

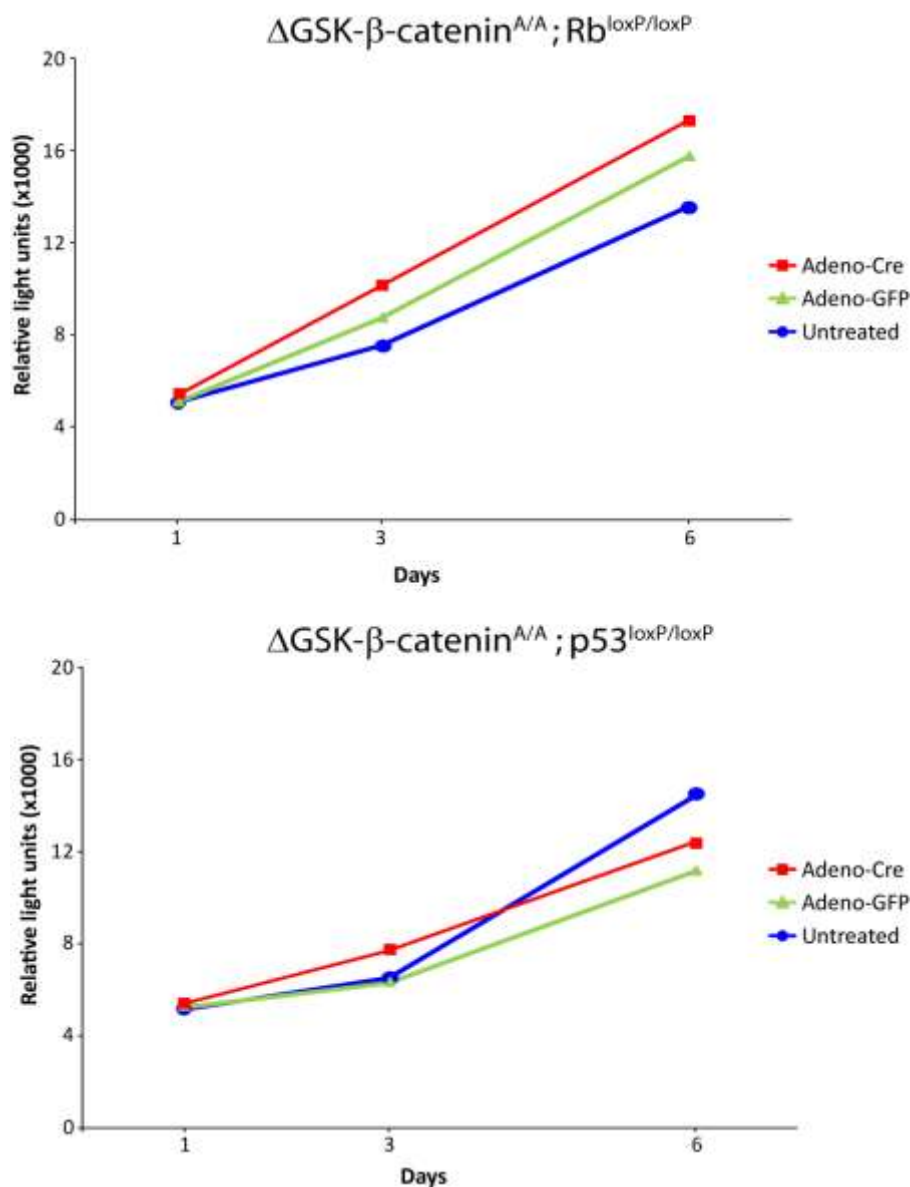


Figure 4.10 Adeno-Cre-infected Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} and Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} NSCs show a slightly enhanced proliferation potential

Neurospheres from Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} (A) or Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} (B) cultures were passaged to a single cell suspension. Cells were plated in quintuplet for each treatment at a density of 3.5×10^3 cells/well. Three identical 96-well plates were prepared. On day one post-plating, Hoechst 33342/DMSO was added to each well of one of the plates and incubated for 30 min at 37 °C. As much medium as possible was removed and replaced with PBS to lower unbound background Hoechst. Fluorescence was measured at 360 nm excitation and 465 nm emission. The same procedure was repeated on days 3 and day 6 post-plating with the remaining 96-well plates. Adeno-Cre-infected NSCs grew slightly faster than controls. This was a single experiment, therefore the statistical significance cannot be determined.

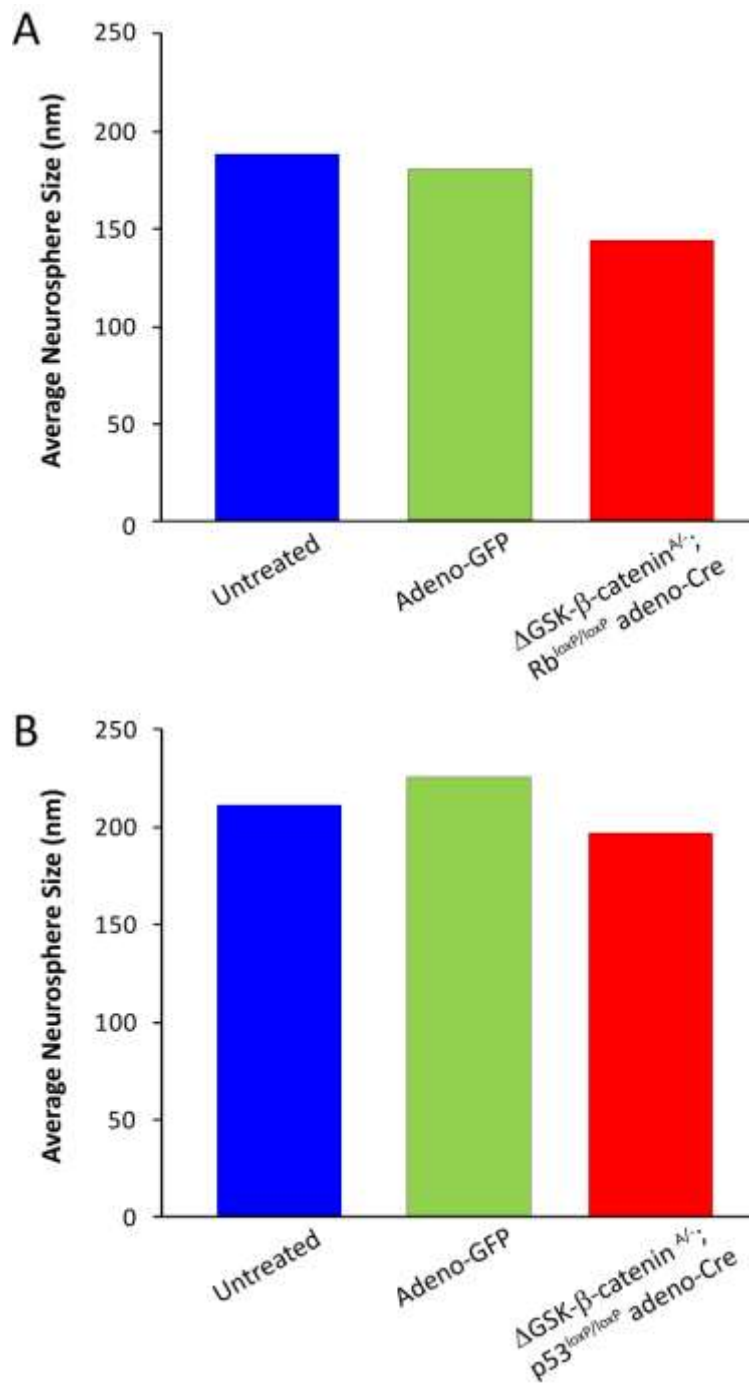


Figure 4.11 Adeno-Cre-infected Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} and Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} neurospheres are smaller than controls

Neurospheres were passaged to a single cell suspension and 0.5×10^6 cells were plated on a 6 cm plate. Ten days after passage, the diameter of the neurospheres was measured using an Axiovert 135 microscope (Zeiss) and the Openlab 5 software. Each experiment was the average of 100 neurospheres. Adeno-Cre-infected Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} (A) or Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} (B) neurospheres grew smaller than controls. This was a single experiment, therefore the statistical significance cannot be determined.

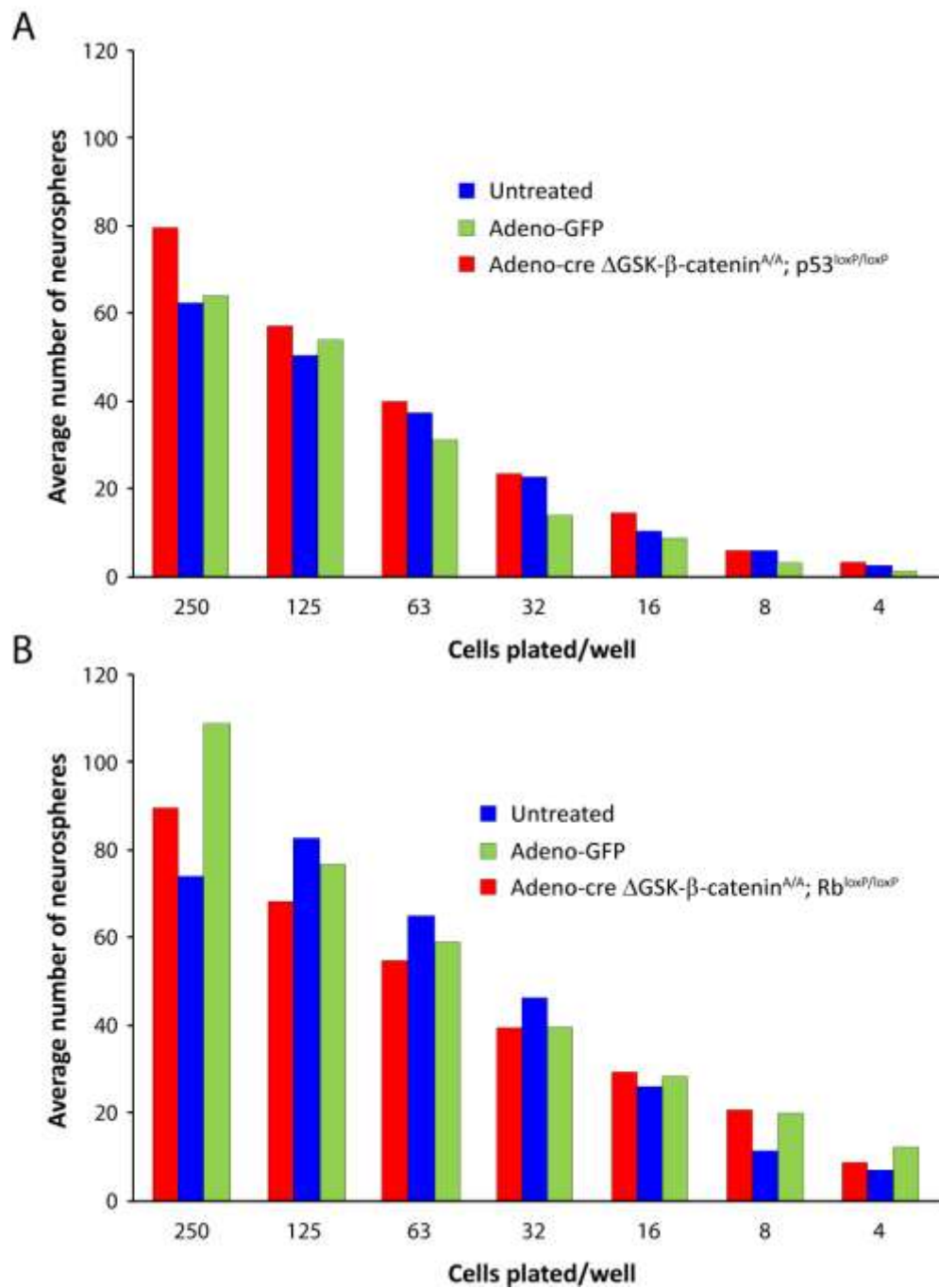


Figure 4.12 Adeno-Cre-infected Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} NSCs show higher self-renewal, but Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} NSCs do not

Neurospheres were passaged to a single cell suspension. About 500 cells were plated into each well of the top row of a 96-well plate. The cells were serially diluted for each row of wells. Ten days after passage, the number of neurospheres was counted. Each result was an average of twelve wells. Adeno-Cre treated Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} (A) grew more spheres than Adeno-GFP controls. Conversely, Adeno-Cre infected Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} grew fewer spheres than Adeno-GFP treated controls (B). This was a single experiment, therefore the statistical significance cannot be determined.

4.2.4 *In vivo* recombination in the SVZ niche of Δ GSK- β -catenin^{A/-}; p53^{flox/flox} mice does not cause CNS neoplasia

An alternative method for inducing recombination *in vivo* is injecting Adeno-Cre virus directly into lateral ventricles, resulting in an infection of cells in the SVZ (Jacques *et al.*, 2010). Nine Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice and nine p53^{loxP/loxP} control mice were injected with Adeno-Cre and culled three hundred days post-infection. No hyperplasias or tumours were found in the SVZ (**Figure 4.13**).

