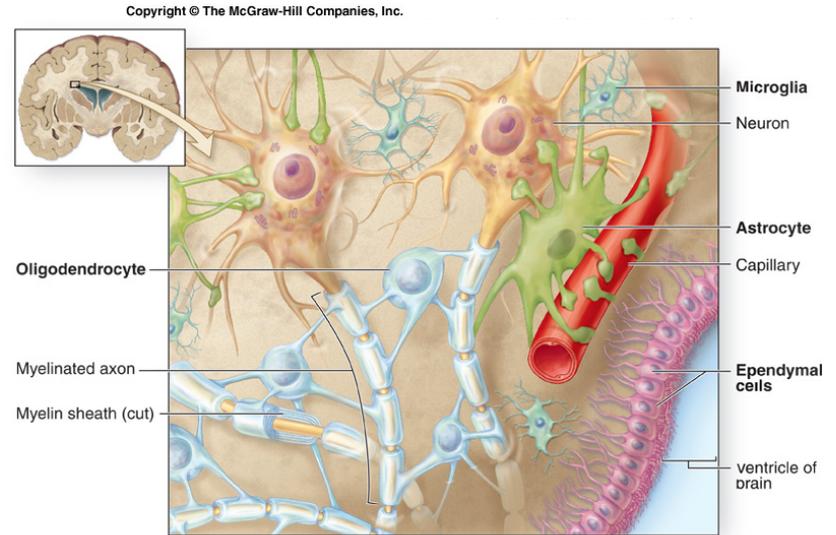
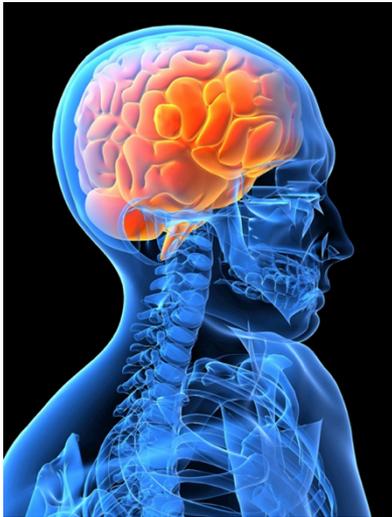


# Neuro-oncology



## MCBO Core Lecture II

### Guido Wollmann

Division of Virology  
March 12 2020

# What is Neuro-oncology?



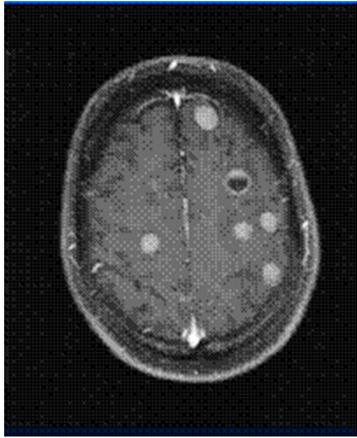
**Primary brain tumors**

**Secondary brain tumors**

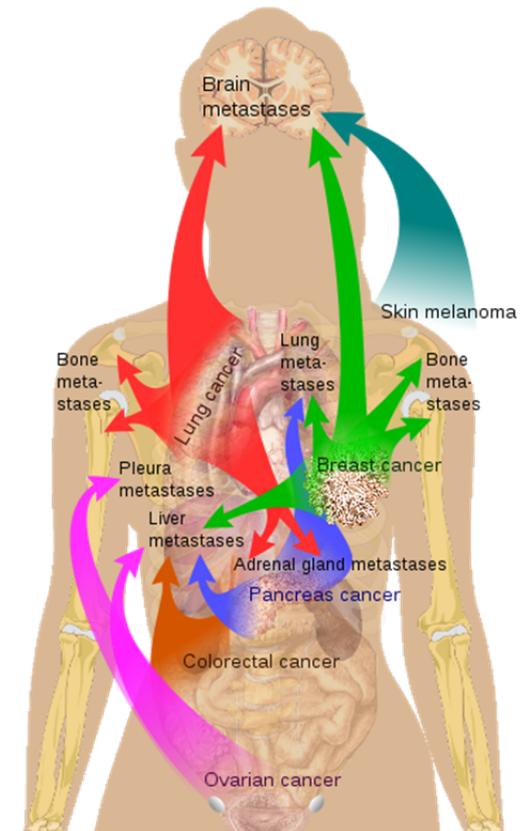
**Neurological symptoms  
of general cancer**

# Neuro-oncology – Terminology

## SECONDARY brain tumors = brain metastasis of non-brain cancers

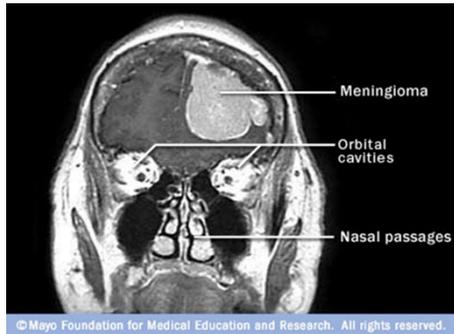


- Most common
- Often multiple lesions
- 25-45% of cancer patients
  - Lung: >50% of all; most common in men
  - Breast: Most common in women
  - Melanoma: Highest risk for brain mets
  - Renal Cell
  - Colorectal

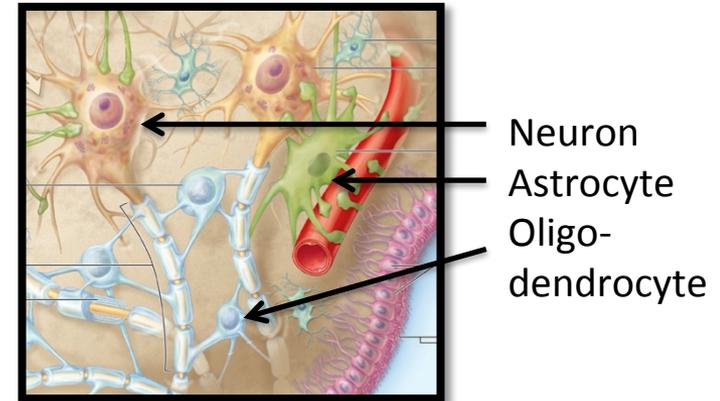
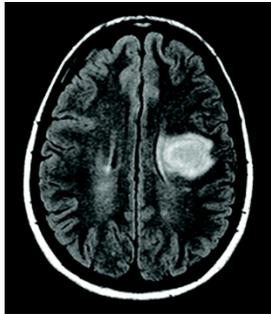
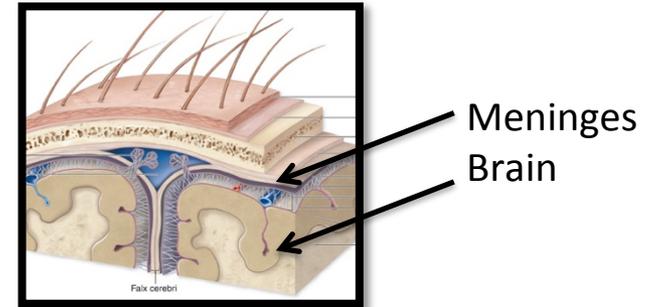


# Neuro-oncology – Terminology

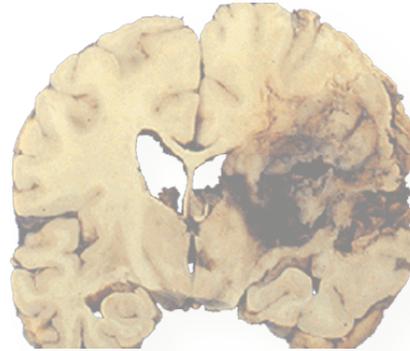
**PRIMARY** brain tumors = originating from brain tissue



- Meningioma (35%)
- Glioma (30%)
  - Astrocytoma
    - Glioblastoma
  - Oligodendroglioma
  - Oligoastrocytoma
  - Ependymoma
- Pituitary Adenoma (13%)



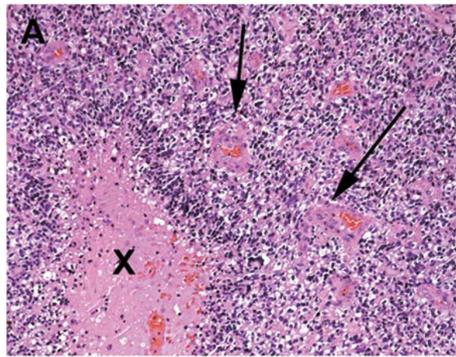
# Glioma – Classification



## WHO classification

(classical classification)

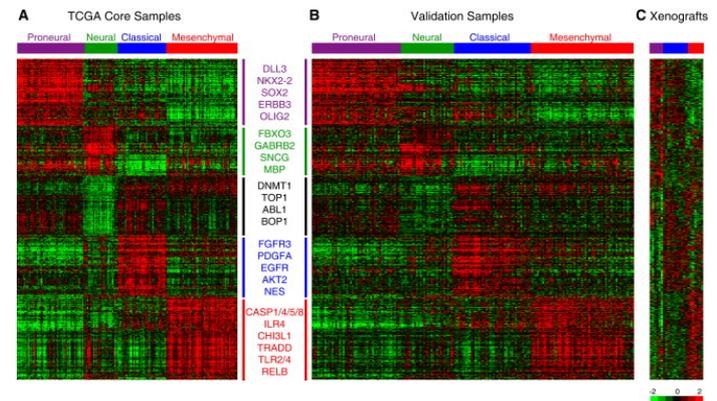
- Based on histopathology
- Grading I, II, III, IV



## Molecular classification

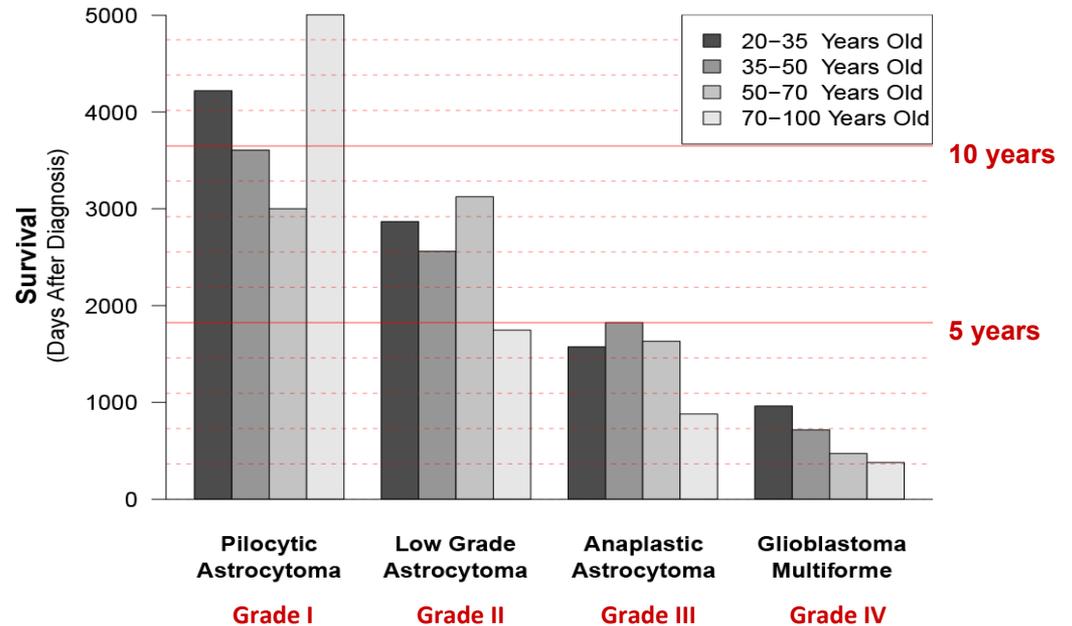
(new classification – since 2010)

