

# Molecular characterization of mesenchymal tumors: promises and challenges

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 ***@kells108***

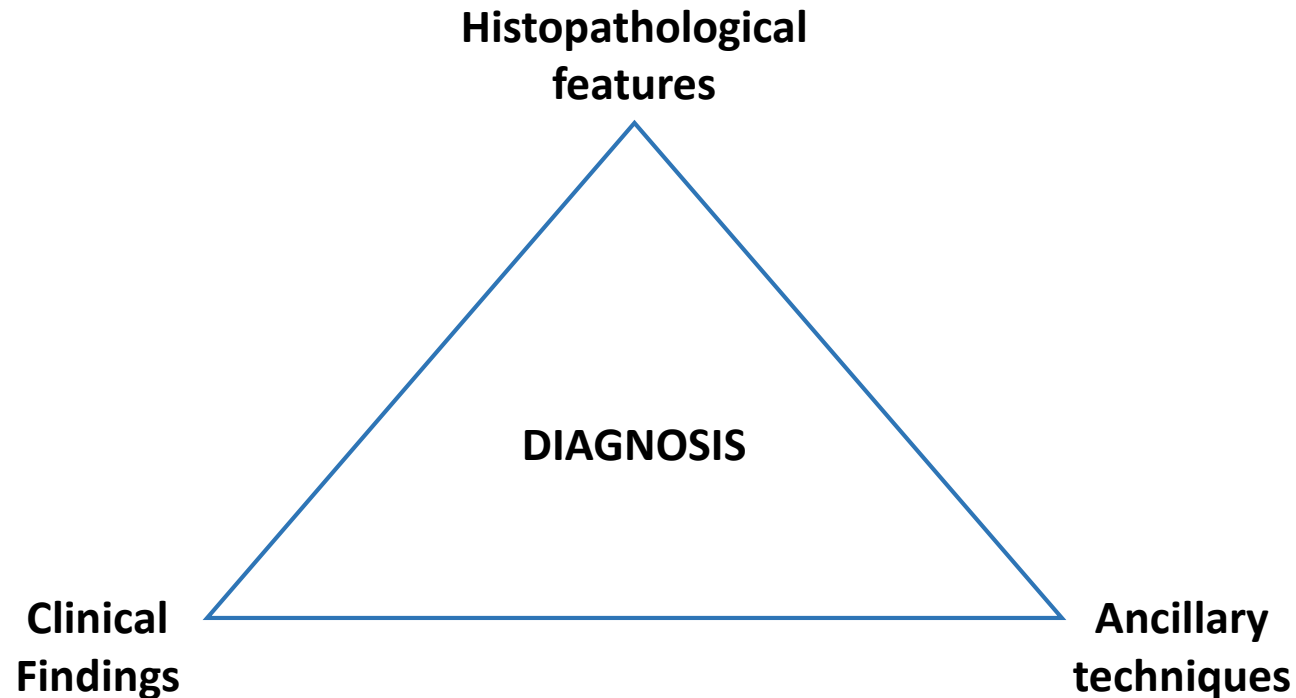
**I, Raul Perret have no conflicts of interest to declare.**

# Objective of the lecture

To discuss the current value and perspectives of genetics in the diagnosis and management of soft tissue tumors

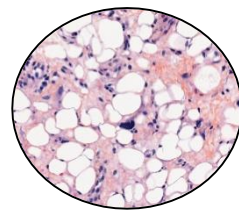
# Take home message

- Molecular biology techniques are valuable tools, in selected cases, but they don't replace our brains

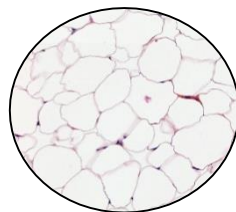


# Overview of Soft Tissue Neoplasms

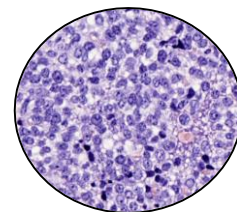
- Sarcomas  $\approx$  1% adult cancers
- Classification based on histology: **Tumor line of differentiation** (*>100 subtypes*)



*Liposarcoma*



*Adipose tissue*



*Ewing Sarcoma*



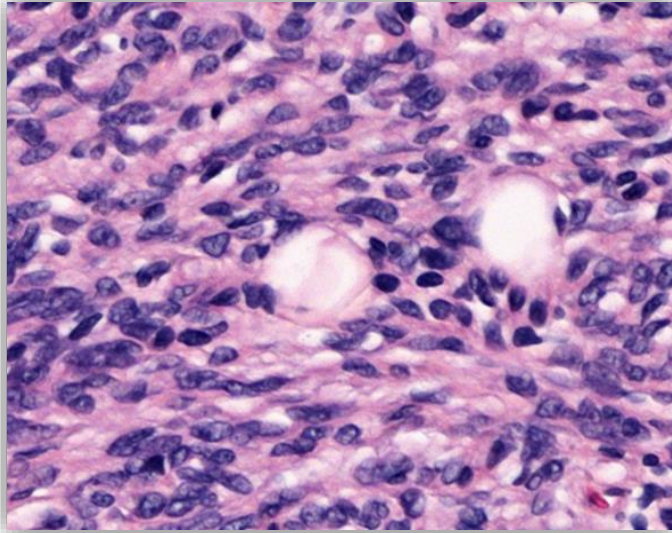
- Classification based on tumour behaviour: **benign, intermediate malignancy, malignant**
- Classification based on genetics: **complex vs simple**

## Simple genetics

No/Minimal chromosomal aberrations

Gene translocations

Point mutations



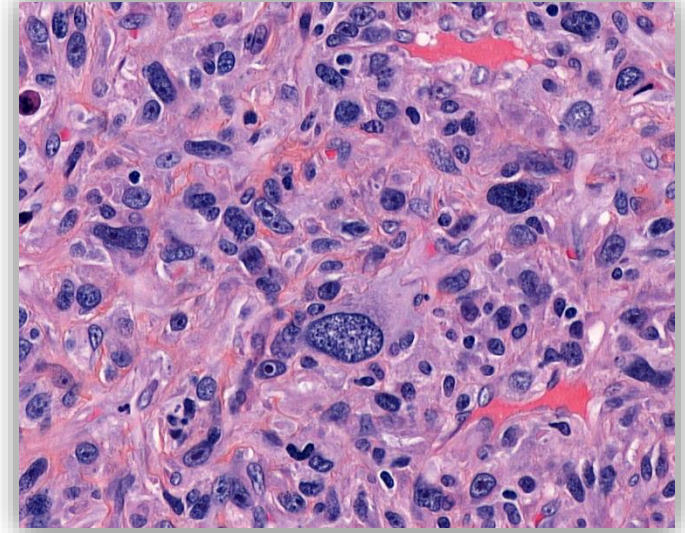
**Dermatofibrosarcoma Protuberans**

## Complex genetics

Numerous chromosomal aberrations

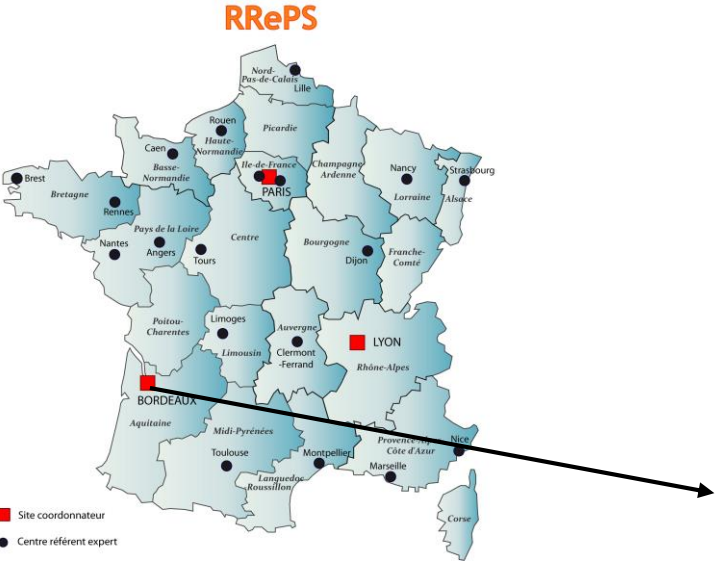
Recurrent

Non-recurrent



**Undifferentiated pleomorphic sarcoma**

Réseau de Référence en Pathologie des Sarcomes



Institut Bergonié (Bordeaux, France)  
Tertiary care center

Biopathology Department  
Available Molecular techniques

| Array-Comparative Genomic Hybridization (aCGH) | Fluorescence in-situ Hybridization (FISH)                              | Massive parallel Sequencing (NGS)  | Sanger-Sequencing                            | RT-PCR |
|--|--|------------------------------------|--|--------|
| CNVs   | MDM2 (Liposarcomas well diff./dediff.)<br>EWSR1 (Ewing sarcoma mainly) | Unclassified or Challenging Tumors | CTNNB1 (desmoid)<br>MYOD1 (spindle cell RMS) |        |