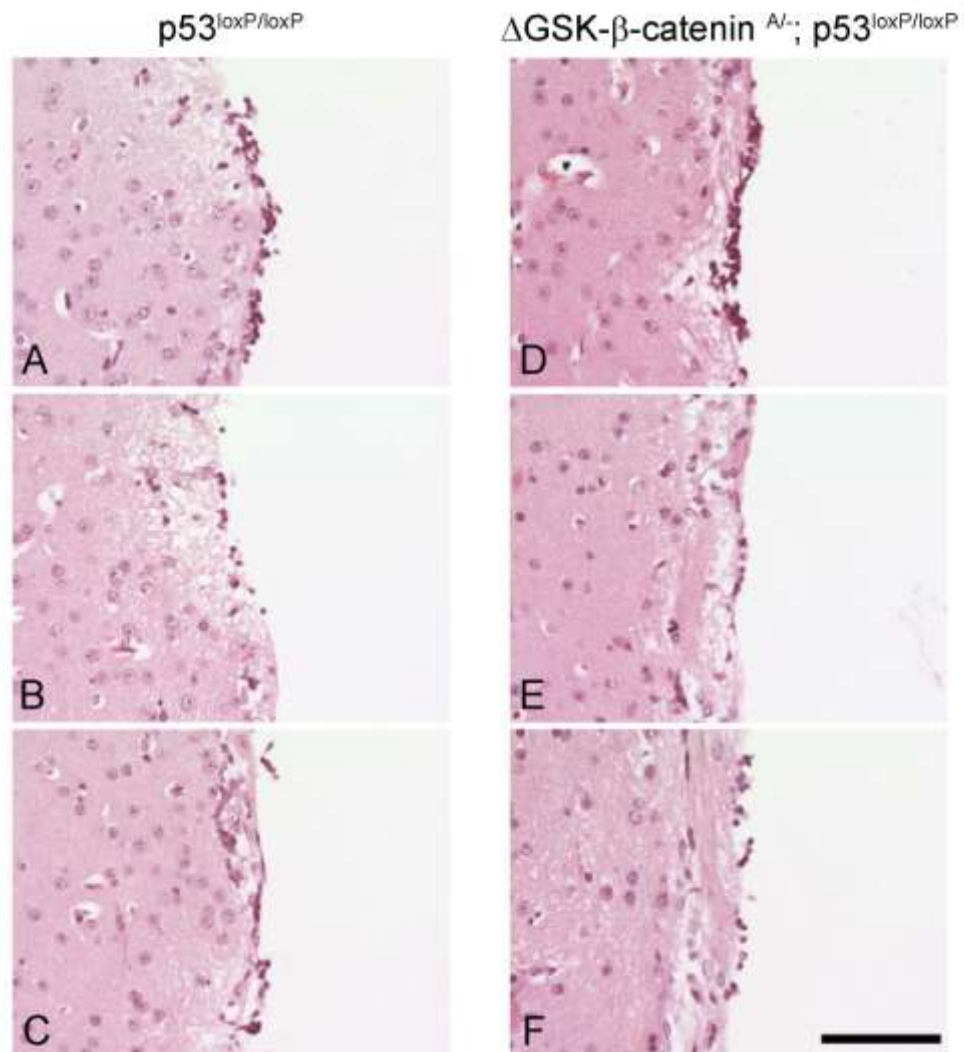


Figure 4.13 SVZ recombined Δ GSK- β -catenin^{A/-}; p53^{flox/flox} mice do not develop abnormal cell proliferations

The lateral ventricles of Δ GSK- β -catenin^{A/-}; p53^{flox/flox} (n=9) (D-F) and control p53^{flox/flox} (n=9) (A-C) mice were injected with Adeno-Cre. Three hundred days post-injection the mice were culled and the brains were processed for histology. Hyperplasia or tumours were not found. The scale bar in F corresponds to 130 μ m.

4.3 Discussion

Nestin- $\Delta 90N$ - β -catenin transgenic mice show severe CNS developmental abnormalities and die prior to birth (Chenn and Walsh, 2002). In this mouse model, expression of $\Delta 90N$ - β -catenin in NSCs increases the proportion of neural stem cells, which continue to proliferate instead of differentiating (Chenn and Walsh, 2002). As previously discussed, Nestin-Cre; Δ GSK- β -catenin mice do not show CNS developmental abnormalities (**chapter 3**). Although the protein is expressed in the brain, the SVZ is not enlarged as would be expected. This may be attributed to the weak expression of Δ GSK- β -catenin. However, the existence of a more subtle phenotype, which may not be detected, by histological examination, cannot be excluded. To investigate this possibility, the effect of Δ GSK- β -catenin expression in NSCs was investigated. For this purpose, NSC cultures were grown from the SVZ of adult Δ GSK- β -catenin mice. To induce Δ GSK- β -catenin expression, NSCs were infected with an Adenovirus expressing Cre-recombinase. An Adenovirus expressing GFP was used as a control. Western blots of NSCs showed that Δ GSK- β -catenin was expressed after Adeno-Cre mediated recombination (**Figure 4.1**). Of the two Δ GSK- β -catenin transgenic mouse lines tested, Δ GSK- β -catenin^{A/-} NSCs expressed significantly more mutant protein than Δ GSK- β -catenin^{C/-} NSCs.

The WST-1 proliferation assay was used to determine NSC growth. In this assay, the WST-1 reagent is metabolised by mitochondria into formazan, a dark red compound. The amount of formazan can be measured by optical density and is proportional to the number of cells in culture. Adeno-Cre recombined Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} NSCs did not show an increased growth potential in comparison to controls. However, the caveat of this method is that growth is not measured directly, but as a by-product of mitochondrial activity. Hence, if expression of Δ GSK- β -catenin alters mitochondrial metabolism, this would have affected the interpretation of the data. Indeed, expression of degradation-resistant β -catenin has been shown to increase the mitochondrial activity of intestinal epithelial and colon cancer cells (Mezhybovska *et al.*, 2009). This suggests that Adeno-Cre recombined Δ GSK- β -catenin NSCs may have an increased rate of formazan production, which could be misunderstood for an increase in proliferation. However, in our studies, Adeno-Cre recombination did not significantly alter formazan formation. This can be explained if Δ GSK- β -catenin expression is not having an effect in these cells. This is in agreement with the results obtained in this chapter.

Another method used to determine NSC growth was to measure NS size. NSCs grown under non-adherent conditions form spherical bodies, termed neurospheres. If a treatment has the potential to affect the growth of NSCs it can be hypothesised that it would also have an impact on the size of the neurospheres. To test this theory, NSCs were grown for ten days

before measuring the diameter of one hundred spheres for each treatment. Adeno-Cre treated Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} neurospheres were not significantly larger or smaller than controls. However, it is possible that neurosphere growth may have reached a plateau by day 10. This would indicate that growth differences may have been missed. Indeed, a report by Mori *et al.* suggests that neurosphere growth starts decreasing at around 250 μ m in diameter (Mori *et al.*, 2006). Moreover, in our study neurospheres rarely reached a size \geq 250 μ m.

One of the key characteristics of stem cells is their ability to self-renew. To assess self-renewal, cells were plated in decreasing concentrations from 250 cells/well to 4 cells/well and grown for 10 days. Only stem cells have the ability to form spheres. Hence, the number of secondary neurospheres is an indication of self-renewal potential. A caveat to this assay is that neurospheres freely fuse with each other (Singec *et al.*, 2006). Coles-Takabe *et al.* (2008), closely studied the formation of non-clonal neurospheres and found that when cells were plated at a density of 131 cells/cm², the percentage of non-clonal spheres was negligible if the cultures were left undisturbed (Coles-Takabe *et al.*, 2008). In the limited dilution assay, cells are grown at 168 cells/cm², for the highest concentration and 1 cell/cm², for the lowest. They are disturbed only twice during the experiment for the addition of fresh medium and growth factors. Therefore, non-clonal sphere formation is likely to be negligible, especially for the lower concentrations. The results presented in this chapter show that there is no significant difference in self-renewal after Adeno-Cre recombination for either Δ GSK- β -catenin^{A/-} and Δ GSK- β -catenin^{C/-} NSCs.

Collectively, the results here largely disagree with published data (Hirabayashi *et al.*, 2004; Qu *et al.*, 2010; Yu *et al.*, 2006). A study investigating the expression of S33Y β -catenin in cortical neural precursors demonstrated that S33Y β -catenin does not affect their growth and self-renewal (Hirabayashi *et al.*, 2004). Although this report provides evidence in favour of the results presented in this chapter, the precursors in the Hirabayashi *et al.* study were from E11.5 embryos, which would have had a different expression pattern and chromatin structure than what occurs in adult NSCs. In disagreement with the data shown here, a report by Yu and colleagues suggests that activation of the Wnt/ β -catenin pathway increases the proliferation and self-renewal of SVZ neural stem cells (Yu *et al.*, 2006). In this report, activation of the pathway was induced by transfection with Wnt3a or Wnt5a. Proliferation was measured by BrdU incorporation, which labelled dividing cells and daughter cells. However, there are a few counter arguments for their results. For example, the medium used to culture the cells contained 10 % FCS, which has been shown to cause the irreversible differentiation of NSCs (Gage *et al.*, 1995; Lee *et al.*, 2006; McKay, 1997; Reynolds and Weiss, 1992). Hence, this may have influenced their results. Additionally, for self-renewal measurement, cells were plated at 2×10^3 cell/cm², which was shown by Coles-Takabe *et al.*, to result in 15-100 % of non-clonal

spheres, depending on how often the plates were disturbed (Coles-Takabe *et al.*, 2008; Yu *et al.*, 2006). However, a recent report by Qu and colleagues agrees with Yu and colleagues results. In this report, expression of $\Delta 90N$ - β -catenin is shown to increase the percentage of BrdU-positive cells from 34 to 49 % in SVZ NSC cultures (Qu *et al.*, 2010). Similarly, expression of Wnt7a also increased proliferation and self-renewal (Qu *et al.*, 2010). In this study, self-renewal was measured by plating single cells under adherent conditions and counting the progeny, thereby removing the risk of non-clonal sphere formation.

Despite expression of Δ GSK- β -catenin protein in NSCs, their growth was not significantly increased. Therefore, mice homozygous for Δ GSK- β -catenin^{A/A} were generated to increase expression levels. Subsequently, these mice were crossed with p53 or Rb conditional knockout mice to promote growth and tumour development. p53 is involved in the cellular response to DNA damage and is often mutated in cancers [reviewed in (Hainaut and Hollstein, 2000)]. With respect to CNS tumours, p53 is mutated in up to 25 % of primary and 65 % of secondary glioblastomas (Ohgaki *et al.*, 2004; Watanabe *et al.*, 1996; Watanabe *et al.*, 1997). Similarly, TP53 is mutated in medulloblastomas, albeit rarely (up to 11 % of cases) (Adesina *et al.*, 1994; Alderson *et al.*, 1996; Ohgaki *et al.*, 1993). However, the p53 pathway is altered by alternative mechanisms in up to 21 % of medulloblastoma cases (Frank *et al.*, 2004). Additionally, several medulloblastoma and PNET mouse models have been generated, which involve p53 inactivation (Frappart *et al.*, 2009; Momota *et al.*, 2008). The RB gene encodes the retinoblastoma protein (Rb), which plays a crucial role in G1→S phase transition (Weinberg, 1995). Loss of heterozygosity at 13q, which affects the RB gene, was found in 12 % of primary and 38 % of secondary glioblastomas (Nakamura *et al.*, 2000). Similarly, promoter hypermethylation of the RB gene, which has been correlated with loss of expression, was found in 43 % of primary and 14 % of secondary glioblastomas (Nakamura *et al.*, 2001a).

In vitro, Adeno-Cre treated Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} and Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} NSCs grew marginally faster than controls. To measure growth, the Hoechst proliferation assay was used. In contrast to the WST-1 proliferation assay which measures mitochondrial metabolism, this assay measures DNA content. The amount of DNA was measured on days 1, 3 and 6 post-plating to more accurately follow the growth of the cells. Neurospheres from Adeno-Cre treated Δ GSK- β -catenin^{A/A}; p53^{loxP/loxP} and Δ GSK- β -catenin^{A/A}; Rb^{loxP/loxP} NSCs grew smaller than controls. Additionally, some differences in self-renewal were observed. However, in general, these effects were very mild.

Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mouse brains were not larger than control and did not show CNS abnormalities. Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} brains showed increased level of gliosis, although this was not the case for Nestin-Cre; Δ GSK- β -catenin^{A/-}

brains. These results imply that gliosis was a result of p53 inactivation and were independent of Δ GSK- β -catenin expression.

Expression of degradation-resistant β -catenin may not be sufficient for neoplastic transformation. For example, *Patched*^{+/-} mice expressing S33Y β -catenin in Nestin-expressing cells do not develop any tumours after eight weeks (Fults *et al.*, 2002). Similarly, *p53*^{-/-} mice expressing S33Y β -catenin in GFAP-expressing cells do not develop tumours within three months (Momota *et al.*, 2008). The latter study was limited to three months due to the development of lymphomas and sarcomas, a known phenotype of p53 knockout mice (Harvey *et al.*, 1993). Collectively, both studies suggest that β -catenin does not promote tumourigenesis. However, degradation-resistant β -catenin may promote tumour formation in the long-term. By using p53 conditional knockout mice the risk of sarcoma and lymphoma development is minimised, since p53 is not inactivated in connective tissue or the lymphatic system in this study. Hence, to address this possibility, the lateral ventricles of a cohort of Δ GSK- β -catenin^{A/-}; *p53*^{loxP/loxP} mice were injected with Adeno-Cre. However, 300 days post-infection no brain tumours or hyperplasia were detected in the SVZ (**Figure 4.13**). Taken together these results suggest that degradation-resistant β -catenin does not have a neoplastic potential. Nonetheless, degradation-resistant β -catenin may be able to affect a tumour phenotype. For example, *p53*^{-/-} mice expressing c-myc in GFAP-expressing cells developed PNET-like tumours with a latency of fourteen weeks (Momota *et al.*, 2008). However, when S33Y β -catenin was co-expressed, the tumour latency shortened to eight weeks (Momota *et al.*, 2008). Furthermore, these tumours showed a larger range of histological features (Momota *et al.*, 2008). This was observed without an increase in the number of tumours detected, suggesting that S33Y β -catenin was not involved in the genesis of these tumours.

4.4 Summary

Expression of Δ GSK- β -catenin did not alter neural stem cell proliferation or self-renewal. In addition, NSC proliferation was not increased, despite Δ GSK- β -catenin expression in conjunction with p53 or Rb inactivation. *In vivo*, Nestin-Cre; Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice did not develop tumours or CNS abnormalities. Similarly, Δ GSK- β -catenin^{A/-}; p53^{loxP/loxP} mice injected with Adeno-Cre into the lateral ventricles did not develop hyperplastic or neoplastic foci. As discussed above, most of these findings are in variance with existing literature. We assumed that the expression level of Δ GSK- β -catenin was responsible for the lack of a phenotype. Deletion of Rb or p53 alone does not show a significant change in stem cell proliferation *in vitro*. Additional activation of β -catenin does not further alter the proliferation of self-renewal of the stem cells. It was therefore concluded that expression of Δ GSK- β -catenin in this model system is not able to elicit a significant biological effect alone or in combination with inactivated Rb or p53 function. It was therefore decided not to further investigate our model system and obtain an alternative transgenic mouse model for expressing degradation-resistant β -catenin.

5 Analysis of β -catenin ^{Δ ex3} expression in the CNS

5.1 Background

As discussed in chapters 3 and 4, the results obtained from the Δ GSK- β -catenin transgenic mouse model do not agree with previous published reports (Chenn and Walsh, 2002; Wrobel *et al.*, 2007). Therefore, an alternative mouse model, in which degradation-resistant β -catenin is conditionally expressed, was utilised. In this model, exon 3 of the β -catenin gene, which encodes the Gsk3 β /Ck1 α phosphorylation site among other domains, is flanked by loxP sites. Cre-mediated recombination excises this exon and degradation-resistant β -catenin ^{Δ ex3} is expressed. Deletion of exon 3 has been identified in some human cancer cell lines (Iwao *et al* 1998, Sparks *et al* 1998). Since the endogenous β -catenin gene is mutated, this model accurately depicts spontaneous mutations in human cancers. Furthermore, the target gene will be expressed at endogenous levels.

