

# Precision diagnostics

miRNAs as non-invasive biomarkers

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Saarbücken, 25.11.2013

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Professor Dr. Andreas Keller

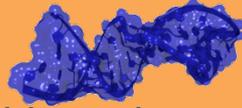
Chair for Clinical Bioinformatics  
Saarland University  
University Hospital



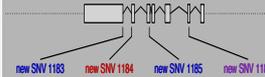
- > Chair for Clinical Bioinformatics
- > Research at a glance



## Non-Invasive Biomarkers



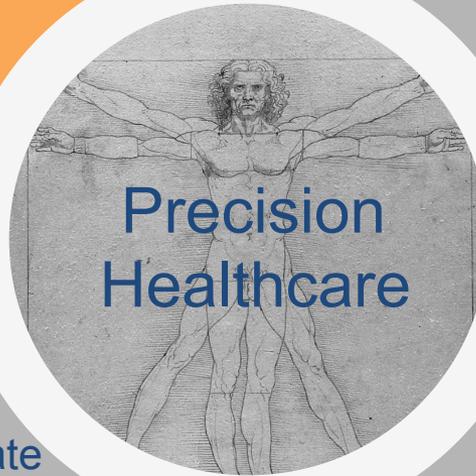
Detection of miRNA and protein biomarker patterns from human blood or serum samples using microarrays, NGS, qRT-PCR & mass spectrometry. Biostatistical evaluation & validation of the complex profiles.



## Genetic Testing by NGS

Whole genome, exome or gene panel sequencing of DNA in order to detect genetic causes for human diseases. Understanding the effect of the respective genetic variants for different disease phenotypes.

# Precision Healthcare



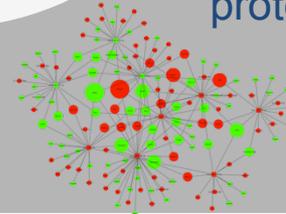
## Bacterial Resistance

Understanding the genetic cause of bacterial resistance and correlate the bacterial resistance to classical culture based tests in order to derive the minimal inhibitory concentration and best therapy with anti bacterial agents.



## Systems Biology

Model and understand how DNA, mRNA, microRNA, methylation and proteins mutually interact in order generate a holistic and multi-scale molecular representation of human pathologies.





A brief intro to biomarkers

Steps in biomarker pipeline

Regulatory basics

miRNAs as markers



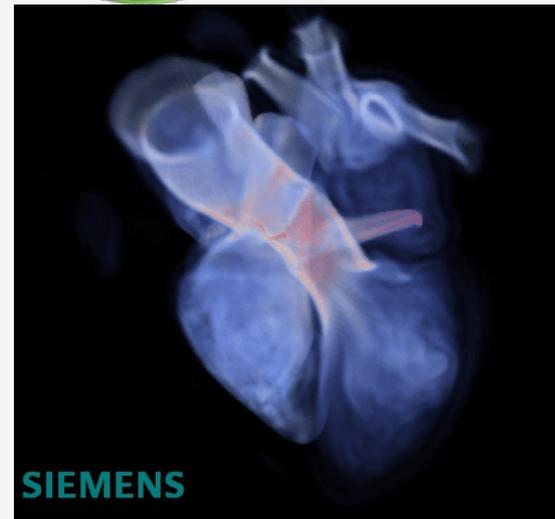
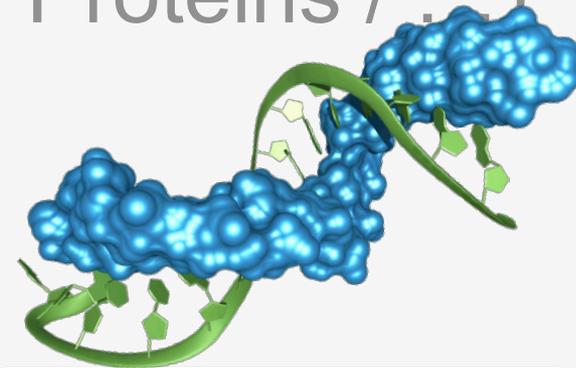


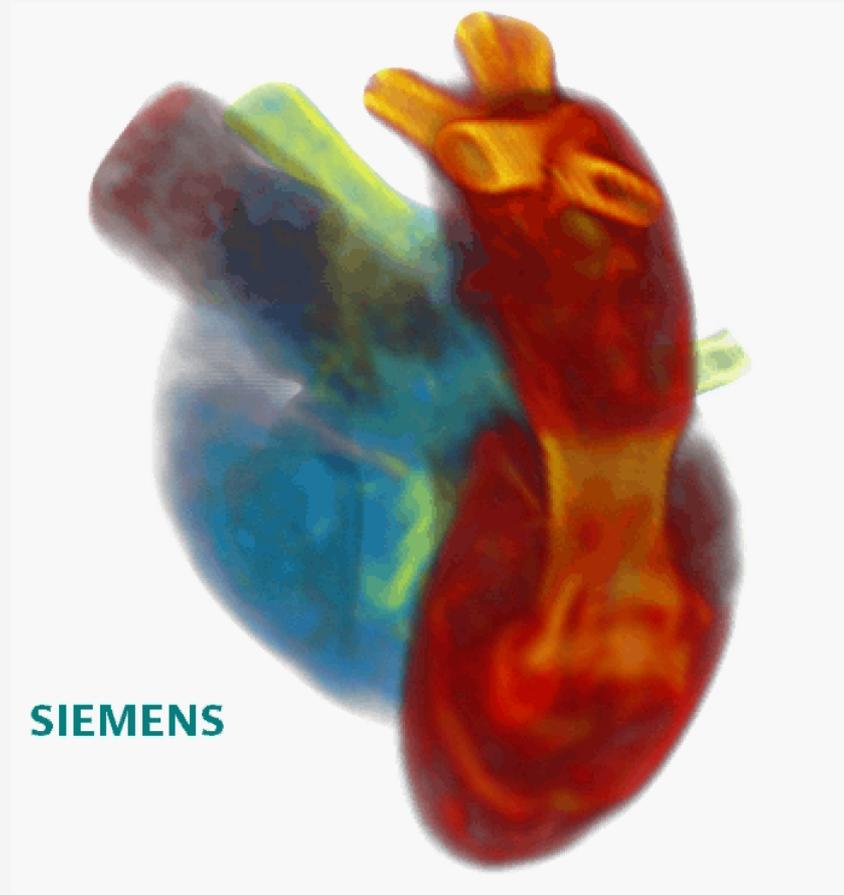
*A biomarker is in general a substance used as an indicator of a biological state. It is a characteristic that is objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacological responses to a intervention.*

*[wikipedia]*



- Molecules (DNA / RNA / Proteins / ...)
- Cells
- Organ function
- ...
  