- Based on molecular profile
- Optimized treatment



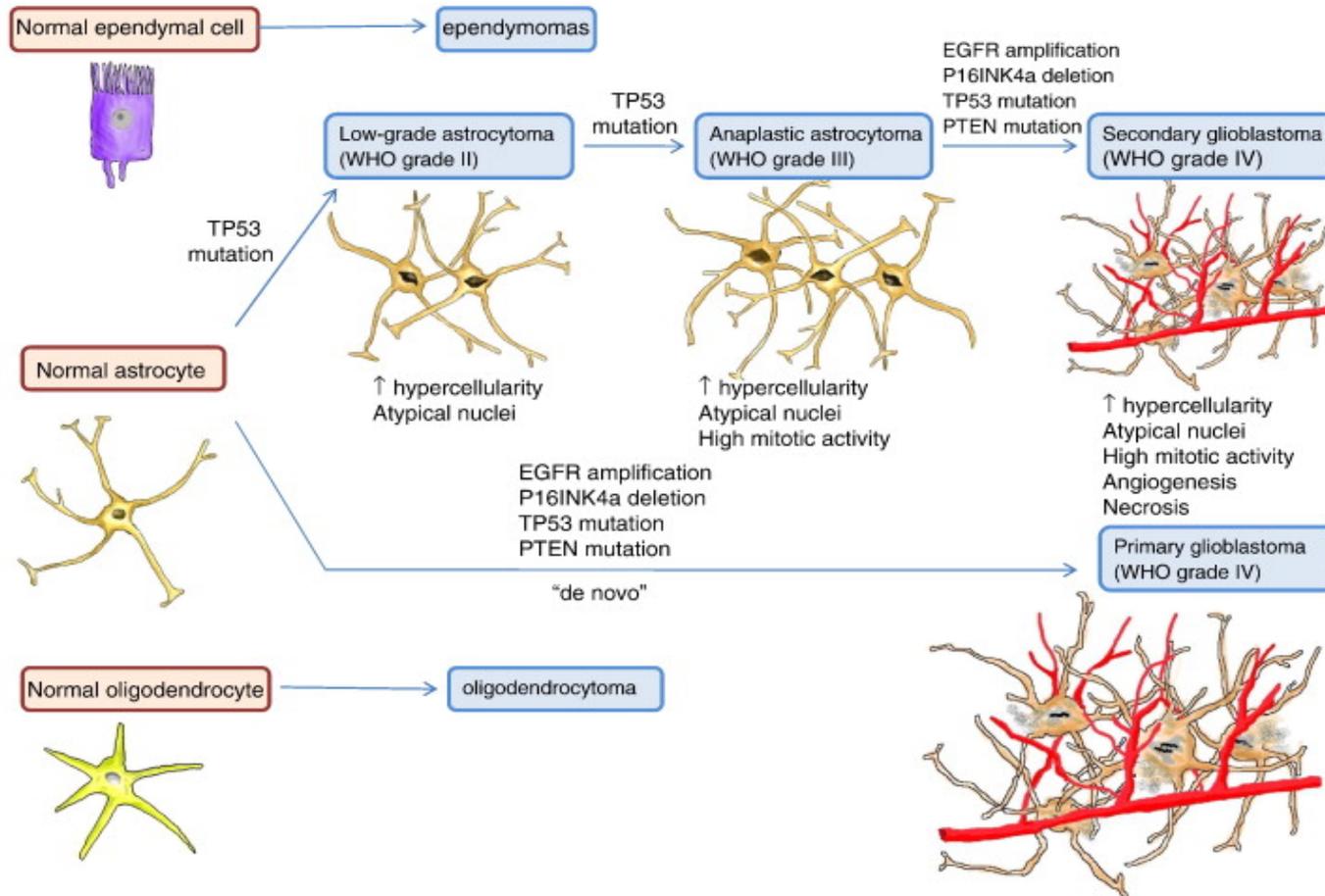
# Glioma – WHO Classification Relative Frequencies

Grade	Tumor Type	Glioma %
I/II	Well-differentiated (low-grade) astrocytoma	15 to 20
III	Anaplastic astrocytoma	30 to 35
IV	Glioblastoma multiforme	40 to 50



<http://www.neurooncology.ucla.edu/>

# Primary vs Secondary GBM



⇒ PRIMARY GBM emerges de-novo as a GBM upon first diagnosis

⇒ SECONDARY GBM evolve from lower grade gliomas first diagnosed years earlier

# Primary vs Secondary GBM

**Table 1.** Primary and secondary glioblastomas: comparison of clinical versus genetic diagnosis

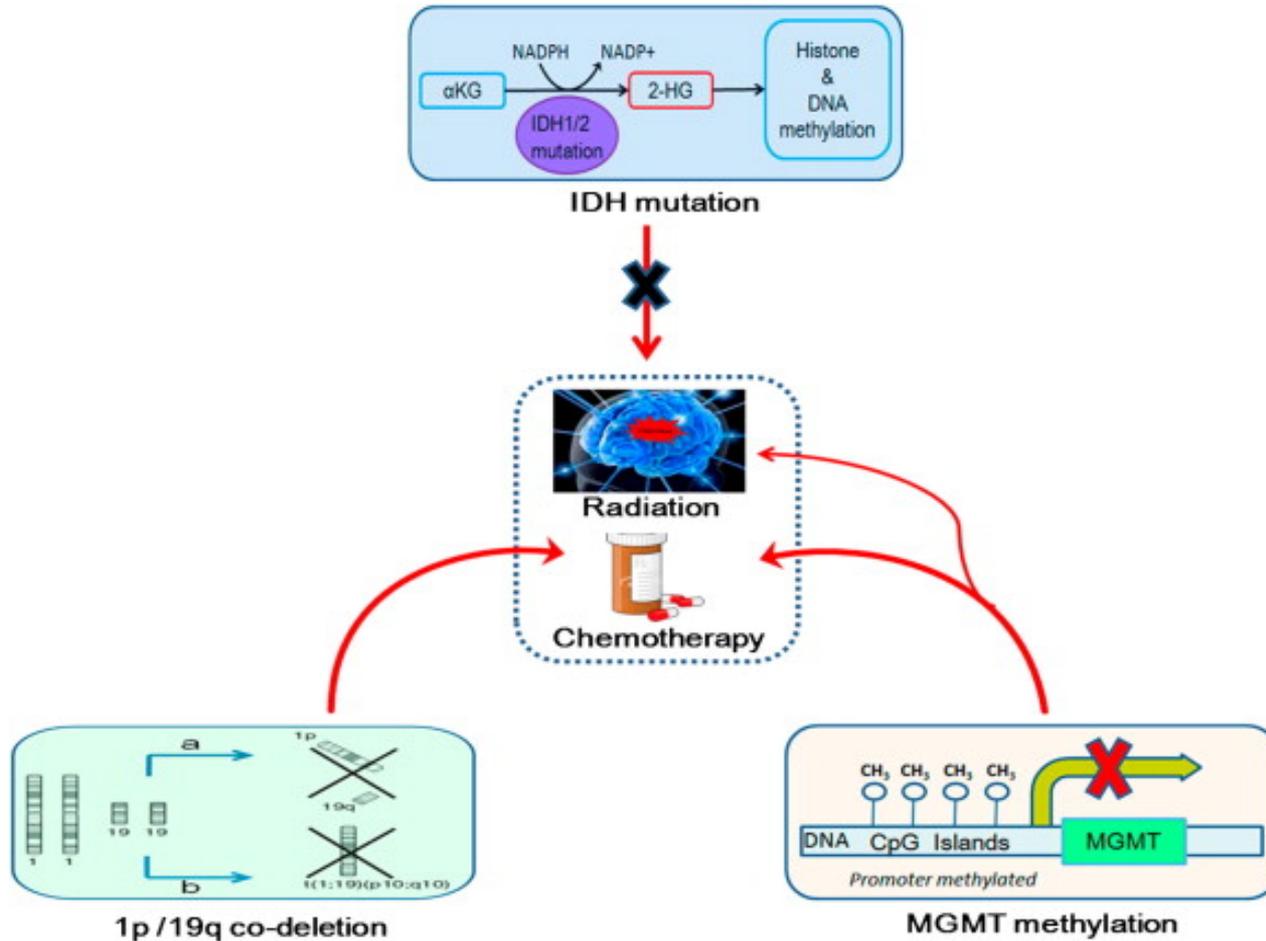
	Primary glioblastoma		Secondary glioblastoma		References
	Clinical criteria <sup>a</sup>	Genetic criteria ( <i>IDH1</i> <sup>wt</sup> )	Clinical criteria <sup>a</sup>	Genetic criteria ( <i>IDH1</i> <sup>mut</sup> )	
Fraction in a population	94.7%	91.2%	5.3%	8.8%	(7, 13)
Mean age, y	59–62	56–61	33–45	32–48	(7, 12, 13, 67, 70)
Male/female ratio	1.33–1.5	1.2–1.46	0.65–2.3	1.0–1.12	(7, 12, 13, 70)
Mean clinical history, mo	6.3	3.9	16.8	15.2	(7, 13)
Median overall survival, mo					(7, 12, 13)
Surgery + radiotherapy	4.7 <sup>b</sup>	9.9	7.8 <sup>b</sup>	24	(7, 13)
Surgery + radio/chemotherapy		15		31	(12)
<i>Histologic features</i>					
Oligodendroglial comp.	18%	20%	42%	54%	(13, 80)
Necrosis	89%	90%	63%	50%	(13, 80)
<i>Genetic alterations</i>					
<i>IDH1</i> mutations	4–7%	0%	73–88%	100%	(10, 12, 13)
<i>TP53</i> mutations	17–35%	19–27%	60–88%	76–81%	(7, 10, 12, 13, 67, 91)
<i>ATRX</i> mutations	4–7%		57–80%		(36, 37)
<i>EGFR</i> amplification	36–45%	35–39%	0–8%	0–6.5%	(7, 10, 12, 13, 91)
<i>CDKN2A</i> deletion	31–52%	30–45%	19–20%	7–22%	(7, 12, 13, 91)
<i>PTEN</i> mutations	23–25%	24–26%	4–12%	0–8%	(7, 12, 13)
19q loss	6%	4%	54%	32%	(9, 13)
1p/19q loss	2–8%		0–13%		(10, 12, 67)
10p loss	47%		8%		(8)
10q loss	70%	67%	63%	73%	(7, 13)

<sup>a</sup>Tumors were considered to be primary if the diagnosis of glioblastoma was made at the first biopsy, without clinical or histological evidence of a preexisting, less malignant precursor lesion, whereas the diagnosis of secondary glioblastoma required histological and/or clinical (neuroimaging) evidence of a preceding low-grade or anaplastic astrocytoma.