The β -catenin^{lox(ex3)} mice were originally generated by the group of Taketo, who demonstrated that expression of β -catenin ^{Δ ex3} promoted intestinal polyposis (Harada *et al.*, 1999). Subsequent reports have indicated that expression of β -catenin ^{Δ ex3} can promote prostate and liver tumourigenesis (**Table 5.1**). Currently, there is limited research into CNS tumourigenesis using the β -catenin^{lox(ex3)} mouse model. Of particular interest, expression of β -catenin ^{Δ ex3} in Nestin-expressing cells has been shown to delay the maturation of radial glia (Wrobel *et al.*, 2007). As a result, there is a gross expansion of the ventricular zone, the precursor to the SVZ, which is equivalent to the phenotype observed in Nestin- Δ 90N- β -catenin mice (Chenn and Walsh, 2002; Wrobel *et al.*, 2007).

5.1.1 Aims

The aim of this study was to assess the role of the Wnt/ β -catenin pathway in the CNS using β -catenin^{lox(ex3)} transgenic mice and to test whether expression of β -catenin ^{Δ ex3} at endogenous levels results in a different biological phenotype.

5.1.2 Methods

NSC cultures were derived from the SVZ and the hippocampus of adult mice (**section 2.4.2**). NSCs were infected with Adeno-Cre to mediate recombination (**section 2.4.3**). Western blot analysis was used to detect β -catenin ^{Δ ex3} and cyclin D1 protein levels (**section 2.6**). NSC growth was assayed using the WST-1 proliferation assay (**section 2.4.4**), Hoechst proliferation assay (**section 2.4.5**) and neurosphere size assay (**section 2.4.6**). Self-renewal was assessed by the limited dilution assay (**section 2.4.7**). Nuclear fractions were obtained from Adeno-Cre, Adeno-GFP and untreated β -catenin^{lox(ex3)/wt} NSC homogenates in order to assess levels of nuclear β -catenin (**section 2.6.1.2**). Neurospheres were differentiated (**section 2.4.8**) and multi-lineage potential of NSCs was analysed by immunocytochemical methods (**section 2.4.9**). En2-Cre; β -catenin ^{Δ ex3} mouse brains were analysed histologically (**section 2.5**). β -catenin^{lox(ex3)} mice were injected intra-cranially with Adeno-Cre to recombine the SVZ (**section 2.1.4**).

Table 5.1 Selected literature regarding β -catenin ^{Δ ex3} transgenic mice

Tissue	Cre expression	Cre expression	Effect	References
Bone	Col2a1-Cre	Chondrocytes	Death ~E18, very severe chondrodysplasia	(Akiyama <i>et al.</i> , 2004)
Breast	WAP-Cre	Mammary alveolar epithelium	Hyperplastic structures and squamous metaplasia	(Miyoshi <i>et al.</i> , 2002)
	Pdgfb-iCreER	Capillary and small vessel endothelial cells	Transcriptional activation of β -catenin accelerates blood-brain-barrier (BBB) maturation	(Liebner <i>et al.</i> , 2008)
CNS	Wnt1-Cre (cell culture)	Neural Crest cells	Sensory neural cell differentiation	(Lee <i>et al.</i> , 2004)
	Nestin-Cre	Neural precursors	Increase in radial glia population resulting in gross enlargement of SVZ,	(Wrobel <i>et al.</i> , 2007)
Embryo	Nes8-Cre	Telencephalon	Up-regulation of dorsal markers and down-regulation of ventral markers	(Backman <i>et al.</i> , 2005)
	Brn4-Cre, Wnt1-Cre	Neural tube	Expansion of the progenitor pool	(Ille <i>et al.</i> , 2007)
Eye	α MHC-CrePR1	Cardiomyocytes	Impaired cardiac growth or cardiac muscular atrophy	(Baurand <i>et al.</i> , 2007)
Heart	Islet1-Cre (E7.0)	Second heart field (SHF) progenitors	Stabilisation resulted in a marked enhancement of SHF progenitors	(Kwon <i>et al.</i> , 2007)
Intestine	Fabpl-Cre, Ck19-Cre	Intestinal epithelium	Cells escape mitotic arrest and apoptosis which results in chromosomal instability	(Aoki <i>et al.</i> , 2007)
Liver	Adeno-Cre (adult)	Injected into tail vein	Stable β -catenin and H-ras promoted hepatocarcinogenesis	(Harada <i>et al.</i> , 2002; Harada <i>et al.</i> , 2004; Mucenski <i>et al.</i> , 2005)
Lung	CCSP-Cre (E14.5)	Respiratory epithelial cells	Goblet cell hyperplasia, and pulmonary tumours	(Mucenski <i>et al.</i> , 2005)
Prostate	PB-Cre	Prostate secretory epithelium	Squamous metaplasia and prostate Adenocarcinoma	(Cheon <i>et al.</i> , 2006)
Thymus	Foxn1-Cre (E10.5)	Thymic epithelial cells	Impaired thymus microenvironment, unable to support T cell development	(Maatouk <i>et al.</i> , 2008)
XY gonads	Sf1-Cre (E11.5)	Gonadal somatic cells	Male to female sex reversal	(Maatouk <i>et al.</i> , 2008)

5.2 Results

5.2.1 Adeno-Cre treated β -catenin^{lox(ex3)/wt} NSCs do not show an enhanced growth potential

NSC cultures were derived from adult β -catenin^{lox(ex3)/wt} mouse brains in order to assess the effect of β -catenin ^{Δ ex3} on these cells. Expression of β -catenin ^{Δ ex3} was induced by infecting the NSCs with Adenovirus-Cre. As expected, Adeno-Cre infected β -catenin^{lox(ex3)/wt} NSCs expressed β -catenin ^{Δ ex3} (**Figure 5.1**). Expression levels were equivalent to those of wild-type β -catenin, confirming efficient infection and recombination. However, there was no increase in cyclin D1 detected (**Figure 5.1**), suggesting that proliferation may not be increased.

Subsequently, growth was measured using the WST-1 and Hoechst proliferation assays. Growth was assessed over the course of three days. Using the standard WST-1 protocol NSC proliferation was found to decrease over this time period (**Figure 5.2**). To this end the starting cell number was optimised to 3.5×10^3 cells/well (**Figure 5.2**). No significant growth difference was detected between Adeno-Cre treated, Adeno-GFP treated or untreated NSCs (n=3) (**Figure 5.3** and **Figure 5.4**). Similarly, no significant difference was found in the diameter of neurospheres (n=3) (**Figure 5.5**).

NSC self-renewal was assessed using the limited dilution assay. Figure 5.6 shows no significant difference between Adeno-Cre and Adeno-GFP infected β -catenin^{lox(ex3)/wt} NSCs (n=3) (**Figure 5.6**).

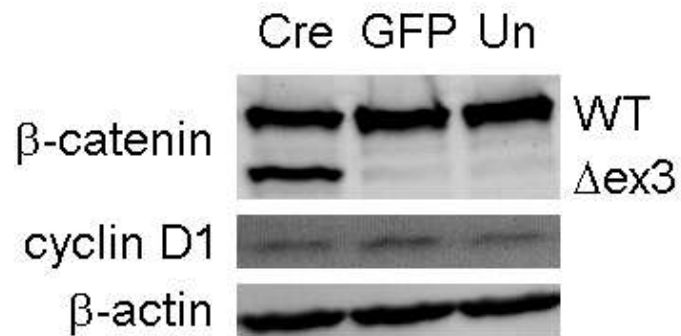


Figure 5.1 Adeno-Cre infected β -catenin^{lox(ex3)/wt} NSCs express β -catenin ^{Δ ex3}, but do not have increased cyclin D1 levels

Untreated (Un), Adeno-GFP (GFP) and Adeno-Cre (Cre)-treated β -catenin^{lox(ex3)/wt} NSC protein extracts were immunoblotted with antibodies against β -catenin (1:500), cyclin D1 (1:2000) and β -actin (1:1000). 10 μ g of total protein was loaded per lane. This is a representative western blot. Adeno-Cre infected β -catenin^{lox(ex3)/wt} NSCs expressed β -catenin ^{Δ ex3} at an equivalent level to that seen with wild-type β -catenin. However, no increase in cyclin D1 was detected. β -actin was used as an internal loading control.

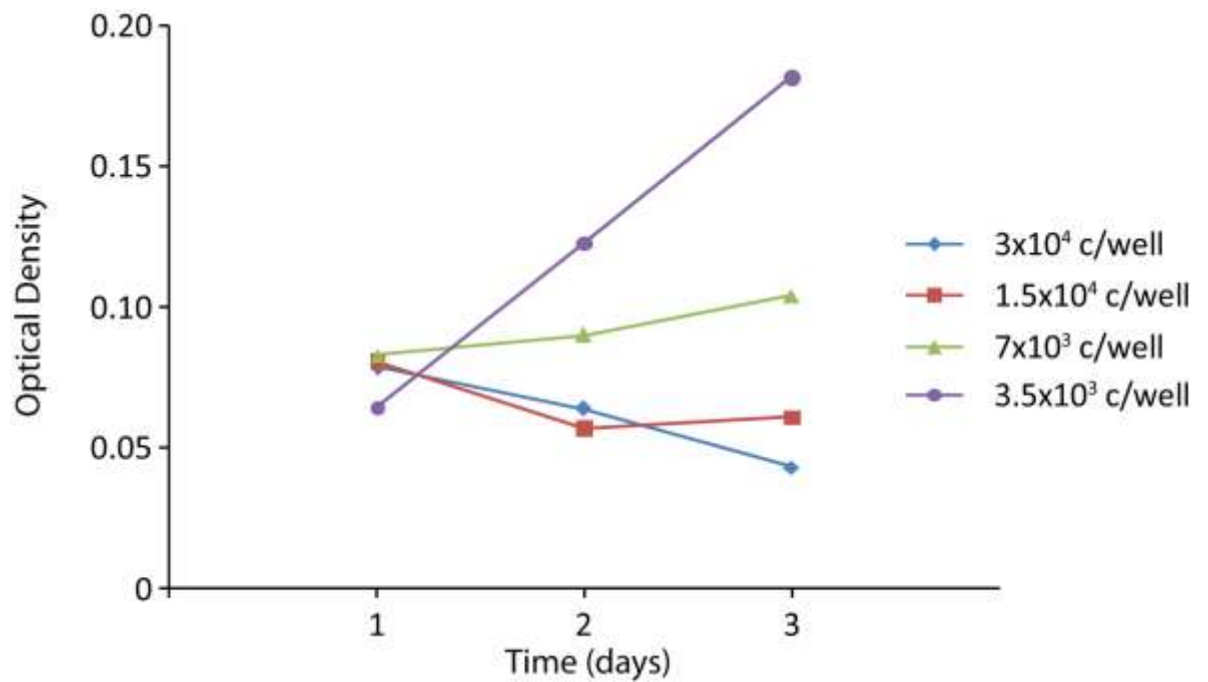


Figure 5.2 The optimal starting cell number for the WST-1 proliferation assay is 3.5×10^3 cells/ml

Neurospheres were passaged to a single cell suspension and untreated β -catenin^{lox(ex3)/wt} cells plated in quintuplet at densities of 3×10^4 , 1.5×10^4 , 7×10^3 , 3.5×10^3 cells/ml in wells of a 96-well plate. Three identical plates were prepared. At day one, two and three after passage, WST-1 reagent was added to one 96-well plate. WST-1 is metabolised by mitochondria into a coloured formazan salt. The OD of the formazan salt can be measured at 440nm and correlates with cell number. Over the course of three days, the proliferation of cells plated at 3×10^4 and 1.5×10^4 cells/ml decreased. The proliferation of cells plated at 7×10^3 cells/ml was found to be marginally increased. In contrast, the proliferation of cells plated at 3.5×10^3 cells/ml was markedly higher.

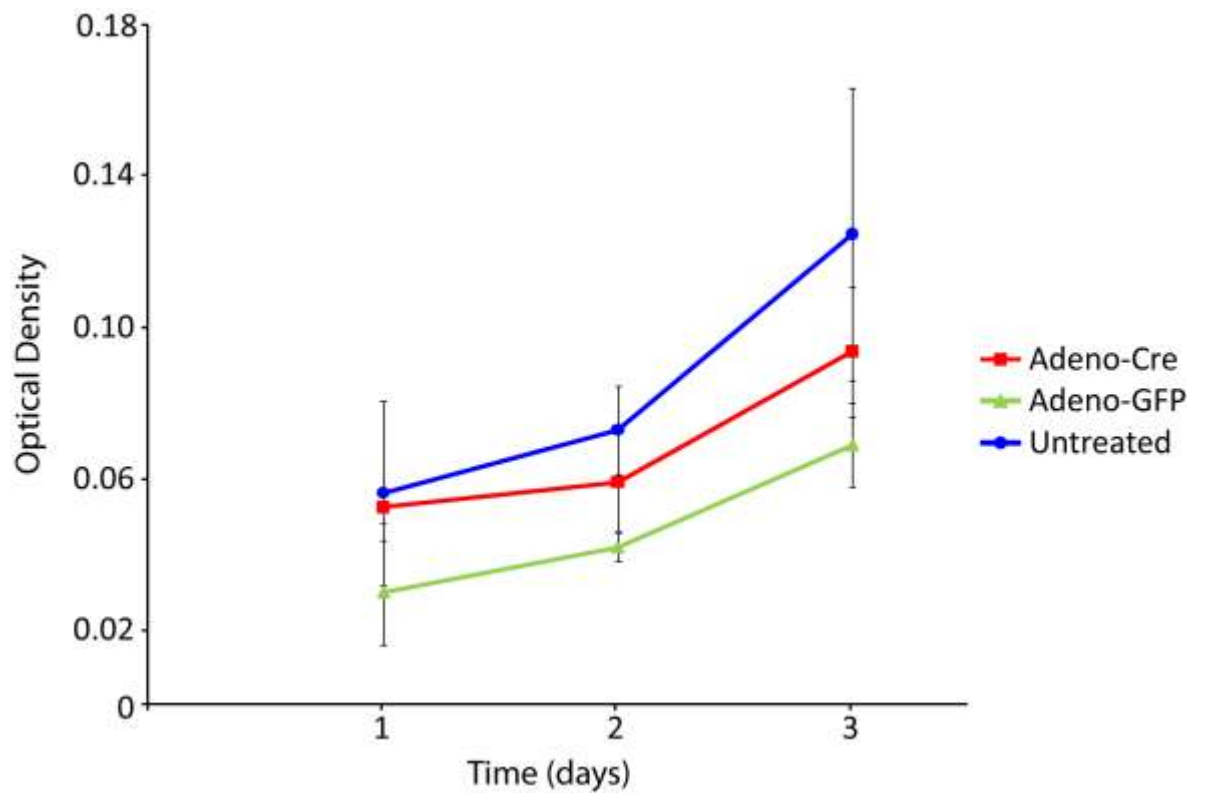


Figure 5.3 No difference in the proliferation of β -catenin ^{Δ ex3} expressing NSCs (WST-1 proliferation assay)

Neurospheres from untreated, Adeno-GFP-treated and Adeno-Cre-treated β -catenin^{lox(ex3)/wt} cultures were passaged to a single cell suspension. Cells were plated in quintuplet for each treatment at 3.5×10^3 cells/well. Three identical 96-well plates were prepared. At day one, two and three after passage, WST-1 reagent was added to one 96-well plate. WST-1 is metabolised by mitochondria into a coloured formazan salt. The OD of the formazan salt can be measured at 440nm and correlates with cell number. The results shown represent the average of three independent cultures. No significant difference in proliferation was detected between any two treatment groups at any time point (two-tailed t-test). OD values were tested for normality and homoscedasticity.