- In-vivo biomarkers

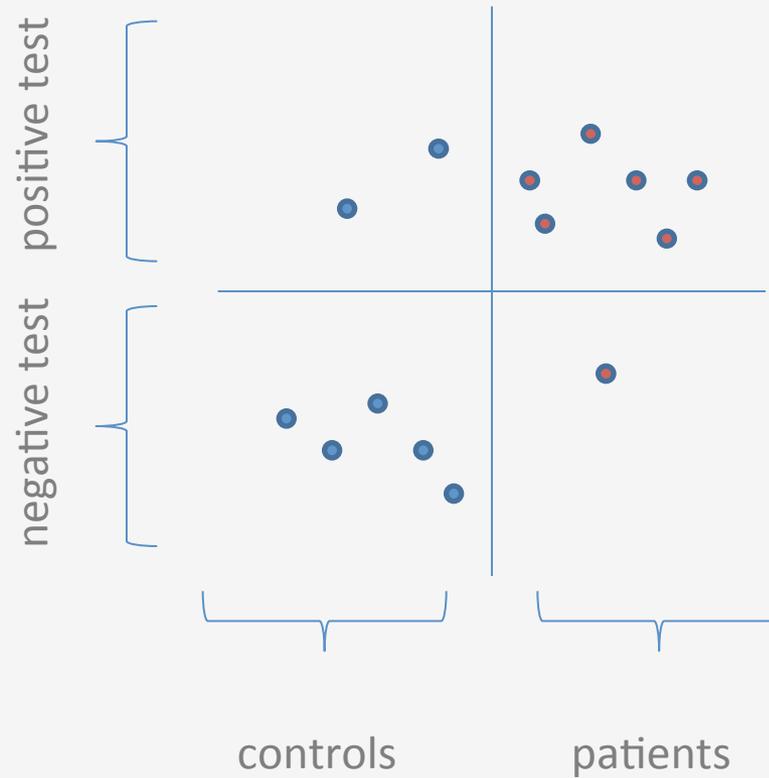




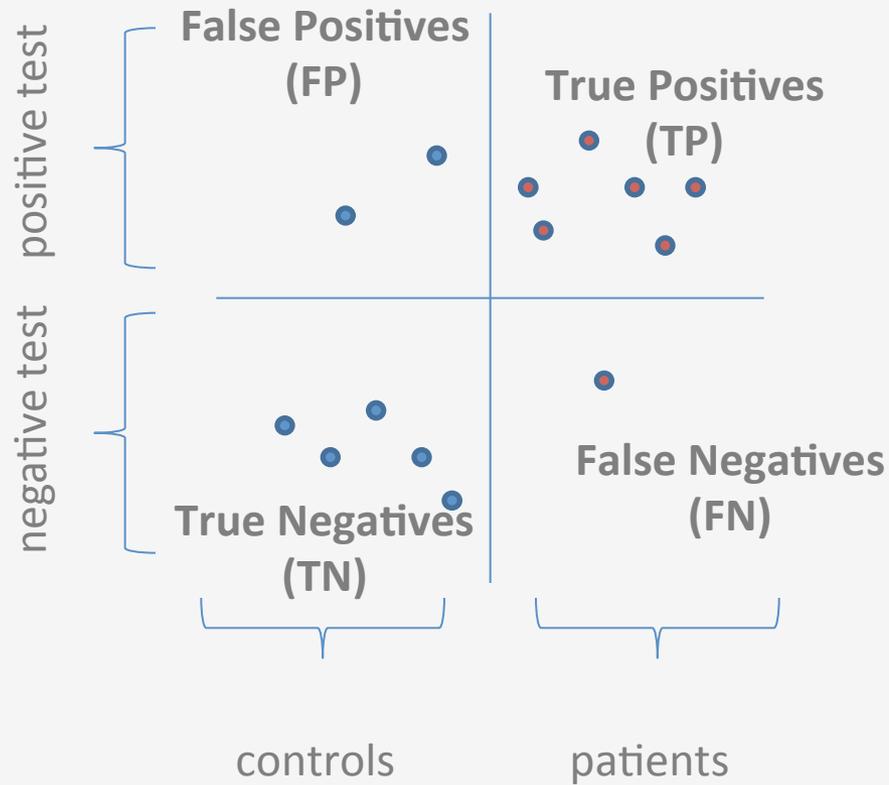


- Specificity
- Sensitivity
- Accuracy
- Positive Predictive Value
- Negative Predictive Value
- Positive Likelihood Ratio
- Negative Likelihood Ratio
- Odds ratio
- Area under the ROC curve
- Wilcoxon Mann-Whitney test
- T-tests

> Example – a diagnostic test



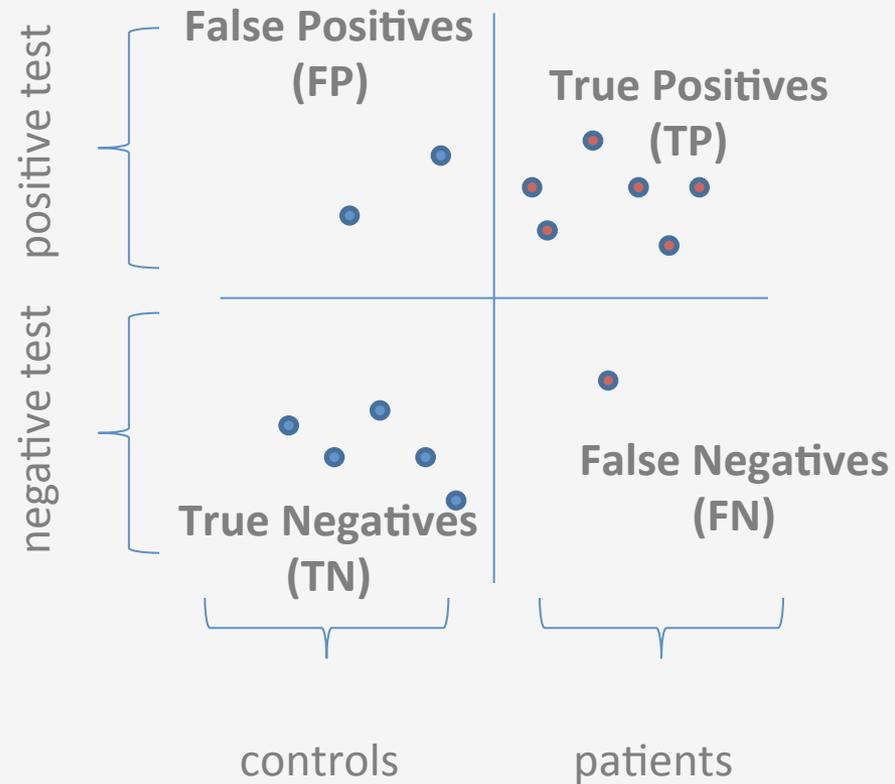
> Example – a diagnostic test



- > Example – a diagnostic test
- > SENSITIVITY



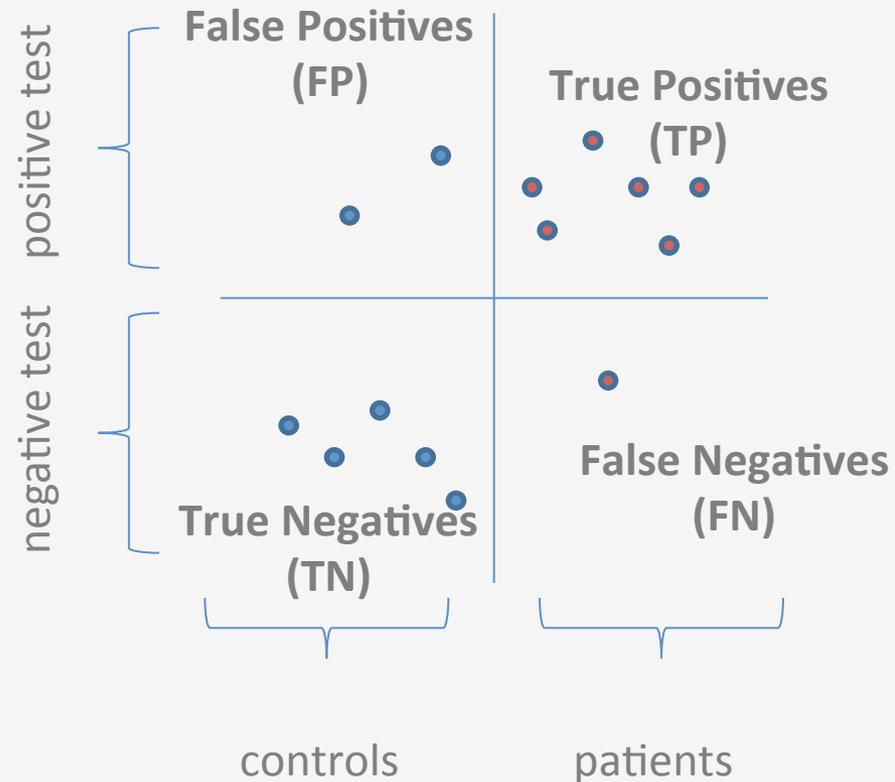
$$\begin{aligned} \text{sens} &= \text{TP} / (\text{TP} + \text{FN}) \\ &= 6 / (6 + 1) \\ &= 85.7\% \end{aligned}$$



- > Example – a diagnostic test
- > SPECIFICITY



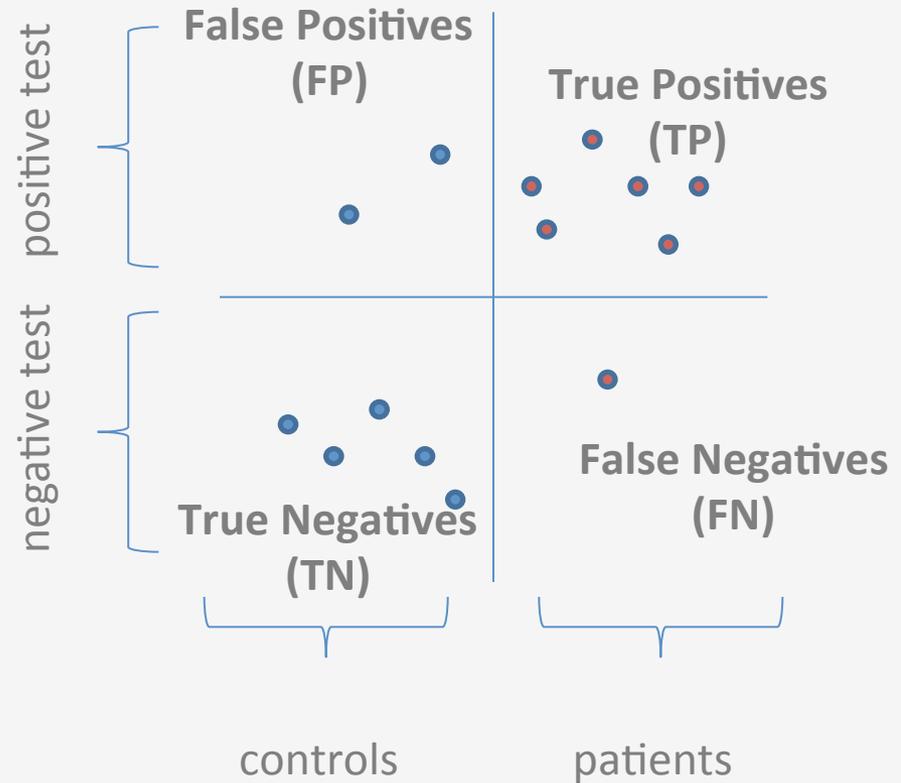
$$\begin{aligned} \text{spec} &= \text{TN} / (\text{TN} + \text{FP}) \\ &= 5 / (5 + 2) \\ &= 71.4\% \end{aligned}$$



