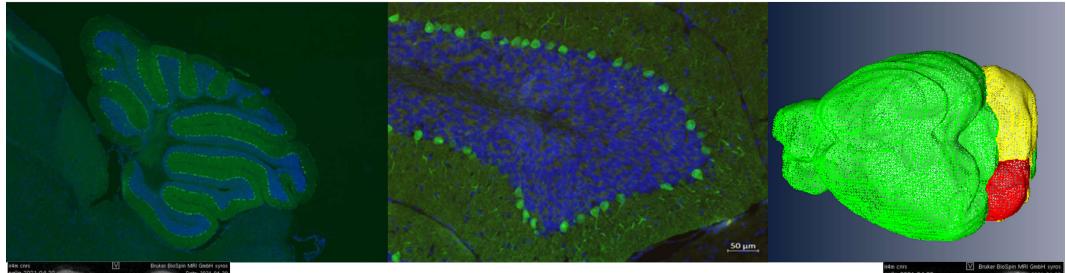
Team: "Signaling and Cancer Progression"





Celio Pouponnot Team: Signaling and Cancer progression Institut Curie ORSAY UMR3347 CNRS/U1021 INSERM/ UPSaclay









universite PARIS-SACLAY

FACULTÉ DES SCIENCES D'ORSAY



Medulloblastoma: an abnormal identity drives cancer progression

Institut Curie
UMR3347 CNRS/U1021 INSERM







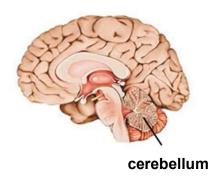


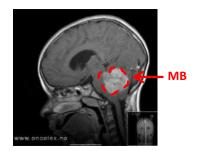
FONDATION DE FRANCE





Medulloblastoma (MB)





Pediatric tumor of the cerebellum (Median age 7 yrs)

Pediatric tumor

In general rare cancers

Represent 1 to 2% of the cancers in total



.

In general rare cancers

Represent 1 to 2% of the cancers in total

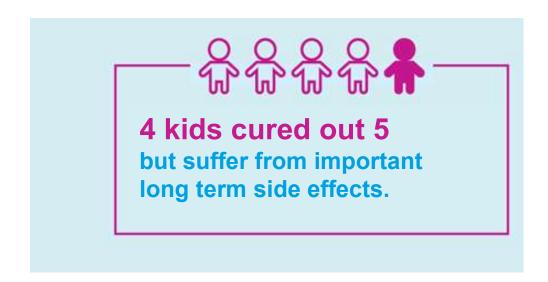


In industrialized countries, represents 2nd cause of mortality betwen 1 to 15 y

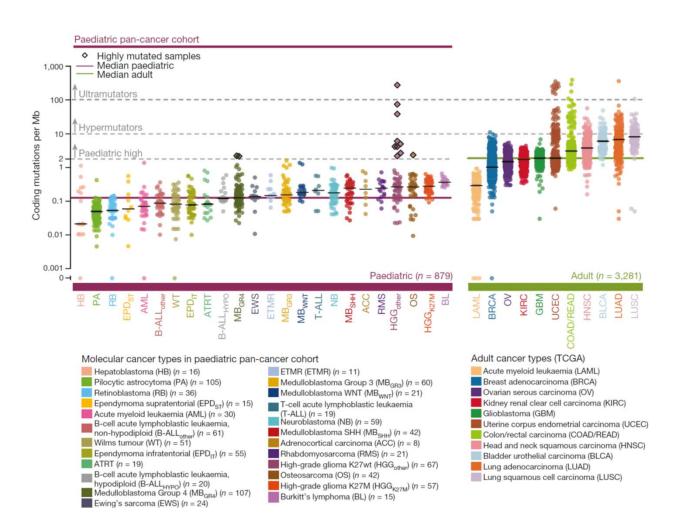
(Less than 1% of death between 0 and 1 year but 20 % between 1 and 14 years)

- 75-80% Cured
 - Better than for adult cancers. But some cancer are of high risk

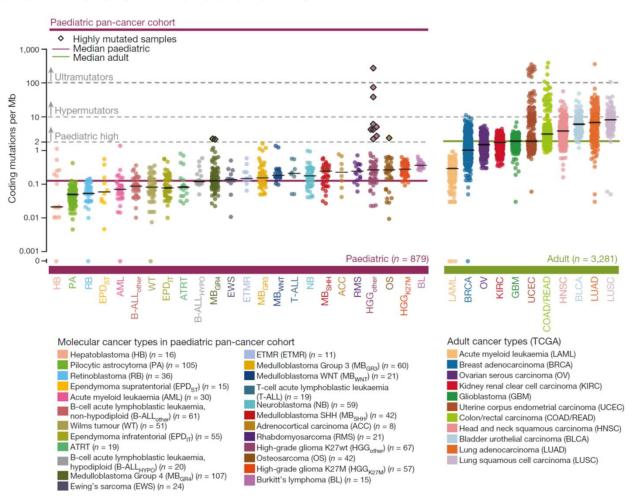
- 75-80% Cured
 - Better than for adult cancers.
 - BUT very important side effects affecting adult life



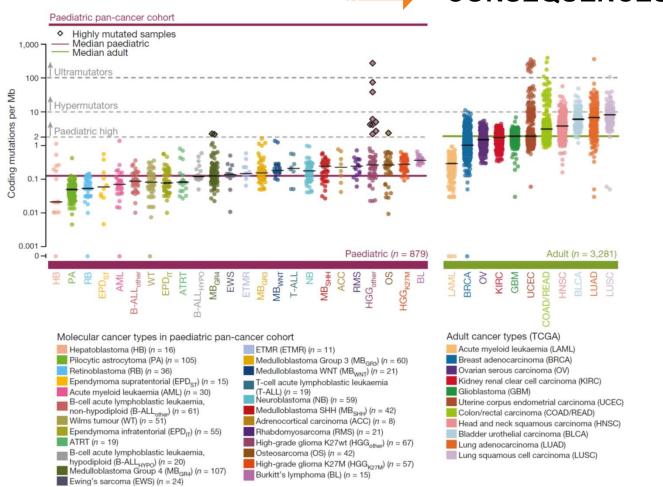
- 75-80% Cured
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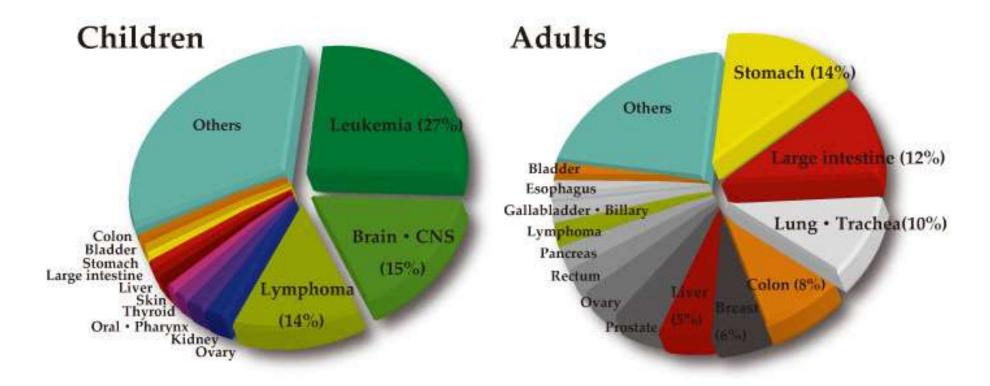
- 75-80% Cured
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 - Important side effects
 - Much less mutations



- 75-80% Cured
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 - Important side effects
 - Much less mutations | consequences?



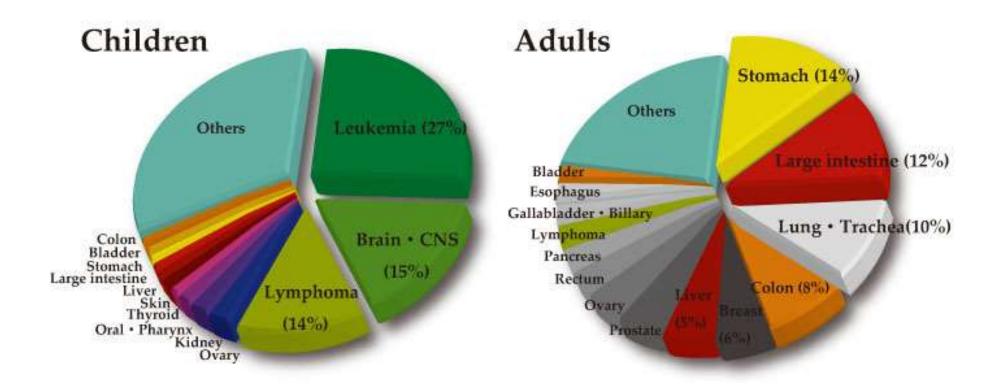
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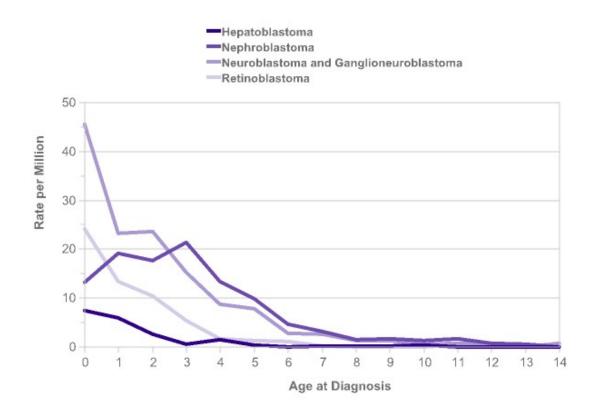
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Different spectrum



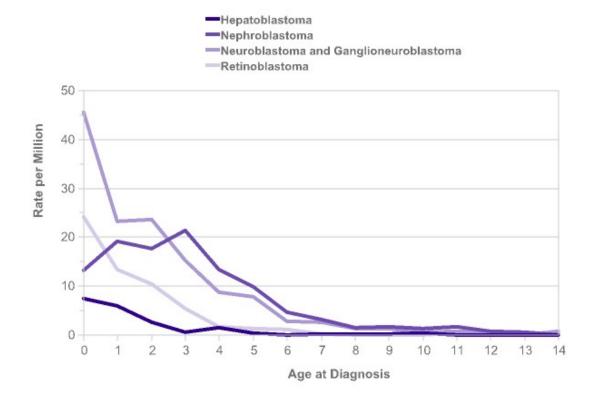
- 75-80% Cured
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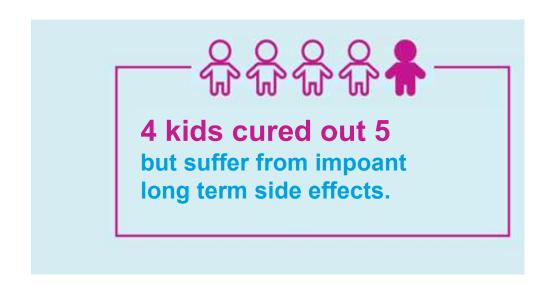
In general rare cancers

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- In a defined window of time



- 75-80% Cured
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In general rare cancers

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How to explain these differences?

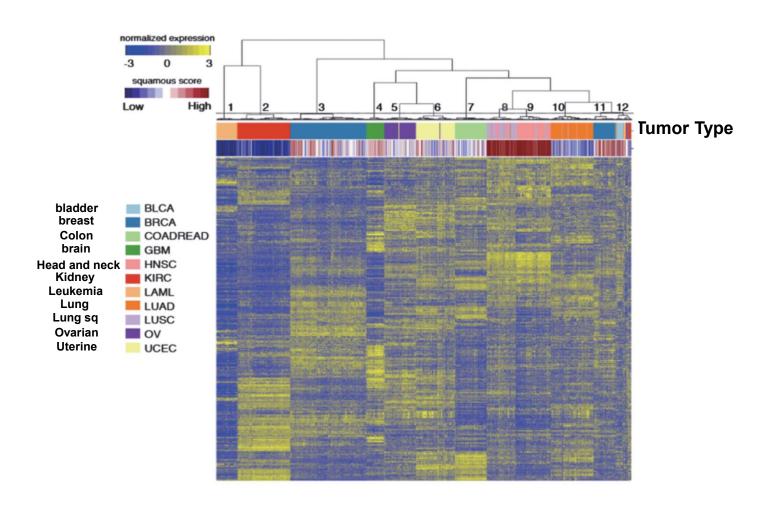
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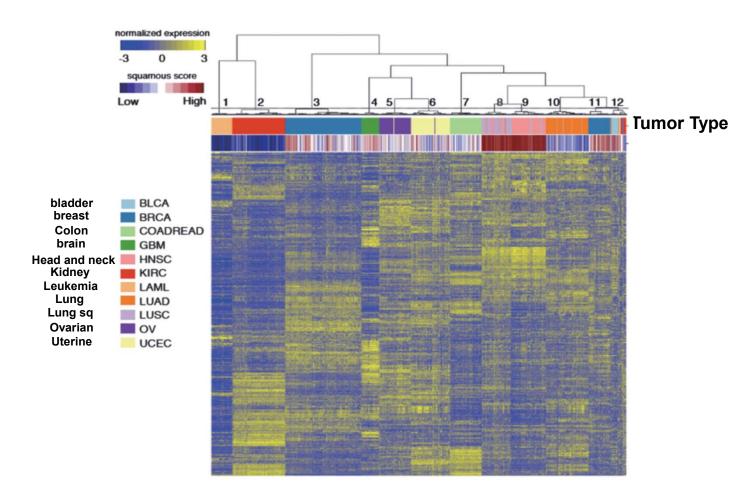