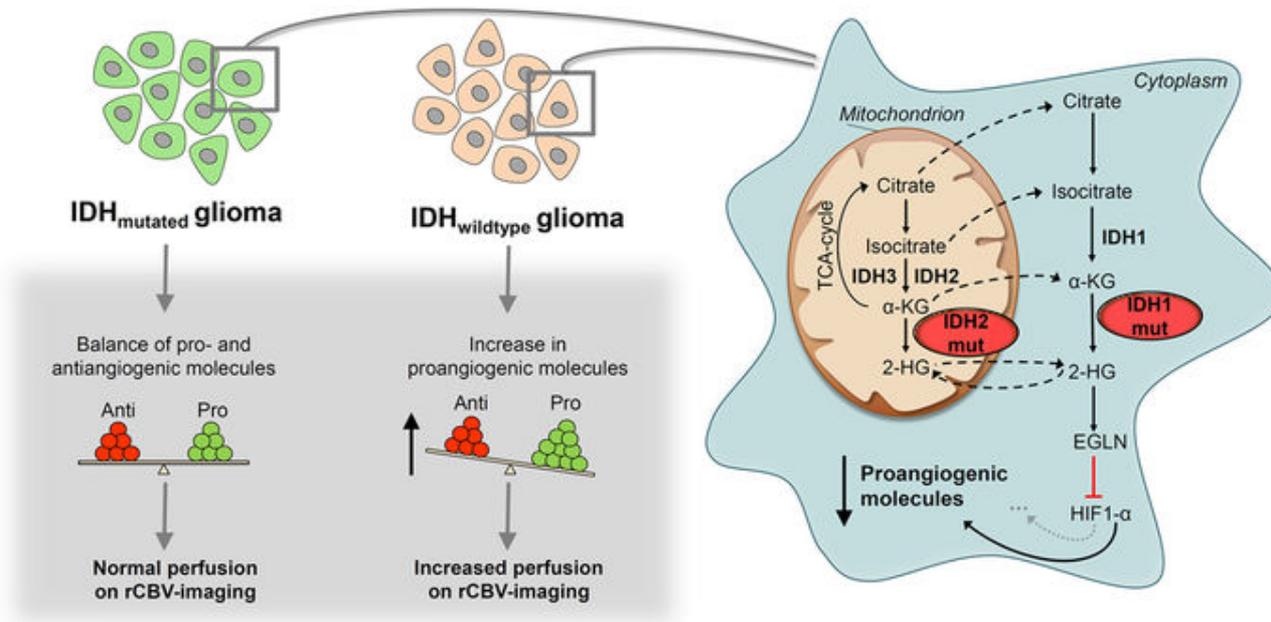
<sup>b</sup>Data from population-based study: all the patients who were treated in different ways were included.

# Molecular Biomarkers

Biomarker: „A functional biochemical or molecular indicator of a biological or disease process that **has predictive, diagnostic, and/or prognostic utility.**“



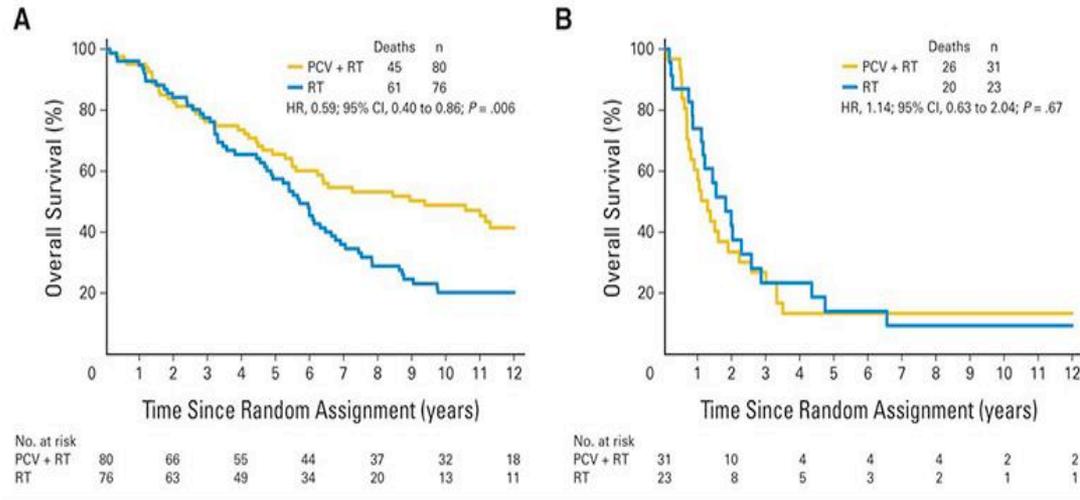
# Molecular Biomarkers: IDH Mutation



-> IDH mutation interferes with hypoxia-inducible factor HIF signaling

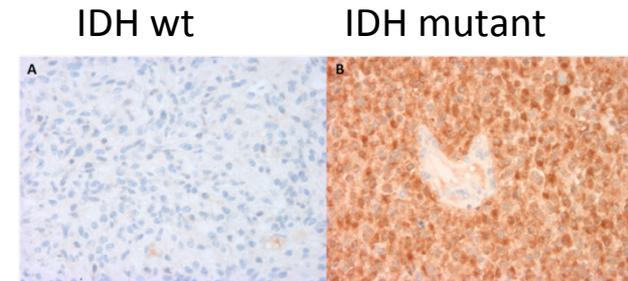
- ⇒ **MOLECULAR marker** for diffusely infiltrating glioma (II and III)
- ⇒ **PROGNOSTIC marker** for better survival
- ⇒ **PREDICTIVE marker** for better response to treatment

# Molecular Biomarkers: IDH Mutation



IDH mutant

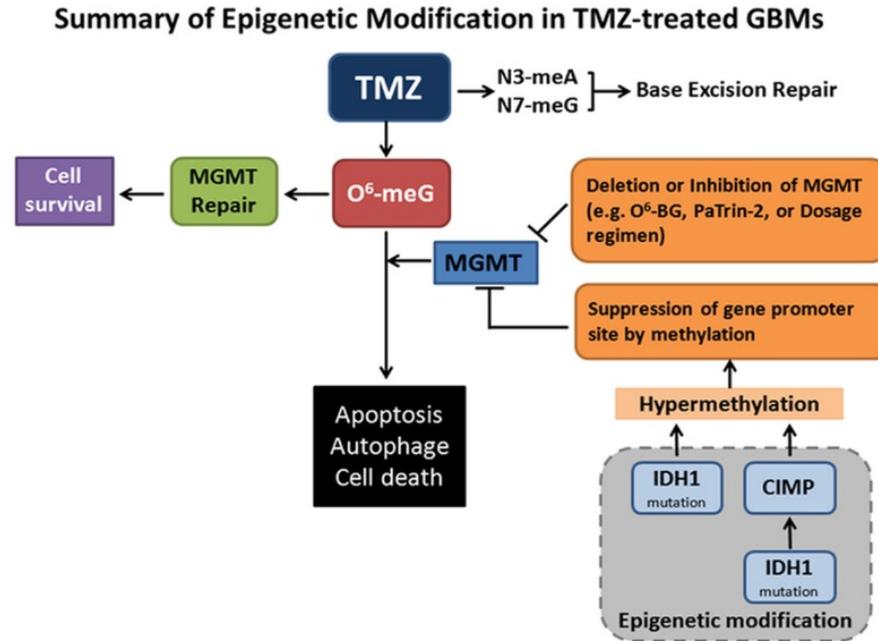
IDH wild type



**Better prognosis and better response to chemotherapy in patients with IDH mutation.**

# Molecular Biomarkers: MGMT Methylation

O6-methylguanine-DNA methyltransferase (MGMT) => DNA repair protein

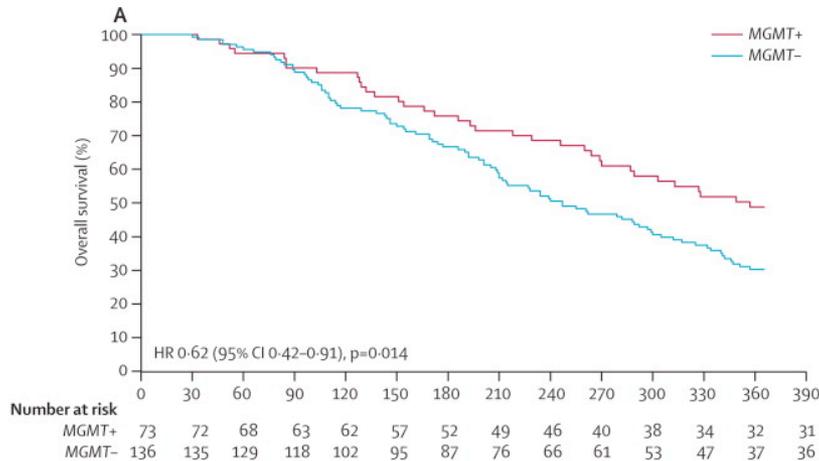


MGMT counteracts the alkylating drug TMZ. Hypermethylation of MGMT promoter region inhibits MGMT repair function and facilitates better chemo-therapeutic responses.