- > Example – a diagnostic test
- > ACCURACY



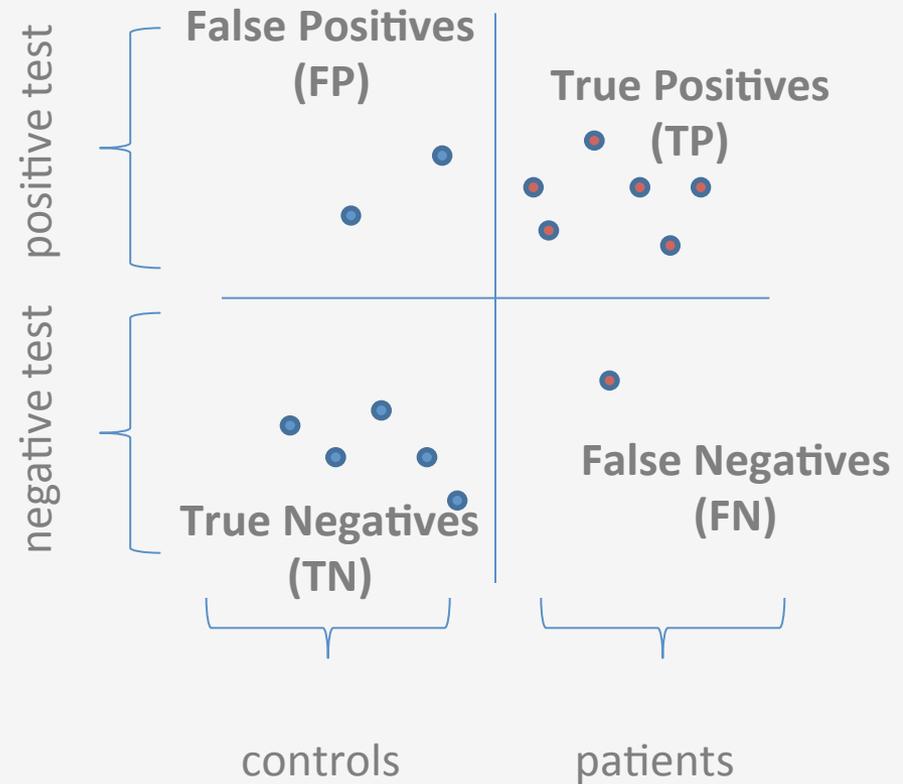
$$\begin{aligned}
 \text{acc} &= (\text{TP} + \text{TN}) / (\text{TP} + \text{FN} + \text{FP} + \text{TN}) \\
 &= (6 + 5) / (6 + 1 + 2 + 5) \\
 &= 78.6\%
 \end{aligned}$$



- > Example – a diagnostic test
- > POSITIVE PREDICTIVE VALUE



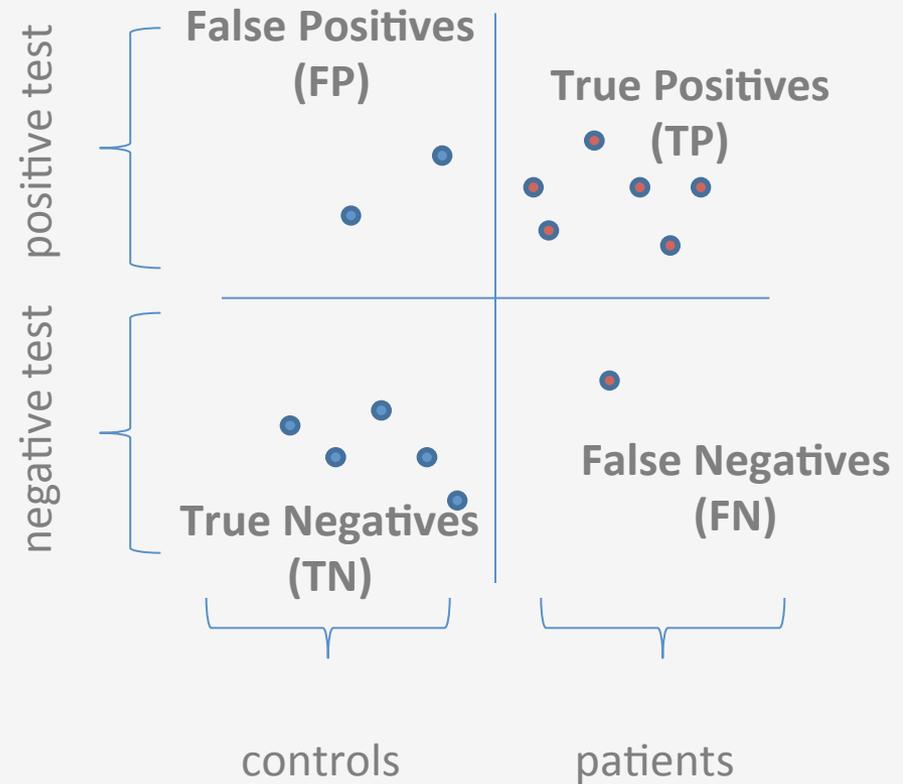
$$\begin{aligned} \text{ppv} &= \text{TP} / (\text{TP} + \text{FP}) \\ &= 6 / (6 + 2) \\ &= 75\% \end{aligned}$$



- > Example – a diagnostic test
- > NEGATIVE PREDICTIVE VALUE



$$\begin{aligned} \text{npv} &= \text{TN} / (\text{TN} + \text{FN}) \\ &= 5 / (5 + 1) \\ &= 83.3\% \end{aligned}$$



- > Example – a diagnostic test
- > PREDICTIVE VALUE PITFAL



in this case, the prevalence of the disease is equal in both classes, in reality, this must not hold and the prevalence has to be included in the consideration

example: test with 80% specificity, 90% sensitivity and prevalence of 1%

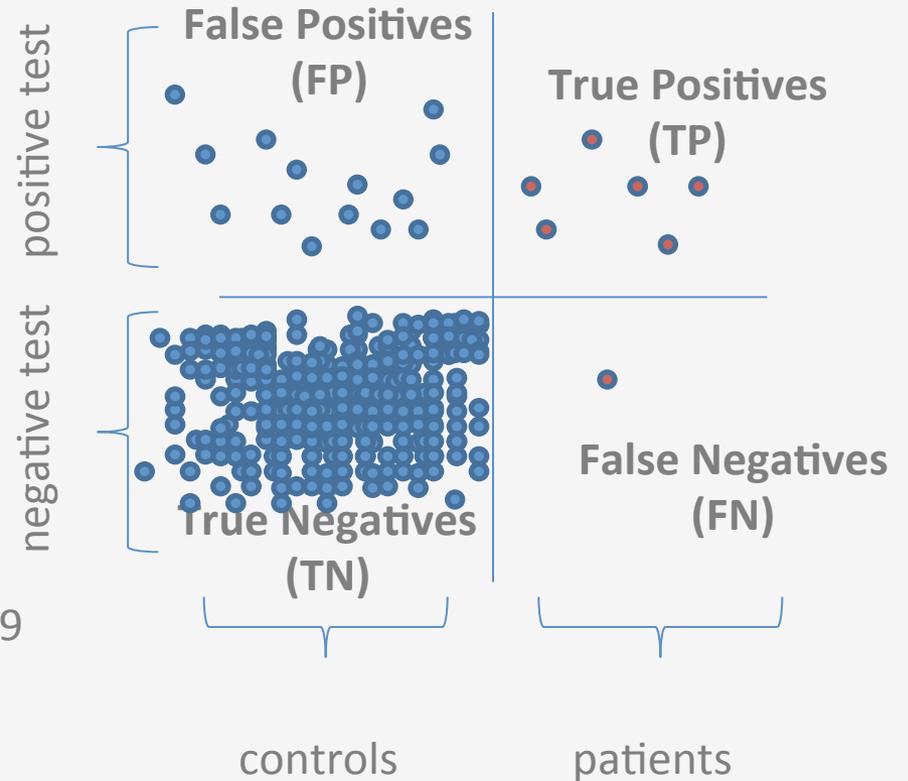
$$ppv = TP / (TP + FP)$$

$$TP = \text{sensitivity} * \text{prevalence} = 0.9 * 0.01 = 0.009$$

$$FP = (1 - \text{specificity}) * (1 - \text{prevalence}) = 0.2 * 0.99 = 0.198$$

$$ppv = 0.009 / (0.009 + 0.198) = 0.043$$

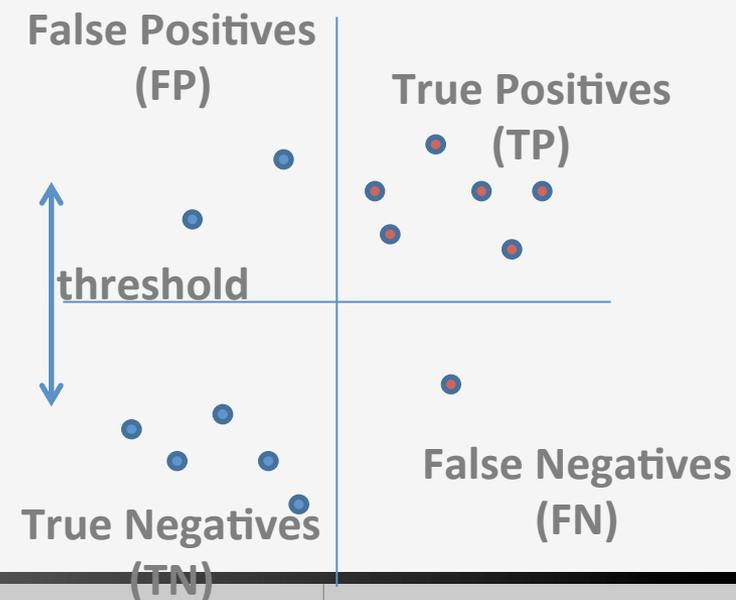
if the test is positive you have a chance of 4.3% to be diseased