How to explain these differences? (tissue context and cell of origin)

Cancers of different locations



Cancers of different locations

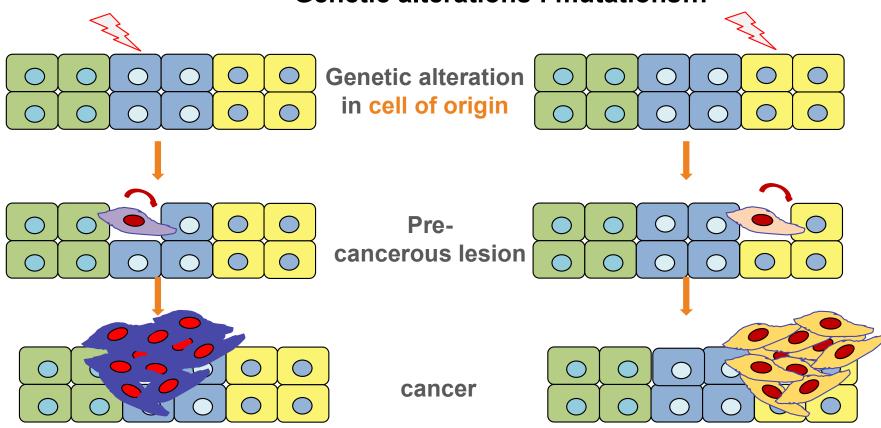


Cancers of a given location cluster together at their transcriptomic level (express similar genes that are representative/specific of the tissue where the tumour develops

Specific lineage markers/cell identity define a tumor type

Tumor progression





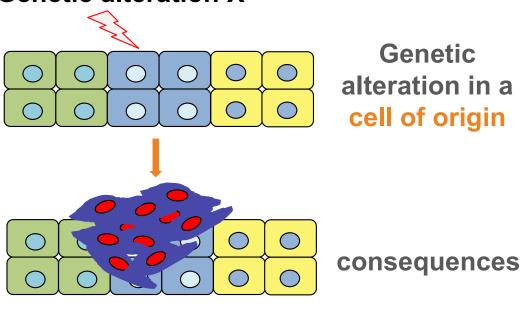
Cell of origin: Identify in which cell the first genetic lesion arises and promotes an pre-cancerous lesion.

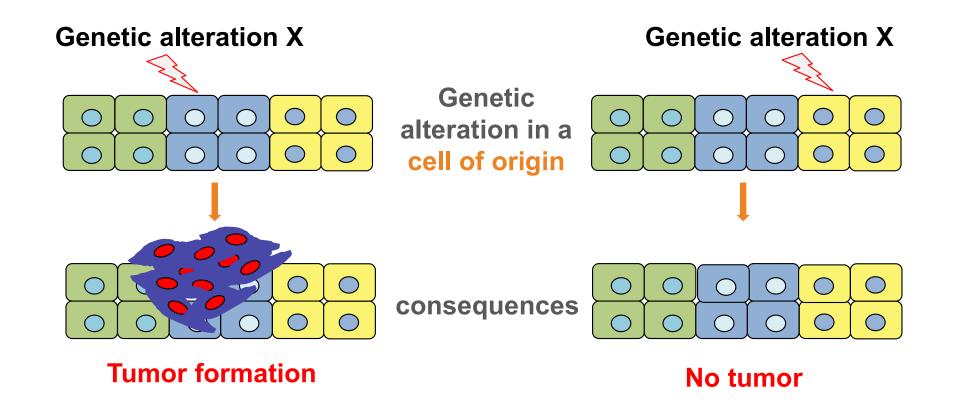
-cell identity and lineage-

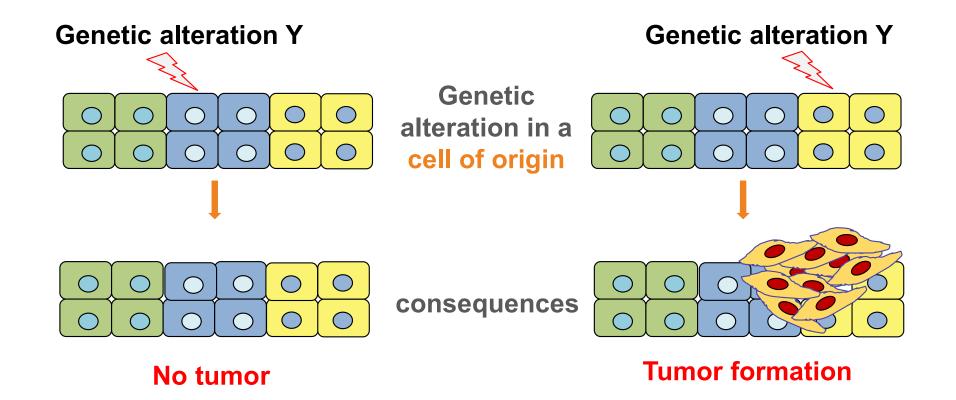


Genetic alteration X

Tumor formation







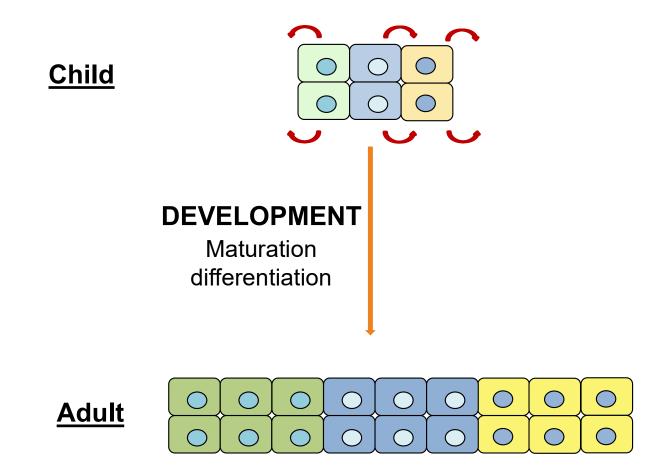
Pediatric cancer:

<u>Child</u> vs <u>Adult</u>

Pediatric cancers arise in a developing tissue

Pediatric cancer:

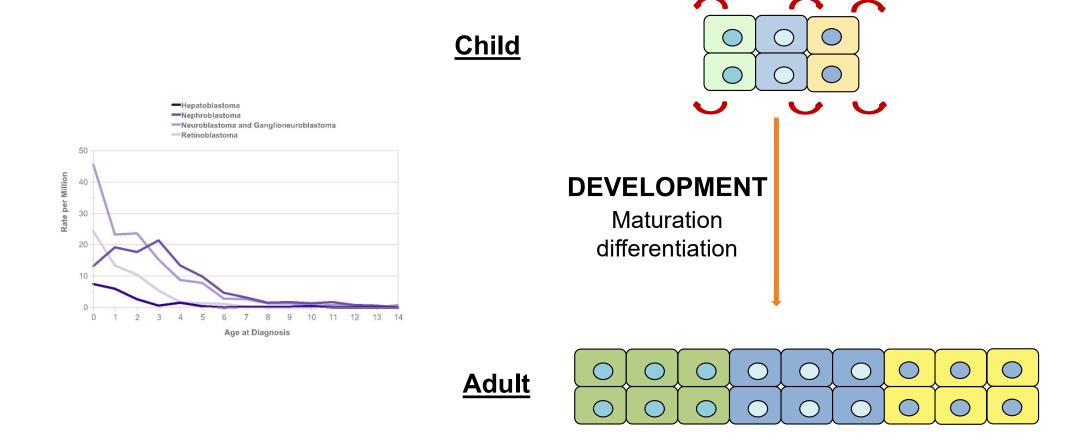
Genetic alteration during development



Pediatric cancers arise in a developing tissue

Pediatric cancer:

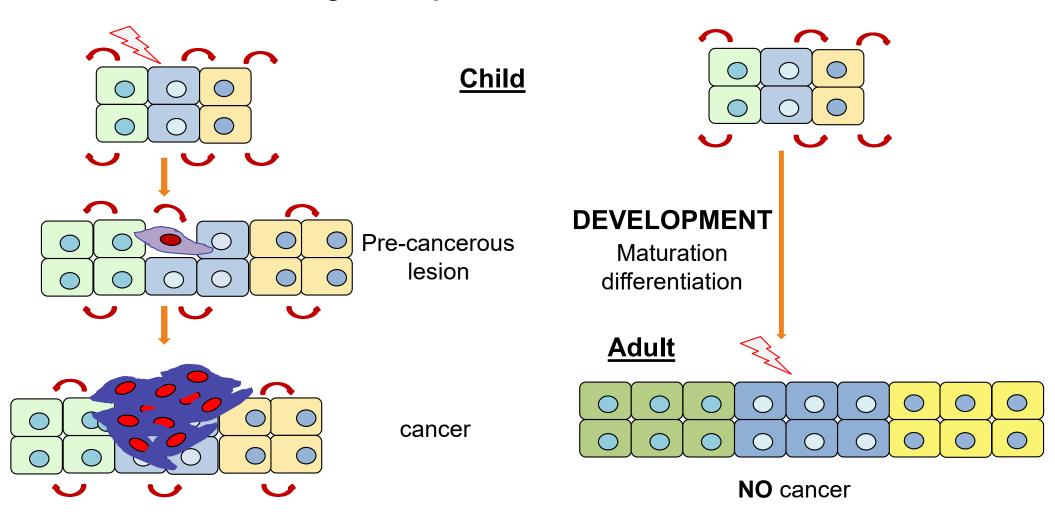
Genetic alteration during development



Pediatric cancers arise in a developing tissue

Pediatric cancer:

Genetic alteration during development

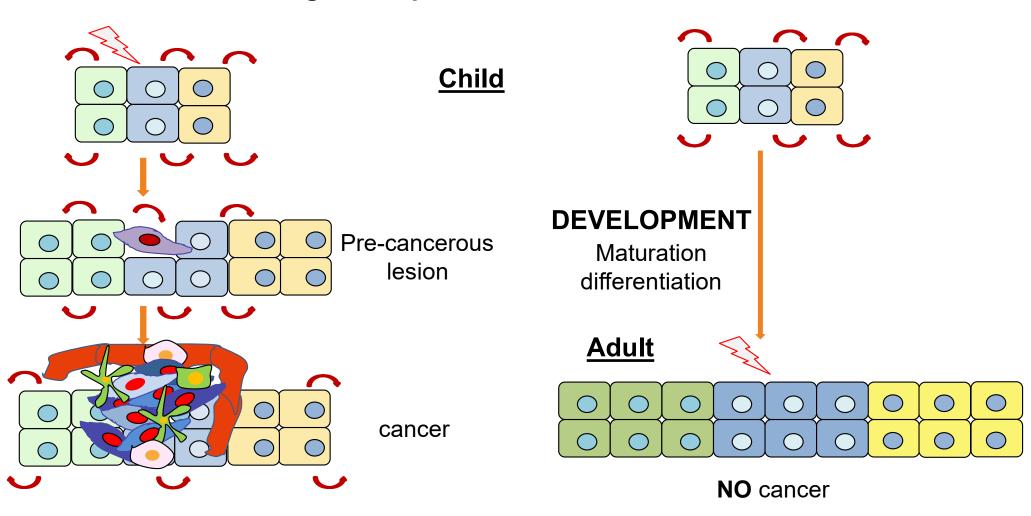


Cell of origin can explain some specificities of pediatric cancers, present in a defined window of time – not present in adult (spectrum)

Pediatric cancers arise in a developing tissue

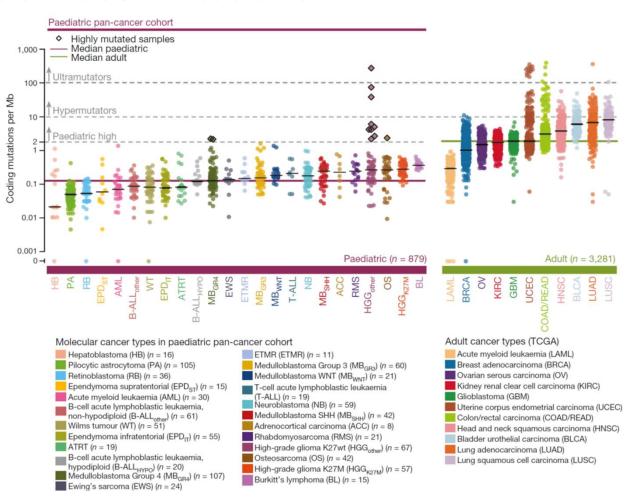
Pediatric cancer:

Genetic alteration during development



Cell of origin can explain some specificities of pediatric cancers, present in a defined window of time – not present in adult (spectrum)

- 75-80% Cured
 - Better than for adult cancers.
 - Important side effects
 - Much less mutations ????