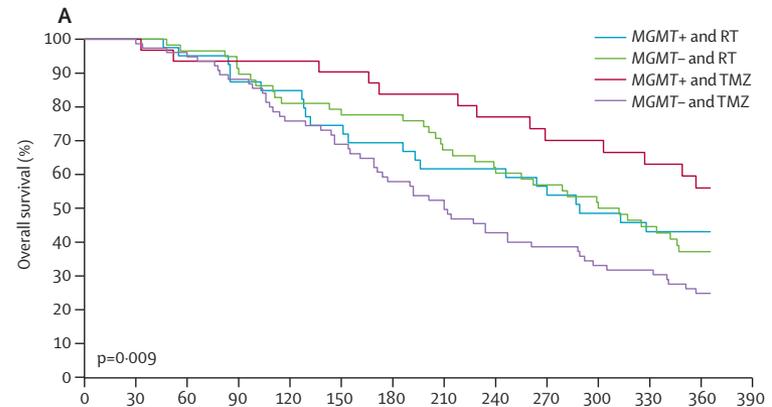
# Molecular Biomarkers: MGMT Methylation

MGMT hypermethylation:

Prognostic marker



Predictiv marker

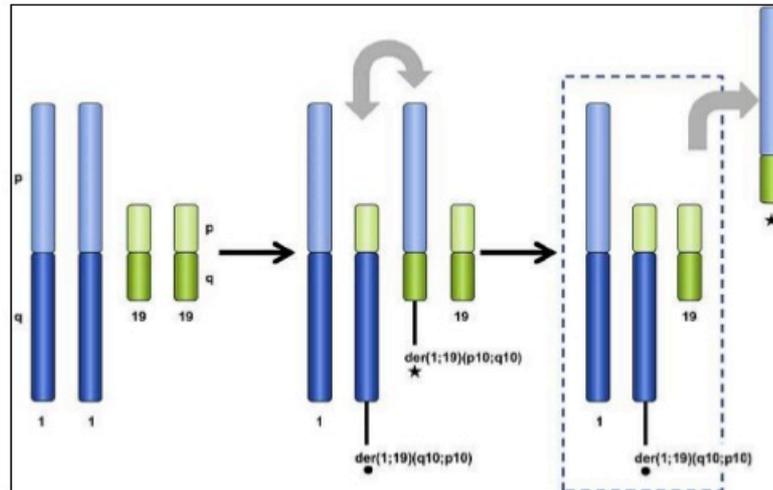


**Better prognosis and better response to chemotherapy in patients with MGMT hypermethylation.**

Lancet Oncol. 2012 13:707-15.

# Molecular Biomarkers: 1p/19q co-deletion

Co-deletion => loss of heterozygosity



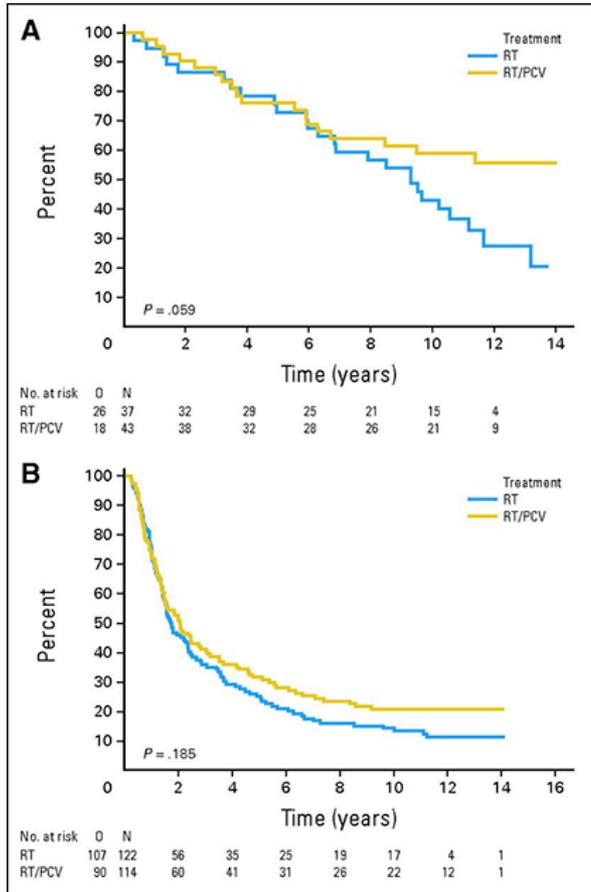
- The first allele is lost (**1st Hit**) due to an imbalanced reciprocal translocation between chromosomes 1 and 19
- The second allele is disrupted (**2nd Hit**) by a somatic mutation capable of inhibiting protein function

⇒ **MOLECULAR** marker for oligodendrogliomas (up to 70% positive for LOH 1p:19q)

⇒ **PROGNOSTIC** marker for better survival

⇒ **PREDICTIVE** marker for better response to treatment

# Molecular Biomarkers: 1p/19q co-deletion



<= LOH 1p:19q

**Better prognosis and better response to chemotherapy in patients with LOH 1p/19q**

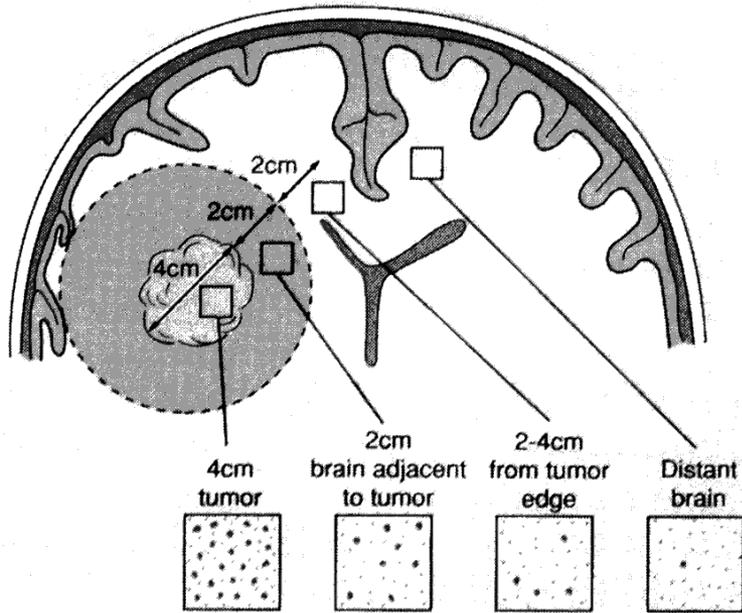
<= normal 1p:19q status

# Glioblastoma – Clinical Challenge

- Mean survival 12-14 months from diagnosis (3 months w/o treatment)
- Mean survival 4-5 months from recurrence
- 2 year survival 10%
- 5 year survival 5%
- Treatment options:
  - Surgery (recurrence within 2 cm of debulking margin in 80% of patients)
  - Radiation (rarely radiosurgery)
  - Chemotherapy:
    - Nitrosureas, PCV, temozolomide, thalidomide, avastin

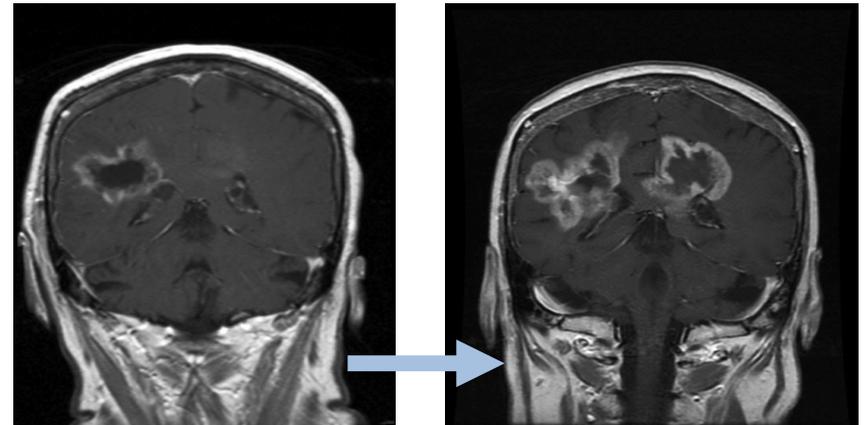
# Glioblastoma – Clinical Challenge

GBM is a “non-surgical disease” => a knife cannot remove the entire tumor



Ratio of tumor cells to total cells	1:1	1:10	1:100	1:1000
Percentage of tumor cell population	92%	6%	1.8%	0.2%

GBM always recurs



12'2010

3'2011

Clin Neurosurg. 1992;38:32.

E.A. Chiocca, 2017, Regis lecture

# Glioblastoma – Standard Therapy

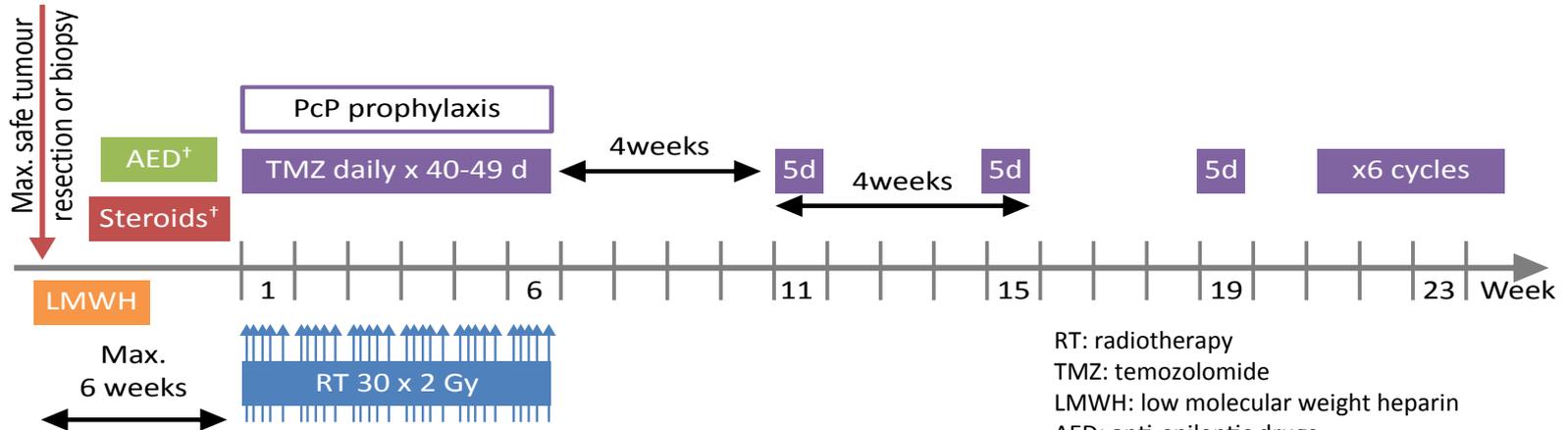
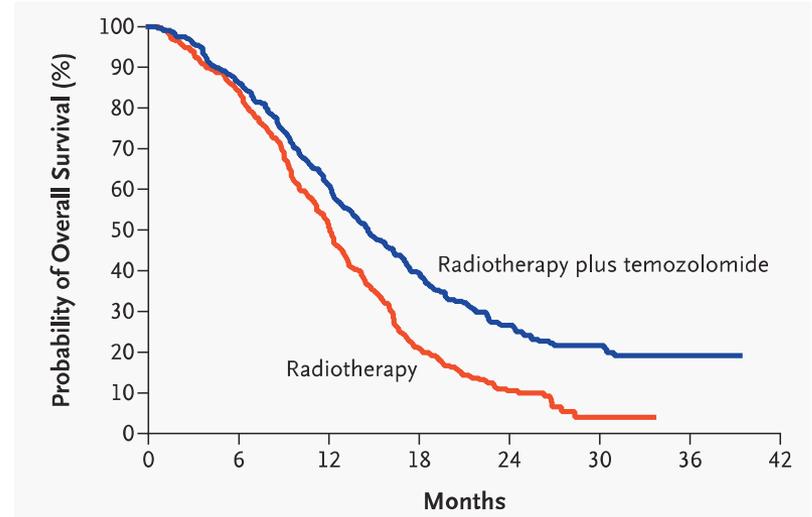
THE NEW ENGLAND JOURNAL OF MEDICINE