# **Molecular Genetics in the pathology department**

## Aims

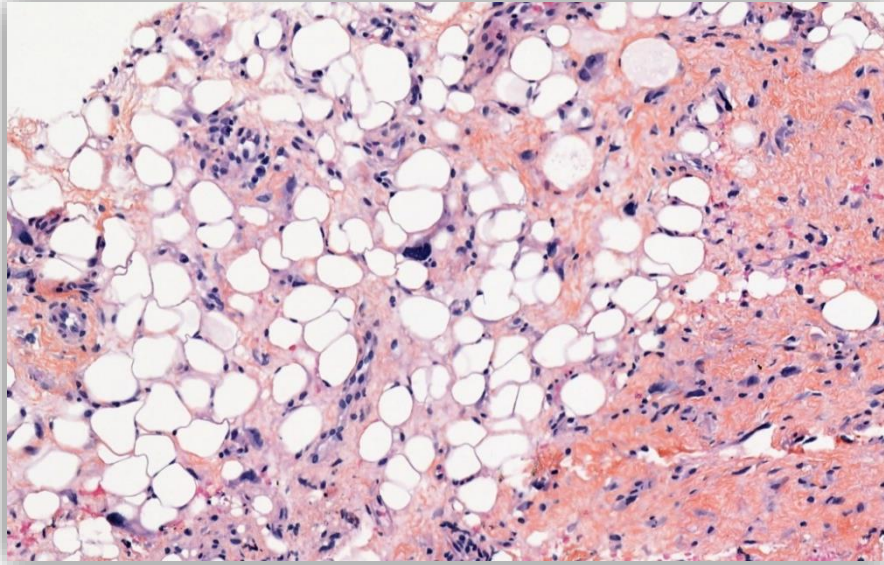
**Increase diagnostic accuracy**

**Identify molecular targets**

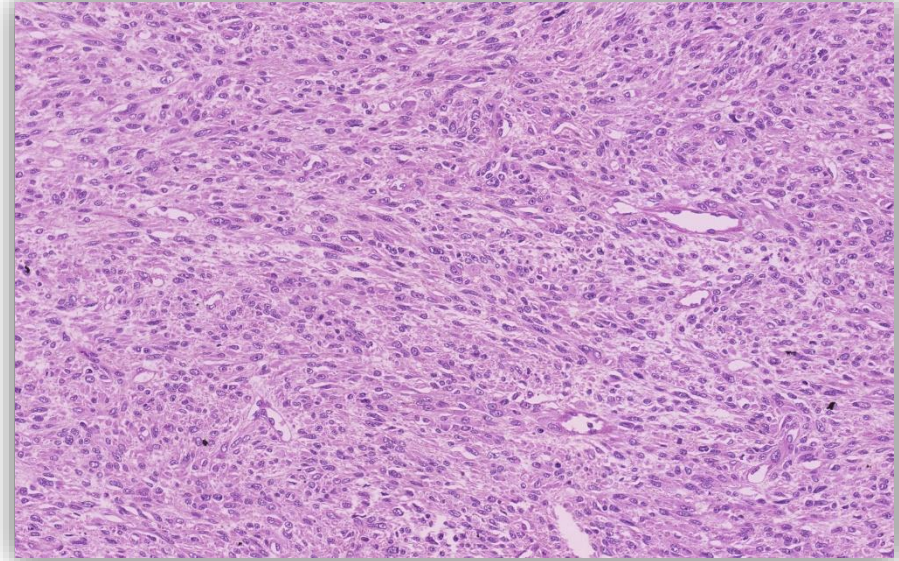
**Predict tumor behavior**



# Adipocytic tumors with *MDM2* amplification



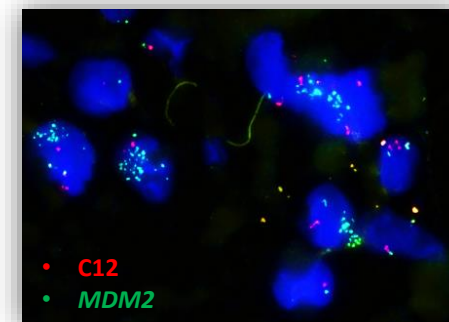
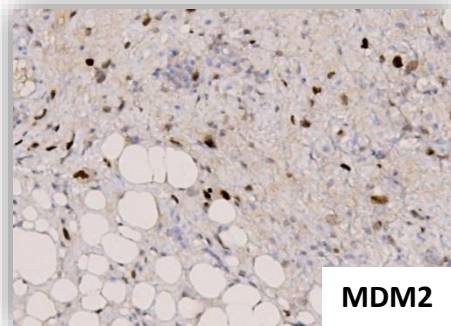
Well differentiated liposarcoma



Dedifferentiated liposarcoma

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Amplification Chr. 12q13-15  
(*MDM2*, *CDK4*, *HMGA2*...)



## Indications of FISH testing for *MDM2* amplification

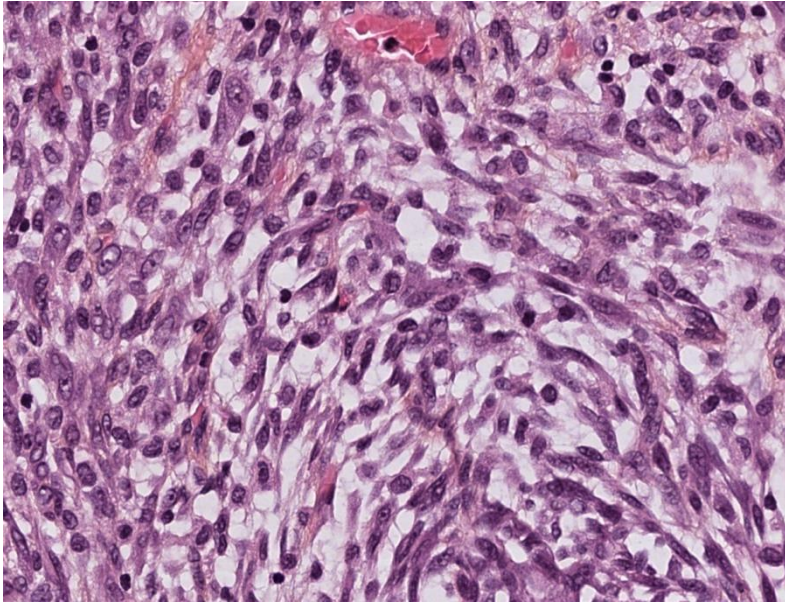
- Recurrent adipocytic tumor
- Deep extremity tumors that are >10 cm in patients >50 years
- Adipocytic tumor with equivocal atypia
- Undifferentiated tumors of the retroperitoneum/pelvis/abdomen
- Core needle biopsies of adipocytic tumors\*

# Is the presence of *MDM2* amplification exclusive of well diff./Dediff. Liposarcoma?

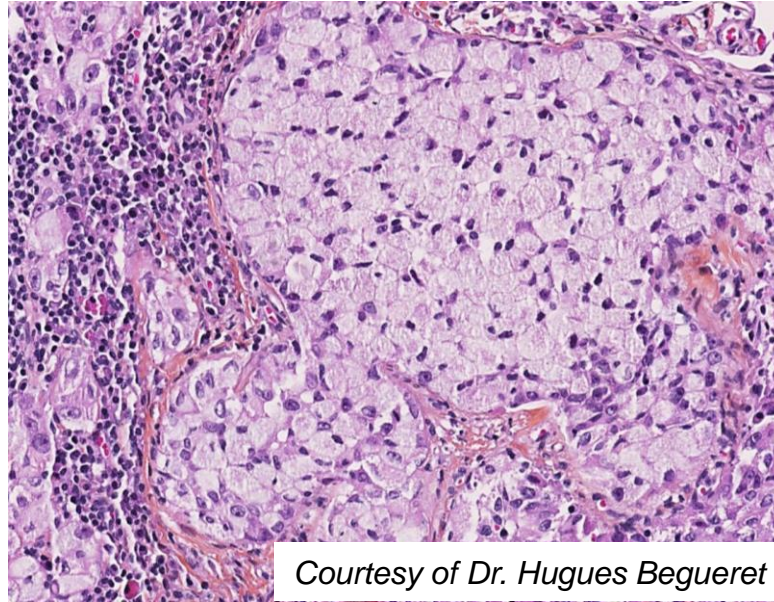
- *Intimal sarcoma*
- *Low grade osteosarcoma*
- *Carcinoma*
- *Gyn Tumors*
- *Melanoma*