Highly mutated samples
 Median paediatric
 Median adult

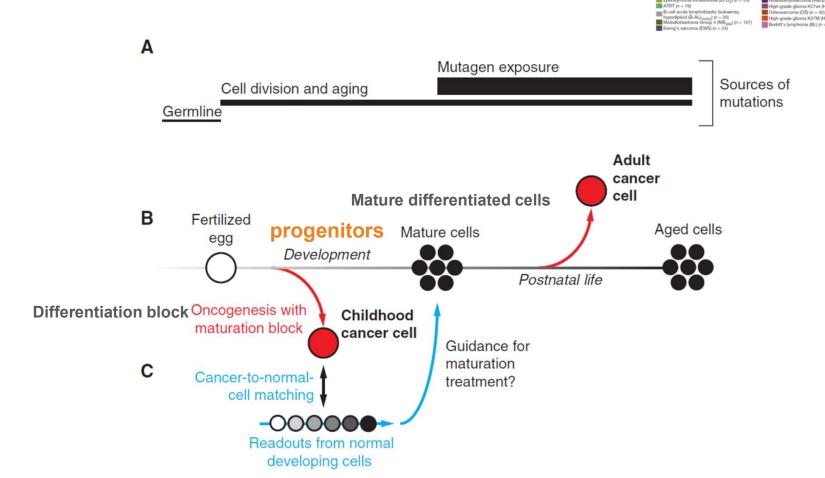
Hepatoblastoma (HB) (n = 16)
Pilocytic astrocytoma (PA) (n = 105)
Retinoblastoma (RB) (n = 36)
Ependymoma supratentorial (EPD_{S1}) (n = 15)

ETMR (ETMR) (n = 11)

Acute myeloid leukaemia (LAML

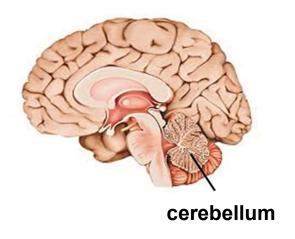
Kidney renal clear cell carcinoma (KIRC)
Giolobastoma (BBM)
Uterine corpus endometrial carcinoma (UCE)
Colon/rectal carcinoma (COAD/READ)
Head and neck squamous carcinoma (PNSC)
Bladder urothelial carcinoma (BLCA)
Lung adenocarcinoma (LUAD)
Lung squamous cell carcinoma (LUSC)

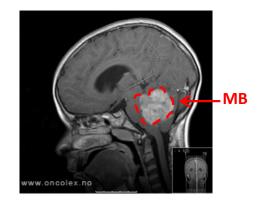
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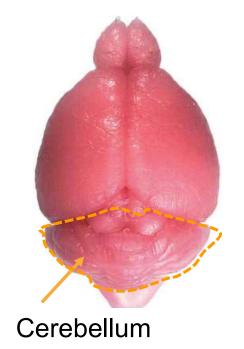
Medulloblastoma Pediatric tumor

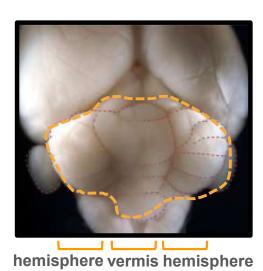
Medulloblastoma (MB)

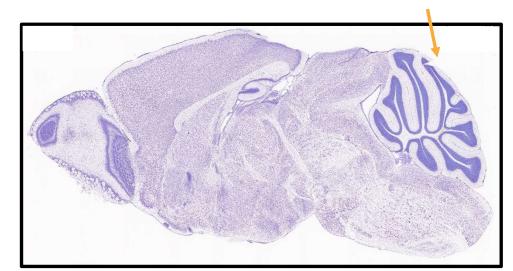




Pediatric tumor of the cerebellum (Median age 7 yrs)





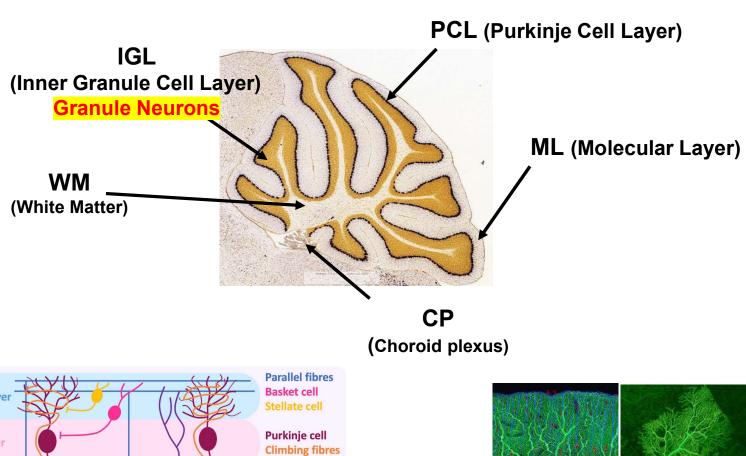


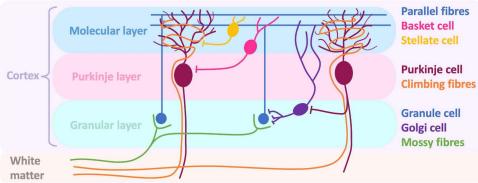
Cerebellum

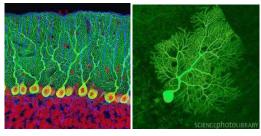
Controls:

Balance, posture Mouvement coordination Some learning functions

Foliated and Stratified structure: Composed of lobules and different layers



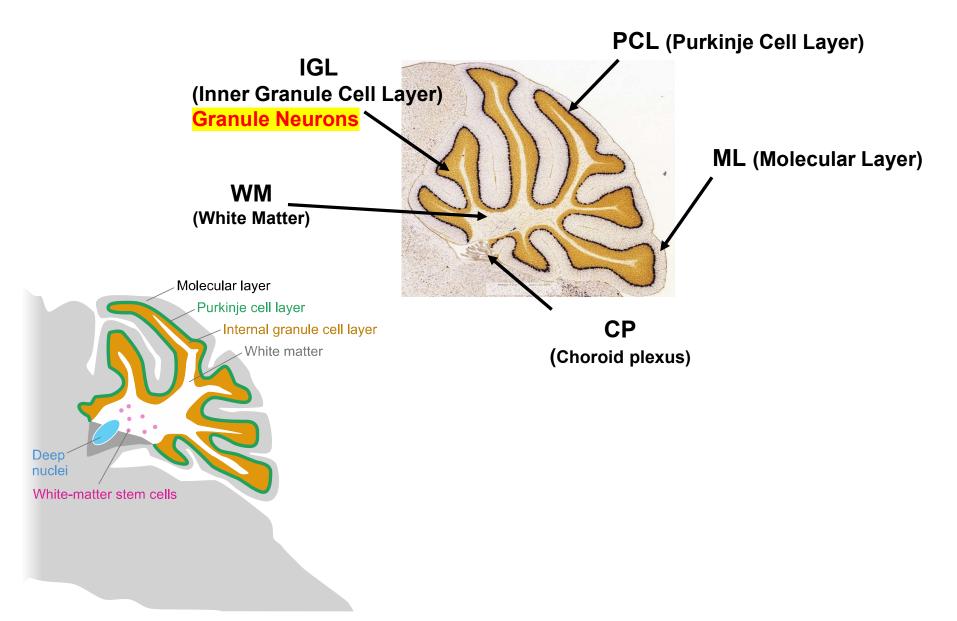




Purkinje cells



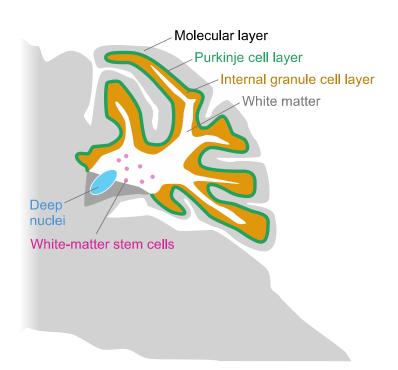
Foliated and Stratified structure: Composed of lobules and different layers



Mature cerebellum

Cell types

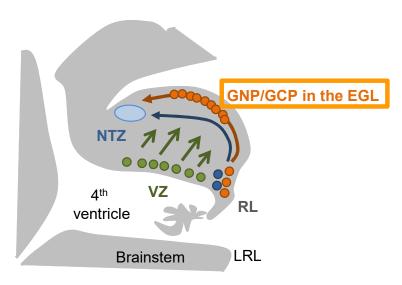
- Granule cells (GC)
- Purkinje cells (PC)
- 6 Interneurons



Developping cerebellum

Germinal zones

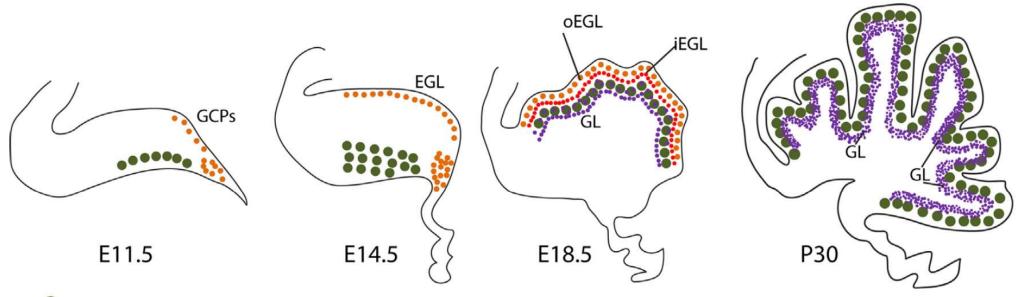
- Ventricular zone (VZ)
 - GABAergic neurons → PCs
- Rhombic Lip (RL)
 - Glutamatergic neurons → GCs



- GABAergic precursors (Purkinje cells and interneurons)
- Precursors of the deep nuclei (glutamatergic)
- Granule cell precursors (GCP or GNP)
 NTZ: nuclear transitory zone

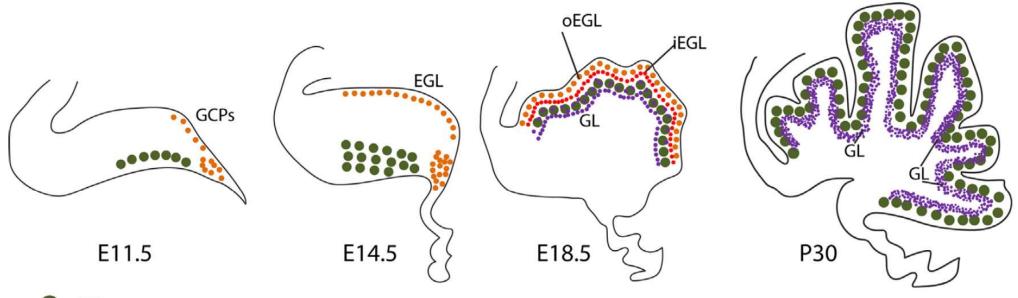
Cerebellar development

Focus on Granule neurons lineages



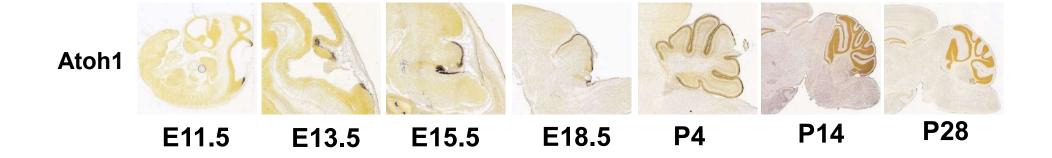
- PCs
- Outer EGL (E14.5 -E18.5)
- Inner EGL

Cerebellar development

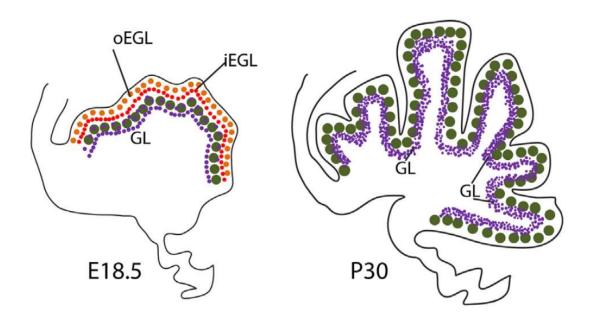


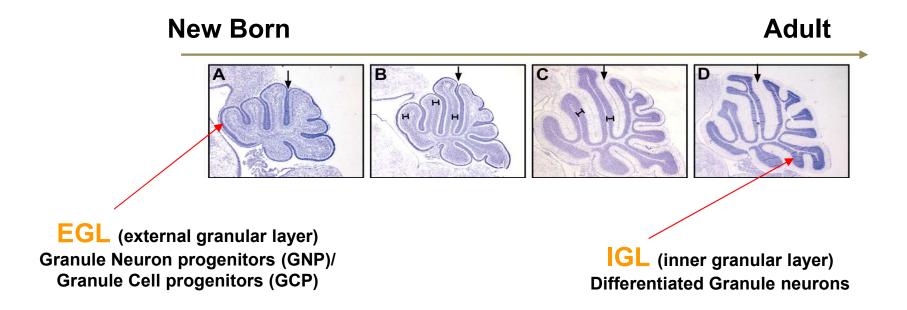
- PCs
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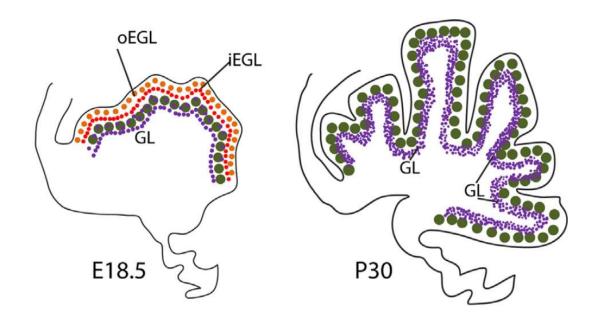
Atoh1 is a master regulator of the GCP