ORIGINAL ARTICLE

## Radiotherapy plus Concomitant and Adjuvant Temozolomide for Glioblastoma

Roger Stupp, M.D., Warren P. Mason, M.D., Martin J. van den Bent, M.D., Michael Weller, M.D., Barbara Fisher, M.D., Martin J.B. Taphoorn, M.D., Karl Belanger, M.D., Alba A. Brandes, M.D., Christine Marosi, M.D., Ulrich Bogdahn, M.D., Jürgen Curschmann, M.D., Robert C. Janzer, M.D., Samuel K. Ludwin, M.D., Thierry Gorlia, M.Sc., Anouk Allgeier, Ph.D., Denis Lacombe, M.D., J. Gregory Cairncross, M.D., Elizabeth Eisenhauer, M.D., and René O. Mirimanoff, M.D., for the European Organisation for Research and Treatment of Cancer Brain Tumor and Radiotherapy Groups and the National Cancer Institute of Canada Clinical Trials Group\*

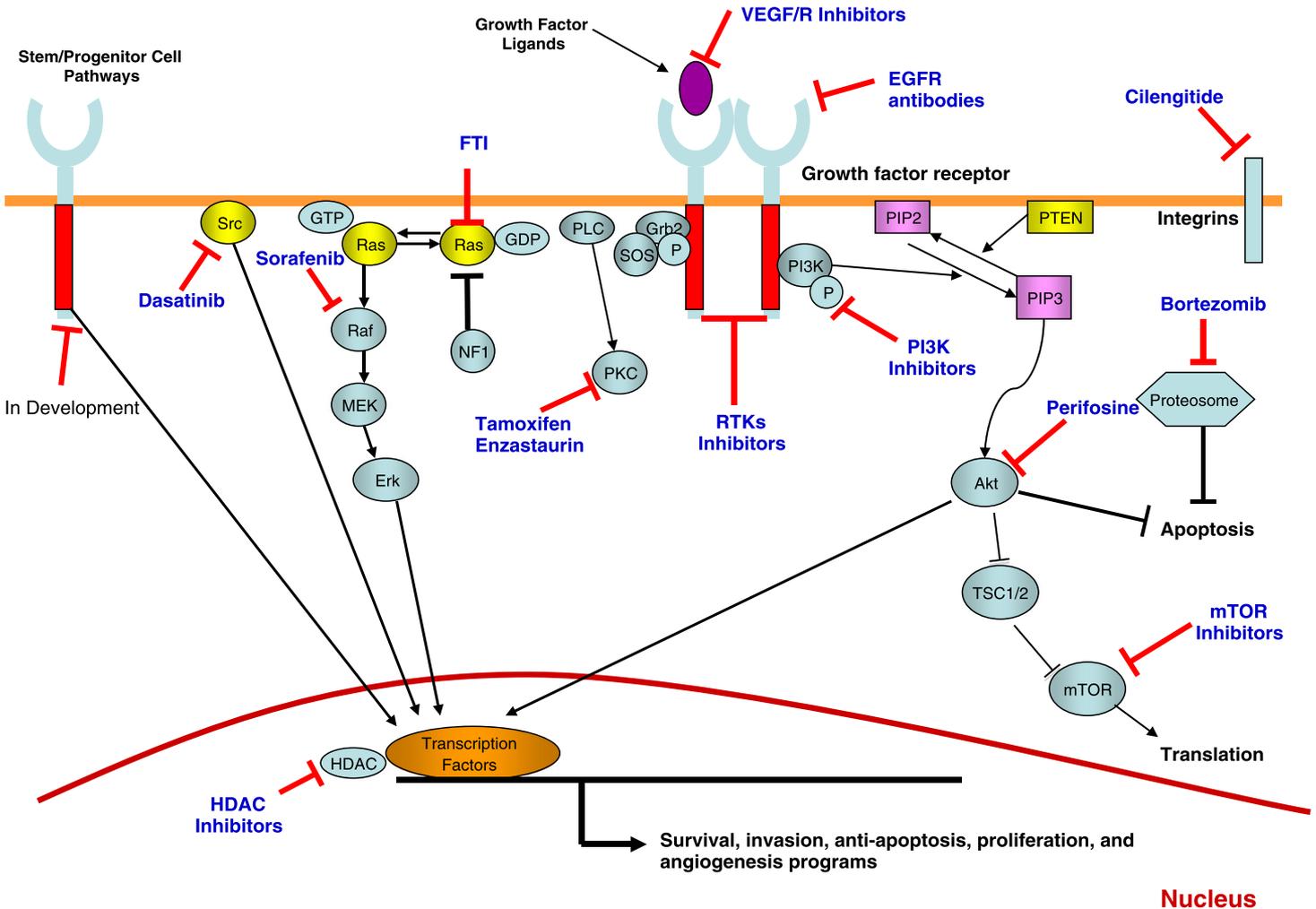
N Engl J Med 352., 987-996



RT: radiotherapy  
 TMZ: temozolomide  
 LMWH: low molecular weight heparin  
 AED: anti-epileptic drugs  
 PcP: pneumocystis jirovicii pneumonia prophylaxis

Ann Neurol 2011;70(1):9–21

# Glioma – Molecular Targets



Hu and Kesari

The Cancer Journal • Volume 18, Number 1, January/February 2012

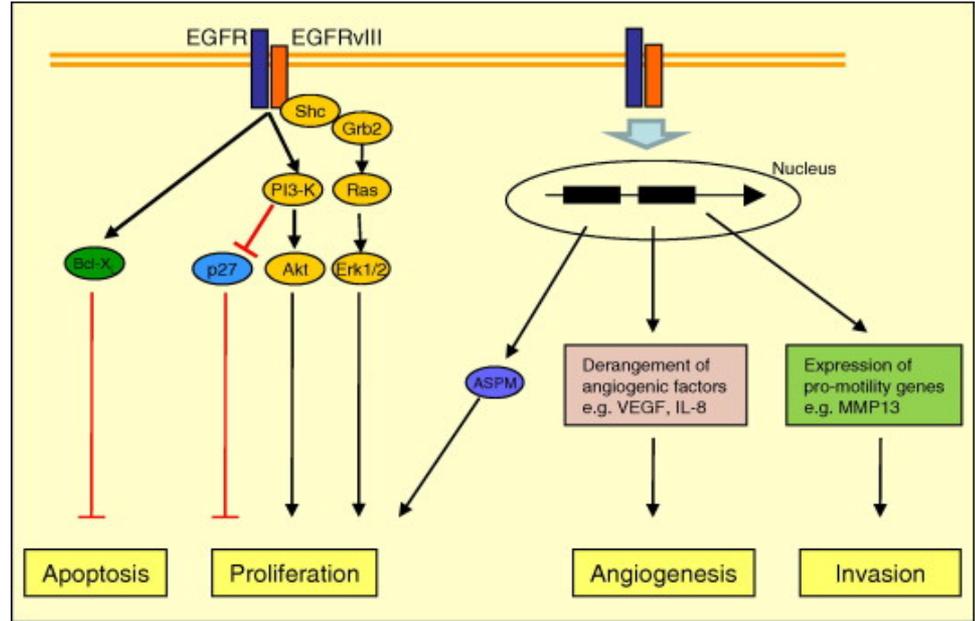
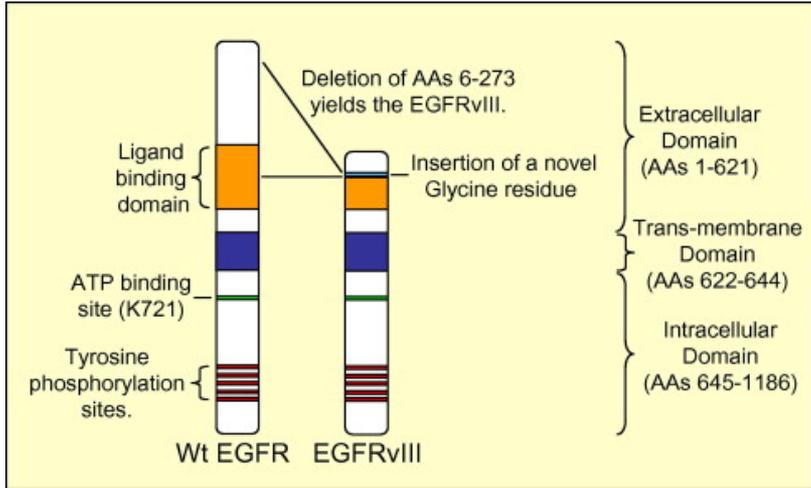
# Glioblastoma – Targeted Therapy

## Challenges in GBM therapy:

- **Redundancy**
  - Not depending on one driver mutation, others can compensate
- **Heterogeneity**
  - Several different driver mutations present in same tumor
- **Resistance**
  - Tumors escape targeting by utilizing new driver mutations

**=> Targeted therapy rarely shows a lasting effect**

# Glioblastoma – EGFR Targeted Therapy



## The rationale for using erlotinib (EGFR blocker) to treat glioblastoma:

- High expression of EGFR in about 50% of GBM
- Blocking EGFR should block glioblastoma growth & invasion
- Small molecule tyrosine kinase inhibitor (TKI) - crosses blood-brain barrier