## ***EML4-ALK* Fusions in various tumor subtypes**

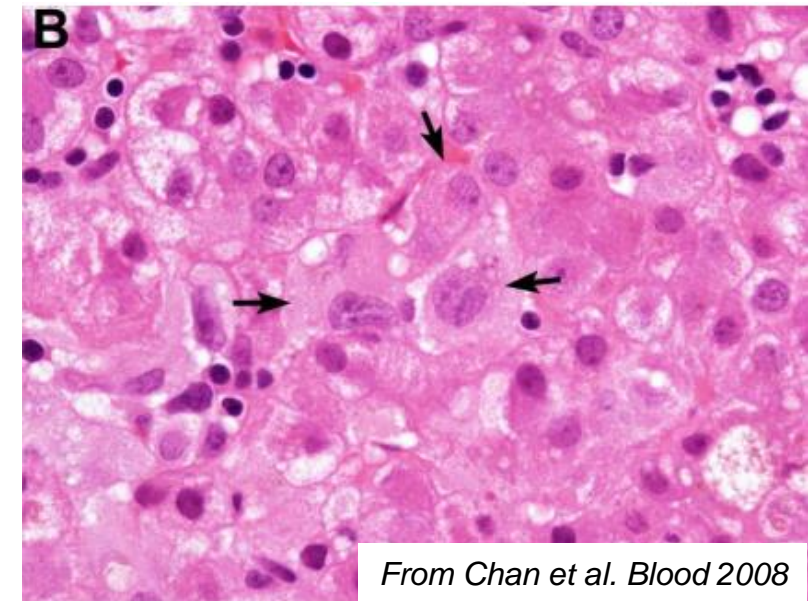


Inflammatory Myofibroblastic Tumor



*Courtesy of Dr. Hugues Begueret*

Lung adenocarcinoma



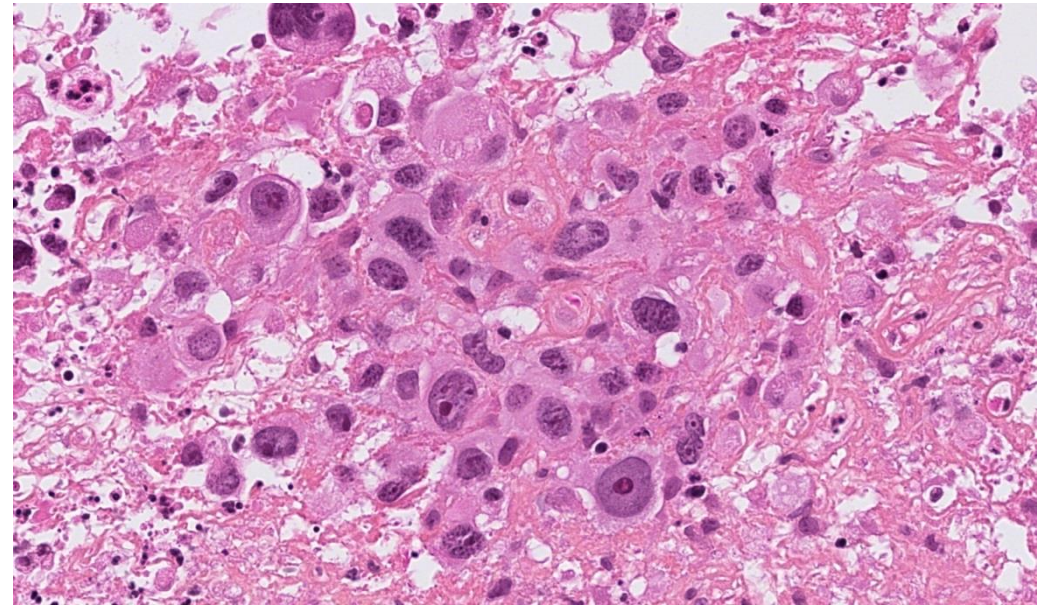
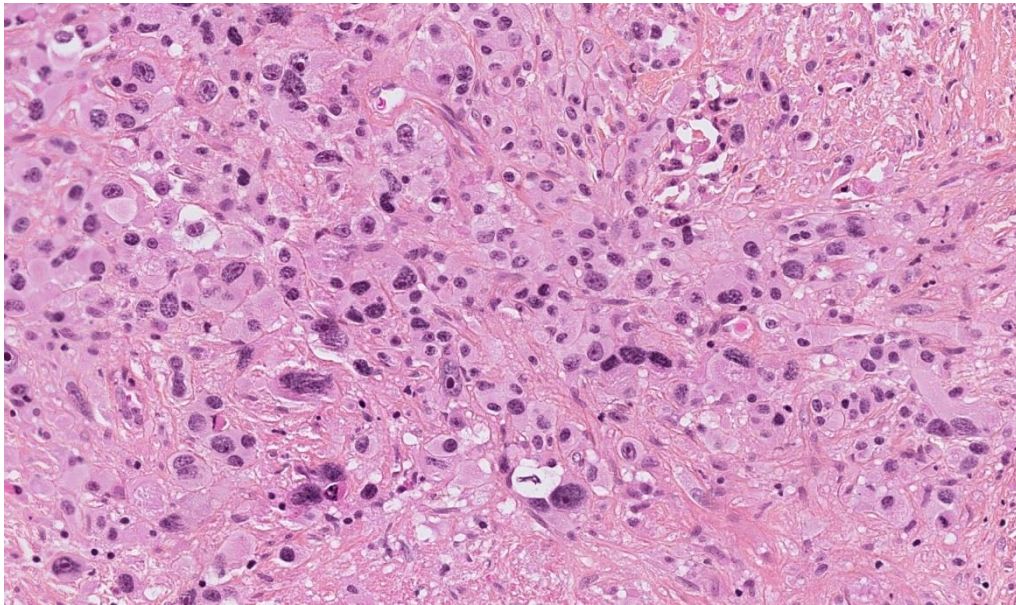
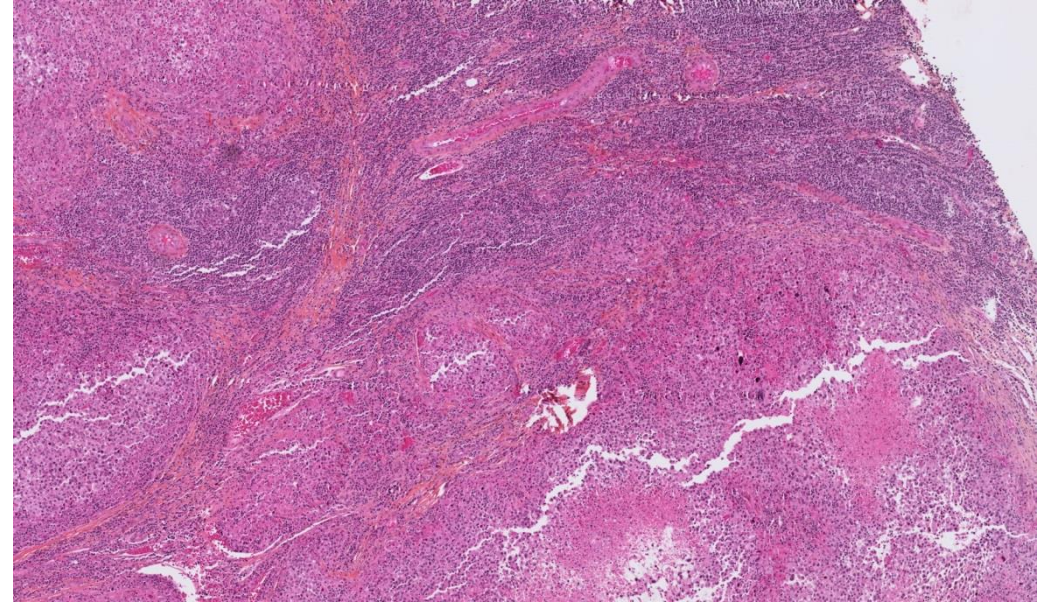
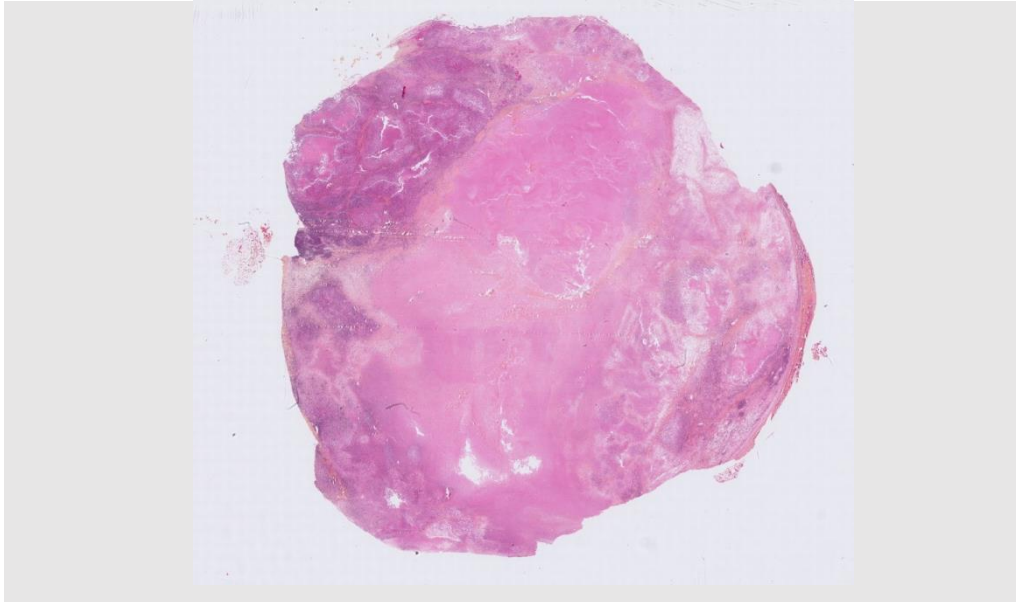
*From Chan et al. Blood 2008*