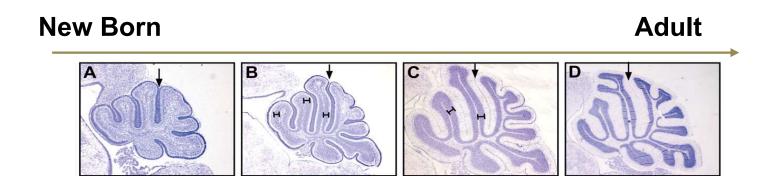


Late post-natal Cerebellar development



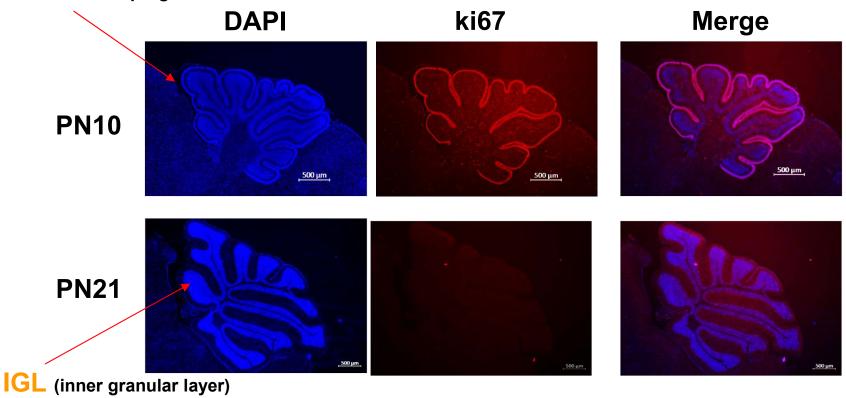


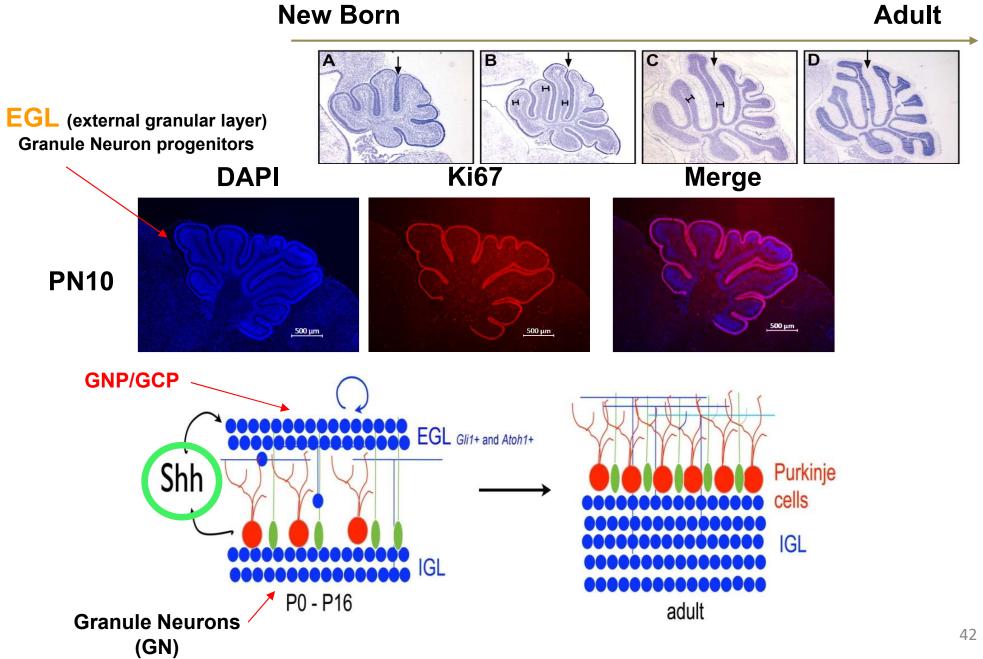


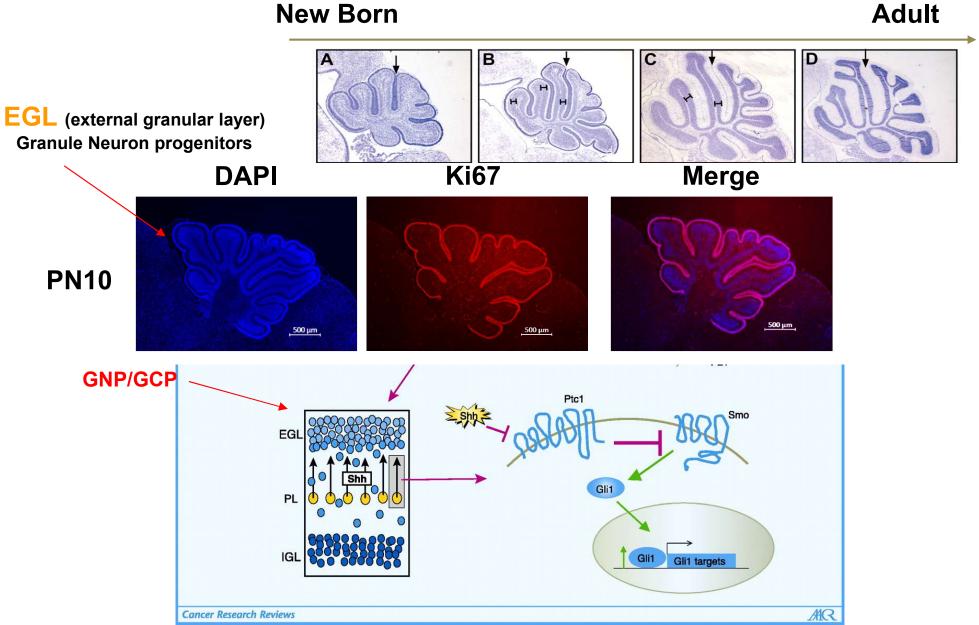


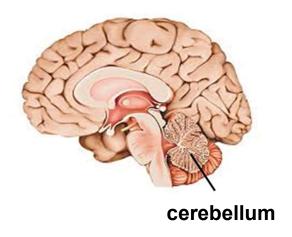
EGL (external granular layer)
Granule Neuron progenitors/GCP

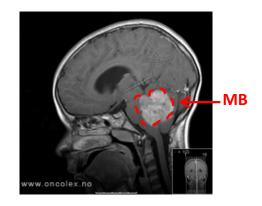
Differentiated Granule neurons



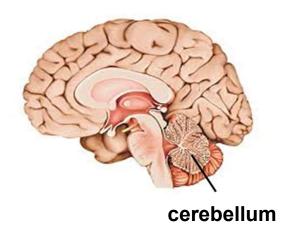


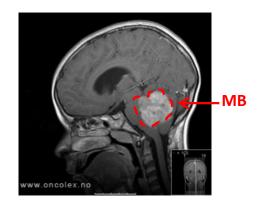






- Pediatric tumor of the cerebellum (Median age 7 yrs)
- Most frequent Malignant brain tumor of childhood (~150 cases/year in France)

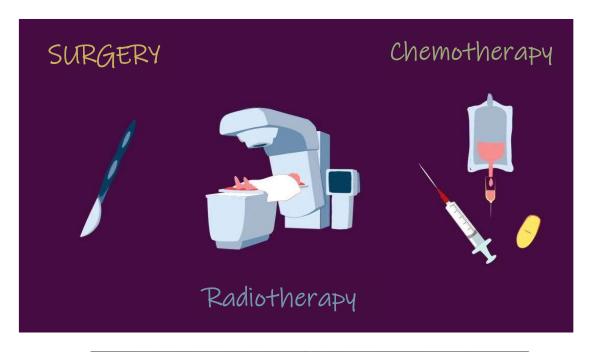




- Pediatric tumor of the cerebellum (Median age 7 yrs)
- Most frequent Malignant brain tumor of childhood (~150 cases/year in France)
- Treatment : surgery, chemotherapy, radiotherapy
 - →70-80% overall survival at 5 years
 - → Important secondary effects

Medulloblastoma Treatment

Current treatment: surgery, radiotherapy and chemotherapy





TREATMENT TOXICITY

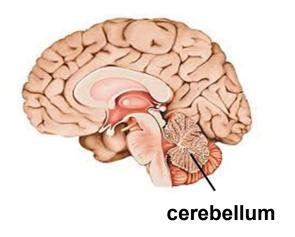
• ~80 % survivors after treatment

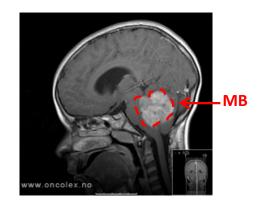
But

Very strong sequeala: TREATMENT TOXICITY

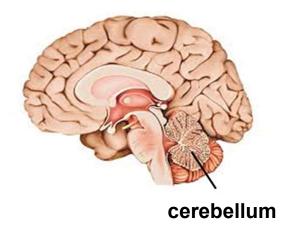
- Mutism
- Hearing deficit, Deafness
- Learning deficit (attention, memory deficit, mental retardation)
- Growth deficit, puberty
- Risk of secondary cancers
- Strong decrease in quality of life in the adult life (social dependency)

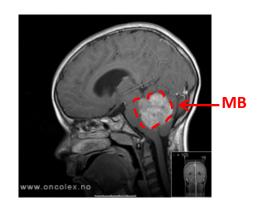
Decrease the secondary effects of therapy



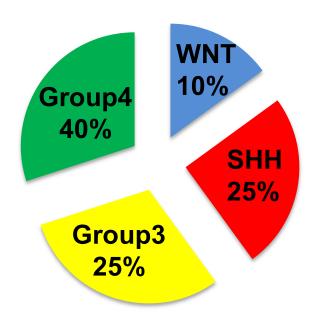


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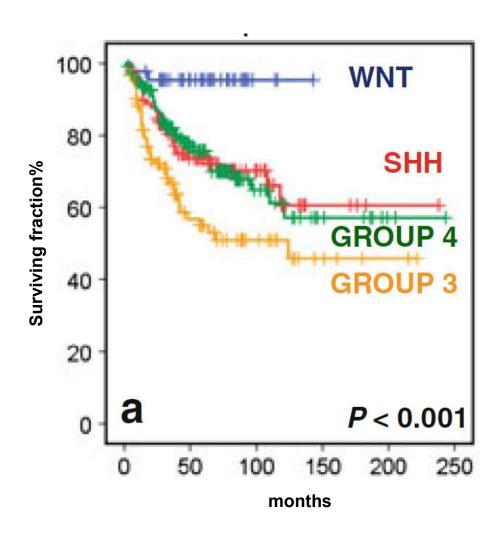




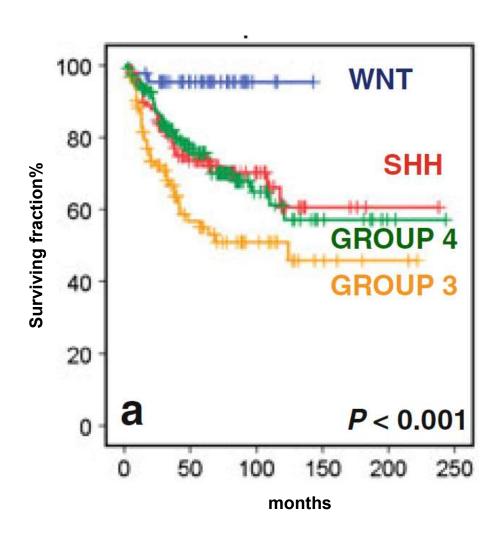
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The different groups of MB (prognostic)



The different groups of MB (prognostic)