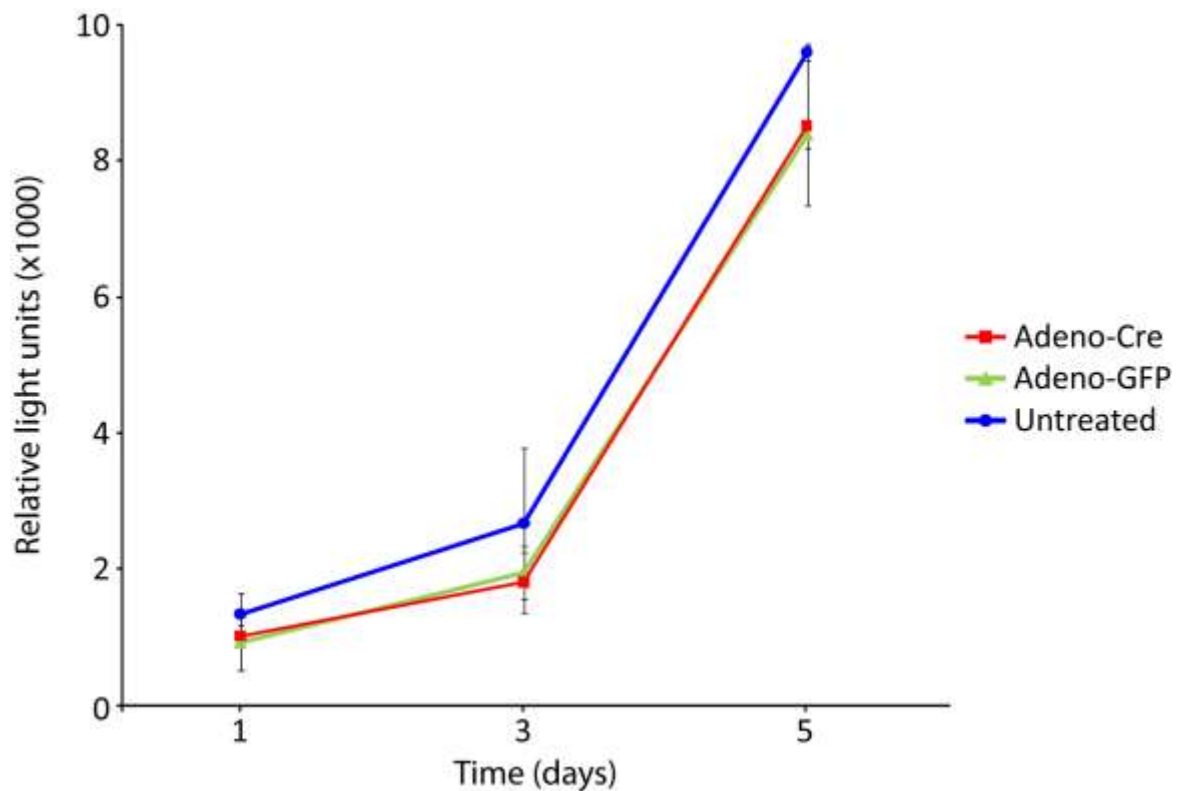


Figure 5.4 No difference in the proliferation of β -catenin ^{Δ ex3} expressing NSCs (Hoechst proliferation assay)

Neurospheres from untreated, Adeno-GFP-treated and Adeno-Cre-treated β -catenin^{lox(ex3)/wt} cultures were passaged to a single cell suspension. Cells were plated in quintuplet for each treatment at a cell density of 3.5×10^3 cells/well. Three identical 96-well plates were prepared. At day one post-plating, 50 ng of Hoechst 33342/DMSO was added to each well of one of the plates and incubated for 30 min at 37°C. The plate was subsequently centrifuged for 1 min at 1000 x g and as much medium as possible was removed and replaced with 1X PBS, which allowed the amount of unbound Hoechst to be lowered. Hoechst fluorescence was detected at 360 nm excitation and 465 nm emission. The same procedure was repeated at days two and three post plating with the remaining 96-well plates. No significant growth difference was detected between any two treatment groups (two-tailed T-test). OD values were tested for normality and homoscedasticity.

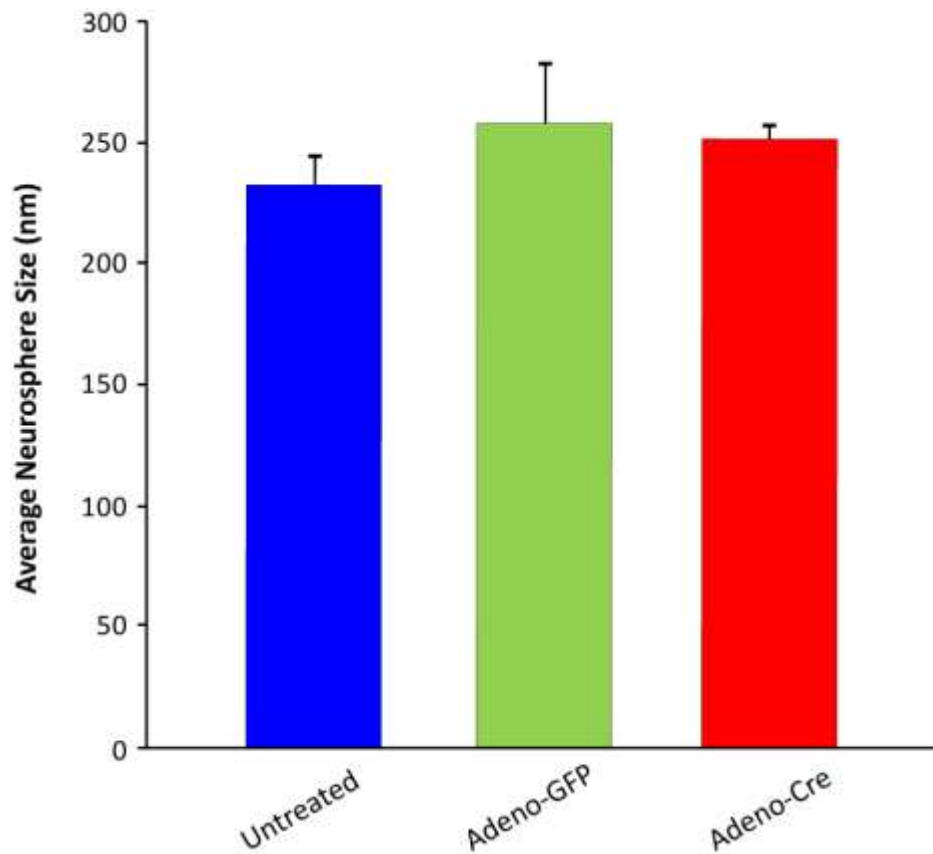


Figure 5.5 No difference in the size of neurospheres from β -catenin ^{Δ ex3} expressing NSCs

Neurospheres from untreated, Adeno-GFP-treated and Adeno-Cre-treated β -catenin^{lox(ex3)/wt} cultures were passaged to a single cell suspension and plated at 0.5×10^6 cells in individual 6 cm diameter plates. Ten days after passaging, the diameter of the neurospheres was measured using an Axiovert 135 microscope (Zeiss) and the Openlab 5 software. The diameter of a 100 neurospheres was measured for each treatment group. An n=3 was calculated from three separate cultures for each treatment group. No significant difference in neurosphere size was found (two-tailed T-test). Neurosphere diameter measurements were checked for normality and homoscedasticity.

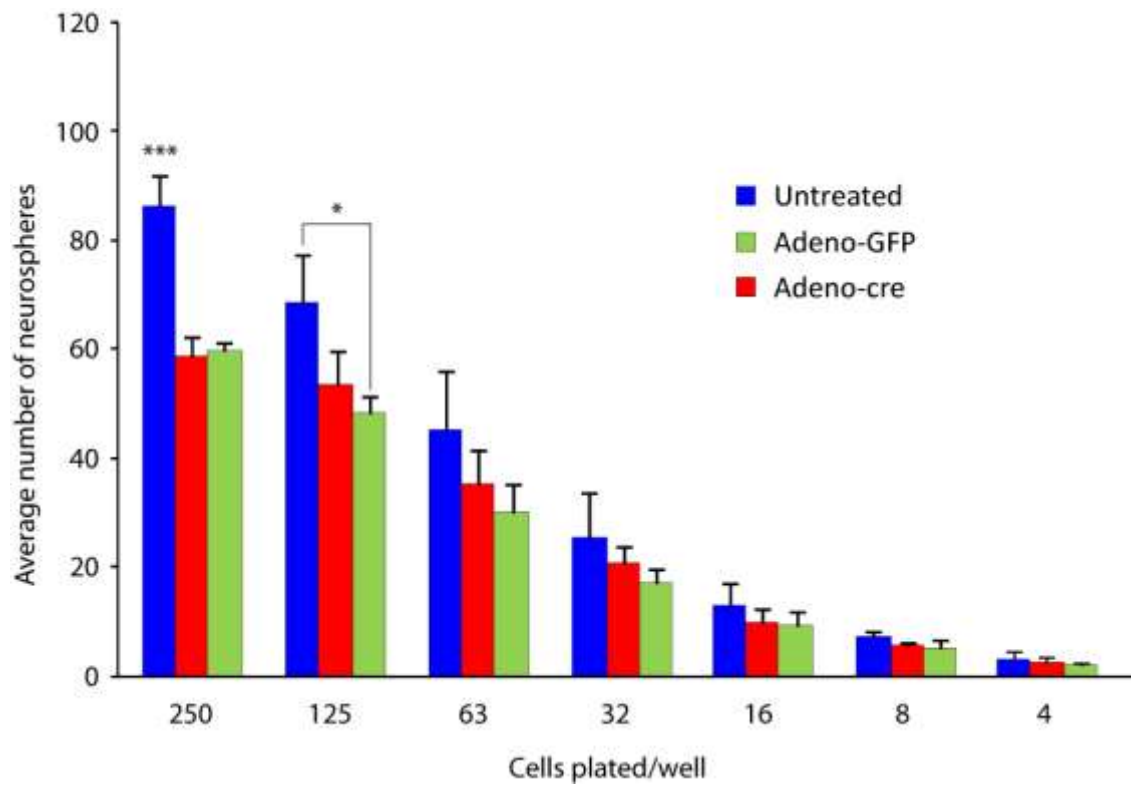


Figure 5.6 There is no difference in self-renewal between Adeno-Cre and Adeno-GFP treated NSCs

Neurospheres from untreated, Adeno-GFP-treated and Adeno-Cre-treated β -catenin^{lox(ex3)/wt} cultures were passaged to a single cell suspension. Around 500 cells were plated into each well of the top row of a 96-well plate. The cells were serially diluted for each row of wells. Ten days after passage the number of neurospheres was counted. The results from each cell concentration were the average of twelve wells. An n=3 was calculated from three individual cultures for each treatment group. No significant difference in self-renewal was detected between Adeno-Cre and Adeno-GFP treated NSCs. The self-renewal of untreated β -catenin^{lox(ex3)/wt} NSCs was significantly higher than Adeno-Cre and Adeno-GFP treated NSCs at 250 cells/well ($p \leq 0.001$). Similarly, the self-renewal of untreated β -catenin^{lox(ex3)/wt} NSCs was significantly higher than Adeno-GFP treated NSCs at 125 cells/well ($p \leq 0.05$).

5.2.2 Expression of β -catenin^{lox(ex3)/wt} does not increase differentiation

The role of the Wnt/ β -catenin pathway in NSC differentiation is not completely understood. To assess the effect of β -catenin ^{Δ ex3} expression in NSC differentiation, Adeno-Cre and Adeno-GFP treated β -catenin^{lox(ex3)/wt} neurospheres were cultured on laminin-coated chamber slides. To promote differentiation, the neurospheres were cultured in media complemented with 10 % foetal calf serum, in the absence of growth factors. Forty eight hours post-culture, cells were immunostained for GFAP (marker for astrocytes), MAP2 (marker for neurones), O4 (marker for oligodendrocytes), Nestin (marker for undifferentiated cells) and β -catenin (**Figure 5.7** and **Figure 5.8**). In view of the fact that MAP2 immunostaining failed for two of the three experiments, quantification was not possible. O4-positive cells were rare in both treatment groups (≤ 1 % of cells per field of view). Interestingly, O4-positive cells were predominantly found near neurospheres. However, the number of neurospheres plated per well was variable. To this end, quantification of O4-positive cells would be biased by the number of neurospheres plated. As expected, nuclear β -catenin was significantly increased in Adeno-Cre treated cells (**Figure 5.9**). No significant difference was detected in the percentage of GFAP- or Nestin-expressing cells (**Figure 5.9**).