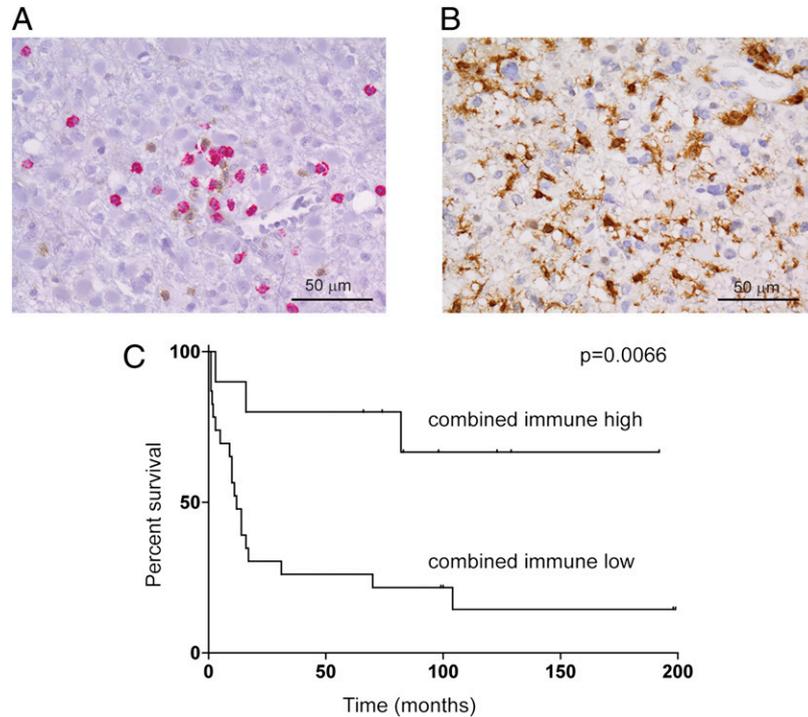
=> In trials, only 10-20% of patients respond

# Glioblastoma – Immunotherapy

- Checkpoint modulation
- Antibody-drug conjugates
- Vaccines
- CAR-T-cells

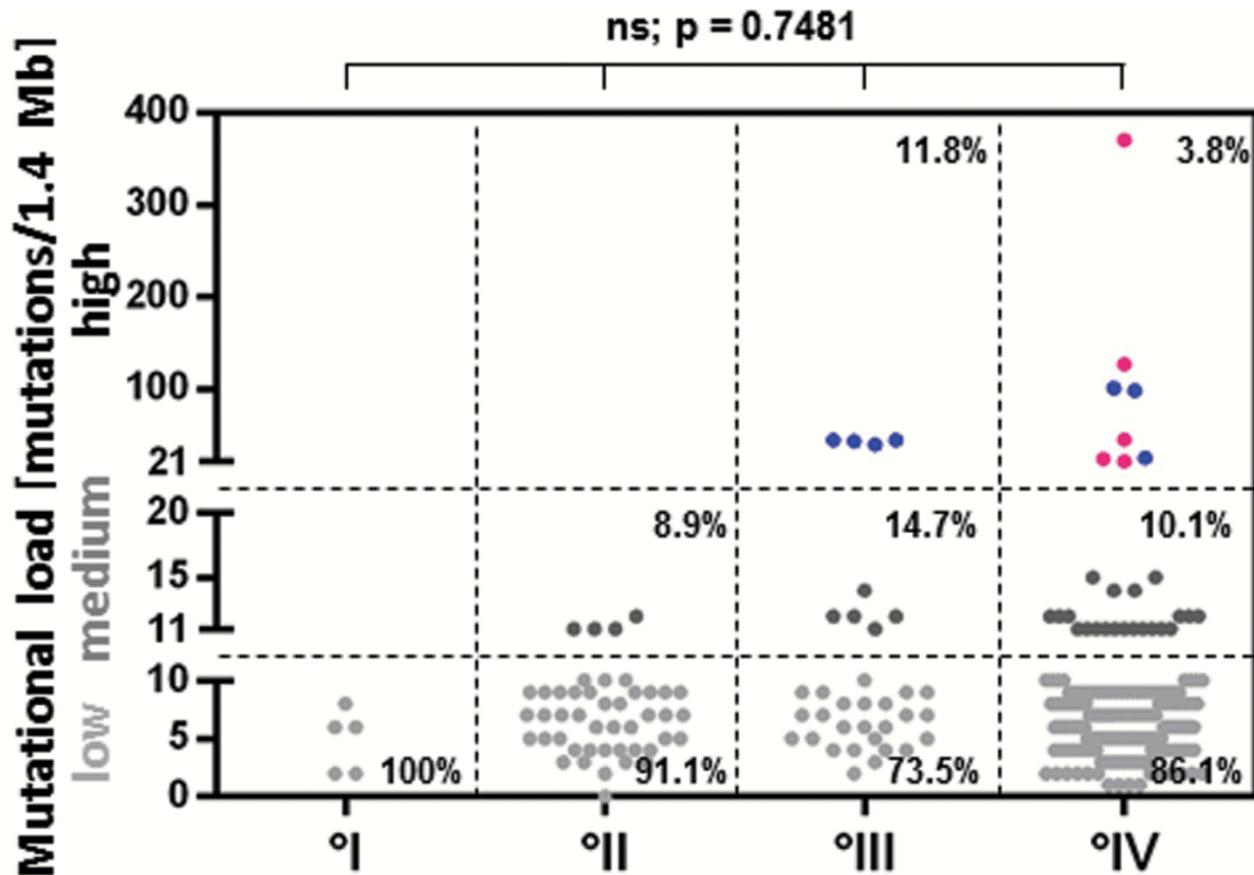
# Glioblastoma – Immunotherapy

**FIGURE 1.** Representative histology of **(A)** greater than median tumor infiltration of cytotoxic T cells (CD8; red) and Th cells (CD4; brown) in long-term survivor HGA11, and **(B)** >75th percentile tumor infiltration of microglia/macrophages (AIF1; brown) in long-term survivor HGA12. IHC was performed using FFPE tumor sections with hematoxylin counterstaining (original magnification  $\times 400$ ). **(C)** Kaplan–Meier survival analysis of combined immune cell infiltration. High combined immune cell infiltration was defined as greater than median cytotoxic T cell or Th cell or >75th percentile microglia/macrophage infiltration. Thirty-three HGA samples were used.



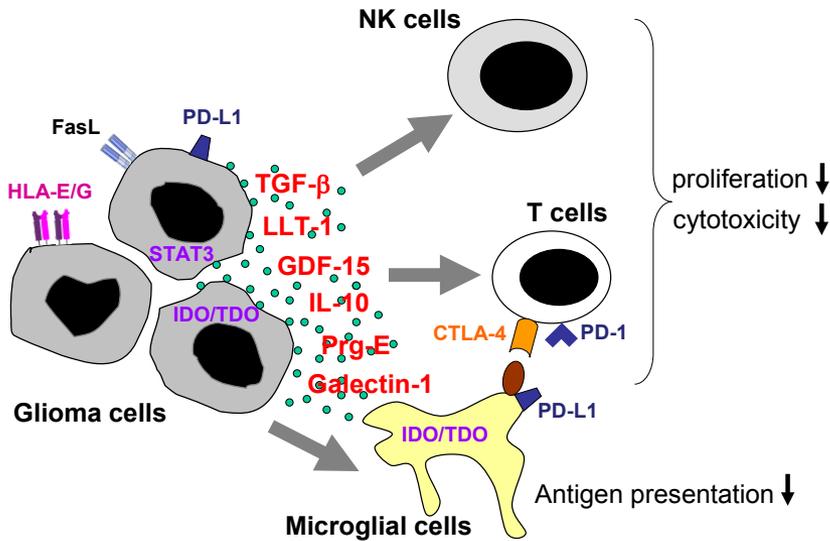
⇒ Higher immunoscore associated with better prognosis  
⇒ Brain not excluded from immunotherapy approaches

# Mutational Load in Glioma



=> Higher grade glioma show higher mutational load

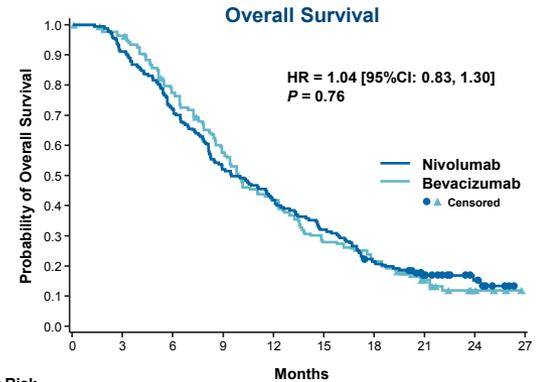
# Checkpoint Immunotherapy



- PD-L1 present in gliomas (in some)
- Anecdotal evidence of successful PD-1 inhibition in some cases
- **Phase III PD-1 inhibitor trial negative** in recurrent glioblastoma
- Clinical trials in newly diagnosed glioblastoma ongoing

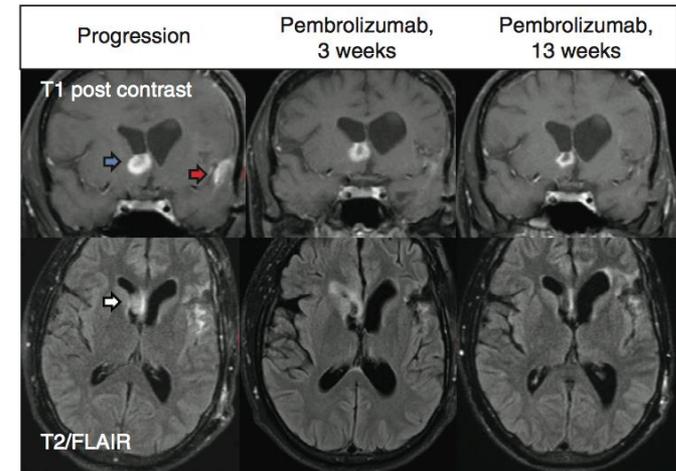
Roth ESMO 2016

	Events, n	Median OS [95% CI], months	12-Month OS Rate [95% CI], months
Nivolumab	154	9.8 [8.2, 11.8]	41.8 [34.7, 48.8]
Bevacizumab	147	10.0 [9.0, 11.8]	42.0 [34.6, 49.3]



No. at Risk	Months									
	0	3	6	9	12	15	18	21	24	27
Nivolumab	184	168	133	96	77	59	39	24	9	0
Bevacizumab	185	169	135	99	72	48	37	14	5	0