Non-Langerhans cell histiocytosis

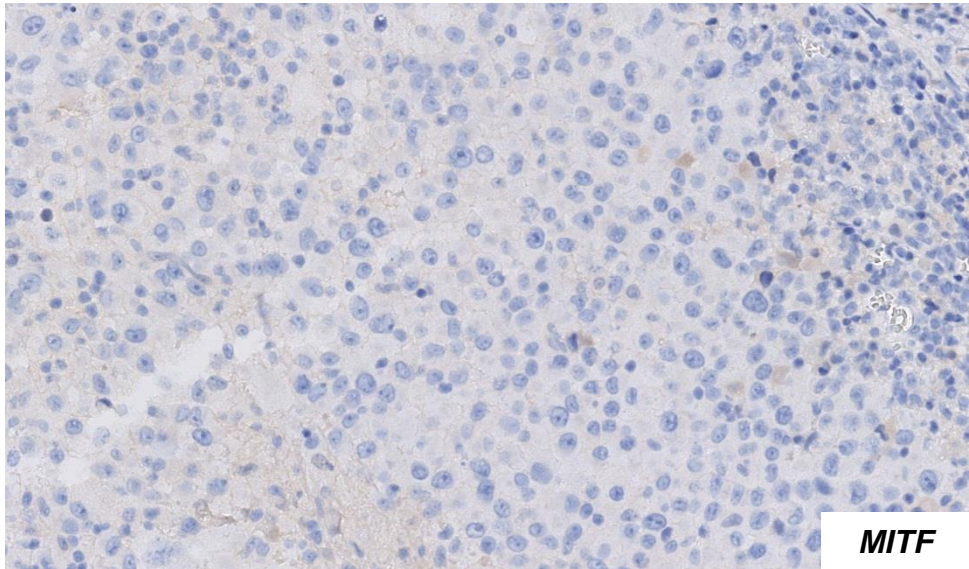
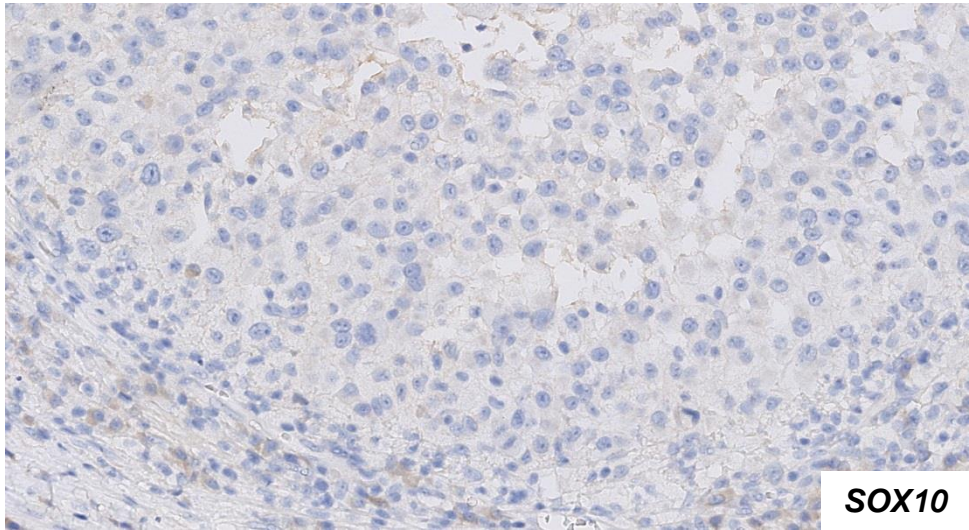
**A molecular alteration does not certify a diagnosis, CPC is mandatory**



*Adult male, axillary adenopathy. Metastasis? Lymphoma?*





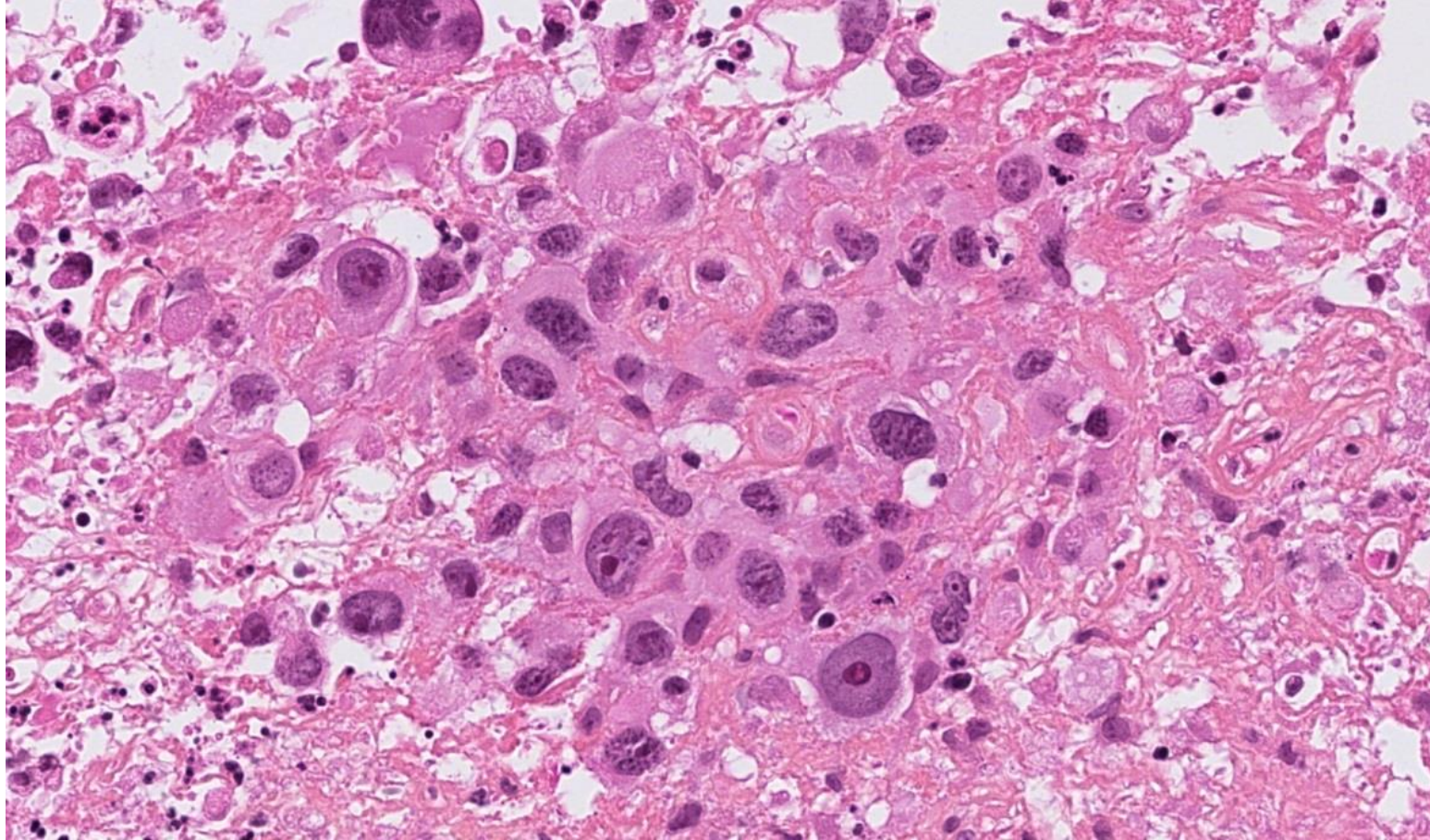


| Other negative markers |              |               |
|------------------------|--------------|---------------|
| S100                   | Myogenin     | CD68          |
| HMB45                  | MDM2         | P40           |
| MelanA                 | CD45         | OCT4          |
| CD34                   | CD20         | MPO           |
| ERG                    | CD3          | Pan-keratin   |
| Desmin                 | CD30         | CK7           |
| H-Caldesmon            | CD5          | CK20          |
| ALK                    | CDX2         | CD138         |
| TTF1                   | PAX8         | CD21          |
| INSM1                  | Chromogranin | Synaptophysin |
| MUC4                   |              |               |