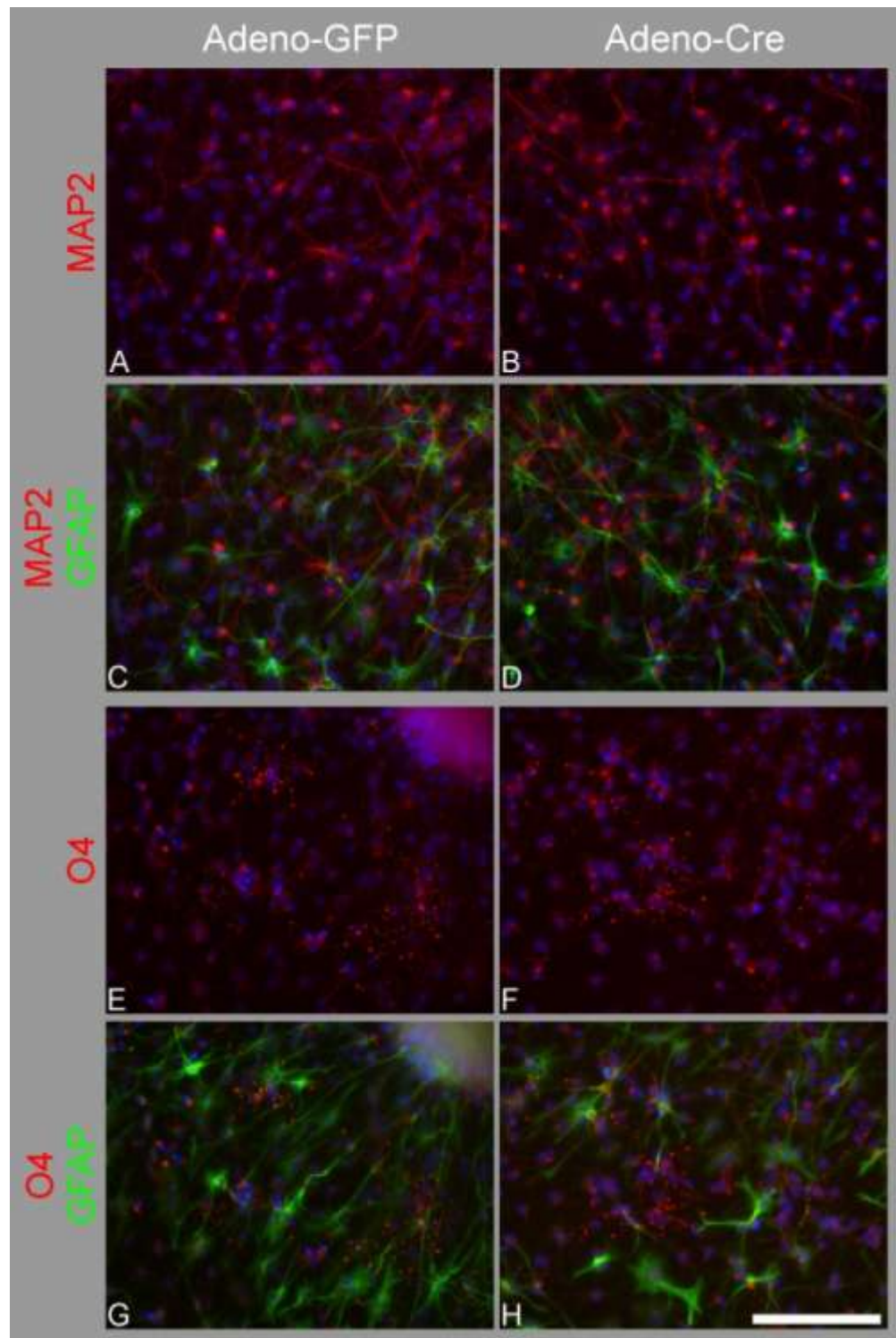


Figure 5.7 β -catenin^{lox(ex3)/wt} NSCs express MAP2, O4 and GFAP

Adeno-Cre and Adeno-GFP treated β -catenin^{lox(ex3)/wt} neurospheres were plated on laminin-coated chamber slides in DMEM/Ham-F12 media supplemented with 10 % foetal calf serum (FCS). Forty eight hours post-culture, cells were fixed with 4 % formaldehyde and immunostained with rabbit polyclonal anti-GFAP (1:500) (C, D, G and H), mouse monoclonal anti-MAP2 (1:500) (A-D) and mouse monoclonal anti-O4 (1:300) (E-H). Hoechst 33342 (1:1000) was added to label the nuclei. The scale bar in H corresponds to 150 μ m

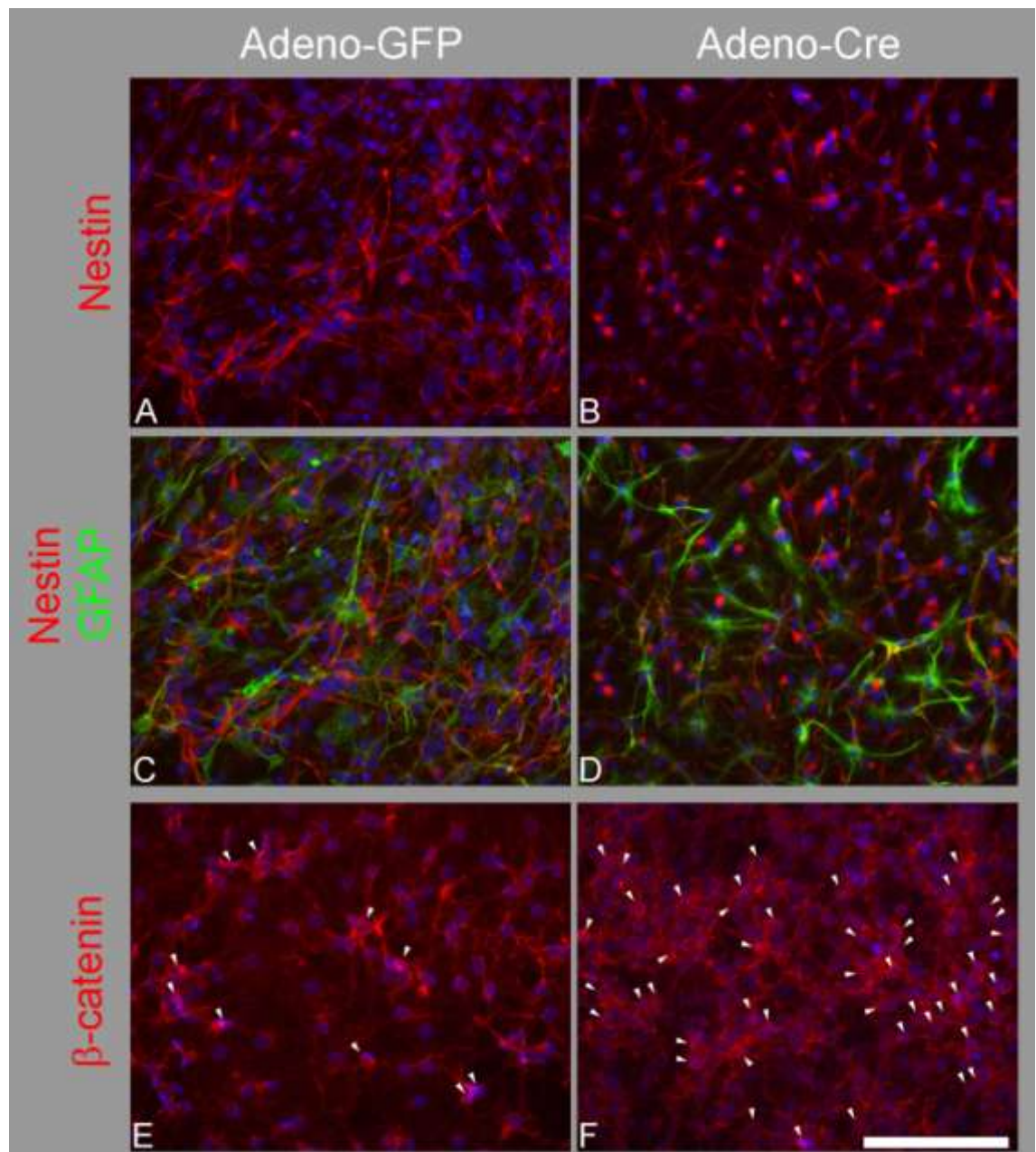


Figure 5.8 β -catenin^{lox(ex3)/wt} NSCs express Nestin, β -catenin and GFAP

Adeno-Cre and Adeno-GFP treated β -catenin^{lox(ex3)/wt} neurospheres were plated on laminin-coated chamber slides in DMEM/Ham-F12 media supplemented with 10 % foetal calf serum (FCS). Forty eight hours post-culture, cells were fixed with 4 % formaldehyde and immunostained with rabbit polyclonal anti-GFAP (1:500) (**C and D**), mouse monoclonal anti-Nestin (1:200) (**A-D**) and mouse monoclonal anti- β -catenin (1:500) (**E and F**). Hoechst 33342 (1:1000) was added to label the nuclei. The white arrows in (**E and F**) represent β -catenin nucleo-positive cells. The scale bar in **F** corresponds to 150 μ m

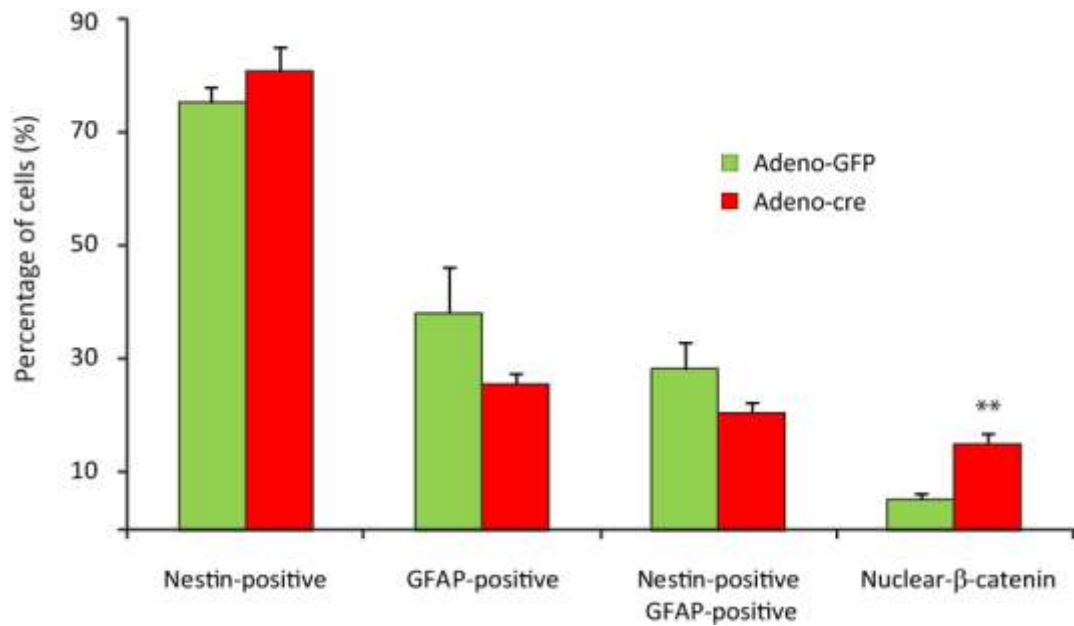
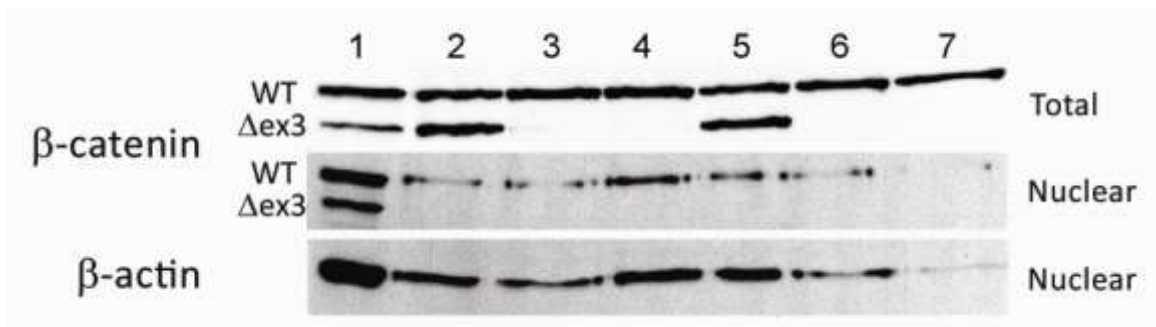


Figure 5.9 No difference in differentiation between Adeno-Cre and Adeno-GFP treated β -catenin^{lox(ex3)/wt} NSCs

Adeno-Cre and Adeno-GFP treated β -catenin^{lox(ex3)/wt} neurospheres were plated on laminin-coated chamber slides in DMEM/Ham-F12 media supplemented with 10 % foetal calf serum (FCS). Forty eight hours post-culture, cells were fixed with 4 % formaldehyde and immunostained for GFAP, Nestin and β -catenin. Cells were counted from three random fields of view for each immunostaining. The results presented are an average from three independent cultures for each treatment. There was no significant difference in the percentage of GFAP and Nestin positive cells between Adeno-Cre and Adeno-GFP treated β -catenin^{lox(ex3)/wt} NSCs. However, the percentage of cells with nuclear β -catenin was significantly higher in Adeno-Cre treated cells ($p= 0.002$) (two-tailed T-test).

5.2.3 Nuclear wild type β -catenin is more abundant than nuclear β -catenin ^{Δ ex3} in Adeno-Cre treated cells

As mentioned previously, Adeno-Cre treated β -catenin^{lox(ex3)/wt} NSCs do not show enhanced growth or self-renewal. These results are different from published data. One possible explanation may be that β -catenin ^{Δ ex3} did not translocate into the nucleus. Although β -catenin ^{Δ ex3} has been shown to translocate into the nucleus of ES cells (Harada *et al.*, 1999), activating mutations in β -catenin are not always associated with nuclear translocation in tumours (Abraham *et al.*, 2001; Anna *et al.*, 2000; Kobayashi *et al.*, 2000). To assess nuclear β -catenin protein levels, Adeno-Cre, Adeno-GFP and untreated β -catenin^{lox(ex3)/wt} NSC nuclear fractions were isolated. Subsequently, protein extracts from these fractions were immunoblotted for β -catenin. Interestingly, all three NSC treatment groups showed high levels of nuclear wild-type β -catenin (**Figure 5.10**). In contrast, no β -catenin ^{Δ ex3} was detected in Adeno-Cre treated cultures (n=2) (**Figure 5.10**). This may explain why no increase in growth and self-renewal was detected in these cells.



- 1 Adeno-Cre β-catenin^{Δex3/wt} total protein control
- 2 Adeno-Cre β-catenin^{Δex3/wt} (I)
- 3 Adeno-GFP β-catenin^{lox(ex3)/wt} (I)
- 4 Untreated β-catenin^{lox(ex3)/wt} (I)
- 5 Adeno-Cre β-catenin^{Δex3/wt} (II)
- 6 Adeno-GFP β-catenin^{lox(ex3)/wt} (II)
- 7 Untreated β-catenin^{lox(ex3)/wt} (II)

Figure 5.10 β-catenin^{Δex3} protein is not detected in the nucleus of Adeno-Cre recombined NSCs

Nuclear fractions from untreated, Adeno-GFP and Adeno-Cre treated β-catenin^{lox(ex3)/wt} NSC were immunoblotted with antibodies against β-catenin (1:500) and β-actin (1:1000). 10 μg of total protein was loaded per lane, except for **lane 7** where nuclear protein yield was low. Control Adeno-Cre treated β-catenin^{lox(ex3)/wt} NSC total protein was loaded into **lane 1**. Nuclear fractions in **lanes 2-4 and 5-7** are from two independent cultures respectively. All treatment groups contained nuclear wild-type β-catenin. However, there was no nuclear β-catenin^{Δex3/wt} detected, despite its strong expression in total protein fractions. β-actin was used as an internal loading control.

5.2.4 En2-Cre; β -catenin^{lox(ex3)/wt} mice show developmental abnormalities

To assess the role of degradation-resistant β -catenin in the CNS, β -catenin^{lox(ex3)/wt} mice were crossed with Nestin-Cre and En2-Cre mice. No Nestin-Cre; β -catenin ^{Δ ex3/wt} double mutant mice were born from this crossing. These results are in agreement with published reports; a recent study demonstrated that Nestin-Cre; β -catenin ^{Δ ex3/wt} mice are embryonic lethal (Wrobel *et al.*, 2007). This phenotype is similar to that observed in Nestin- Δ 90N- β -catenin mice (Chenn and Walsh, 2002).