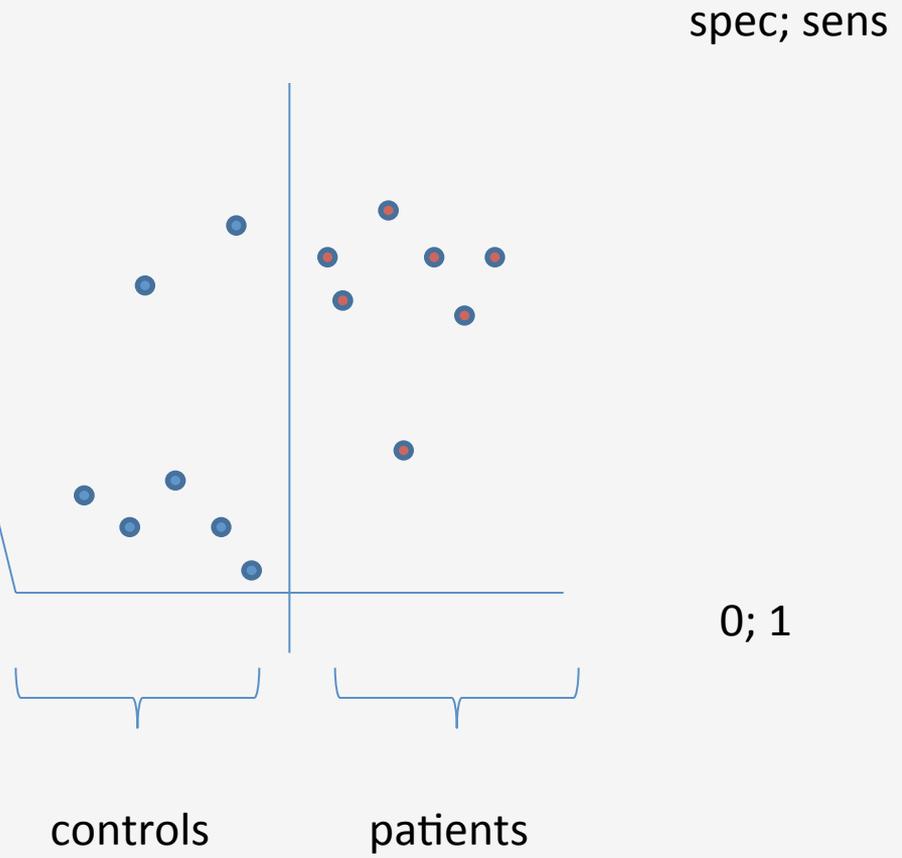
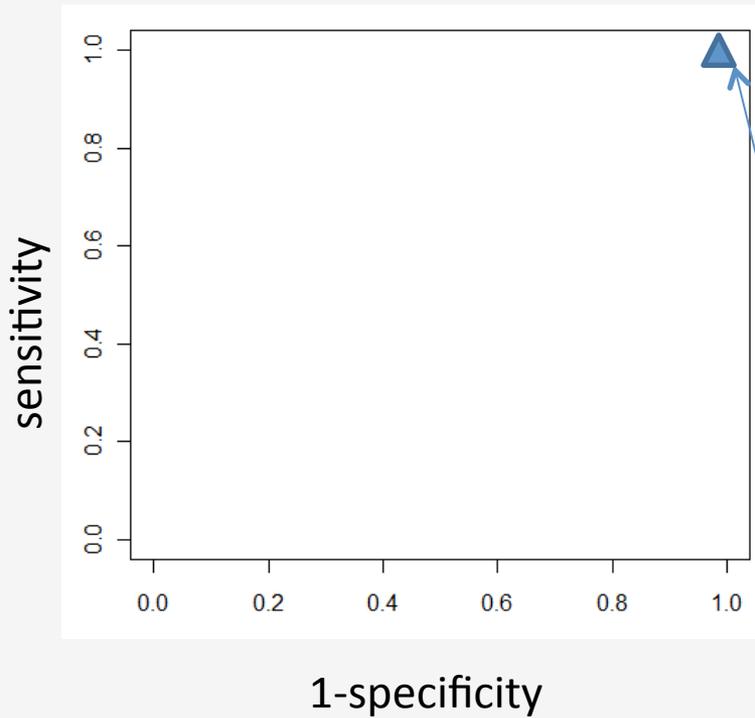
- > Example – a diagnostic test
- > ROC / AUC



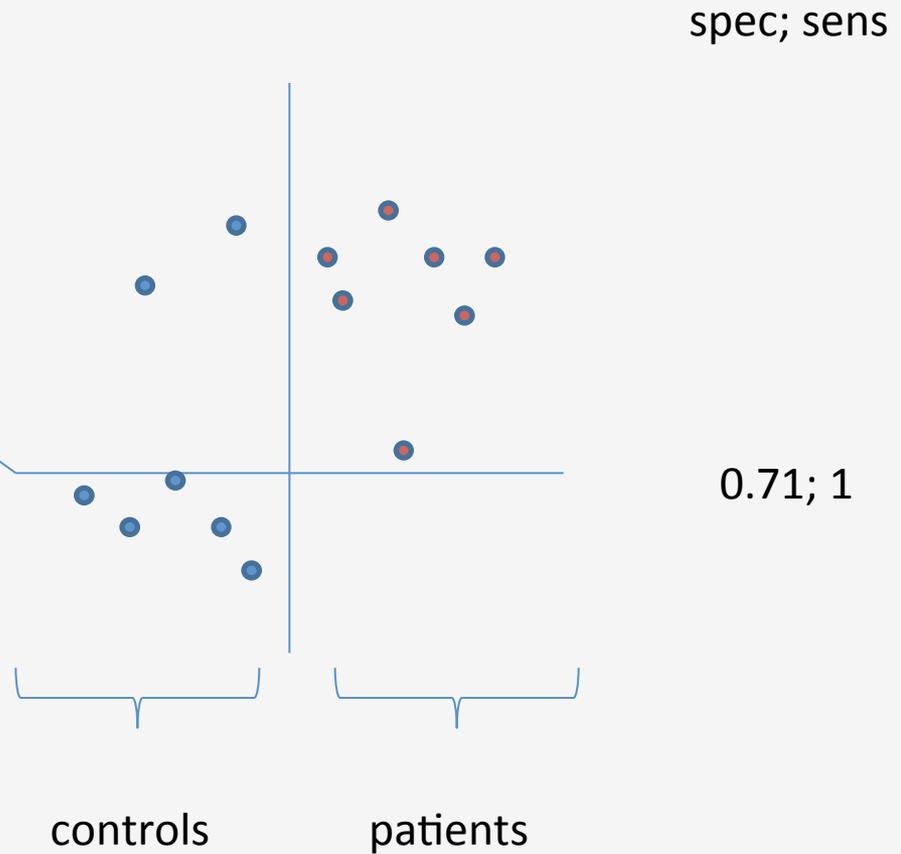
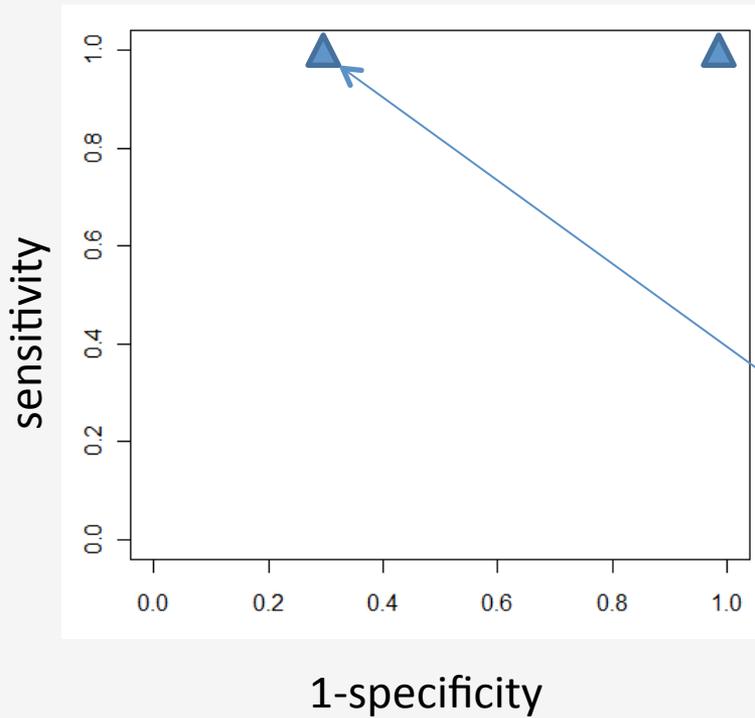
- ROC (receiver operator characteristics) curve is a plot of sensitivity versus  $1 - \text{specificity}$
- Specificity and Sensitivity are computed depended on a threshold for a binary classifier
- ROC analysis helps to find the optimal classification threshold
- The closer the area under the curve (AUC) to 1 the better the classifier