Reardon et al., WFOS meeting 2017



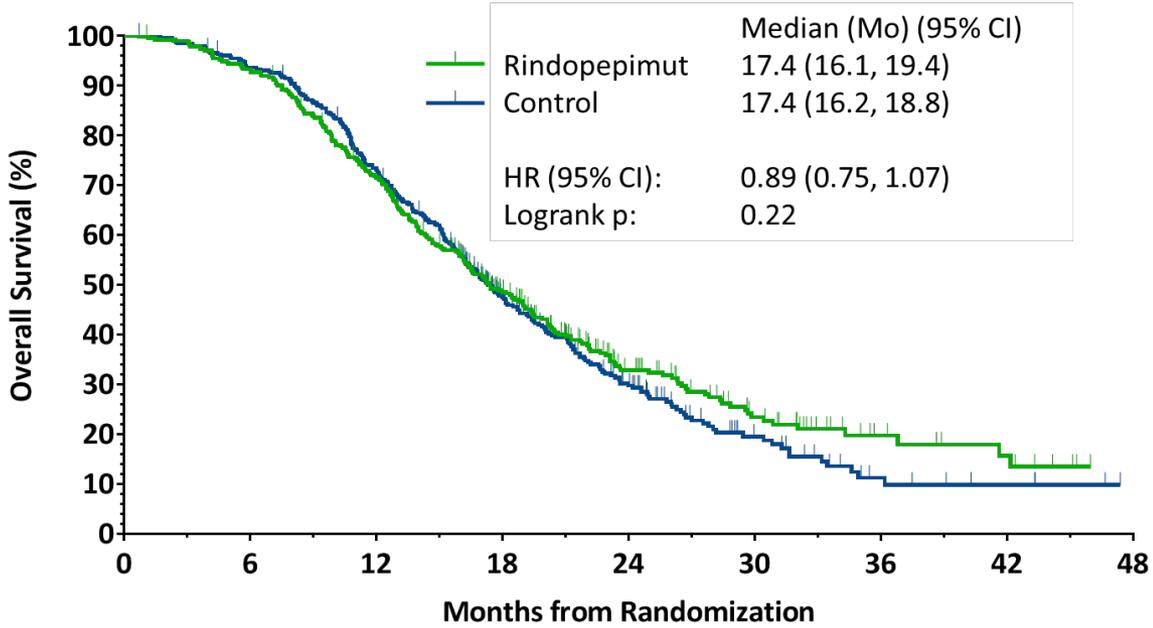
Johans, Cancer Discovery 2016

# Glioblastoma Cancer Vaccination

- Vaccine approaches: tumor cell lysate, RNA, peptides, DC
- Strong adjuvants required
- Promising data from preclinical models
- Clinical trials dissapointing

# Glioblastoma – EGFRviii vaccination

## EGFRviii vaccination



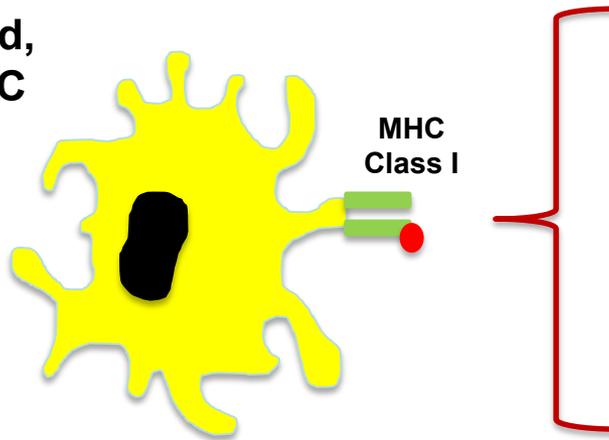
Number at Risk	0	6	12	18	24	30	36	42	48
Rindopepimut	371	345	261	159	72	32	12	7	0
Control	374	347	268	149	73	25	8	4	0

Weller et al., SNO meeting 2016

# Glioblastoma – DC vaccine

Example for a DC based vaccine

**Matured, activated,  
peptide-loaded DC**

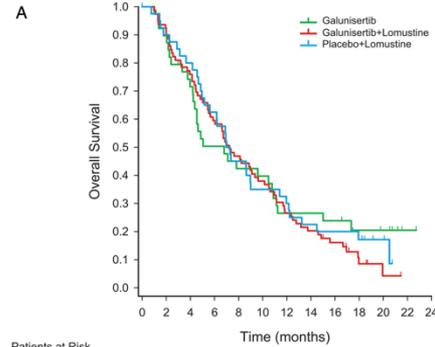
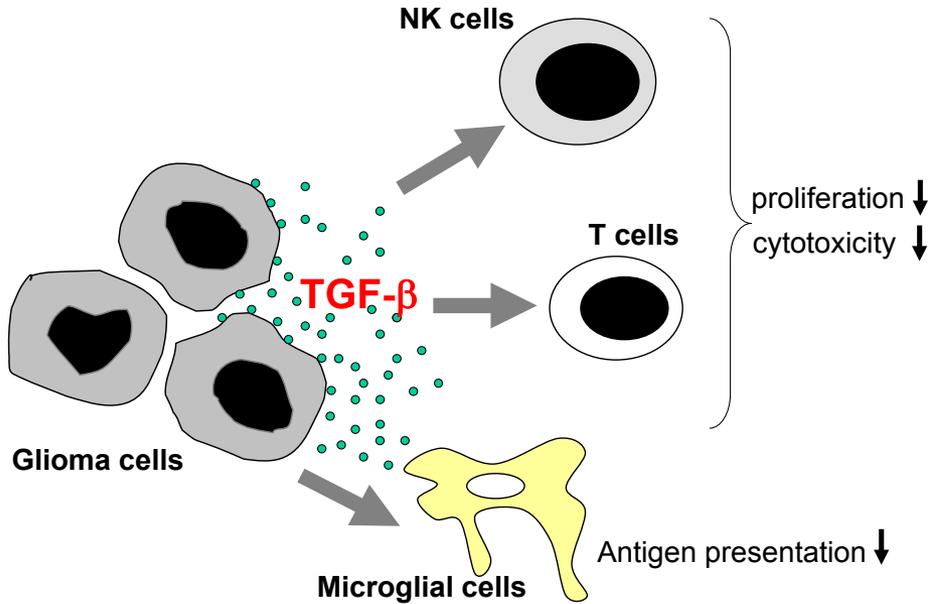


**Six 9-10 amino acid antigen epitopes**

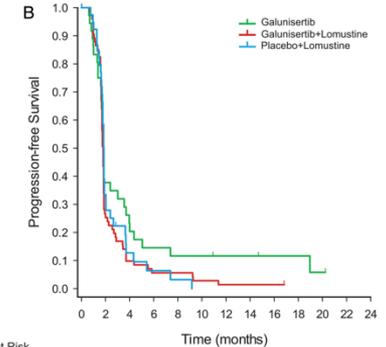
- MAGE-1 (HLA - A1)
- AIM-2 (A1)
- gp100 (HLA - A2)
- IL-13R $\alpha$ 2 (A2)
- HER2/neu (A2)
- TRP-2 (A2)

- Targeting multiple antigens
- Promising data in a randomized phase II trial
- Phase III trial ongoing: ICT-107 or placebo in addition to temozolomide-based radiochemotherapy in patients with newly diagnosed glioblastoma

# Glioblastoma – TGF- $\beta$ inhibition



Patients at Risk													
Galunisertib	39	35	27	19	16	15	10	10	9	6	5	1	0
Galunisertib+Lomustine	79	73	60	47	37	30	21	16	11	4	1	0	0
Placebo+Lomustine	40	36	32	25	18	14	12	9	8	6	3	0	0



Patients at Risk													
Galunisertib	39	13	8	5	4	4	3	3	2	2	1	0	0
Galunisertib+Lomustine	79	19	7	4	4	2	1	1	1	0	0	0	0
Placebo+Lomustine	40	12	4	2	1	0	0	0	0	0	0	0	0

=> No impact on median survival in TGF- $\beta$  targeting treatment groups

# The Year 2010

**Introduction of a novel GBM classification  
based on molecular signatures**



## Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in *PDGFRA*, *IDH1*, *EGFR*, and *NF1*

Roel G.W. Verhaak,<sup>1,2,17</sup> Katherine A. Hoadley,<sup>3,4,17</sup> Elizabeth Purdom,<sup>7</sup> Victoria Wang,<sup>8</sup> Yuan Qi,<sup>4,5</sup> Matthew D. Wilkerson,<sup>4,5</sup> C. Ryan Miller,<sup>4,6</sup> Li Ding,<sup>9</sup> Todd Golub,<sup>1,10</sup> Jill P. Mesirov,<sup>1</sup> Gabriele Alexe,<sup>1</sup> Michael Lawrence,<sup>1,2</sup> Michael O'Kelly,<sup>1,2</sup> Pablo Tamayo,<sup>1</sup> Barbara A. Weir,<sup>1,2</sup> Stacey Gabriel,<sup>1</sup> Wendy Winckler,<sup>1,2</sup> Supriya Gupta,<sup>1</sup> Lakshmi Jakkula,<sup>11</sup> Heidi S. Feiler,<sup>11</sup> J. Graeme Hodgson,<sup>12</sup> C. David James,<sup>12</sup> Jann N. Sarkaria,<sup>13</sup> Cameron Brennan,<sup>14</sup> Ari Kahn,<sup>15</sup> Paul T. Spellman,<sup>11</sup> Richard K. Wilson,<sup>9</sup> Terence P. Speed,<sup>7,16</sup> Joe W. Gray,<sup>11</sup> Matthew Meyerson,<sup>1,2</sup> Gad Getz,<sup>1</sup> Charles M. Perou,<sup>3,4,8</sup> D. Neil Hayes,<sup>4,5,\*</sup> and The Cancer Genome Atlas Research Network

<sup>1</sup>The Eli and Edythe L. Broad Institute of Massachusetts Institute of Technology and Harvard University, Cambridge, MA 02142, USA

<sup>2</sup>Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, MA 02115, USA

<sup>3</sup>Department of Genetics

<sup>4</sup>Lineberger Comprehensive Cancer Center

<sup>5</sup>Department of Internal Medicine, Division of Medical Oncology

<sup>6</sup>Department of Pathology and Laboratory Medicine

University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA

<sup>7</sup>Department of Statistics

<sup>8</sup>Group in Biostatistics

University of California, Berkeley, CA 94720, USA

<sup>9</sup>The Genome Center at Washington University, Department of Genetics, Washington University School of Medicine, St. Louis, MO 63108, USA

<sup>10</sup>Department of Pediatric Oncology, Center for Cancer Genome Discovery, Dana-Farber Cancer Institute, Boston, MA 02115, USA

<sup>11</sup>Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA

<sup>12</sup>Department of Neurological Surgery, University of California, San Francisco, CA 94143, USA

<sup>13</sup>Department of Radiation Oncology, Mayo Clinic, Rochester, MN 55905, USA

<sup>14</sup>Department of Neurosurgery, Memorial Sloan-Kettering Cancer Center, New York, NY 10065, USA