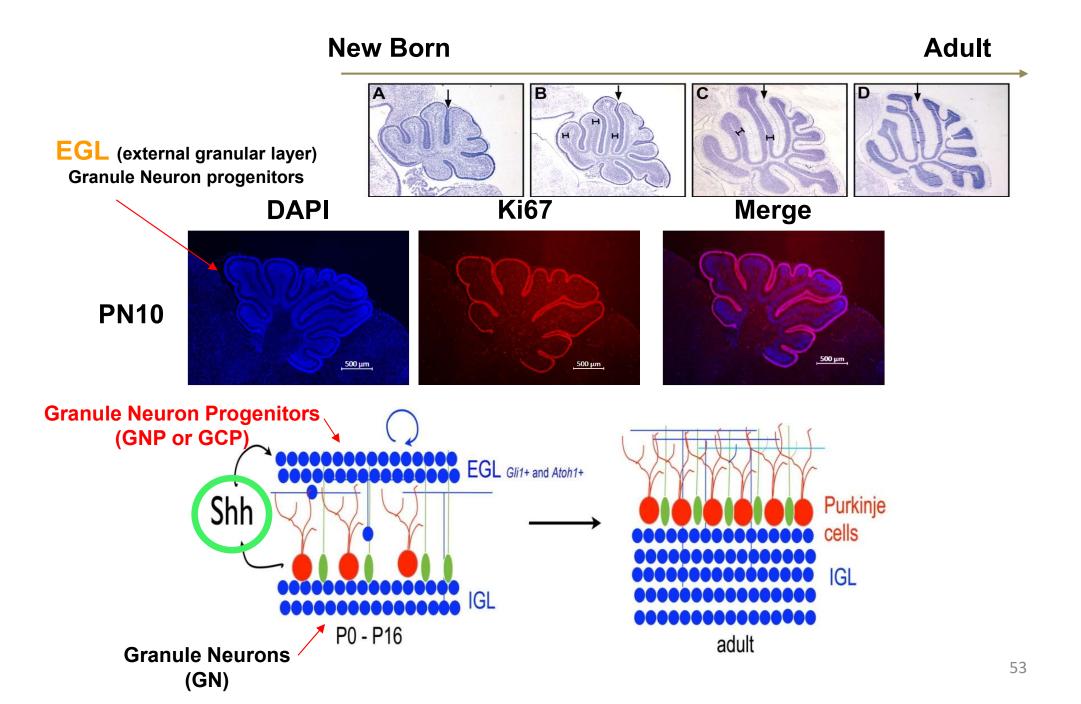


G3 has the worse prognosis

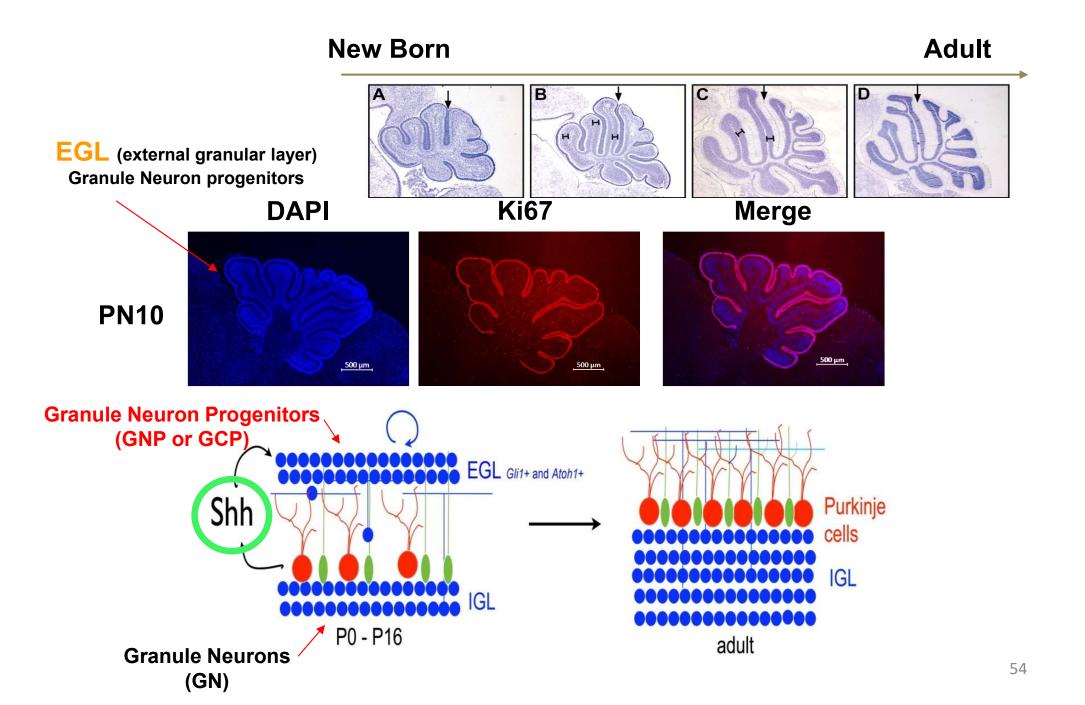
➤ Based on gene expression profile : 4 different molecular groups

MB subtype		WNT	SHH	3	4
Clinical features	Age distribution	1.0	0.5 Infant Childhood Adult	Infant Childhood Adult	1.0
	incidence	10%	25%	25%	40%
	histology	Classic (very rare LCA)	Classic > desmoplastic/ nodular> LCA	Classic>LCA	Classic; rarely LCA
	Metastasis at diagnosis	rare 5-10%	intermediate 15-20%	frequent 40-45%	frequent 35-40%
	Overall survival (5years)	Very good	Intermediate 75%	Bad 50%	intermediate
	Cell of origin	Lower rhombic lip precursor	?	Unknown	
Genomic features	Driver pathway/genes	WNT/βCAT CTNNB1 mutation	SHH PTCH1 mutation	MYC amplification OTX2 amplification	MYCN & CDK6 amplification
	Expression signature	WNT signaling	SHH signaling	MYC & GABAergic & photoreceptor signature	Neuronal & glutamatergic signature

Cell of origin SHH medulloblastoma



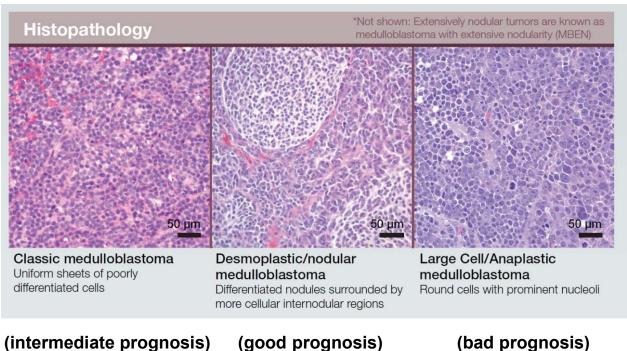
Are the GCP the cell of origin SHH medulloblastoma?



➤ Based on gene expression profile : 4 different molecular groups

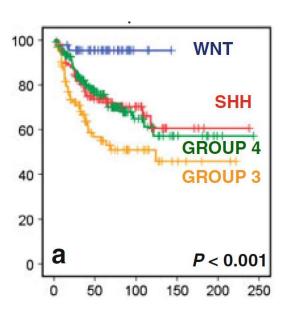
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	Cell of origin	Lower rhombic lip precursor	Granular cell progenitor	Unknown	
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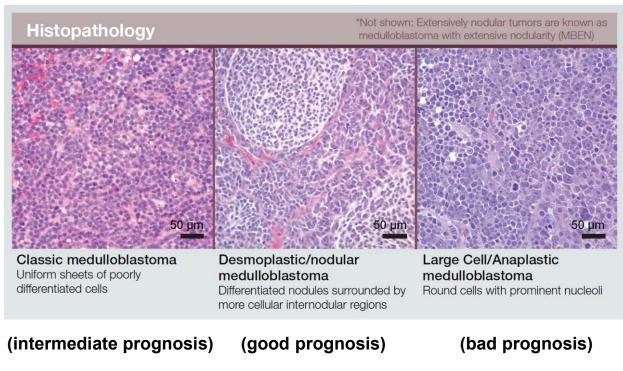
Histological classification



(intermediate prognosis) (good prognosis)

Histological classification



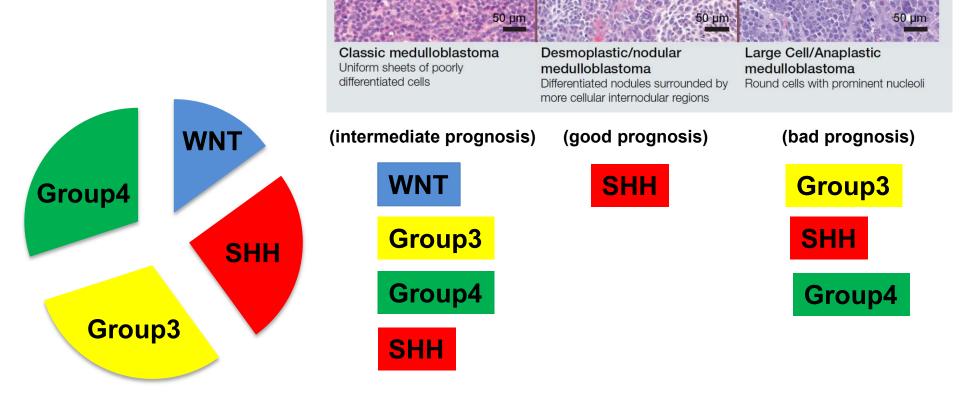


Histopathology

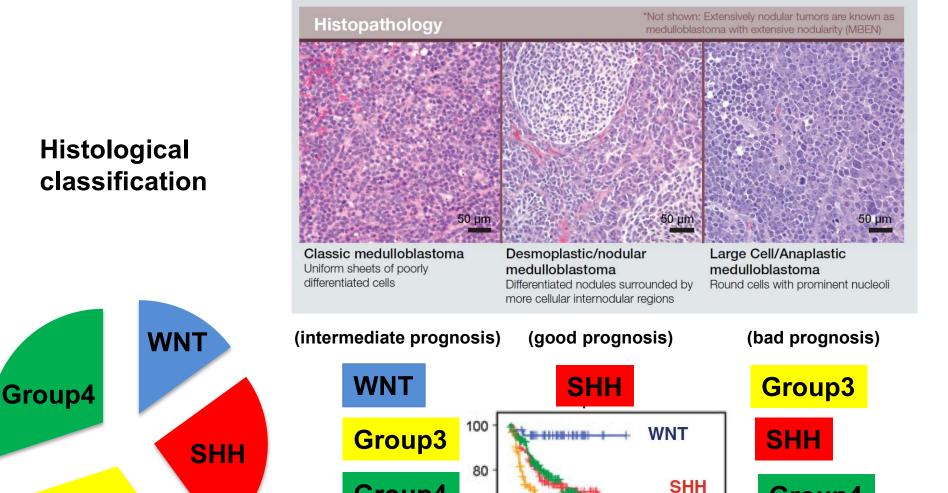
*Not shown: Extensively nodular tumors are known as

medulloblastoma with extensive nodularity (MBEN)





Transcriptomic classification



Group4

SHH

60

40

20

Transcriptomic classification

Group3

Group4

GROUP 4

GROUP 3

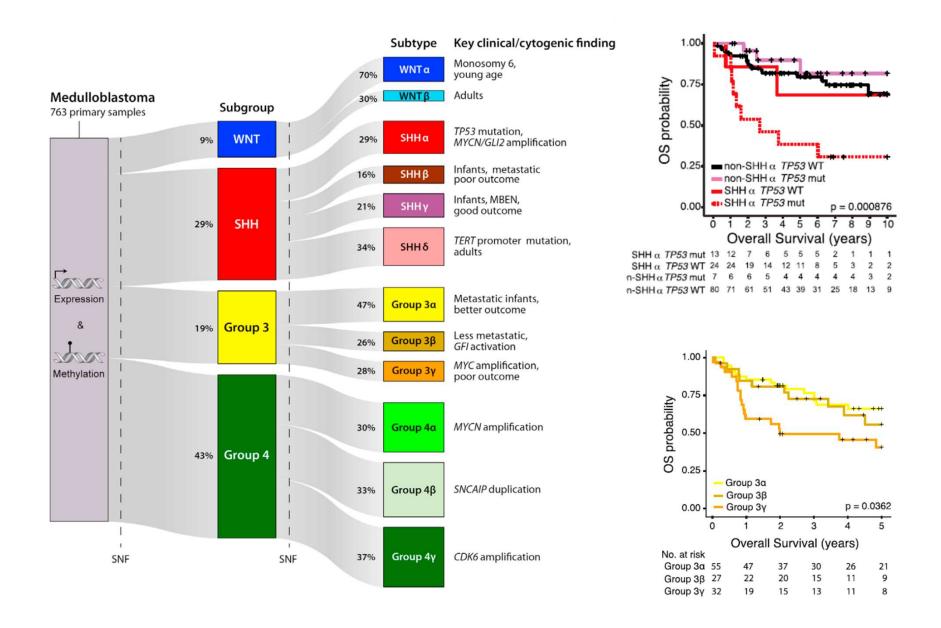
P < 0.001

200

100

150

MB groups can be stratified in subtypes



How to test that the GCP/GNP are the cell of origin of SHH medulloblastoma?

Are the GCP the cell of origin SHH medulloblastoma?

How to test that the GCP are the cell of origin of SHH medulloblastoma?