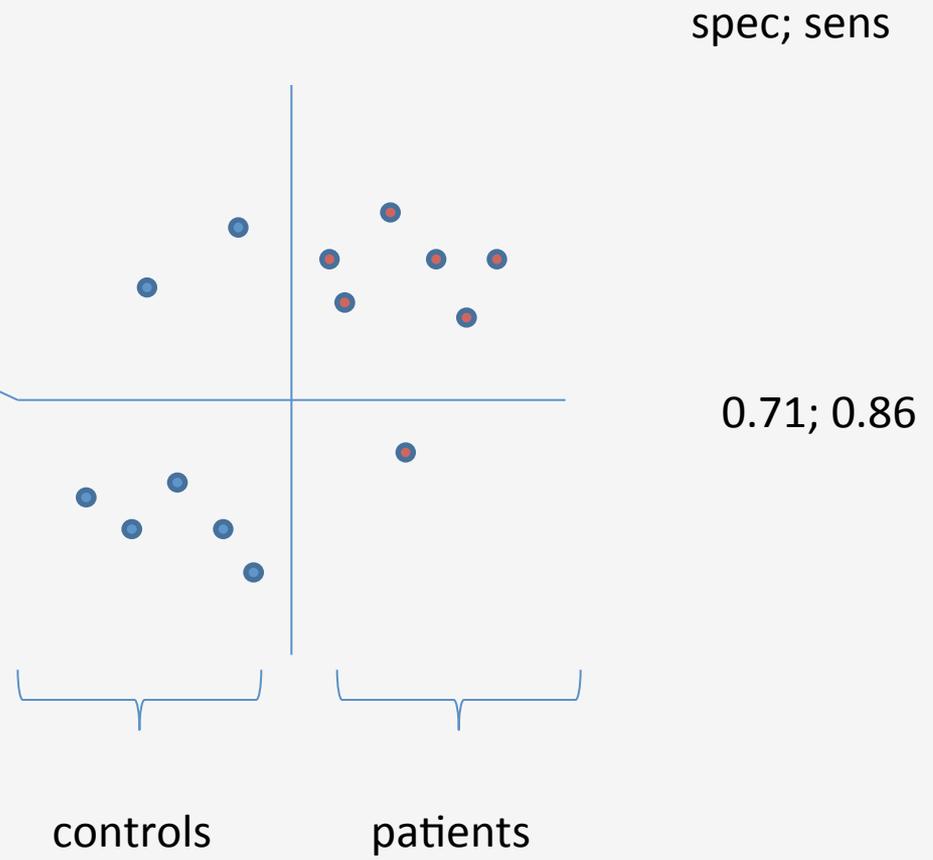
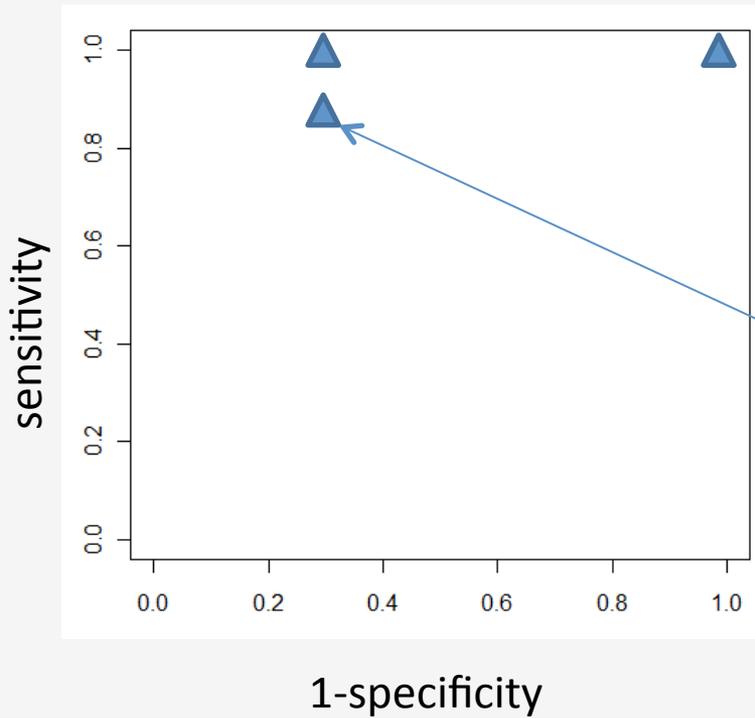
- > Example – a diagnostic test
- > ROC / AUC



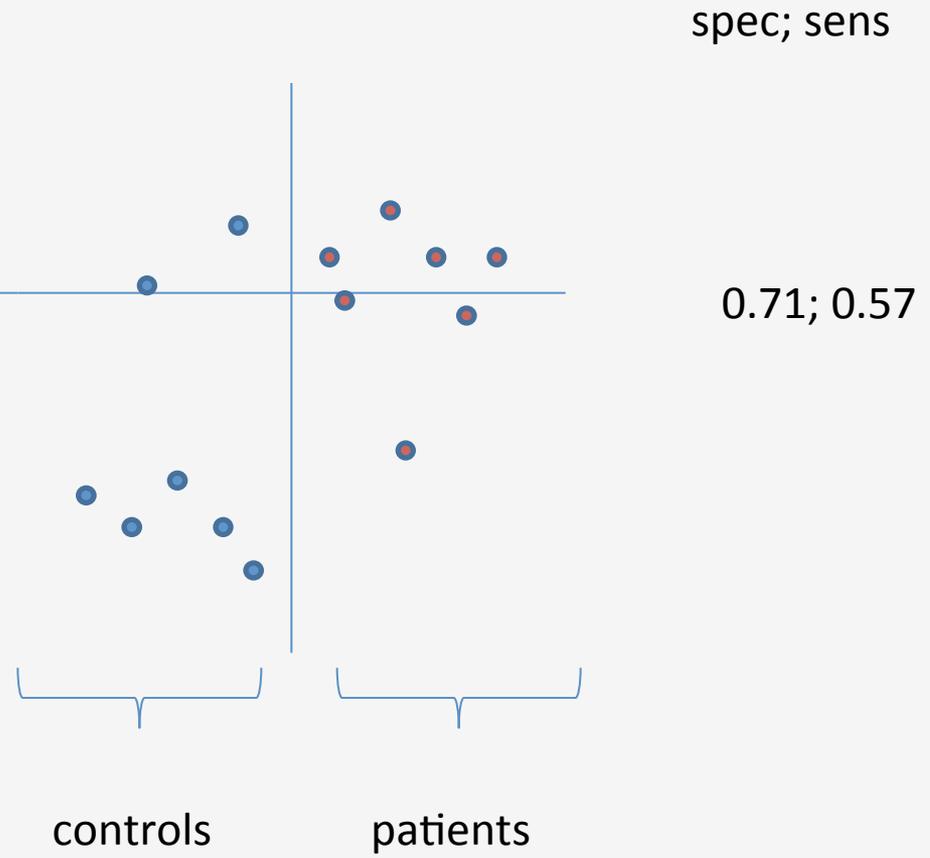
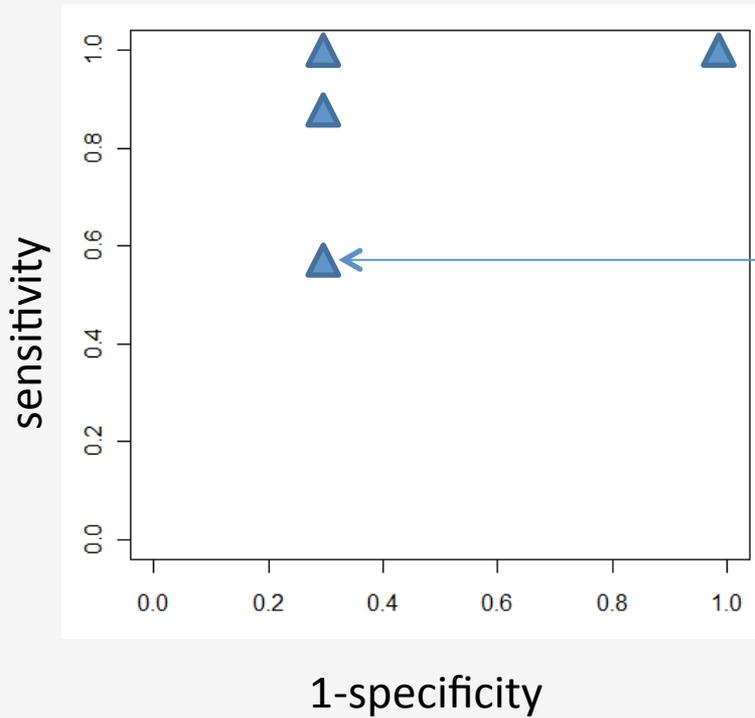
- > Example – a diagnostic test
- > ROC / AUC