Ki67 75%

INI1 and BRG1 conserved expression

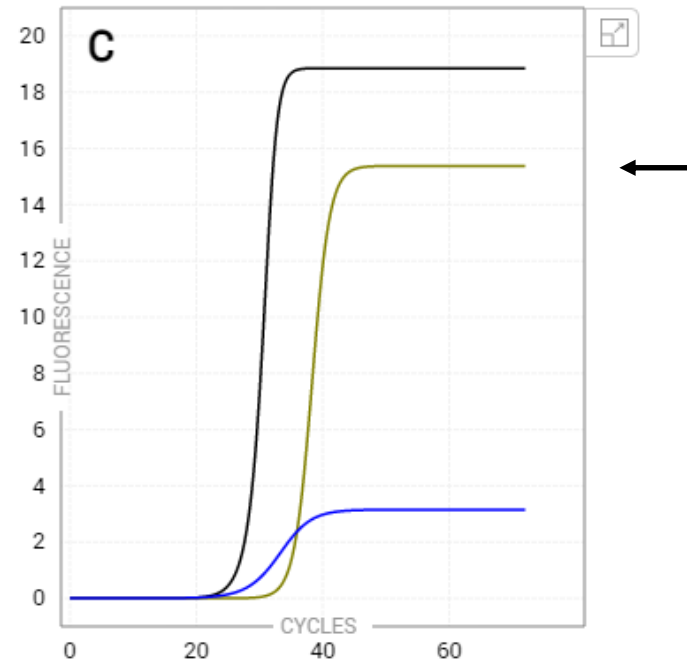




***Next Step?***



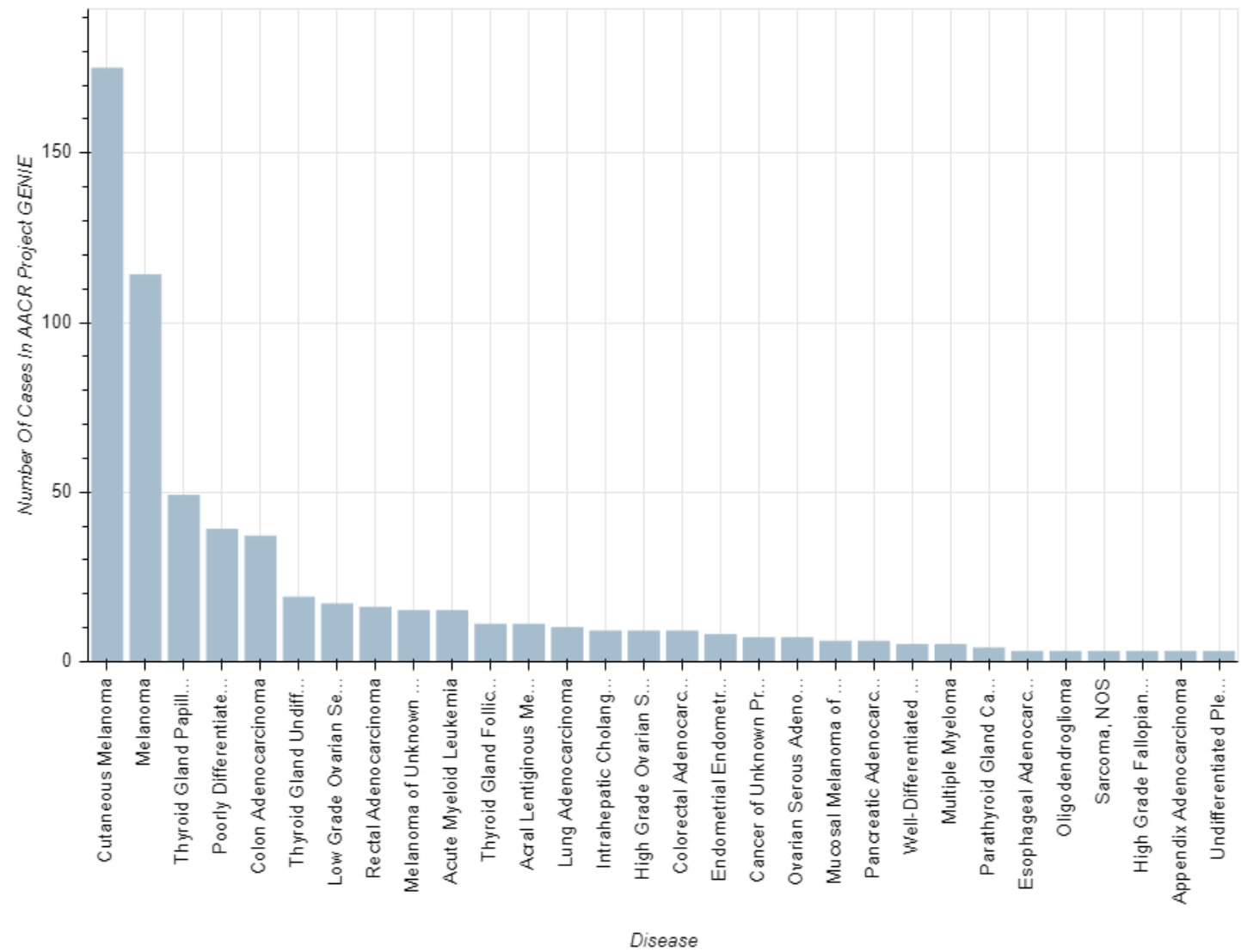
# Molecular screening for *BRAF*/*NRAS* mutations



| TARGET               |   | CQ    | $\Delta$ CQ |
|----------------------|---|-------|-------------|
| ● BRAF Total         | + | 30.35 | -           |
| → ● <u>NRAS Q61R</u> | + | 36.79 | 7.61        |
| ● NRAS Total         | + | 29.18 | -           |



*NRAS Q61R is present in 0.77% of AACR GENIE cases, with cutaneous melanoma, melanoma, thyroid gland papillary carcinoma, poorly differentiated thyroid gland carcinoma, and colon adenocarcinoma having the greatest prevalence<sup>4</sup>.*



Diagnosis: undifferentiated malignant epithelioid tumor,  
favor undifferentiated melanoma (probable metastatic location)

# Dedifferentiated and Undifferentiated Melanomas

## *Report of 35 New Cases With Literature Review and Proposal of Diagnostic Criteria*

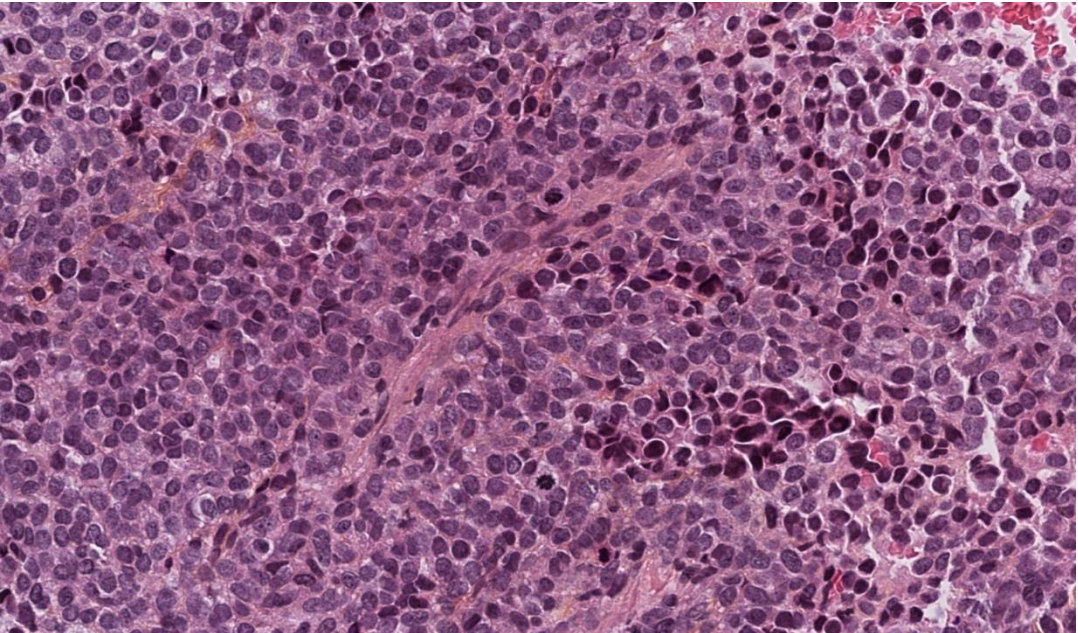
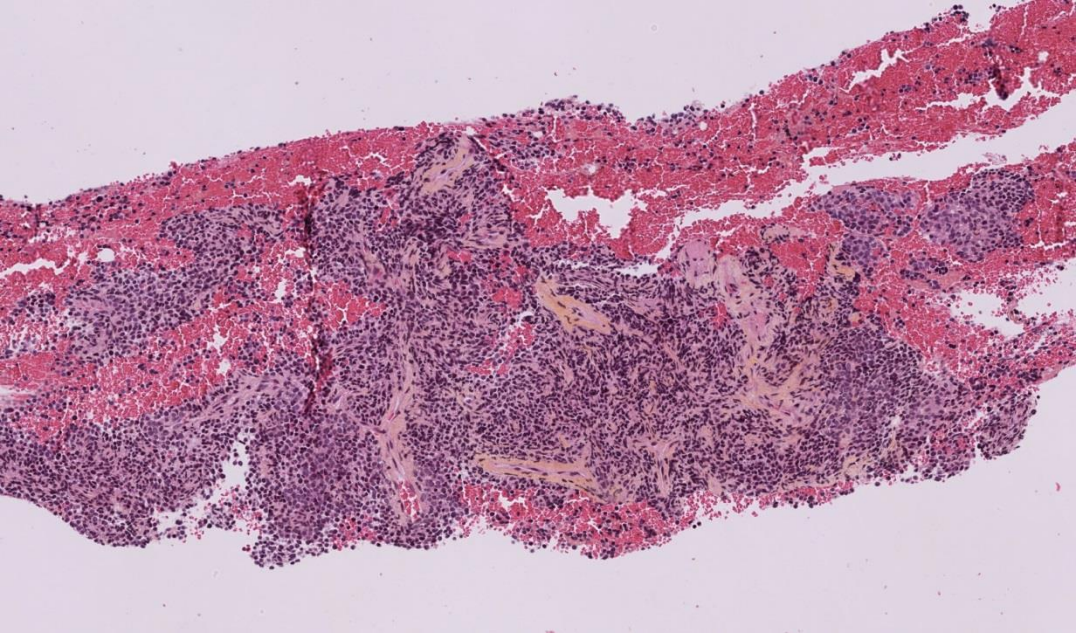
*Abbas Agaimy, MD,\* Robert Stoeckl, PhD,\* Annkathrin Hornung, MD,† Judith Popp, MD,†  
Michael Erdmann, MD,† Lucie Heinzerling, MD,†‡ and Arndt Hartmann, MD\**