- -match the transcriptome of SHH medulloblastoma to that of different normal cerebellar progenitors during development
- -use mouse genetics

Cell of origin of SHH-MB

GCP/GNP is the cell of origin of SHH-MB









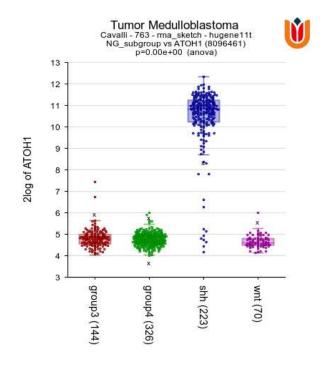








Atoh1 expression across MB groups



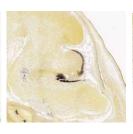
Cell of origin of SHH-MB

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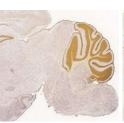






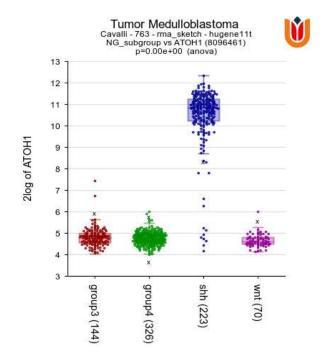






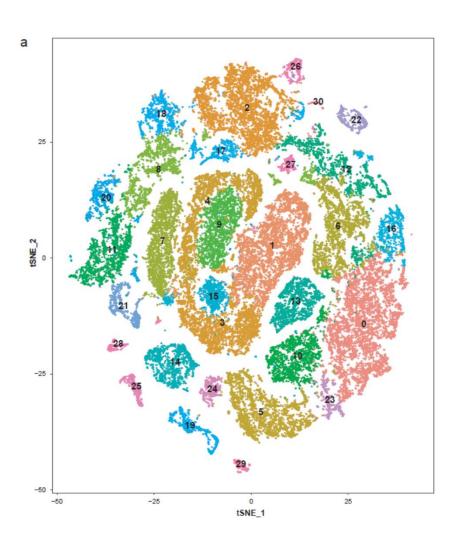


Atoh1 expression across MB groups



ATOH1 expression is enriched in SHH- group

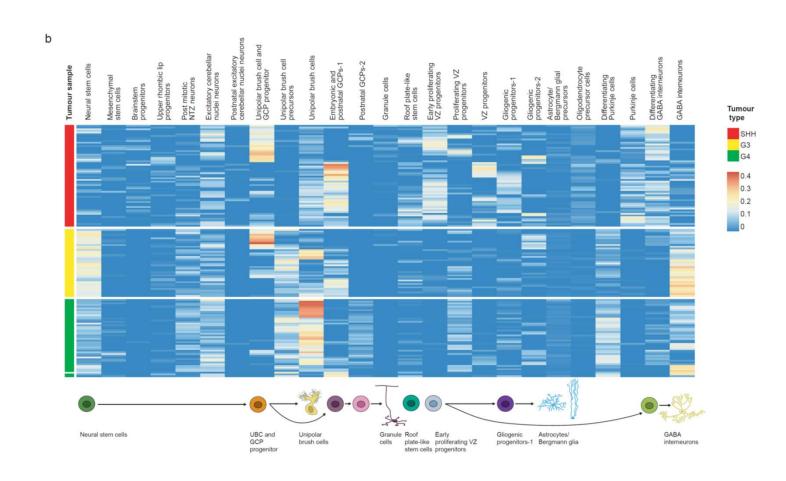
matching the transcriptome:



- 0- Excitatory cerebellar nuclei neurons
- 1- Embryonic and postnatal GCPs-1
- 2- Neural stem cells
- 3- Unipolar brush cell and GCP progenitor
- 4- Unipolar brush cells
- 5- GABA interneurons
- 6- Brainstem progenitors
- 7- Granule cells
- 8- VZ progenitors
- 9- Unipolar brush cell precursors
- 10- Differentiating Purkinje cells
- 11- Gliogenic progenitors-1
- 12- Upper rhombic lip progenitors
- 13- Mesenchymal stem cells-1
- 14- Purkinje cells
- 15- Postnatal GCPs-2
- 16- Post mitotic NTZ neurons
- 17- Roof plate-like stem cells
- 18- Proliferating VZ progenitors
- 19- Oligodendrocyte progenitor cells
- on our congruence of the programme
- 20- Gliogenic progenitors-2
- 21- Astrocyte/Bergmann glia precursors
- 22- Endothelial cells
- 23-Postnatal excitatory cerebellar nuclei neurons
- 24- GABA interneuron precursors
- 25- Pericytes
- 26- Early proliferating VZ progenitors
- 27- Mesencgymal stem cells-2
- 28- Microglia
- 29- Meninges
- 30- Red blood cells

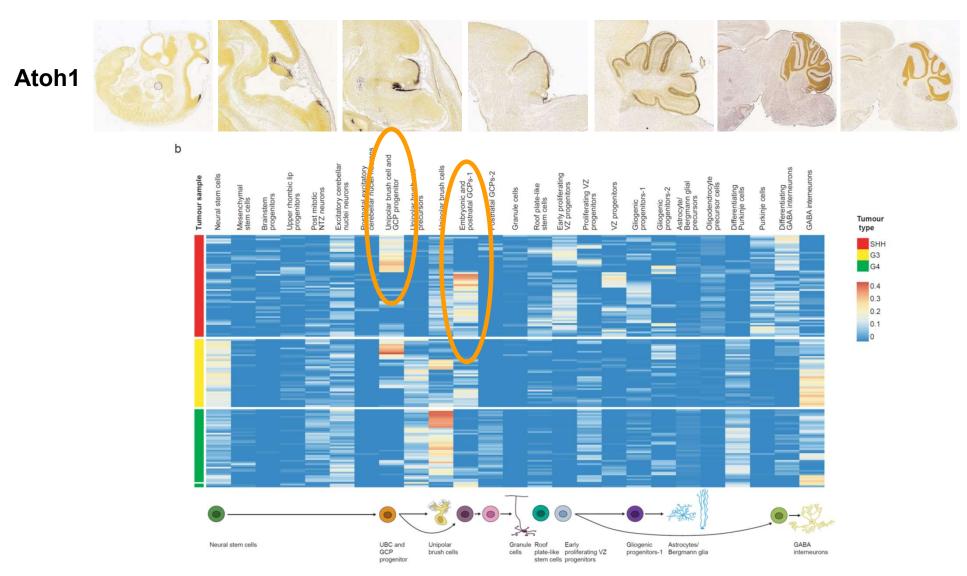
scRNAseq of cerebellar cells

matching the transcriptome:



Matching the MB to cerebellar cell transcriptomes

matching the transcriptome:



Mouse genetics:

















Mouse genetics:

Atoh1









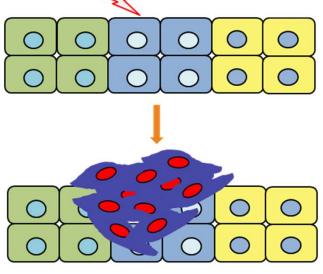




Genetic alteration SHH



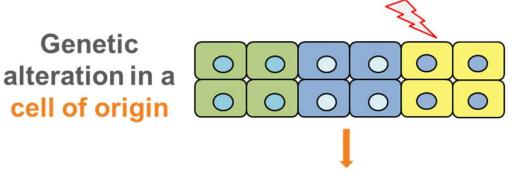




Tumor formation

consequences

Genetic



No tumor

Mouse genetics:

Atoh1





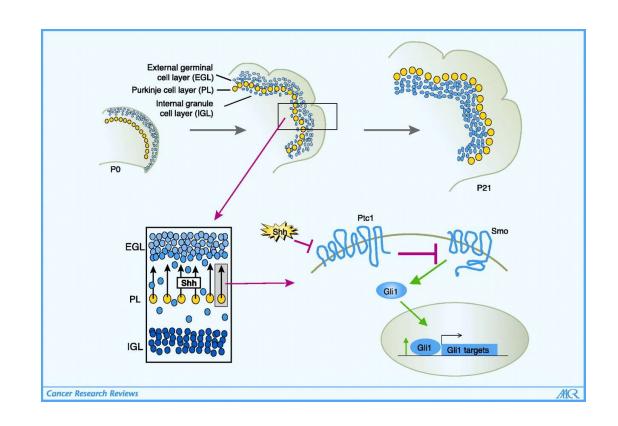










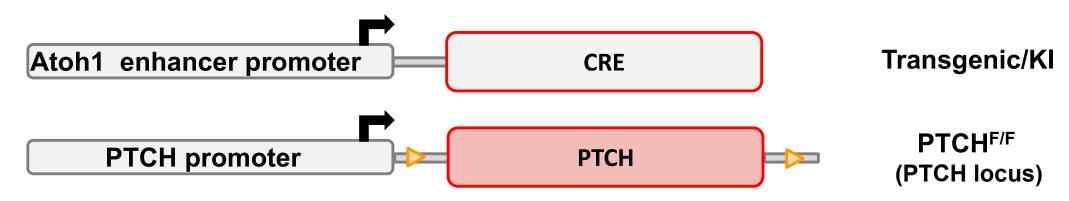


Mouse genetics:

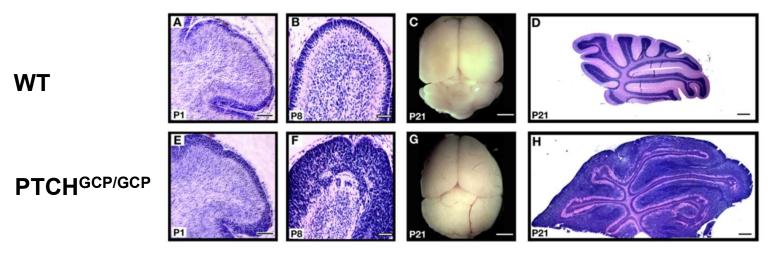


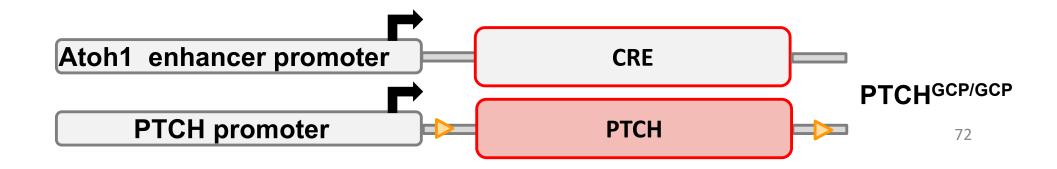
Mouse

Atoh1-cre::PTCH^{F/F} to generate the PTCH^{GCP/GCP} mice



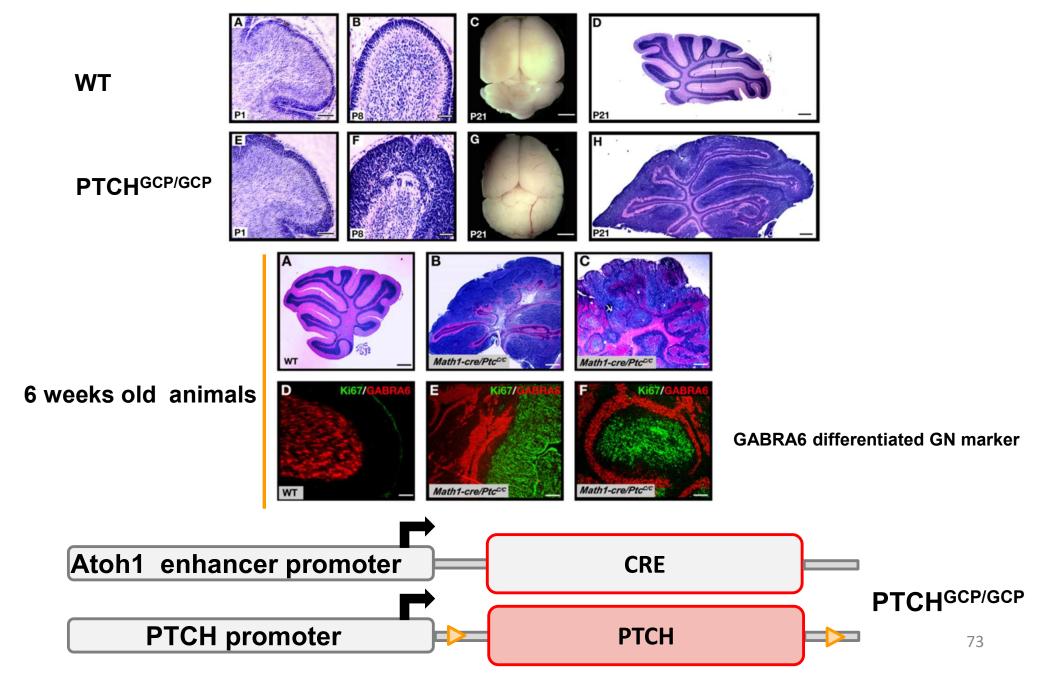
Atoh1Cre::PTCHF/F:





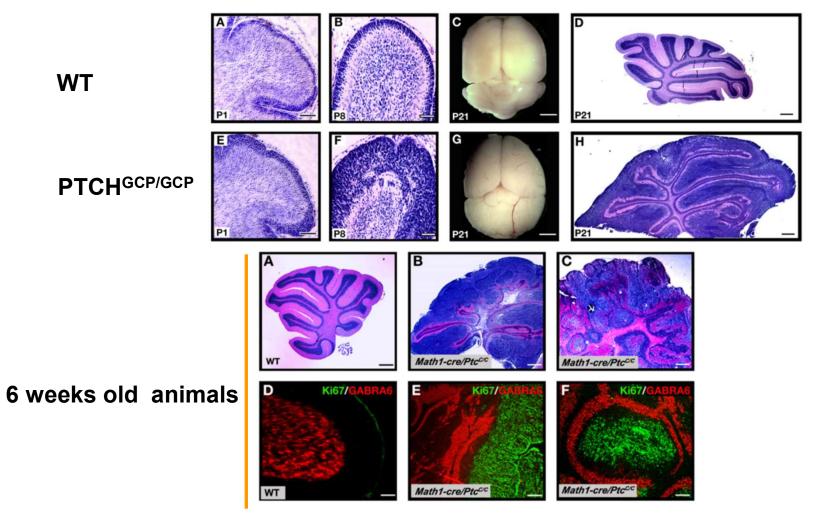
Cell of origin SHH group

Atoh1Cre::PTCH^{F/F}:



Cell of origin SHH group

Atoh1Cre::PTCHF/F:



PTCH inactivation (activation of SHH pathway) in GCP leads to MB formation

GCP/GNP is the cell of origin of SHH-MB

GCP/GNP is the cell of origin of SHH-MB



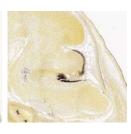
Atoh1 is expresssed in granule cell progenitors (GCP) Atoh1 is a specific marker of the GCP lineage