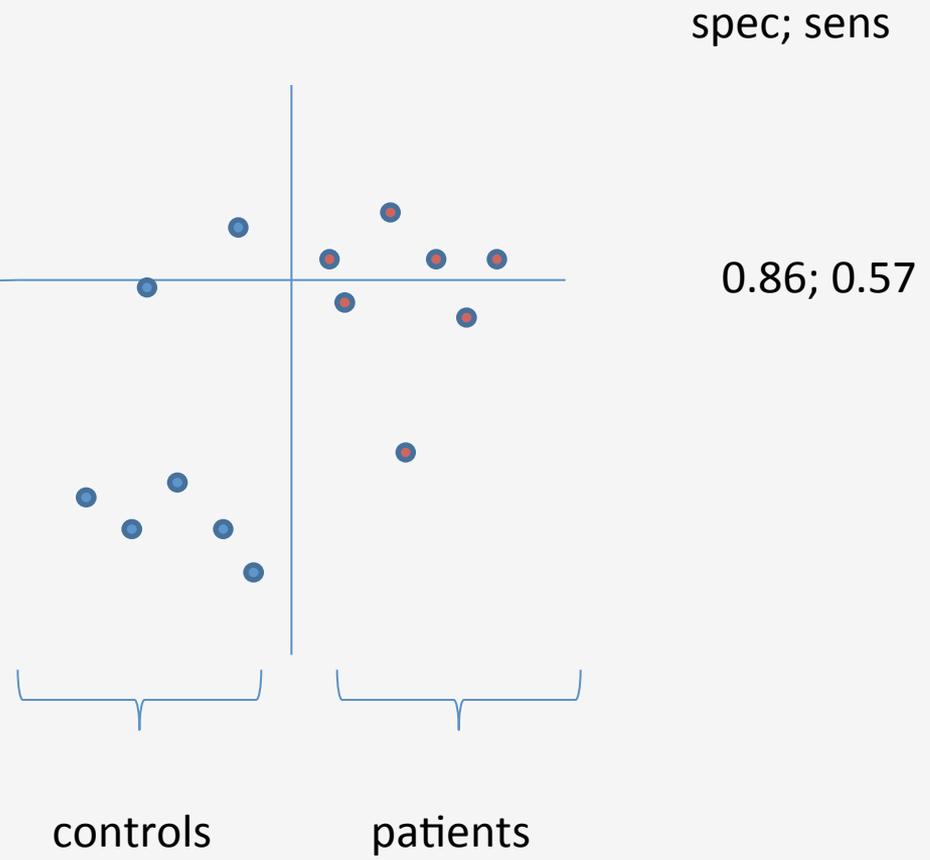
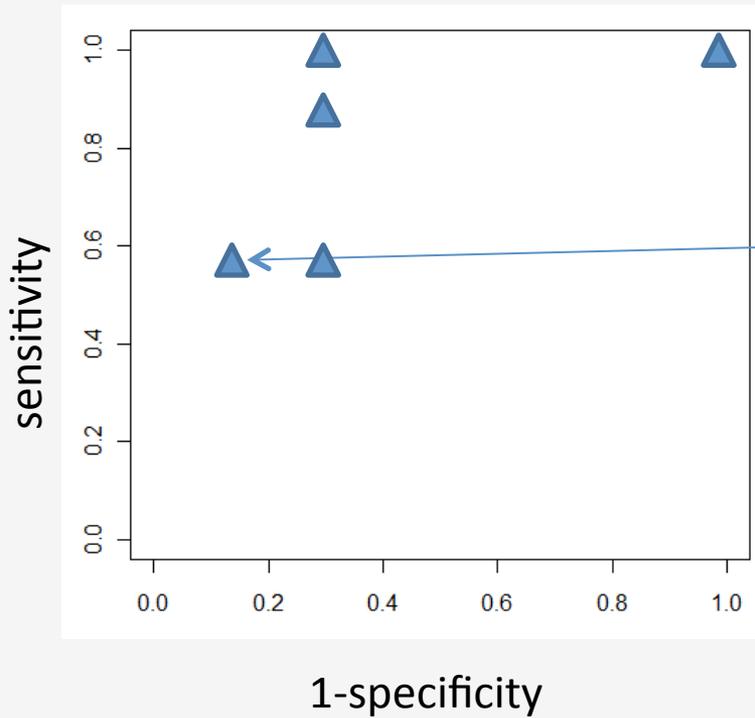
- > Example – a diagnostic test
- > ROC / AUC



- > Example – a diagnostic test
- > ROC / AUC

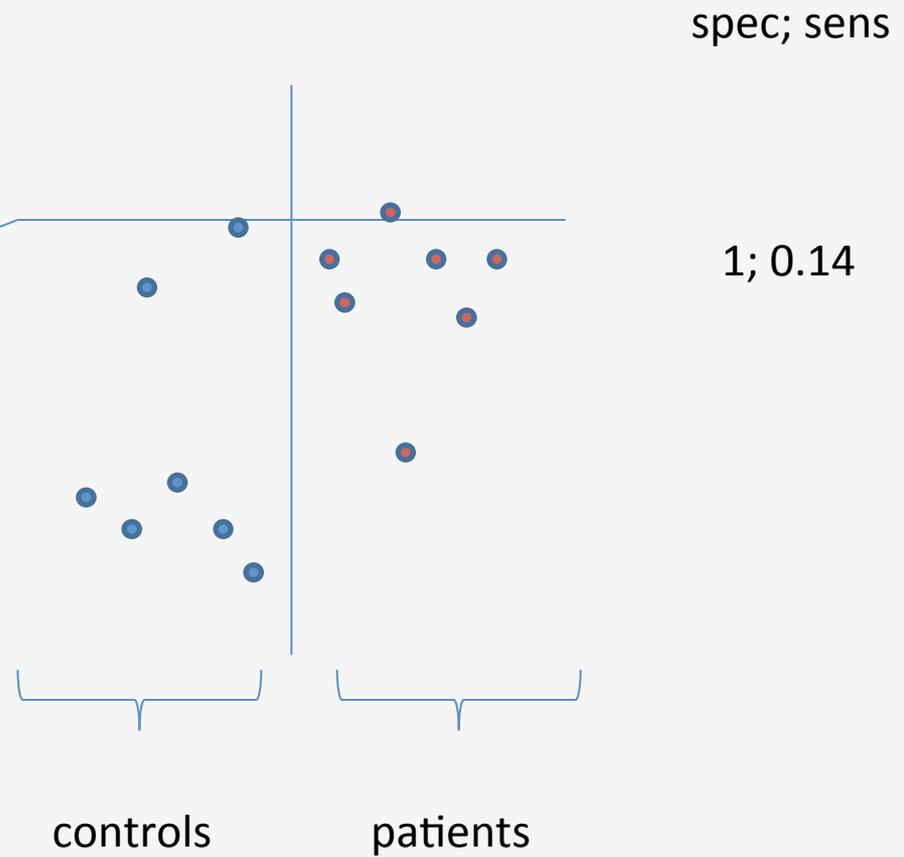
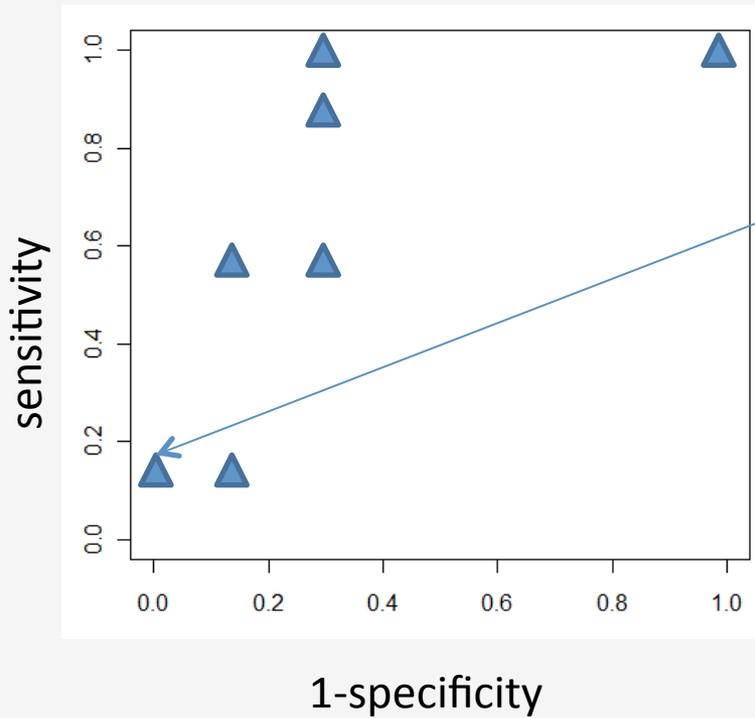


- > Example – a diagnostic test
- > ROC / AUC

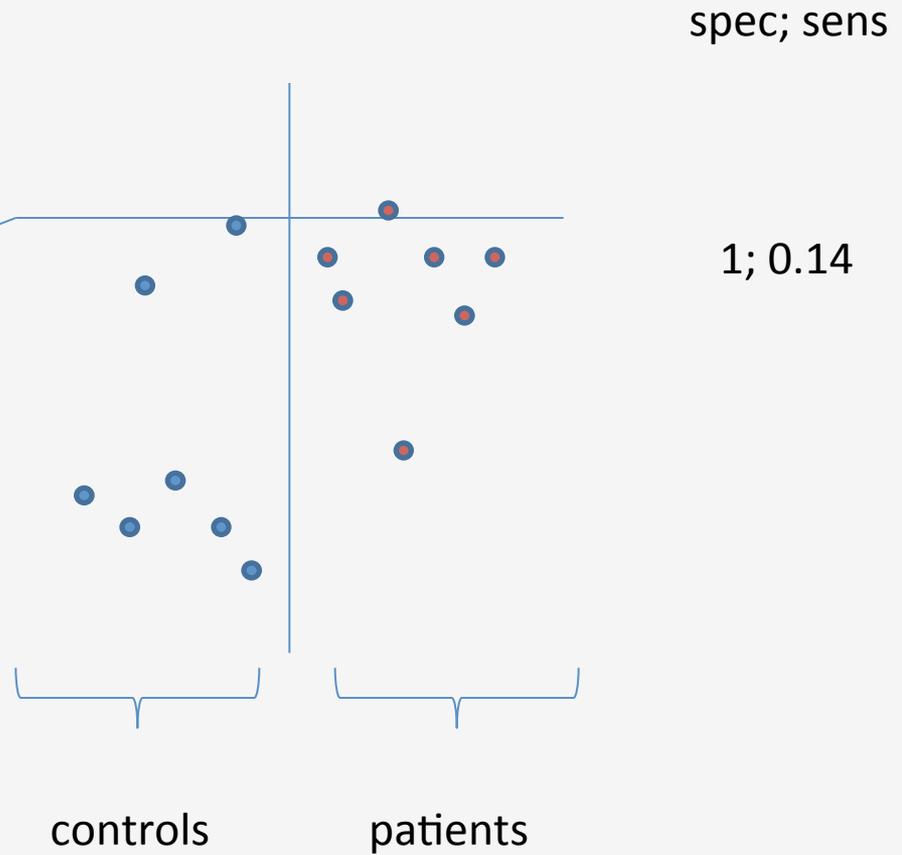
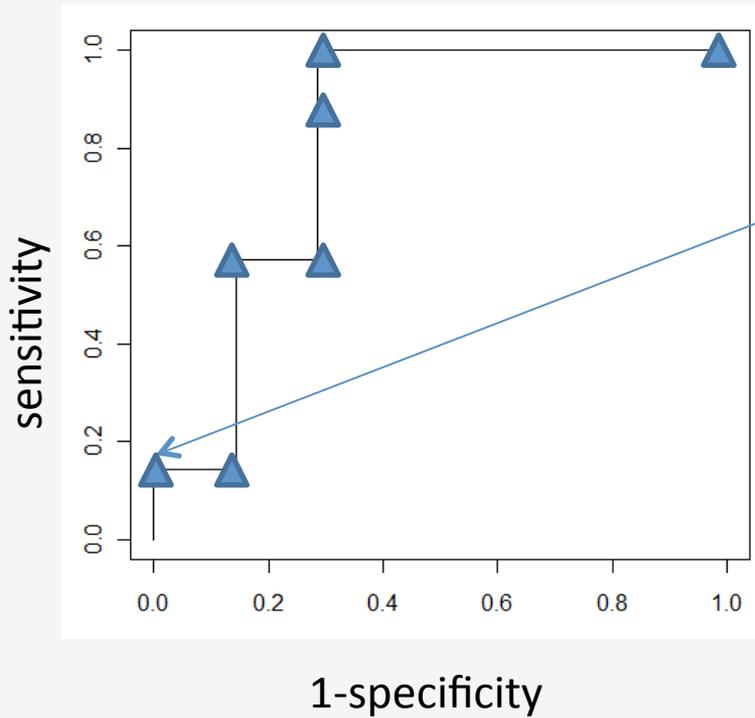