*Am J Surg Pathol • Volume 45, Number 2, February 2021*

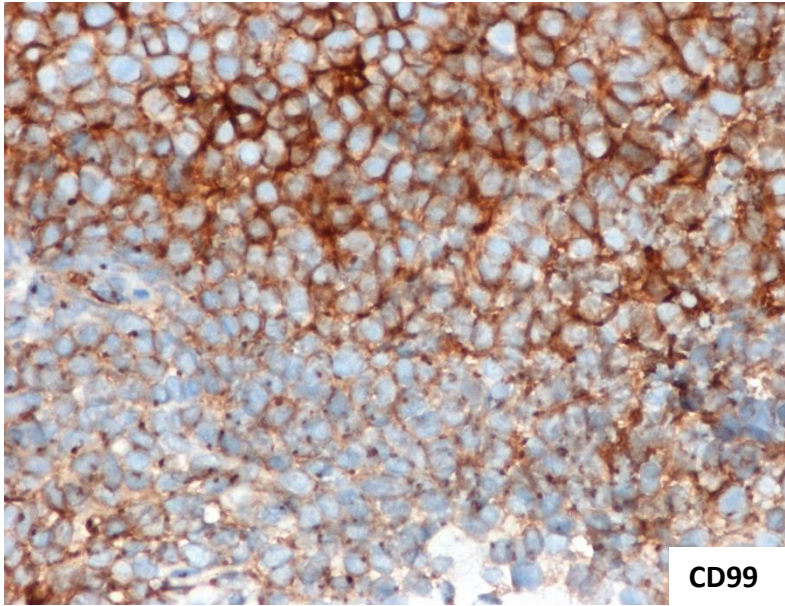
Clues to the diagnosis of dedifferentiated and undifferentiated melanoma :

- Presence of minimal differentiated clone in dedifferentiated melanoma
- Earlier history of melanoma
- Undifferentiated histology that does not fit any defined entity
- Locations at sites that are unusual for undifferentiated/unclassified pleomorphic sarcoma (axilla, inguinal, neck, digestive system, etc.)
- Unusual multifocal disease typical of melanoma spread
- Detection of a melanoma-compatible gene mutation
- Absence of another genuine primary (eg, anaplastic carcinoma) in other organs.

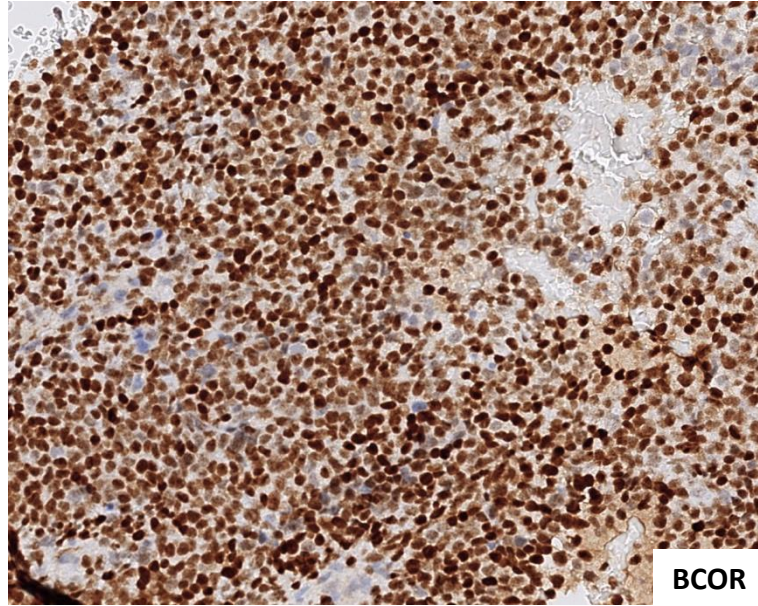
Adult male, popliteal fossa



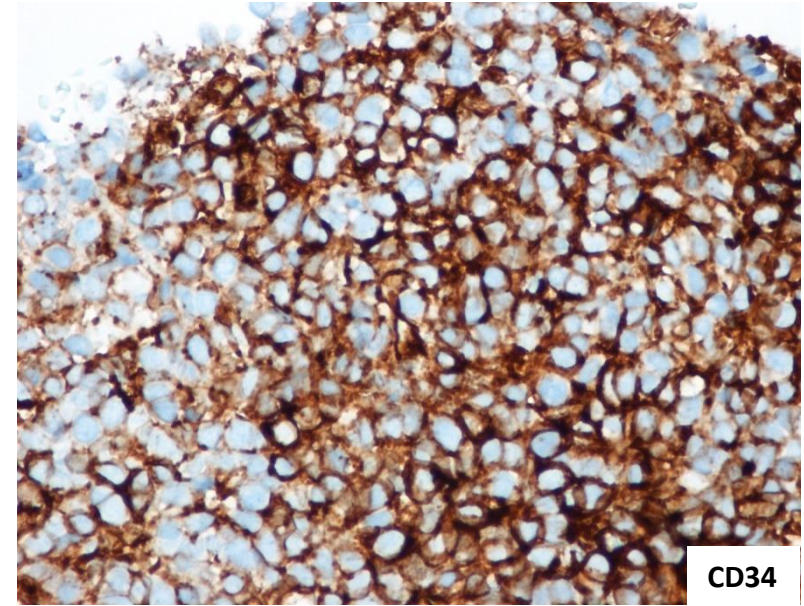




CD99



BCOR




















CD34

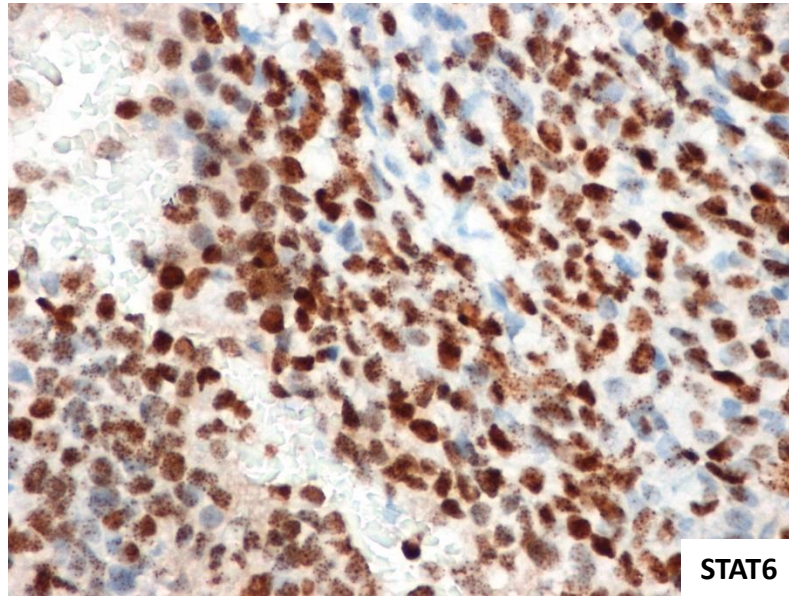
| Other markers                      |            |                 |
|------------------------------------|------------|-----------------|
| S100 -                             | Desmin -   | CD3 -           |
| Pan-keratin +/-                    | WT1 -      | CD20 -          |
| EMA -                              | ETV4 -     | CD79A -         |
| ERG -                              | NKX2-2 -   | MPO -           |
| NUT -                              | SATB2 -    | Synaptophysin - |
| SMA -                              | SS18-SSX - | Chromogranin -  |
| INI1 and BRG1 conserved expression |            |                 |