GCP/GNP is the cell of origin of SHH-MB









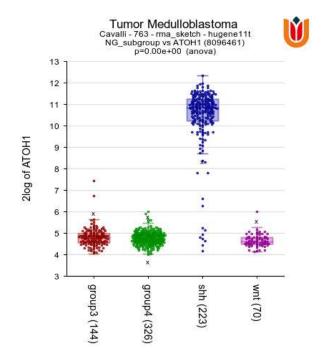








Atoh1 expression across MB groups





GCP/GNP is the cell of origin of SHH-MB

















Atoh1 expression across MB groups

Tumor Medulloblastoma
Cavallii -763 - ma_sketch - hugene11t
NG_subgroup vs ATOH1 (8096461)
p=0.00e+00 (anova)

13
12
11
10
9
8
7
6
5
4
3

Figure 1

Figure 2

Figure 2

Figure 3

Figure 3

Figure 3

Figure 3

Figure 4

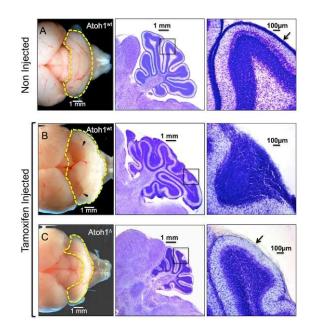
Figure 3

Figure 4

Figure 3

Figure 4

Atoh1 and SHH-MB formation (PTCH-/-)



GCP/GNP is the cell of origin of SHH-MB

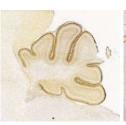
















Atoh1 expression across MB groups

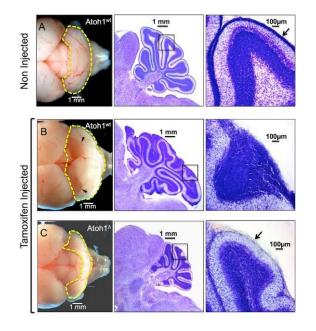
Tumor Medulloblastoma
Cavalli 763 - ma sketch - hugene11t
NG_subgroup vs ATOH1 (8096461)
p=0.00e+00 (anova)

13
12
11
10
9
4
3

group3 (1444)

y
group3 (1444)

Atoh1 and MB formation

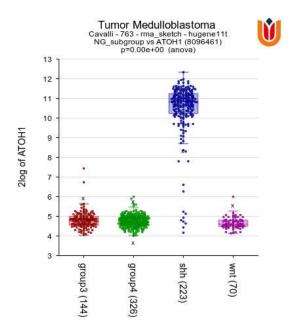


Deletion of Atoh1
Prevents MB formation

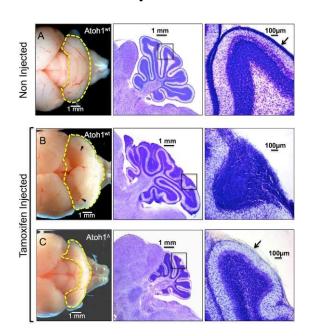
GCP/GNP is the cell of origin of SHH-MB

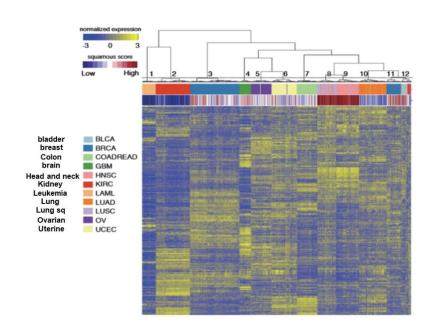


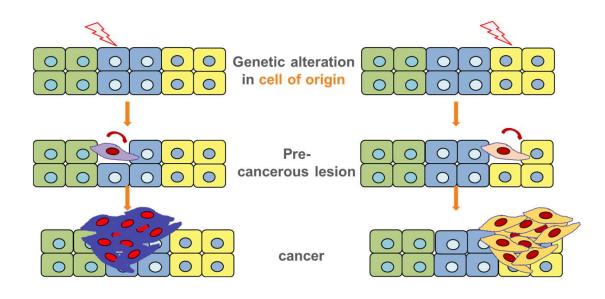
Atoh1 is expressed in SHH-MB



Atoh1 is required for SHH-MB formation







•LINEAGE ADDICTION IN CANCER:

- → Cancer are classified by their localization (organ specificity)
- → Close association between cell lineage and cancer phenotype (Cancer cells expressed specific lineage markers representative of cell of origin)
- → Lineage markers are key for tumour progression (Lineage dependency (ex: Atoh1in SHH-MB))

Medulloblastoma (MB)

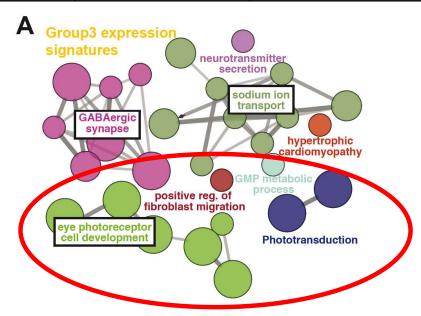
➤ Based on gene expression profile : 4 different molecular groups

MB subtype		WNT	SHH	3	4
	Age distribution	1.0	0.5 Infant Childhood Adult	Infant Childhood Adult	1.0
Clinical features	incidence	10%	25%	25%	40%
	histology	Classic (very rare LCA)	Classic > desmoplastic/ nodular> LCA	Classic>LCA	Classic; rarely LCA
	Metastasis at diagnosis	rare 5-10%	intermediate 15-20%	frequent 40-45%	frequent 35-40%
	Overall survival (5years)	Very good	Intermediate 75%	Bad 50%	intermediate
	Cell of origin	Lower rhombic lip precursor	Granular cell progenitor	Unknown	
Genomic features	Driver pathway/genes	WNT/βCAT CTNNB1 mutation	SHH PTCH1 mutation	MYC amplification OTX2 amplification	MYCN & CDK6 amplification
	Expression signature	WNT signaling	SHH signaling	MYC & GABAergic & photoreceptor signature	Neuronal & glutamatergic signature

Medulloblastoma (MB)

➤ Based on gene expression profil : 4 different molecular groups

MB subtype	WNT	нн	3	4
incidence	10%	25%	25%	40%
Overall survival	Very good	Intermediate	Bad (meta+++)	Intermediate (meta++)
Driver pathway	WNT	нн	MYC amplification OTX2 amplification	MYCN & CDK6 amplification
Expression signature	WNT signaling	SHH signaling	Photoreceptor markers	Neuronal & glutamatergic signature



Group 3 Medulloblastoma (MB)



Group 3 Medulloblastoma



Group 3 MB displays an abnormal identity (photoreceptors of the retina)

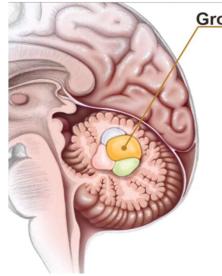
 Identity unrelated to the tissue of origin: retina fate in a cerebellar tumor

•LINEAGE ADDICTION IN CANCER:

- → Cancer are classified by their localization (organ specificity)
- → Close association between cell lineage and cancer phenotype (Cancer cells expressed specific lineage markers representative of their localization)
- → Lineage markers are key for tumour progression (Lineage dependency can guide treatment (ex ER in breast Cancer))

Challenge the concept of lineage addiction in cancer

Group 3 Medulloblastoma (MB)



Group 3 Medulloblastoma

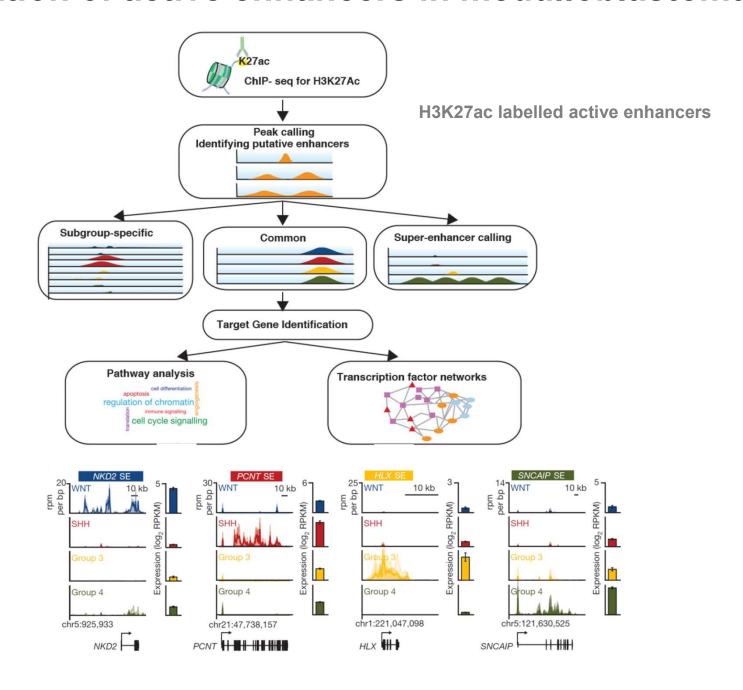


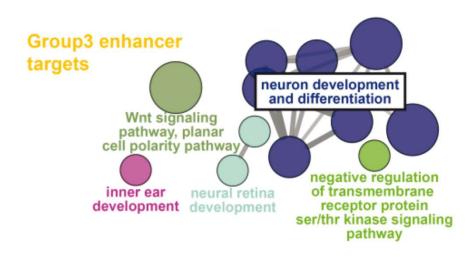
Group 3 MB displays an abnormal identity (photoreceptors of the retina)

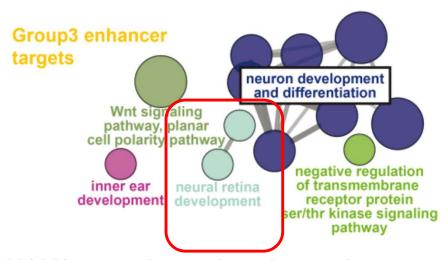
 Identity unrelated to the tissue of origin: retina fate in a cerebellar tumor

- Challenge the concept of lineage addiction in cancer
 - How this abnormal identity is established?
 - Is there an addiction to this abnormal identity?

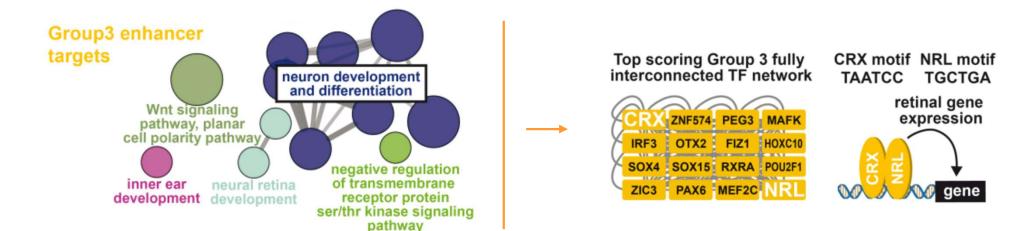
Identification of active enhancers in medulloblastoma





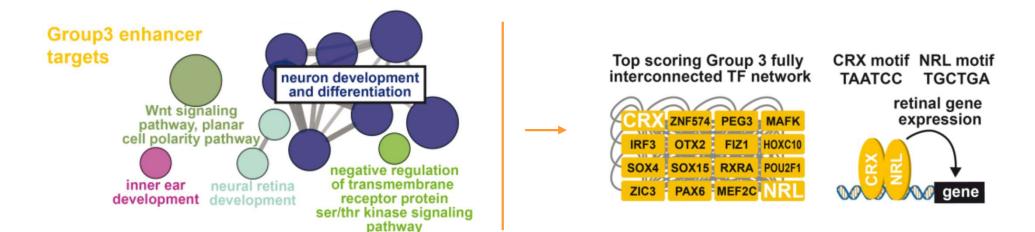


H3K27ac labelled active enhancers (Identification of G3 enhancers) Controlled genes involved in retina development



H3K27ac labelled active enhancers (Identification of G3 enhancers) Controlled genes involved in retina development

Look for enrichment of binding sites for TFs on these enhancers



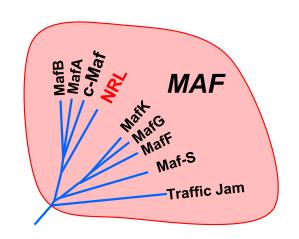
H3K27ac labelled active enhancers (Identification of G3 enhancers) Controlled genes involved in retina development

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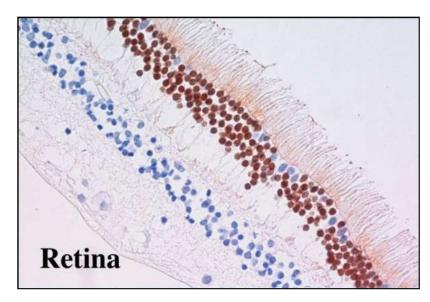
NRL and CRX binding sites are enriched in Group 3 enhancers NRL AND CRX are lineage restricted photoreceptor TFs

NRL in Medulloblastoma





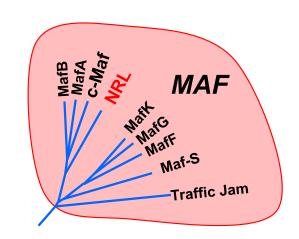
NRL expression is restricted to the photoreceptors of the retina



(immunohistochemistry (IHC))