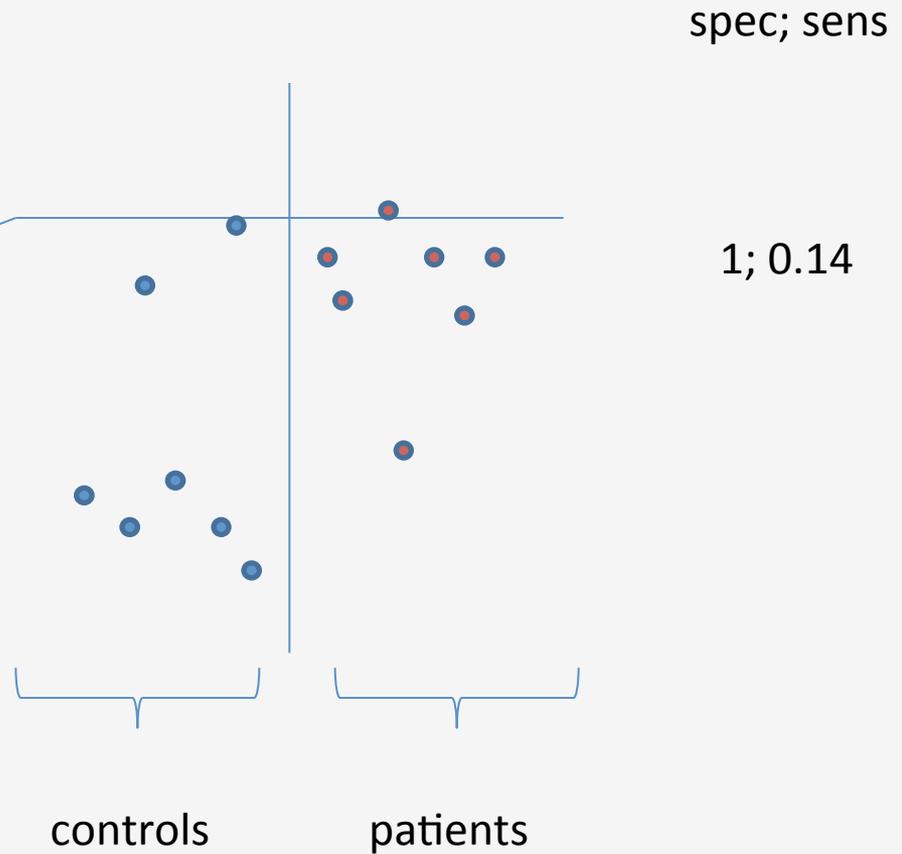
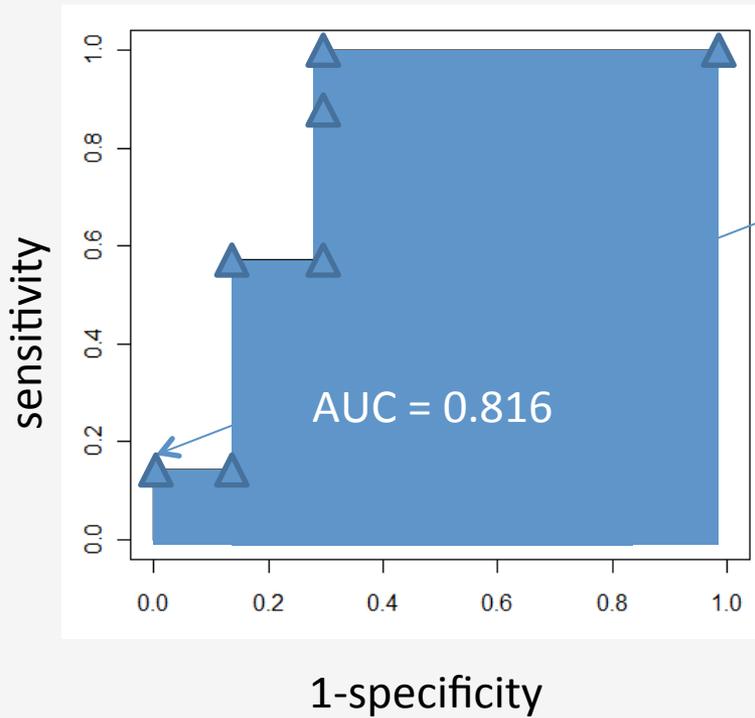
- > Example – a diagnostic test
- > ROC / AUC