<sup>15</sup>SRA International, Fairfax, VA 22033, USA

<sup>16</sup>Walter and Eliza Hall Institute, Parkville, Victoria 3052, Australia

<sup>17</sup>These authors contributed equally to the work

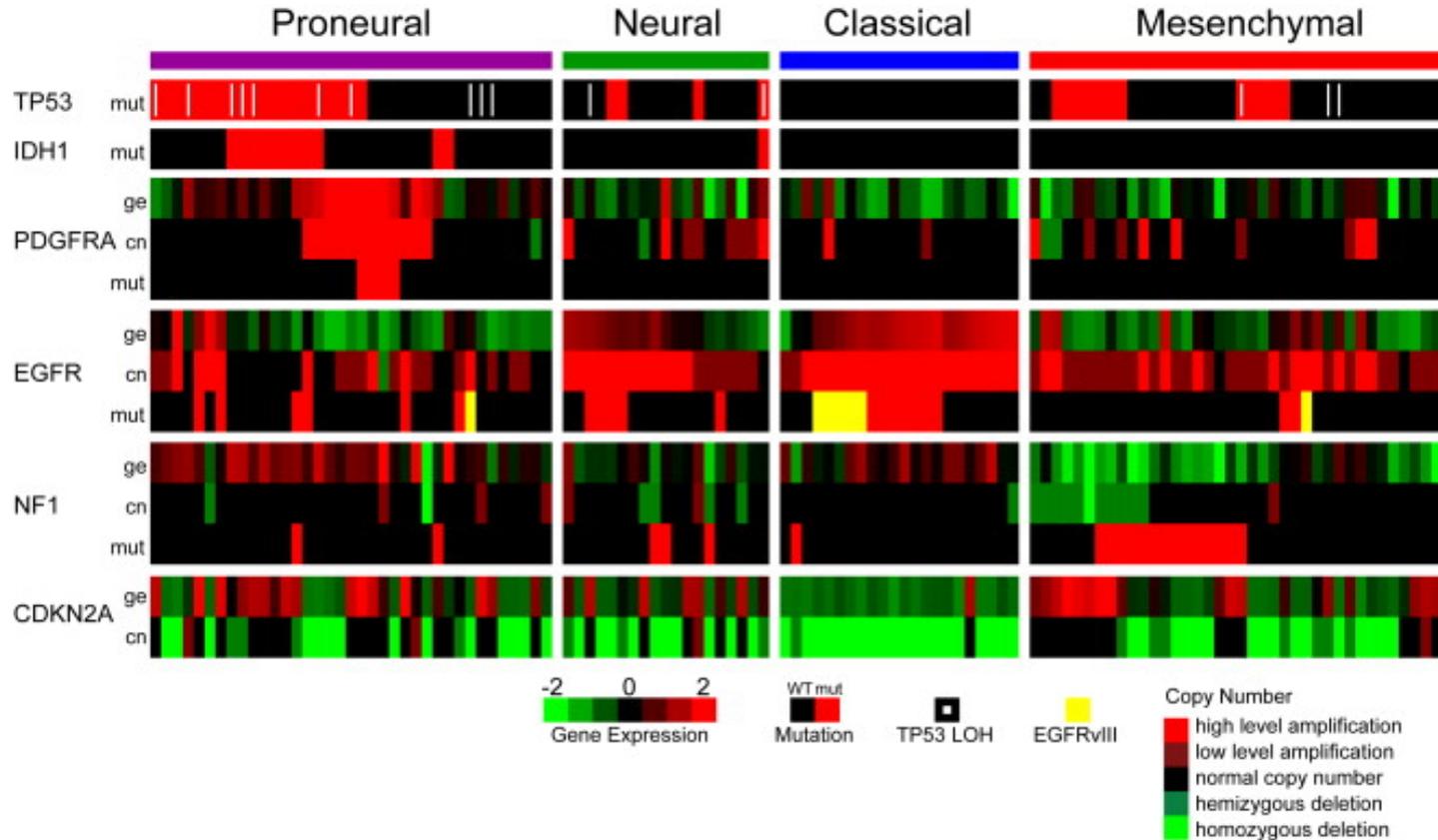
\*Correspondence: [hayes@med.unc.edu](mailto:hayes@med.unc.edu)

DOI 10.1016/j.ccr.2009.12.020

Cancer Cell 17, 98–110, January 19, 2010

# Glioma – Molecular Classification

Analysis from The Cancer Genome Atlas ( $\approx$  600 GBM tumors)



Cancer Cell 17, 98–110, January 19, 2010

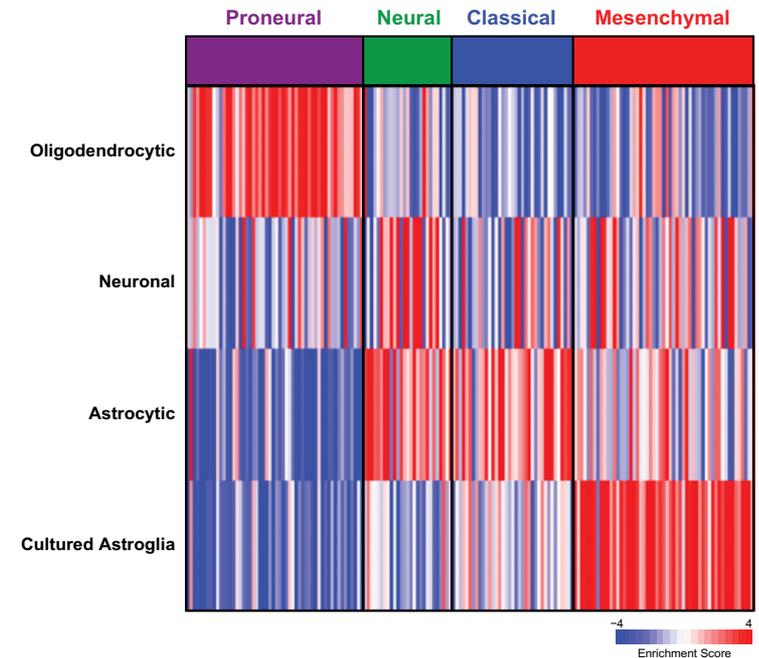
# Glioma – Molecular Classification

**Table 3. Distribution of Frequently Mutated Genes across GBM Subtypes**

Gene	Proneural (n = 37)	Neural (n = 19)	Classical (n = 22)	Mesenchymal (n = 38)	Total No. of Mutations
<i>TP53</i>	<b>20 (54%)</b>	4 (21%)	<b>0 (0%)</b>	12 (32%)	36
<i>PTEN</i>	6 (16%)	4 (21%)	5 (23%)	12 (32%)	27
<i>NF1</i>	2 (5%)	3 (16%)	1 (5%)	<b>14 (37%)</b>	20
<i>EGFR</i>	6 (16%)	5 (26%)	7 (32%)	2 (5%)	20
<i>IDH1</i>	<b>11 (30%)<sup>a</sup></b>	1 (5%)	0 (0%)	0 (0%)	12
<i>PIK3R1</i>	7 (19%)	2 (11%)	1 (5%)	0 (0%)	10
<i>RB1</i>	1 (3%)	1 (5%)	0 (0%)	5 (13%)	7
<i>ERBB2</i>	2 (5%)	3 (16%)	1 (5%)	1 (3%)	7
<i>EGFRvIII</i>	1 (3%)	0 (0%)	5 (23%)	1 (3%)	7
<i>PIK3CA</i>	3 (8%)	1 (5%)	1 (5%)	1 (3%)	6
<i>PDGFRA</i>	4 (11%)	0 (0%)	0 (0%)	0 (0%)	4

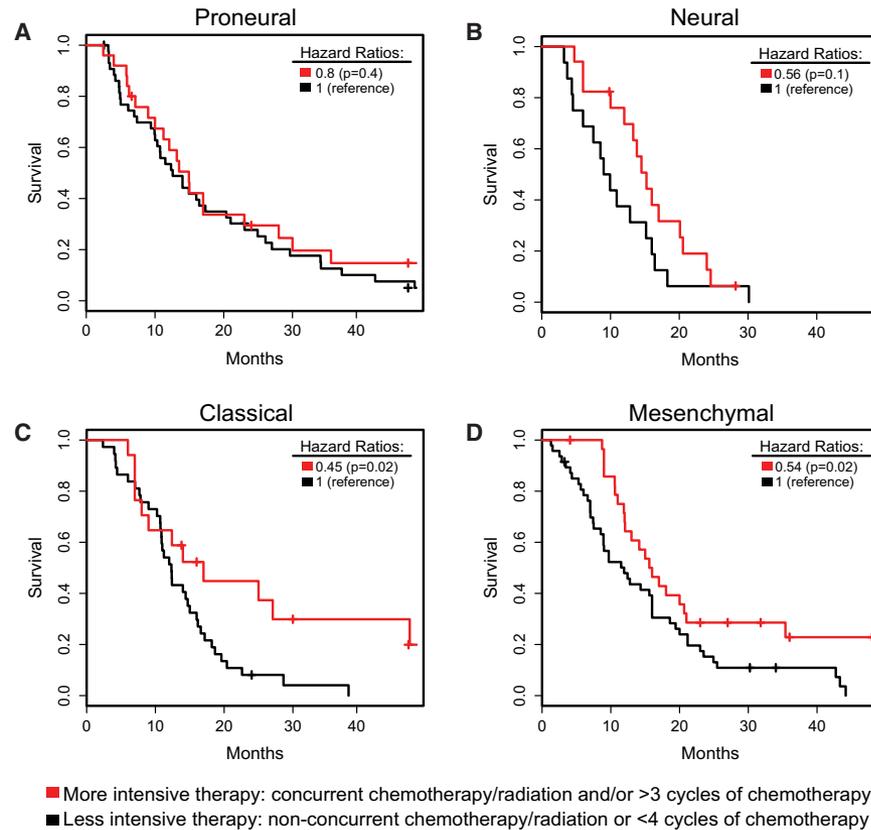
Significance of the difference in number of events between subtypes and remainder of the subtypes was determined using a two-sided Fisher's exact test, corrected for multiple testing using a Familywise Error Rate. Bold type indicates p values significant at an 0.1 level. Also see [Figure S5](#) and [Tables S2, S4, and S6](#).

<sup>a</sup> p value significant at 0.01 level.



Correlation between GBM subtype and cultured cell types

# Glioma – Molecular Classification



- ⇒ The “CLASSICAL” subtype responds best, the “PRONEURAL” subtype worst to intensified treatment.
- ⇒ Later studies found proneural to have best and mesenchymal subtype to have worst overall prognosis

# Glioma – Molecular vs WHO Classification

## Genetic pathways to primary and secondary glioblastomas