*10 -14 days later...*

## Targeted RNA-Sequencing results

| Actions  | Classification  | Report  | Artifact  | Genes                    | SS                       | Reads           | %Reads | Strong | Brkpt | Cat         | Type                          | InFrame     | TO | Rept  | Artf | Tier I | Tier II | Tier III | Tier IV | Germ |
|--|---|---|---|--------------------------|--------------------------|-----------------|--------|--------|-------|-------------|-------------------------------|-------------|----|-------|------|--------|---------|----------|---------|------|
|                           |  |  |  | <input type="checkbox"/> | <input type="checkbox"/> | NAB2 → STAT6    | 151    | 4900   | 45.0  | True        | chr12:57487381,chr12:57493223 | Fusion      |    | True  | 1    | 0      | 0       | 0        | 0       | 0    |
| GSP2s  |   |   |   |                          |                          |                 |        |        |       |             |                               |             |    |       |      |        |         |          |         |      |
| Filters  |   |   |   |                          |                          |                 |        |        |       | Reads (#/%) |                               | Start Sites |    |       |      |        |         |          |         |      |
| STAT6_chr12_57493177_23+_A1_GSP2<br>STAT6_chr12_57492825_24+_A1_GSP2<br>STAT6_chr12_57492632_23+_A1_GSP2 |   |   |   |                          |                          |                 |        |        |       | 4900 / 45.0 |                               | 151         |    |       |      |        |         |          |         |      |
|                        |   |   |   |                          |                          |                 |        |        |       |             |                               |             |    |       |      |        |         |          |         |      |
|                           |  |  |  | <input type="checkbox"/> | <input type="checkbox"/> | KANSL1 → ARL17B | 54     | 82     | 10.8  | True        | chr17:44171926,chr17:44430296 | Fusion      |    | False | 86   | 0      | 5       | 0        | 0       | 0    |
|                           |  |  |  | <input type="checkbox"/> | <input type="checkbox"/> | NAB2 → STAT6    | 48     | 69     | 0.6   | True        | chr12:57486978,chr12:57493223 | Fusion      |    | True  | 1    | 0      | 0       | 0        | 0       | 0    |
|                           |  |  |  | <input type="checkbox"/> | <input type="checkbox"/> | NAB2 → STAT6    | 10     | 10     | 0.1   | True        | chr12:57487357,chr12:57493223 | Fusion      |    | True  | 1    | 0      | 0       | 0        | 0       | 0    |

## *NAB2-STAT6* fusion



Diagnosis: Solitary fibrous tumor, high-risk based on Demicco et al. (PMID: 28731041)

**Molecular genetics can be very helpful for characterizing diagnostically challenging tumors**



# Other potentially useful applications of molecular profiling

- Prediction of tumor aggressiveness :

[Nat Med](#). 2010 Jul;16(7):781-7. doi: 10.1038/nm.2174. Epub 2010 Jun 27.

## **Validated prediction of clinical outcome in sarcomas and multiple types of cancer on the basis of a gene expression signature related to genome complexity.**

[Chibon F](#)<sup>1</sup>, [Lagarde P](#), [Salas S](#), [Pérot G](#), [Brouste V](#), [Tirode F](#), [Lucchesi C](#), [de Reynies A](#), [Kauffmann A](#), [Bui B](#), [Terrier P](#), [Bonvalot S](#), [Le Cesne A](#), [Vince-Ranchère D](#), [Blay JY](#), [Collin F](#), [Guillou L](#), [Leroux A](#), [Coindre JM](#), [Aurias A](#).

- Sarcoma classification based on RNA or DNA-methylome tumor profiling:

[J Pathol](#). 2018 May;245(1):29-40. doi: 10.1002/path.5053. Epub 2018 Mar 30.

## **Transcriptomic definition of molecular subgroups of small round cell sarcomas**

[Sarah Watson](#)<sup>1 2</sup>, [Virginie Perrin](#)<sup>1 2</sup>, [Delphine Guillemot](#)<sup>3</sup>, [Stephanie Reynaud](#)<sup>3</sup>, [Jean-Michel Coindre](#)<sup>4 5</sup>, [Marie Karanian](#)<sup>6</sup>, [Jean-Marc Guinebretière](#)<sup>7</sup>, [Paul Freneaux](#)<sup>8</sup>, [François Le Loarer](#)<sup>4 5</sup>, [Megane Bouvet](#)<sup>3</sup>, [Louise Galmiche-Rolland](#)<sup>9 10</sup>, [Frédérique Larousserie](#)<sup>11</sup>, [Elisabeth Longchamp](#)<sup>12</sup>, [Dominique Ranchere-Vince](#)<sup>6</sup>, [Gaelle Pierron](#)<sup>3</sup>, [Olivier Delattre](#)<sup>1 2 3 13</sup>, [Franck Tirode](#)<sup>1 2 14</sup>

[Nat Commun](#). 2021 Jan 21;12(1):498. doi: 10.1038/s41467-020-20603-4.

## **Sarcoma classification by DNA methylation profiling**

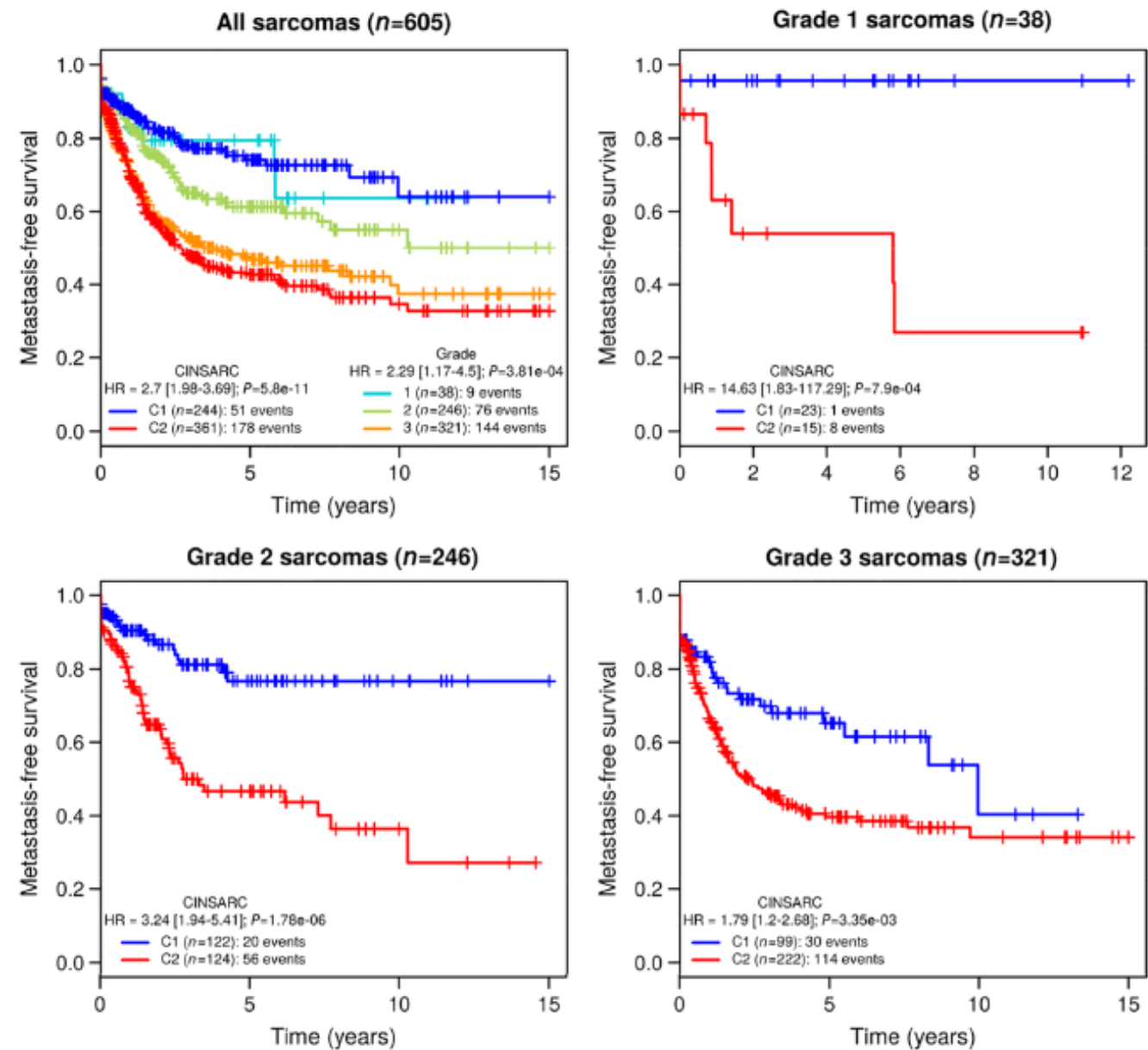
[Christian Koelsche](#)<sup># 1 2 3</sup>, [Daniel Schrimpf](#)<sup># 1 2</sup>, [Damian Stichel](#)<sup># 2</sup>, [Martin Sill](#)<sup># 4 5</sup>, [Felix Sahm](#)<sup>1 2</sup>, [David E Reuss](#)<sup>1 2</sup>, [Mirjam Blattner](#)<sup>4 6</sup>, [Barbara Worst](#)<sup>4 6 7</sup>, [Christoph E Heilig](#)<sup>8</sup>, [Katja Beck](#)<sup>8 9</sup>, [Peter Horak](#)<sup>8</sup>, [Simon Kreutzfeldt](#)<sup>8</sup>, [Elke Paff](#)<sup>4 6 7</sup>, [Sebastian Stark](#)<sup>4 6 7</sup>, [Pascal Johann](#)<sup>4 6 7</sup>, [Florian Selt](#)<sup>4 7 10</sup>, [Jonas Ecker](#)<sup>4 7 10</sup>, [Dominik Sturm](#)<sup>4 6 7</sup>, [Kristian W Pajtler](#)<sup>4 5 7</sup>, [Annekathrin Reinhardt](#)<sup>1 2</sup>, [Annika K Wefers](#)<sup>1 2</sup>, [Philipp Sievers](#)<sup>1 2</sup>, [Azadeh Ebrahimi](#)<sup>2</sup>, [Abigail Suwala](#)<sup>1 2</sup>, [Francisco Fernández-Klett](#)<sup>1 2</sup>, [Belén Casalini](#)<sup>2</sup>