Instead, En2-Cre; β -catenin ^{Δ ex3/wt} double mutant mice were viable. Engrailed 2 (En2) belongs to a family of evolutionary conserved transcription factors. During early development, En2 is expressed in spatially-restricted domains across the mid/hind-brain junction, the region from which the cerebellum develops (Davis and Joyner, 1988; Davis *et al.*, 1988; Davis *et al.*, 1991; Davidson *et al.*, 1988). En2-Cre; β -catenin ^{Δ ex3/wt} mouse brains showed marked reduction of the cerebellar vermis, resulting in a tissue defect (**Figure 5.11** and **Figure 5.12**). The phenotype was so pronounced that the vermis was not fused at the midline (**Figure 5.11**). Furthermore, the cerebella showed severe lobular abnormalities. In **Figure 5.12 A**, all lobules but the tenth were missing. Similarly, in **Figure 5.12 B**, only lobules III, IX and X are visible. However, in this example lobule III and IX are clearly abnormal when compared to controls (**Figure 5.12 C**). Of note, lobule II fails to fold back resulting in the inner granule layer meeting with the inferior colliculus (**Figure 5.12**).

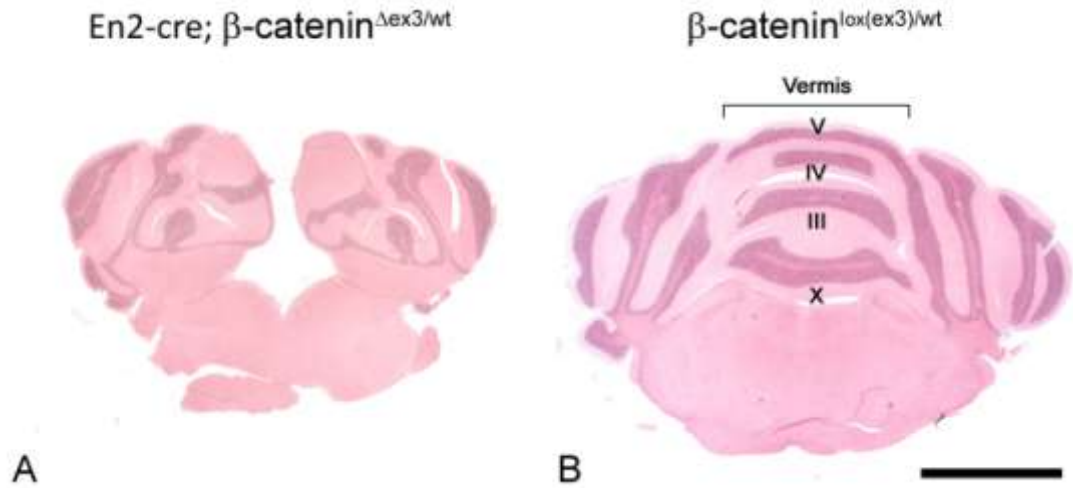


Figure 5.11 The cerebella of En2-Cre; β-catenin^{Δex3/wt} mice show signs of severe hypoplasia (coronal)
 Coronal sections of cerebella from En2-Cre; β-catenin^{lox(ex3)/wt} (A) and control β-catenin^{lox(ex3)/wt} (B) mice were stained for H&E. Compared to the control, the En2-Cre; β-catenin^{Δex3/wt} cerebellum is showing severe hypoplasia in the vermis. The roman numerals represent the different cerebellar lobules. The scale bar in B corresponds to 1500 μm.

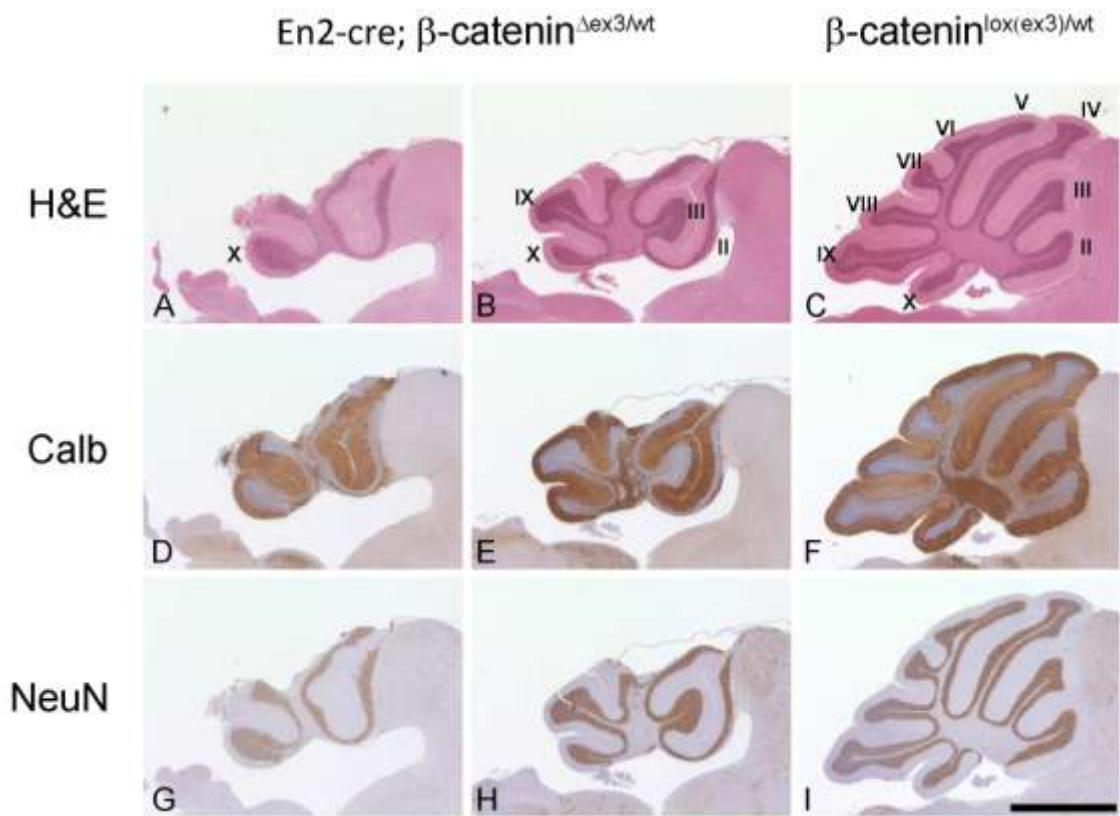


Figure 5.12 The cerebella of En2-Cre; β -catenin^{lox(ex3)/wt} mice show signs of severe hypoplasia (sagittal) Sagittal sections of cerebella from En2-Cre; β -catenin^{lox(ex3)/wt} (A-B; D-E; G-H) and β -catenin^{lox(ex3)/wt} (C, F, I) mice were stained for H&E (A-C), calbindin (Calb) (D-F) and NeuN (G-I). The roman numerals represent the different cerebellar lobules. En2-Cre; β -catenin^{Δex3/wt} cerebella (A) show severe lobular abnormalities compared to the control. Although lobules III and IX are present in (B), they are abnormal. Lobule X appears unaffected in En2-Cre; β -catenin^{Δex3/wt}. Interestingly, lobule II fails to fold back in En2-Cre; β -catenin^{Δex3/wt} mice, resulting in the internal granule layer fusing with the inferior colliculus. The scale bar in I corresponds to 1300 μ m.

5.2.5 β -catenin^{lox(ex3)/wt} mice develop SVZ hyperplasia, but no neoplasia following Adeno-Cre injection

To express β -catenin ^{Δ ex3} in the SVZ, the ventricles of adult β -catenin^{lox(ex3)/wt} mice were injected with Adeno-Cre virus. 100 days post-infection, mice were injected with BrdU and then sacrificed (n=5). The brains were then sectioned coronally and stained for GFAP (astrocytes), Synatophysin (SYP; neurones) and BrdU (dividing cells and daughter cells). Small growths were detected in the SVZ of Adeno-Cre injected β -catenin^{lox(ex3)/wt} mice. These growths consisted of an underlying layer of GFAP+/SYP-/BrdU+ cells and a mass of GFAP-/SYP-/BrdU- cells, which protruded into the ventricle (**Figure 5.13**). Although GFAP+/SYP-/BrdU+ cells share the expression profile of SVZ neural stem cells, more work is needed for confirmation (Doetsch, *et al* 1999). In contrast, the identity of the GFAP-/SYP-/BrdU- cells was not clear. It is unlikely that they were transit-amplifying daughter cells, as such cells have a high proliferative potential and would have stained strongly for BrdU.

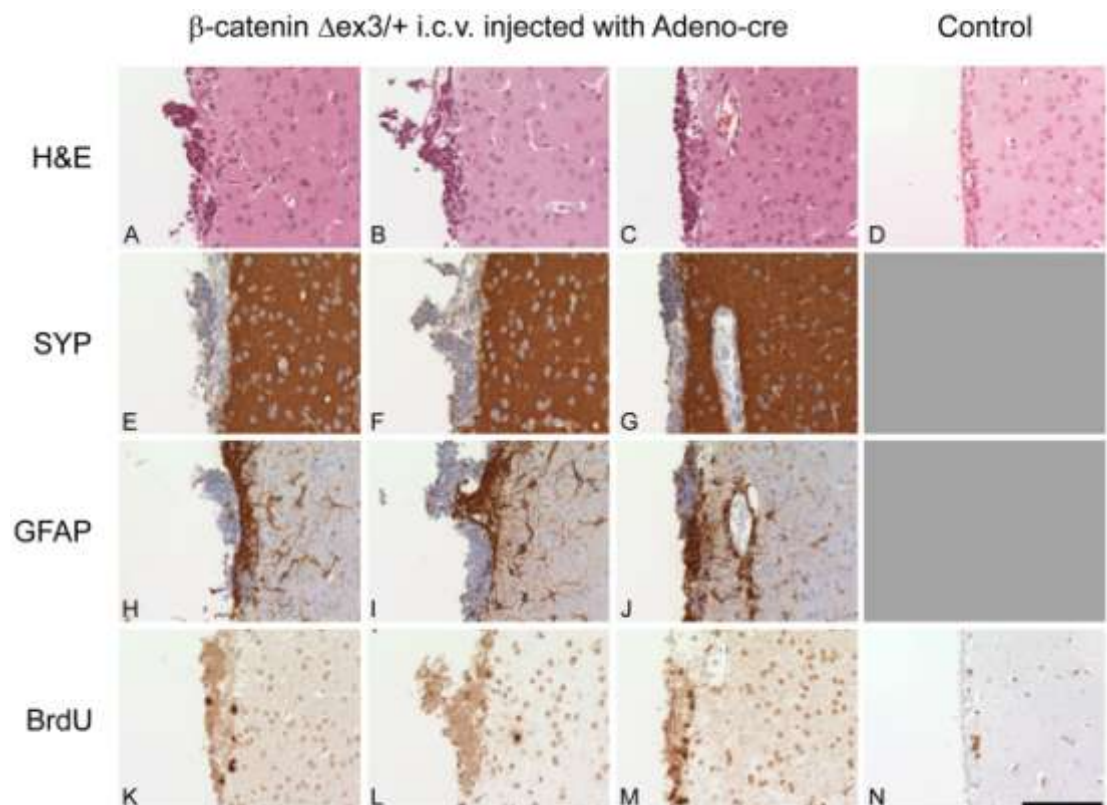


Figure 5.13 β -catenin^{lox(ex3)/wt} mice develop SVZ enlargements after Adeno-Cre intra cranial (i.c.) injections

β -catenin^{lox(ex3)/wt} mice were injected with Adeno-Cre into the ventricles. After 100 days, mice were injected with BrdU and culled. SVZ staining for H&E (**A-C**), synaptophysin (SYP) (**E-G**), GFAP (**H-J**) and BrdU (**K-M**) shows abnormal growths. These growths are composed of a layer of GFAP+/SYP-/BrdU+ cells and GFAP-/SYP-/BrdU- cells. The GFAP+/SYP-/BrdU+ cells may be stem cells. The identity of the GFAP-/SYP-/BrdU- cells is unclear. The control panels (**D and N**) correspond with a Rosa26 LacZ mouse injected with Adeno-Cre (90 days incubation). The scale bar in **N** corresponds to 130 μ m.

5.3 Discussion

Results from the Δ GSK- β -catenin mouse model and NSC cultures, presented in chapters 3 and 4, did not show a significant phenotype and after careful testing it was decided to use an alternative mouse model. The β -catenin^{lox(ex3)/wt} mouse model is the most commonly used model for studying the effect of degradation-resistant β -catenin (Harada *et al.*, 1999). In this model, exon 3 of the endogenous β -catenin gene, which encodes the phosphorylation motif of β -catenin is flanked by loxP sites. Following Cre-mediated recombination, exon 3 is deleted and degradation-resistant β -catenin ^{Δ ex3} is expressed. This model confers two key advantages. First, as β -catenin ^{Δ ex3} expression is controlled by the endogenous β -catenin promoter and regulatory elements, this model depicts β -catenin mutations in cancer more accurately than the Δ GSK- β -catenin mouse model. Second, as β -catenin ^{Δ ex3} is 76 aa smaller than wild-type β -catenin, they can be distinguished from one another by simple immunoblotting based on size (using the same antibody).

To assess the role of β -catenin ^{Δ ex3} expression on NSCs *in vitro*, neurospheres were derived, expanded and recombined as described in chapter 2. Immunoblotting analysis of Adeno-Cre-treated NSCs showed expression of β -catenin ^{Δ ex3}, the protein levels of which were similar to those of wild-type β -catenin (expressed by the other allele), and confirmed efficient recombination. However, expression of β -catenin ^{Δ ex3} did not elicit an increase of cyclin D1 protein levels. Similarly, Adeno-Cre-treated cells did not grow significantly faster or larger than controls and no differences were detected in NSC self-renewal. One possible explanation for these results is that β -catenin ^{Δ ex3} may not translocate into the nucleus of our cultured cells. β -catenin ^{Δ ex3} protein has been shown to translocate into the nucleus of ES cells (Harada *et al.*, 1999). However, activating mutations in β -catenin are not always associated with nuclear translocation in tumours (Abraham *et al.*, 2001; Anna *et al.*, 2000; Kobayashi *et al.*, 2000). Therefore, to test this hypothesis, nuclear extracts were isolated from Adeno-Cre, Adeno-GFP and untreated β -catenin^{lox(ex3)/wt} NSCs. Western blotting analysis (using an anti- β -catenin antibody) demonstrated high levels of wild-type β -catenin, but not β -catenin ^{Δ ex3}. This is in contrast to the results obtained with total protein fractions. One reason for this could be loss of protein during nuclear fractionation. However, no β -catenin ^{Δ ex3} was detected in either of the Adeno-Cre treated NSC nuclear protein fraction samples. These results suggest that in undifferentiated NSC cultures, β -catenin ^{Δ ex3} does not appear to translocate into the nucleus. This would explain the lack of any significant differences in growth and self-renewal, but more evidence is needed to substantiate these results.