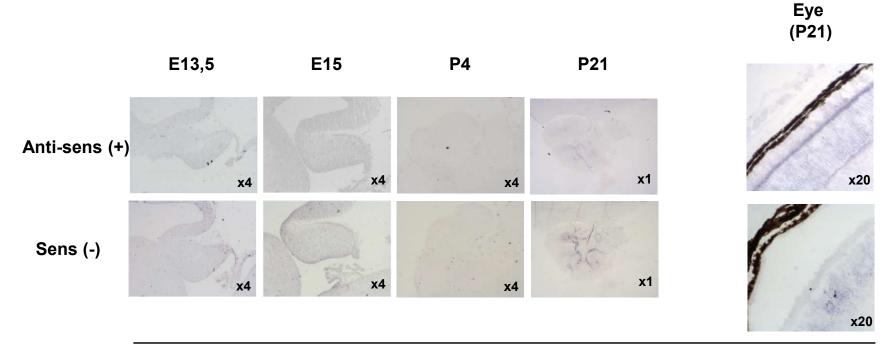
NRL in Medulloblastoma





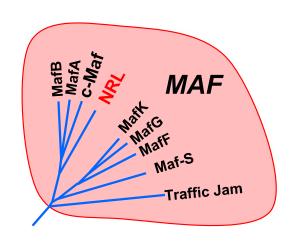
NRL expression is restricted to the photoreceptors of the retina

(not expressed in the cerebellum)



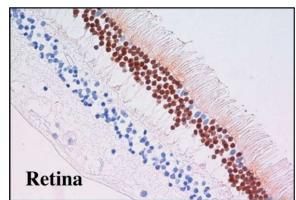
NRL in Medulloblastoma





 NRL expression is restricted to the photoreceptors of the retina (not expressed in the cerebellum)

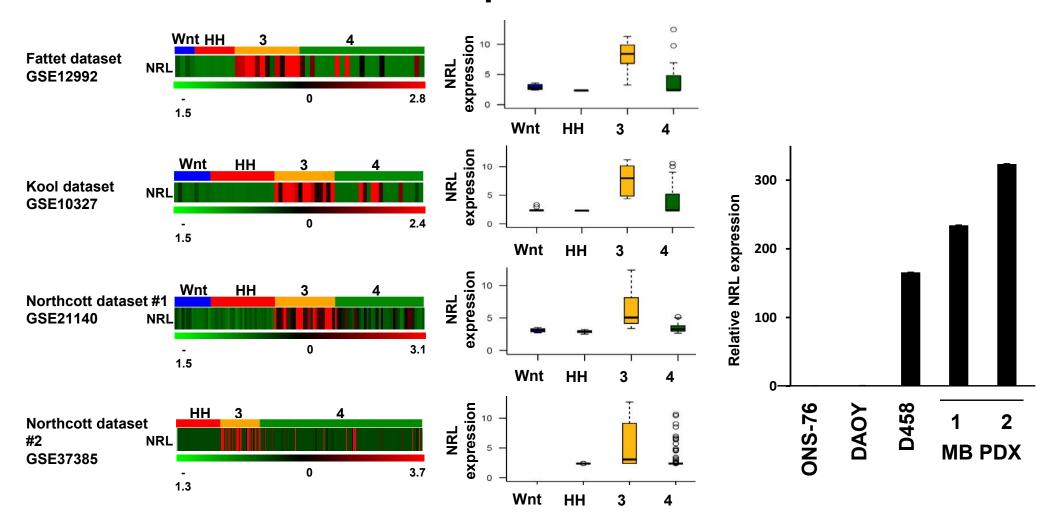
 Role in photoreceptor terminal differentiation (KO NRL: lack of a subset of photoreceptors)
 Mutations of NRL in human (retinitis pigmentosa)



Role of NRL in medulloblastoma?

→ NRL has not yet been demonstrated to be involved in oncogenesis

NRL overexpression in MB



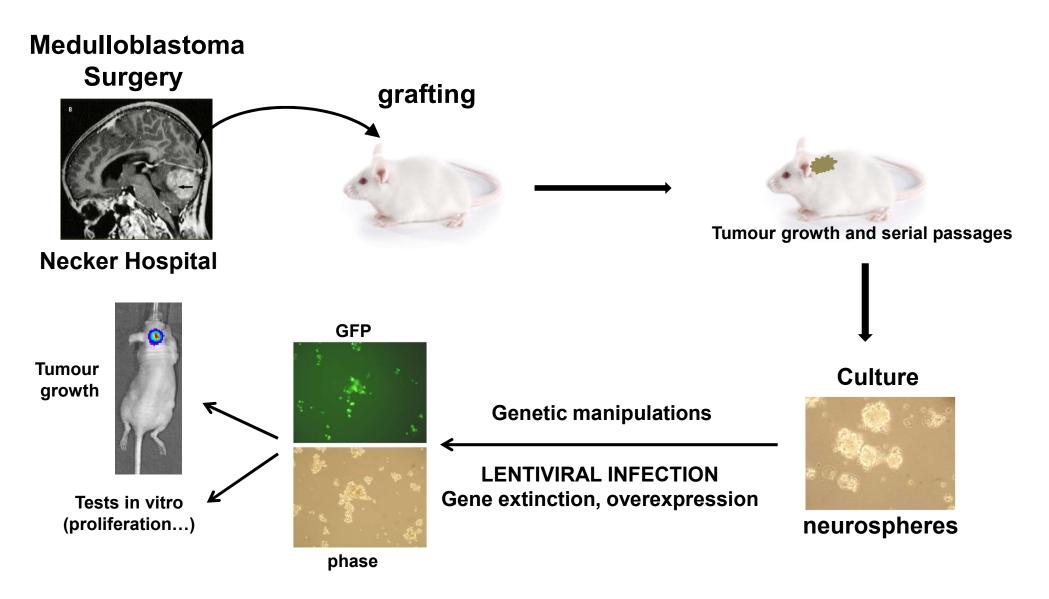
NRL is overexpressed in the metastatic MB group 3

Group 3 MB PDXs

PDX: Patient-derived xenograft

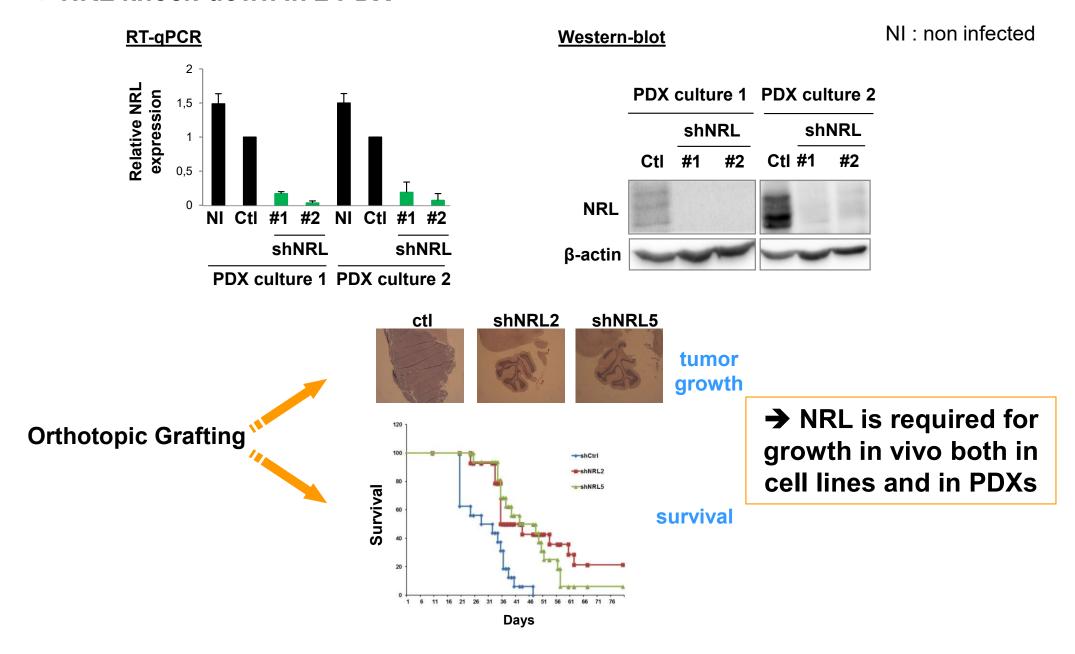
Group 3 MB PDXs

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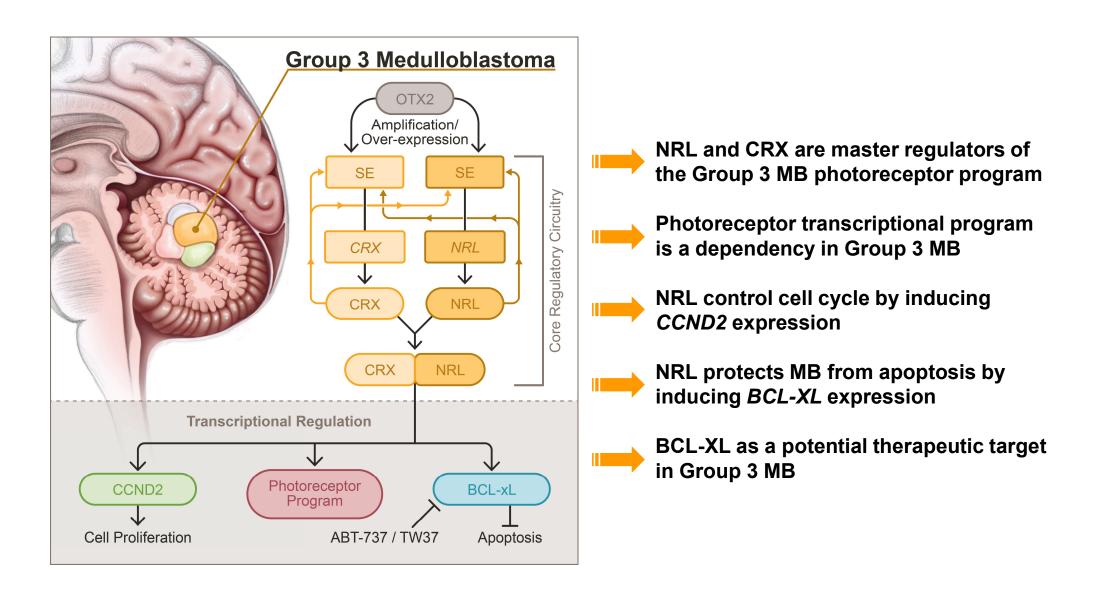


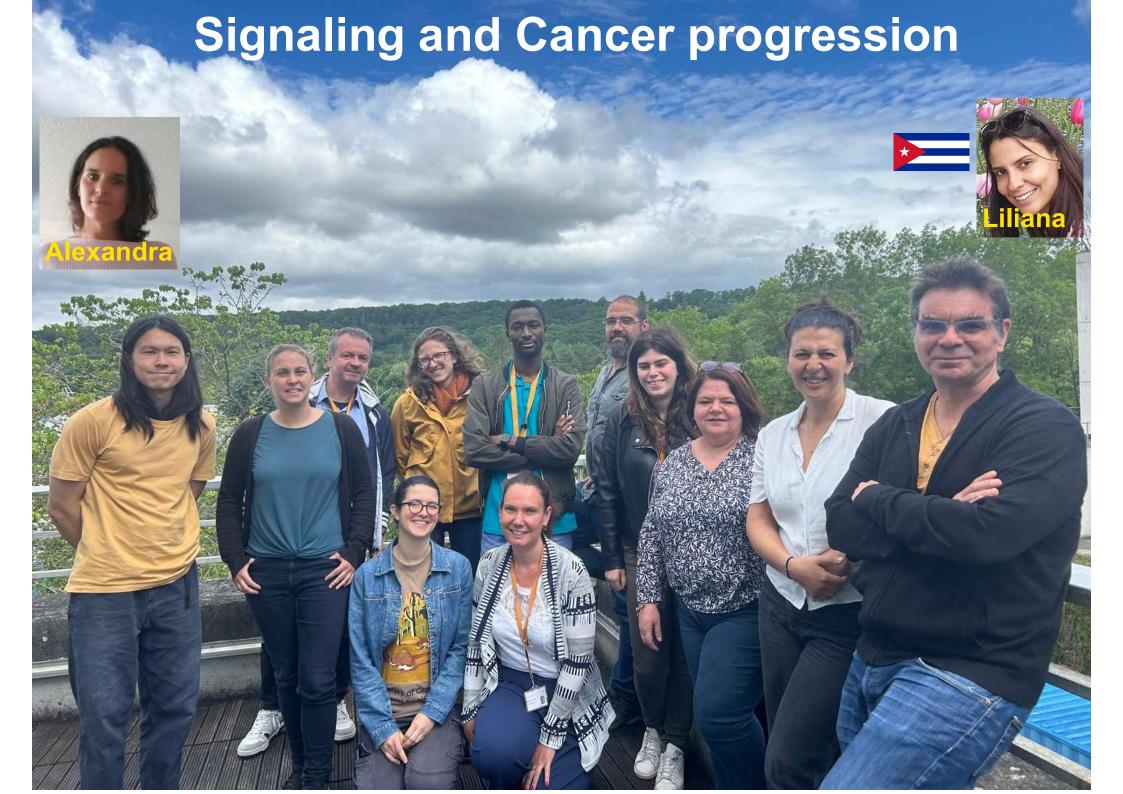
NRL is required for MB growth in vivo

►NRL knock-down in 2 PDX



Model







Pediatric Cancers

In general rare cancers

- 75-80% Cured
 - Better than for adult cancers.
 - Important side effects
 - Much less mutations ????