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- Cancer grading system based on a gene expression signature related to genome complexity
- Stratification of tumors in two groups: low risk and high risk of metastasis



# CINSARC

## *Advantages*

- Probably gives additional prognostic information
- Reproducibility
- Dichotomic
- Can be performed in very small samples and after neo-adjuvant treatment

## *Disadvantages*

- Expensive
- Not a perfect system
- Not useful for every sarcoma subtype

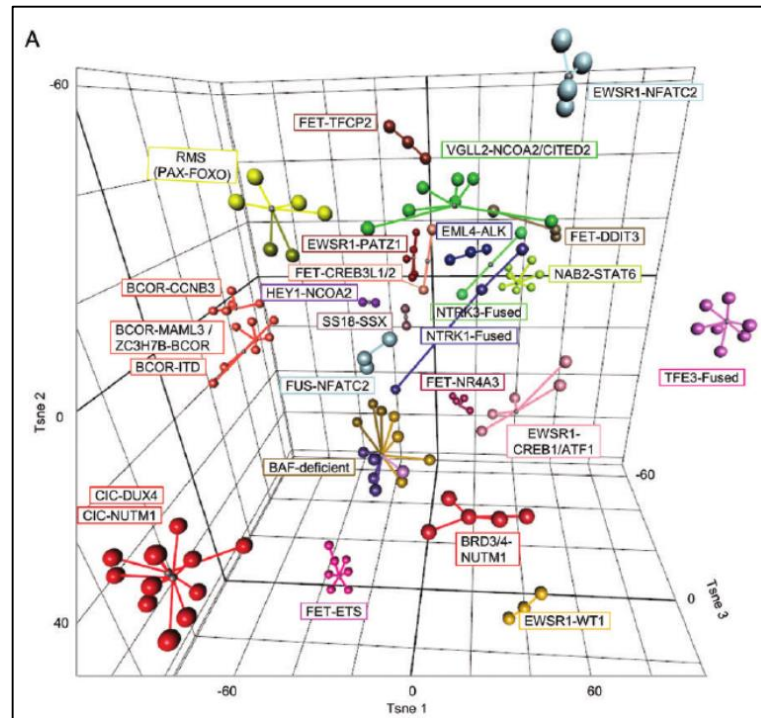
Utility in clinical practice? Don't know yet...

# Sarcoma classification based on on RNA or DNA-methylome tumor profiling

► J Pathol. 2018 May;245(1):29-40. doi: 10.1002/path.5053. Epub 2018 Mar 30.

## Transcriptomic definition of molecular subgroups of small round cell sarcomas

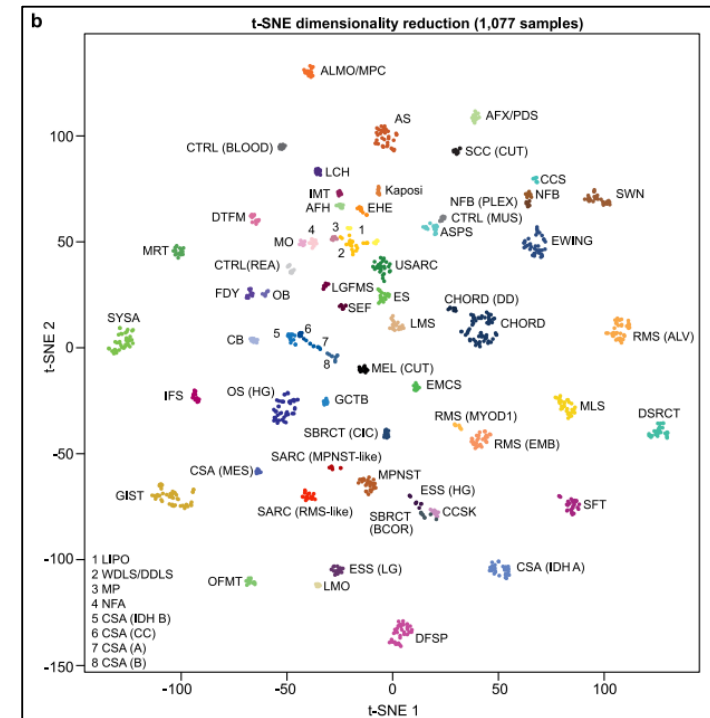
Sarah Watson <sup>1 2</sup>, Virginie Perrin <sup>1 2</sup>, Delphine Guillemot <sup>3</sup>, Stephanie Reynaud <sup>3</sup>, Jean-Michel Coindre <sup>4 5</sup>, Marie Karanian <sup>6</sup>, Jean-Marc Guinebretière <sup>7</sup>, Paul Freneaux <sup>8</sup>, François Le Loarer <sup>4 5</sup>, Megane Bouvet <sup>3</sup>, Louise Galmiche-Rolland <sup>9 10</sup>, Frédérique Larousserie <sup>11</sup>, Elisabeth Longchamp <sup>12</sup>, Dominique Ranchere-Vince <sup>6</sup>, Gaëlle Pierron <sup>3</sup>, Olivier Delattre <sup>1 2 3 13</sup>, Franck Tirode <sup>1 2 14</sup>



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## Sarcoma classification by DNA methylation profiling

Christian Koelsche <sup># 1 2 3</sup>, Daniel Schrimpf <sup># 1 2</sup>, Damian Stichel <sup># 2</sup>, Martin Sill <sup># 4 5</sup>, Felix Sahn <sup>1 2</sup>, David E Reuss <sup>1 2</sup>, Mirjam Blattner <sup>4 6</sup>, Barbara Worst <sup>4 6 7</sup>, Christoph E Heilig <sup>8</sup>, Katja Beck <sup>8 9</sup>, Peter Horak <sup>8</sup>, Simon Kreutzfeldt <sup>8</sup>, Elke Paff <sup>4 6 7</sup>, Sebastian Stark <sup>4 6 7</sup>, Pascal Johann <sup>4 6 7</sup>, Florian Selt <sup>4 7 10</sup>, Jonas Ecker <sup>4 7 10</sup>, Dominik Sturm <sup>4 6 7</sup>, Kristian W Pajtl <sup>4 5 7</sup>, Annekathrin Reinhardt <sup>1 2</sup>, Annika K Wefers <sup>1 2</sup>, Philipp Sievers <sup>1 2</sup>, Azadeh Ebrahimi <sup>2</sup>, Abigail Suwala <sup>1 2</sup>, Francisco Fernández-Klett <sup>1 2</sup>, Belén Casalini <sup>2</sup>



*Useful techniques to interpreted with caution (CPC)*

## Conclusion

- Molecular techniques are valuable tools that can provide additional diagnostic, prognostic and therapeutic data
- Multidisciplinary expertise is needed for its correct implementation
- Molecular genetics don't replace the basic diagnostic process of disease





*La cité du vin – Bordeaux, France*

*Thank you*



*Le pont de Pierre – Bordeaux, France*

*Gracias*



*Glaciar Perito Moreno – Santa Cruz, Argentina*

*Merci*



*Saltos del Moconá – Misiones, Argentina*