Results presented in this chapter contradict with published data. Expression of degradation-resistant β -catenin has been shown to increase the proliferation and self-renewal

of NSCs *in vitro* (Lie *et al.*, 2005; Qu *et al.*, 2010; Yu *et al.*, 2006). A possible explanation for this discrepancy could be the NSC culture conditions in our system. For example, in the study by Yu *et al.*, NSCs were cultured in medium containing DMEM/HAMS F12, EGF, FGF, B27 supplement and 10 % FCS. Of note, serum has been shown to cause irreversible differentiation of NSCs and therefore was not considered as a suitable condition (Gage *et al.*, 1995; Lee *et al.*, 2006; McKay, 1997; Reynolds and Weiss, 1992). Similarly, during isolation of adult hippocampal NSCs by Lie and colleagues (2005), cultures were treated with DMEM/HAMS F12 and 10 % FCS for 24 hours before treatment with media supplemented with N2 and FGF (Lie *et al.*, 2005). Apart from irreversible differentiation, culturing NSCs in FCS allows for the permanent decrease of NSC proliferation (Lee *et al.*, 2006). Another study however, disagrees with these findings and their interpretation. In a study by Qu and colleagues, NSCs were cultured under similar conditions as in our study (Qu *et al.*, 2010). However, the NSCs grew in monolayers and not as free-floating spheres. It is possible that the cells in the study of Qu and colleagues were grown in laminin-coated culture plates. It remains to be shown whether growth as a monolayer influences the translocation of degradation-resistant β -catenin into the nucleus.

The Wnt/ β -catenin pathway plays a complex role in differentiation and maintenance of NSCs. To assess the role of β -catenin ^{Δ ex3} expression in differentiation, NSCs were grown in laminin-coated chamber slides and cultured in differentiation medium (DMEM/HAMS F12 supplemented with 10 % FCS). 48h post-culture, cells were immunostained for GFAP (astrocytes), MAP2 (neurons), O4 (oligodendrocytes), β -catenin and Nestin (undifferentiated cells). Expression of β -catenin ^{Δ ex3} increased the fraction of cells with nuclear β -catenin. However, there was no significant difference in the fraction of GFAP-positive or Nestin-positive cells. Results from MAP2 immunostaining were inconclusive. O4-positive cells were rare, ranging from 0-5 cells per field of view. They were more prominently found in close proximity to neurospheres. However, the number of neurospheres plated per well was variable. Therefore, it was not possible to accurately compare the O4 immunostaining between the different treatment groups. Taking into account the lack of a significant difference in Nestin staining, these results suggest that expression of β -catenin ^{Δ ex3} is not increasing differentiation. This is in disagreement with known roles of the Wnt/ β -catenin in NSC differentiation. The Wnt/ β -catenin pathway appears to have a dual role in differentiation depending on the developmental stage of cells. Constitutive activation of the Wnt/ β -catenin pathway during early development appears to inhibit NSC differentiation without an increase in proliferation (Chenn and Walsh, 2002; Wrobel *et al.*, 2007). Similarly, during adulthood, low-level Wnt/ β -catenin pathway activity has been proposed to maintain NSCs in an undifferentiated state (Wexler *et al.*, 2009). However, constitutive activation of the pathway during late development

and in adult NSCs increases neuronal differentiation (Hirabayashi *et al.*, 2004; Lie *et al.*, 2005; Wexler *et al.*, 2008). These results could be explained by an increase in the proliferation of cell committed to neuronal differentiation rather than by a putative increase in differentiation. Lie *et al.* reported that Wnt3 can increase the amount of new neurons by five- to ten-fold under non-proliferating conditions. However, even under such conditions, five percent of cells were found to still be proliferating (Lie *et al.*, 2005). These authors do not mention the percentage of cells proliferating without Wnt3 treatment. Therefore, the possibility remains that five percent of proliferating cells could give rise to this increase in neurogenesis. In this case the prospect that the Wnt/ β -catenin pathway may promote the proliferation of neuronally committed precursor cells rather than increasing proliferation is still possible. If so, it may explain why the percentage of cells expressing Nestin were not decreased in NSC cultures expressing β -catenin ^{Δ ex3}.

To assess the effect of β -catenin ^{Δ ex3} in the CNS, β -catenin^{lox(ex3)/wt} mice were crossed with two CNS Cre-recombinase-expressing mouse lines: Nestin-Cre (expression in neural precursors and adult neural stem cells) and En2-Cre, which drives expression in spatially-restricted domains across the mid/hind-brain junction, which develop into the cerebellum (Davis and Joyner, 1988; Davis *et al.*, 1988; Davis *et al.*, 1991; Davidson *et al.*, 1988). As expected, no Nestin-Cre; β -catenin ^{Δ ex3/wt} double mutant mice were born. These mice have been reported to be embryonic lethal due to abnormalities in the maturation of radial glia (Wrobel *et al.*, 2007). Instead, En2-Cre; β -catenin ^{Δ ex3/wt} double mutant mice were viable and showed ataxia after 3 weeks, caused by a defect in the cerebellar vermis, where the Cre transgene is expressed (Zinyk *et al.*, 1998). Furthermore, most of the cerebellar lobules were either missing or were abnormal, except for the tenth lobule. Interestingly, this phenotype was similar to that observed in mice that express orthodenticle homeobox 2 (Otx2), a gene involved in cerebellar patterning, under the control of Engrailed 1 (En1^{wt/Otx2LacZ} mice) (Broccoli *et al.*, 1999). Like in En2-Cre; β -catenin ^{Δ ex3/wt} cerebella, the vermis of these mice was reduced and not fused at the midline (Broccoli *et al.*, 1999). Furthermore, only the posterior lobules VIII, IX and X are present (Broccoli *et al.*, 1999). In order to compare these two transgenic mouse models it is necessary to discuss certain aspects of cerebellar development.

From anterior to posterior, the neural tube is composed of the prosencephalon, the mesencephalon, the metencephalon and the myelencephalon. Studies in quail-chick chimaeras have indicated that both the mesencephalon and metencephalon contribute to cerebellum development (Hallonet *et al.*, 1990; Hallonet and Le Douarin, 1993; Hatten and Heintz, 1995). The isthmus organizer (IO), located just caudally to the junction of these two regions, functions in releasing signalling proteins required for the correct patterning of the mid-hindbrain (Bally-

Cuif *et al.*, 1992; Bally-Cuif and Wassef, 1994; Martinez *et al.*, 1991) (**Figure 5.14**). The IO is in turn organised by a complex gene expression pattern. Specifically, the negative interaction of two genes, namely Otx2 and gastrulation brain homeobox 2 (Gbx2), defines IO positioning in the brain (Broccoli *et al.*, 1999; Katahira *et al.*, 2000; Millet *et al.*, 1999). One of the main signalling proteins originating from the IO is Fgf8, which induces Wnt1 expression (Adams *et al.*, 2000; Reifers *et al.*, 1998). Subsequently, Wnt1 regulates the expression of En1 and En2 (Bally-Cuif *et al.*, 1992; McMahon *et al.*, 1992).

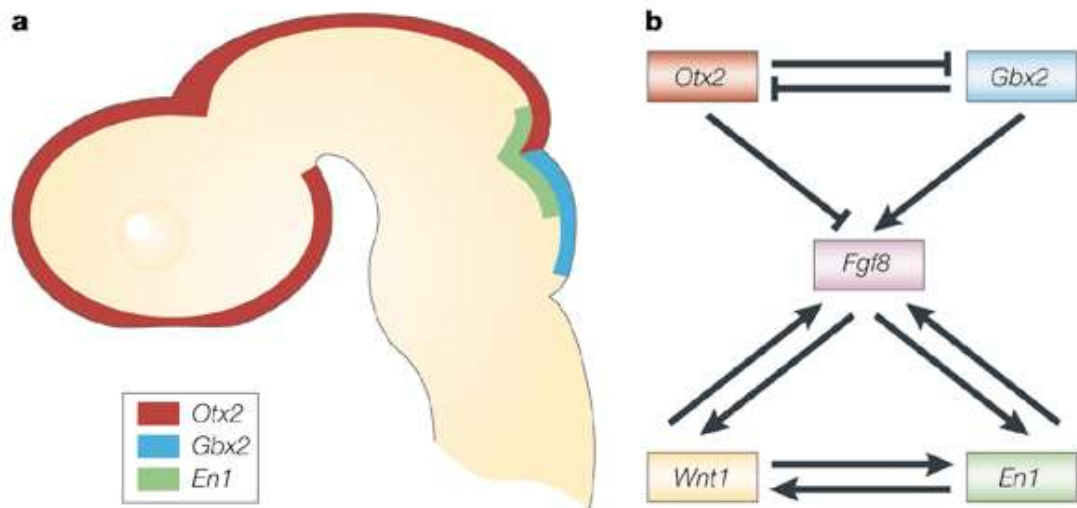


Figure 5.14 Patterning of the midbrain/hindbrain region⁵

(a) Formation of the mid-/hindbrain region is dependent on proper functioning of the isthmus organizer, which is formed by the interaction, or reciprocal repression, of Otx2 and Gbx2. En1 is expressed in both the mid- and hindbrain regions. (b) The genetic interactions among Otx2, Gbx2, Fgf8, Wnt1 and En1. En1, engrailed 1; Fgf8, fibroblast growth factor 8; Gbx2, gastrulation brain homeobox 2; Otx2, orthodenticle homologue 2.

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In $En1^{wt/Otx2LacZ}$ transgenic mice, Otx2 expression is pushed caudally (Broccoli *et al.*, 1999). As a result, Wnt1 expression is shifted into the rhombic lip, the germinal area from which granule neurones, glutamergic deep nuclear neurones and unipolar brush cells originate (Alder *et al.*, 1996; Englund *et al.*, 2006; Fink *et al.*, 2006; Machold and Fishell, 2005; Wang *et al.*, 2005) (**Figure 5.15**). In the $En1^{wt/Otx2LacZ}$ mouse model, Wnt1 is expressed in the anterior region of the rhombic lip. Interestingly, mapping experiments have shown that precursors from this area give rise to the cerebellar vermis (Sgaier *et al.*, 2005). Furthermore, Wnt1 acts through the canonical pathway in cerebellar development (Panhuysen *et al.*, 2004). Collectively, these studies suggest that activation of the Wnt/ β -catenin pathway in the rhombic lip is detrimental to cerebellar development. This is in agreement with the data obtained from the En2-Cre; β -catenin ^{$\Delta ex3/wt$} mouse model presented here. Of note, conditional APC loss-of-function in neural crest-derived cells results in a massive apoptosis of neural crest cells (Hasegawa *et al.*, 2002). Hence, activation of the Wnt/ β -catenin pathway may promote the apoptosis of cerebellar rhombic lip precursors.

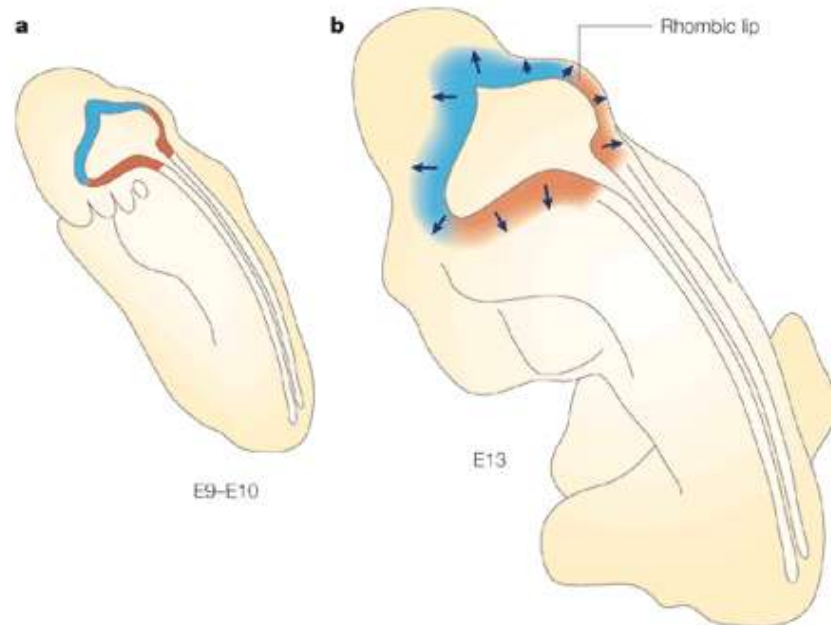


Figure 5.15 Granule neurone development in mice⁶

(a) At embryonic day (E) 9, the rhombic lip (blue and orange) is a zone of proliferation between the fourth ventricle and the neural tube. The cells in the blue region give rise to the cerebellar granule neurons and pontine nucleus, whereas cells in the red region yield other rhombic lip derivatives such as the inferior olivary nucleus. (b) At about E13, cells from the rhombic lip migrate outwards to populate the cerebellar anlage.

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De-regulation of the Wnt/ β -catenin pathway has been documented for tumours of the CNS (**Table 1.5**). Previous reports have documented that constitutive activation of the Wnt/ β -catenin pathway in SVZ neural stem cells was not sufficient to elicit tumours (Fults *et al.*, 2002; Momota *et al.*, 2008). However, the latest time point in these studies was three months. Jacques *et al.* showed that conditional inactivation of two or even three tumour suppressor genes in the SVZ results in brain tumours after up to eight months (Jacques *et al.*, 2010). Therefore, constitutive activation of the Wnt/ β -catenin pathway may still promote tumourigenesis in the long-term. To assess this, β -catenin^{lox(ex3)/wt} mice were injected with Adenovirus-Cre into the lateral ventricles, where the SVZ is located. This experiment is currently ongoing. However, a cohort of mice was culled for analysis 100 days post-infection. Encouragingly, these mice showed abnormal enlargements in the SVZ. Immunohistochemical staining of these growths for GFAP, BrdU and synaptophysin (SYP) indentified two cell populations. The first population consisted of GFAP+/SYP-/BrdU+ cells, which correspond with markers expressed by type B neuronal stem cells. The second population consisted of GFAP-/SYP-/BrdU- cells, which do not match with markers for either type C transit-amplifying cells or type A neuroblasts. Hence, these preliminary results presented here suggest that activation of the Wnt/ β -catenin pathway in the SVZ promotes neural stem cell expansion *in vivo*. However, one year post injection the mice did not develop any tumours (Brandner, S, private communication).

5.4 Summary

Expression of β -catenin ^{Δ ex3} in NSCs does not significantly increase growth or self-renewal potential *in vitro*. This may be attributed to β -catenin ^{Δ ex3} not translocating into the nucleus. However, more data is needed to confirm this result. However, mice, which expressed β -catenin ^{Δ ex3} under the control of the En2 promoter, had a developmental defect in the area corresponding to embryonal Cre expression, which later becomes the cerebellar vermis. Finally, activation of dominant active β -catenin^{lox(ex3)/wt} mice in the stem/progenitor cell compartment of the SVZ in the lateral ventricles resulted in small hyperplasias, but no neoplastic lesions in the SVZ. Experiments are ongoing to assess the collaboration with other oncogenic signals, such as p53 or RB pathway inactivation.

6 Conclusion and future work

6.1 Summary

To study the role of the Wnt/ β -catenin pathway in the CNS, we generated transgenic mice that conditionally express degradation-resistant β -catenin (Δ GSK- β -catenin). However, as described in chapter 3 and 4, Δ GSK- β -catenin expression in developing and the adult CNS did not result in detectable developmental abnormalities (with or without p53 expression). *In vitro* expression of Δ GSK- β -catenin did not alter the proliferation or self-renewal of adult NSCs. Similarly, additional deletion of the tumour suppressor genes Tp53 or Rb did not convincingly alter the proliferation or self-renewal of these cells. To directly recombine the SVZ neural stem cells, Δ GSK- β -catenin; p53^{loxP/loxP} mice were injected with Adeno-Cre into the lateral ventricles. Nonetheless, no mice were found to have developed hyperplasias or tumours as late as one year after intraventricular injection. The most plausible explanation for the absence of a phenotype is that the expression levels of Δ GSK- β -catenin might have been insufficient to elicit an effect. However, this hypothesis has not been confirmed experimentally. Instead, we obtained an alternative transgenic mouse model for expressing degradation-resistant β -catenin; these were β -catenin^{lox(ex3)/wt} transgenic mice. Expression of β -catenin ^{Δ ex3} in NSCs did not significantly alter growth or self-renewal. This may be attributed to β -catenin ^{Δ ex3} not translocating into the nucleus. However, more data is needed to confirm this result. *In vivo*, no Nestin-cre; β -catenin ^{Δ ex3} were born as expected, whilst mice expressing β -catenin ^{Δ ex3} under the control of the En2 promoter survived to term. These mice showed severe cerebellar vermis abnormalities. The cause for this phenotype was not determined in this study as time did not permit. However, existing literature suggests that constitutive activation of the Wnt/ β -catenin pathway during early development can cause severe apoptosis of neuronal crest derived cells. Finally, β -catenin^{lox(ex3)/wt} mice injected with Adeno-Cre into the lateral ventricles developed growths in the SVZ one hundred days post-injection. These growths did not appear to be highly proliferative, but there are mice available for analysis at later time-points.

6.2 Future work

6.3 Synergism between Wnt/ β -catenin, p53, PTEN and Rb pathways in CNS tumours

One of the goals of this study was to investigate the synergism between the Wnt/ β -catenin pathway and the p53, Rb and PTEN pathway in brain tumourigenesis. However, due to complications with the Δ GSK- β -catenin mice this was not achieved. Therefore, the alternative mouse model, β -catenin^{lox(ex3)/wt}, should be used to ascertain the role of the abovementioned pathways in tumourigenesis.

6.3.1 TP53, PTEN and RB in gliomas

Astrocytic gliomas progress from low-grade diffuse astrocytomas (WHO grade II) to anaplastic astrocytomas (WHO grade III) and subsequently to (secondary) glioblastomas (WHO grade IV). TP53 is mutated in more than 60 % of diffuse astrocytomas (Okamoto *et al.*, 2004; Reifenberger *et al.*, 1996; Watanabe *et al.*, 1996). The frequency of these mutations does not change during tumour progression, which suggests that TP53 mutations are important for tumourigenesis (Sidransky *et al.*, 1992; von *et al.*, 1992; Watanabe *et al.*, 1996; Watanabe *et al.*, 1997).

The RB1 gene encodes the retinoblastoma protein, which plays a crucial role in G1 to S phase transition during proliferation (Weinberg, 1995). The RB1 gene is found at chromosome 13q, which is lost in 12 % of primary and 38 % of secondary glioblastomas (Nakamura *et al.*, 2000). Additionally, promoter hypermethylation occurs in 12 % of primary and 43 % of secondary glioblastomas (Nakamura *et al.*, 2001a). Interestingly, de-regulation of the Rb pathway also occurs in anaplastic astrocytomas (Reifenberger *et al.*, 1994; Schmidt *et al.*, 1994). These findings suggest that the pathway is important for progression from diffuse astrocytomas to anaplastic astrocytomas.

PTEN is a tumour suppressor that antagonises the phosphatidylinositol-3-kinase (PI3K) pathway (Maehama and Dixon, 1998). Loss of chromosome 10q, where PTEN is located, occurs in 70 % of glioblastomas (Ohgaki *et al.*, 2004). This incidence is similar between primary and secondary glioblastomas (Tohma *et al.*, 1998). Loss of chromosome 10q is infrequent in low grade gliomas, but has been reported in 35 % to 60 % of anaplastic astrocytomas, suggesting a role in progression (Balesaria *et al.*, 1999; Bigner and Vogelstein, 1990; Ichimura *et al.*, 1998; James *et al.*, 1988).

β -catenin is rarely mutated in gliomas (Gotze *et al.*, 2009). However, β -catenin, TCF4, LEF1, c-myc and cyclin D1 expression increases with glioma malignancy grade (Sareddy *et al.*, 2009b). This effect may be partially attributed to an increase in promoter hypermethylation of Wnt antagonists (Gotze *et al.*, 2009). Similarly, Wnt antagonist promoter hypermethylation is common in secondary glioblastomas (Gotze *et al.*, 2009). These results suggest that activation of the Wnt/ β -catenin pathway may be involved in both glioma progression and spontaneous development of primary glioblastomas.

In summary, aberrations in the p53 pathway are vital for glioma tumourigenesis. On the other hand mutations in the PTEN, Rb and Wnt/ β -catenin pathways also seem to play a role in tumour progression. Taking these findings into account, it is unlikely that β -catenin^{lox(ex3)/wt}; Rb^{loxP/loxP} or β -catenin^{lox(ex3)/wt}; PTEN^{loxP/loxP} mice will develop gliomas. However, β -catenin^{lox(ex3)/wt}; p53^{loxP/loxP} mice might develop gliomas, which would shed some light into the role of the Wnt/ β -catenin pathway in these tumours.

Finally, p53^{loxP/loxP}; Rb^{loxP/loxP} and p53^{loxP/loxP}; PNET^{loxP/loxP} mice develop PTEN-like and glioma-like tumours (Jacques *et al.*, 2010). Therefore it would be interesting to determine how the expression of β -catenin ^{Δ ex3} may influence the tumour phenotype of these mice.

6.3.2 TP53, PTEN and RB in medulloblastomas

TP53 mutations are rare in medulloblastomas (5-10 %), but if present are associated with poor prognosis (Adesina *et al.*, 1994; Alderson *et al.*, 1996; Ohgaki *et al.*, 1993) (Tabori *et al.*, 2010). Additionally, the p53 pathway is altered by alternative mechanisms in up to 21 % of medulloblastomas (Frank *et al.*, 2004). Interestingly, mice null for double-strand break repair genes and p53 develop medulloblastomas (Frappart *et al.*, 2009; Yan *et al.*, 2006). These tumours often acquire mutations in components of the Shh pathway (Frappart *et al.*, 2009; Yan *et al.*, 2006). This is relevant since mutations in the Wnt and Shh pathways are mutually exclusive events in medulloblastoma (Thompson *et al.*, 2006). This suggests that mutations in the p53 pathway may not correlate with medulloblastomas with Wnt/ β -catenin pathway deregulation. Hence, β -catenin^{lox(ex3)/wt}; p53^{loxP/loxP} mice may not be biologically relevant for modelling medulloblastomas.

PTEN mutations are also rare in medulloblastomas (Rasheed *et al.*, 1997). However, loss of 10q is found in 18 % to 42 % of medulloblastoma cases (Avet-Loiseau *et al.*, 1999; Gilhuis *et al.*, 2000; Mendrzyk *et al.*, 2005; Reardon *et al.*, 1997; Shlomit *et al.*, 2000). Furthermore, PTEN promoter hypermethylation can be detected in 50 % of medulloblastomas (5/10 cases investigated) (Hartmann *et al.*, 2006).

No mutations in the RB gene have been detected in medulloblastomas (Lee *et al.*, 1987). However, mice with conditional deletions of Rb and p53 in GFAP-expressing cells develop tumours with medulloblastoma features and combined inactivation of Rb and p53 in SVZ stem/progenitor cells give rise to PNETs, which are histologically similar to medulloblastomas (Jacques *et al.*, 2010; Marino *et al.*, 2000). Hence, de-regulation of the Rb pathway may play a role in medulloblastoma development.

As discussed in chapter 1, activation of the Wnt/ β -catenin pathway has been reported in around 23 % of medulloblastomas (**Table 1.5**). Interestingly, medulloblastomas with nuclear β -catenin immunoreactivity tend to:

1. Have β -catenin mutations (92 %, 23/25)
2. Have lost of a copy of chromosome 6 (70 %, 14/20)
3. Show few other chromosomal abnormalities
4. Show histological features of classical medulloblastomas (85 %, 40/47)

(Clifford *et al.*, 2006; Ellison *et al.*, 2005; Thompson *et al.*, 2006). This suggests that loss of chromosome 10 and 13, which are associated with PTEN and Rb loss, does not correlate with the Wnt/ β -catenin pathway in medulloblastomas. However, genes lost on chromosome 6 may be involved in the p53, PTEN or Rb pathway. Hence, β -catenin^{lox(ex3)/wt}; Rb^{loxP/loxP} or β -catenin^{lox(ex3)/wt}; PTEN^{loxP/loxP} or β -catenin^{lox(ex3)/wt}; p53^{loxP/loxP} mice might develop medulloblastomas.

6.3.3 Tumour suppressor genes on chromosome 6

Full or partial loss of chromosome 6 has been reported for other types of cancer, including breast cancer, lymphomas and melanomas (Noviello *et al.*, 1996; Offit *et al.*, 1993; Trent *et al.*, 1983). This suggests that important tumour suppressor genes are present on this chromosome. In support of this argument, microcell-mediated transfer of chromosome 6 into the breast cancer cell line MDA-MB-231, resulted in reduced *in vitro* invasion and tumourigenic potential (Theile *et al.*, 1996). Some tumour suppressor genes located on chromosome 6 are summarised in (Table 6.1).

Table 6.1 Selection of tumour suppressor genes located on the human chromosome 6

Human gene	Abbreviation	Chromosomal position
Cyclin-dependent kinase inhibitor 1A	CDKN1A	6p21.2
Nucleolar protein 7	NOL7	6p23
Absent in melanoma 1	AIM1	6q21
Cyclin C	CCNC	6q21
Protein tyrosine phosphatase, receptor type K	PTPRK	6q22.33
Pleiomorphic Adenoma gene-like 1	PLAGL1	6q24.2
SAM and SH3 domain containing 1	SASH1	6q24.3
Large tumour suppressor, <i>Drosophila</i> homolog 1	LATS1	6q25.1

Of the genes listed in Table 6.1, LATS1 and PLAGL1 are of particular interest. LATS1 is the human homolog of *Drosophila* warts (wts), a member of the Hippo pathway (Justice *et al.*, 1995). In *Drosophila*, the Hippo pathway inhibits cell proliferation and promotes proliferation by inhibiting Yorkie (Yki) (Huang *et al.*, 2005). The mammalian homolog of Yki is Yes-associated protein 1 (YAP1), which is phosphorylated and inhibited by LATS1 (Dong *et al.*, 2007; Oh and Irvine, 2009). Interestingly, YAP1 is up-regulated in medulloblastomas with an active Wnt/ β -catenin pathway (Fernandez *et al.*, 2009). This suggests that de-regulation of the Hippo pathway may be an important event in medulloblastomas with Wnt/ β -catenin pathway activation. The Hippo pathway partly regulates proliferation by negatively regulating the Wnt/ β -catenin pathway. Small interfering RNA knockdown of LATS1 in a human embryonal kidney cell line (HEK293T) increased the Wnt3a-dependent expression of AXIN2 and enhanced the luciferase expression of the TOPflash Wnt/ β -catenin pathway reporter plasmid (Varelas *et al.*, 2010). Interestingly, TEA domain 1 (TEAD1), the major transcriptional partner of YAP1, is also up-regulated in medulloblastomas (Fernandez *et al.*, 2009; Zhao *et al.*, 2008). TEAD1 is negatively regulated by p38 α MAPK, which is located on chromosome 6 (Ambrosino *et al.*,

2006). Therefore, deregulating the Hippo pathway seems an attractive target for studying Wnt/ β -catenin medulloblastomas.

PLAGL1 is a member of the novel subfamily of zinc-finger transcription factors, consisting of PLAG1, PLAGL1 and PLAGL2. PLAGL1 has been shown to induce apoptosis and G1 arrest, in a manner similar to p53 (Spengler *et al.*, 1997). Subsequently, it was found that PLAGL1 could directly bind to p53 and significantly enhance the expression of p53-responsive genes (Huang *et al.*, 2001). This effect was not observed in the absence of p53, suggesting that PLAGL1 is a transcriptional co-factor of p53 (Huang *et al.*, 2001). In the cerebellum, PLAGL1 expression was detected in the external granule layer from postnatal (P) day 2 to 7 (Ciani *et al.*, 2003). Nuclear PLAGL1 was also detected in Purkinje cells at P7 (Ciani *et al.*, 2003). In the adult cerebellum, PLAGL1 expression is low and primarily found in Purkinje cells (Ciani *et al.*, 2003). Interestingly, PLAGL1 expression co-localises with neuronal stem cell markers (Nestin, GFAP, proliferating cell nuclear antigen [PCNA] and BrdU) during CNS development (Valente *et al.*, 2005). Furthermore, promoting PLAGL1 expression by raising cyclic Adenosine monophosphate (cAMP) decreased BrdU incorporation in cerebellar granule neurons (Contestabile *et al.*, 2005). These results suggest that PLAGL1 has a key role in controlling neuronal stem cell proliferation. The PLAGL1 gene is paternally imprinted in mice and humans (Kamiya *et al.*, 2000; Smith *et al.*, 2002). This means that PLAGL1 is only expressed from the paternal chromosome 6. Medulloblastomas with Wnt/ β -catenin pathway activation tend to lose one copy of chromosome 6. It would be interesting to assess if this is the copy of chromosome 6 that is lost in these tumours.

No conditional knockout mouse models have been published for either of these genes. Once they have been generated, it will be interesting to cross them with β -catenin^{lox(ex3)/wt} mice to determine if they can synergistically promote medulloblastoma development.

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