- > Example – a diagnostic test
- > ROC / AUC



- > Example – a diagnostic test
- > ROC / AUC



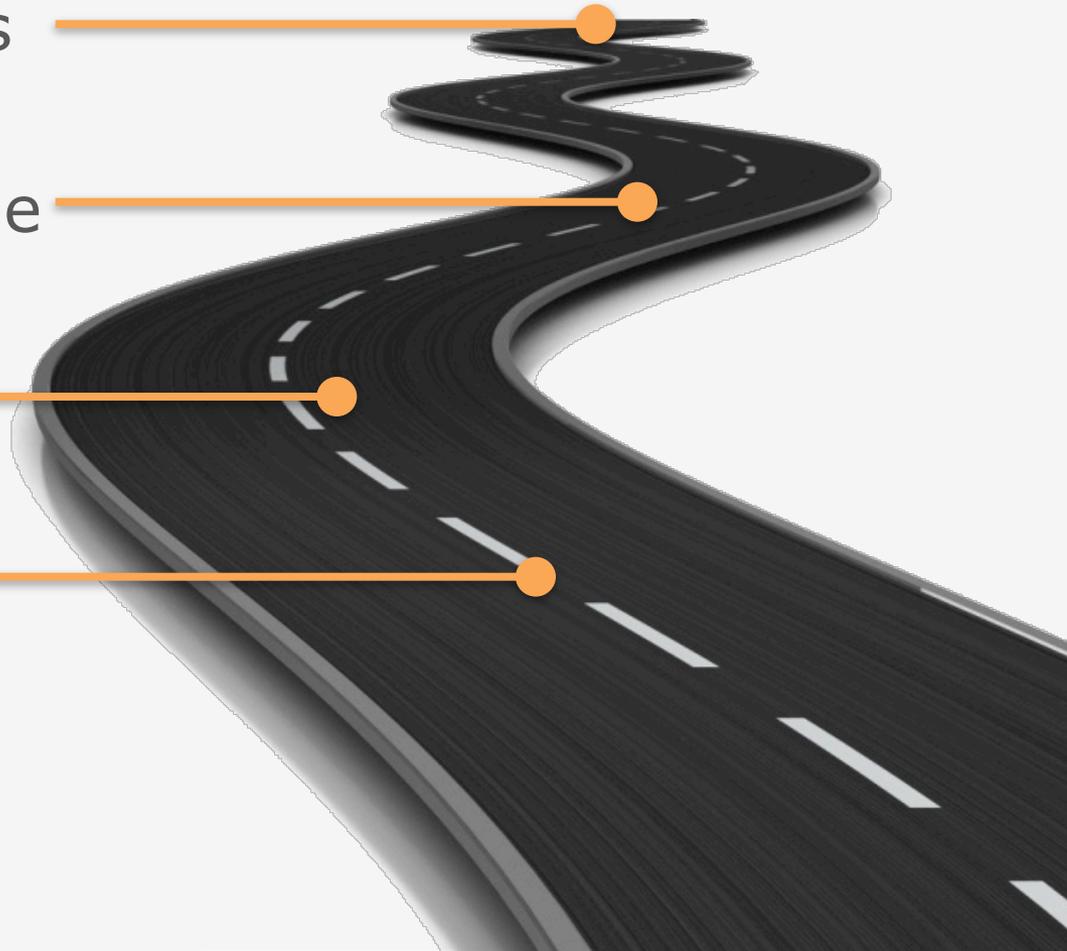


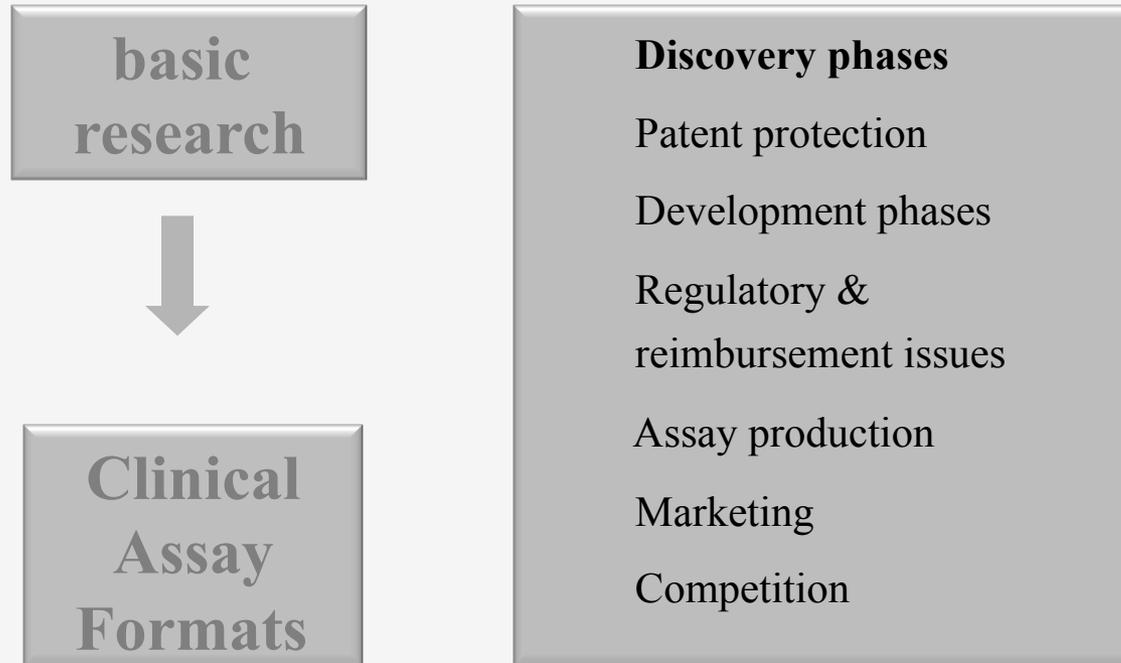
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Steps in biomarker pipeline

Regulatory basics

miRNAs as markers





many hurdle to overcome



- > Steps for a typical IVD assay
- > Example: ELISA



## Predevelopment

## Assay Development



- Specifications

- IP issues

- Make immunogens (inject, wait, fuse, screen, repeat)

- Candidate antibodies

- Conjugation and reagent research (prototype assays)

- Select antibodies

- Reagent components

- Assay configuration

- Reagent manufacturing processes

- Begin stability studies

- Repeat until final design achieved

- Design verification testing

- Validation lots

- produced

- Submit 510K/PMA

- Complete design validation

- Inventory build

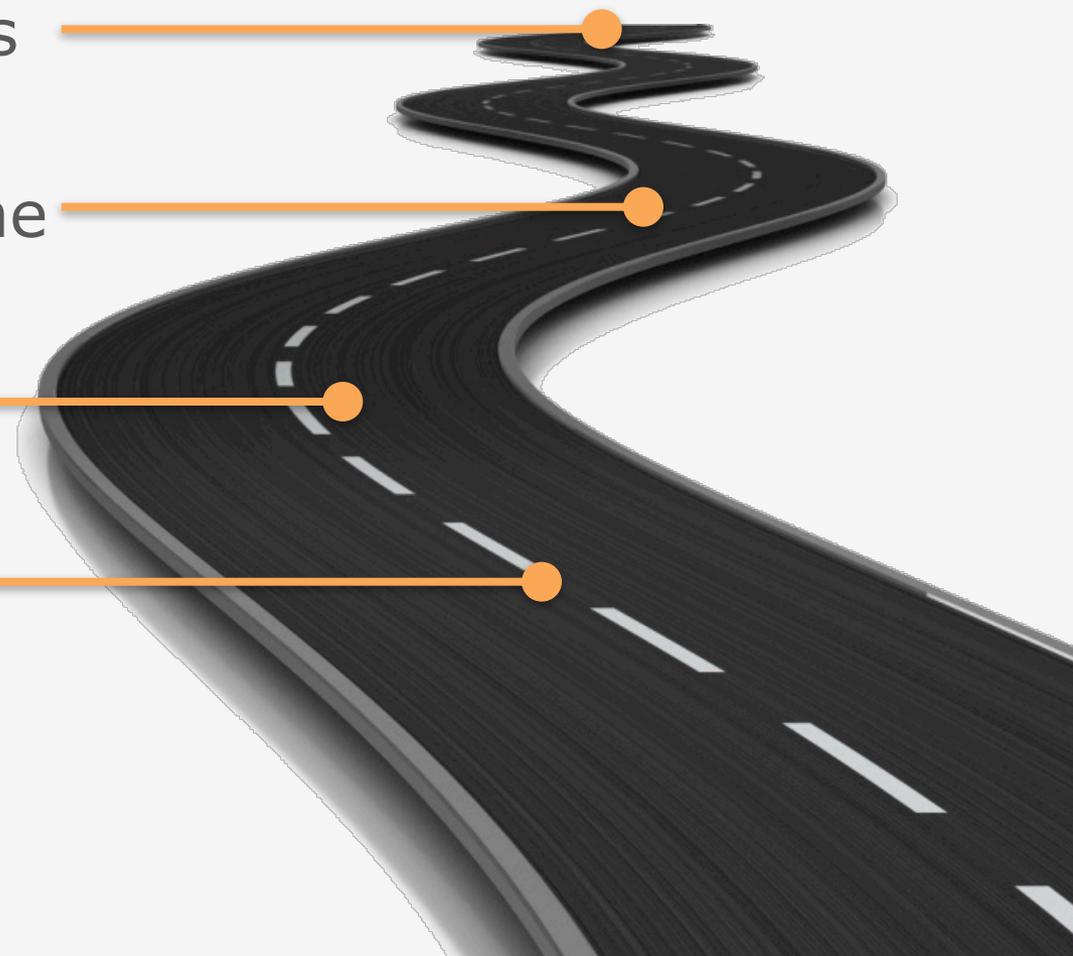


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- In the US 3 classes of medical devices exist:
  - Class I: Devices that do not require premarket approval or clearance but must follow general controls.
  - Class II: Devices that are cleared using the 510(k) process, which uses a similar approved device in the market (predicate device) for comparison. The process is referred as Premarket Notification (PMN).
  - Class III: Devices are approved by the Premarket Approval (PMA) process, similar to new drug approvals. These include devices to sustain human life and are of substantial importance in preventing impairment of human health. (Section 515)

> FDA: determining the class



Medical Specialty	Regulation Citation (21CFR)
73 Anesthesiology	Part 868
74 Cardiovascular	Part 870
75 Chemistry	Part 862
76 Dental	Part 872
77 Ear, Nose, and Throat	Part 874
78 Gastroenterology and Urology	Part 876
79 General and Plastic Surgery	Part 878
80 General Hospital	Part 880
81 Hematology	Part 864
82 Immunology	Part 866
83 Microbiology	Part 866
84 Neurology	Part 882
85 Obstetrical and Gynecological	Part 884
86 Ophthalmic	Part 886
87 Orthopedic	Part 888
88 Pathology	Part 864
89 Physical Medicine	Part 890
90 Radiology	Part 892
91 Toxicology	Part 862

21 CFR 866 -- IMMUNOLOGY AND MICROBIOLOGY DEVICES  
 part C--Microbiology Devices

Sec. 866.2300 Multipurpose culture medium.

*Identification.* A multipurpose culture medium is a device that consists primarily of liquid or solid biological materials intended for medical purposes for the cultivation and identification of several species of pathogenic microorganisms without the need of additional nutritional supplements. Test sults aid in the diagnosis of disease and also provide epidemiological information on diseases caused by these microorganisms.

*Classification.* Class I (general controls). The device is exempt from the premarket notification procedures in subpart E of part 807 of this chapter subject to the limitations in 866.9.

**Subpart C--Microbiology Devices**

- § 866.2050 - Staphylococcal typing bacteriophage.
- § 866.2120 - Anaerobic chamber.
- § 866.2160 - Coagulase plasma.
- § 866.2170 - Automated colony counter.
- § 866.2180 - Manual colony counter.
- § 866.2300 - Multipurpose culture medium.
- § 866.2320 - Differential culture medium.
- § 866.2330 - Enriched culture medium.
- § 866.2350 - Microbiological assay culture medium.
- § 866.2360 - Selective culture medium.

<http://www.fda.gov/MedicalDevices/DeviceRegulationandGuidance/Overview/ClassifyYourDevice/ucm051530.htm>

# > FDA: determining the class



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86 Ophthalmic	Part 886
87 Orthopedic	Part 8
88 Pathology	Part 8
89 Physical Medicine	Part 8
90 Radiology	Part 8
91 Toxicology	Part 8

**PART 866 -- IMMUNOLOGY AND MICROBIOLOGY DEVICES**

**Subpart G--Tumor Associated Antigen immunological Test Systems**

Sec. 866.6040 Gene expression profiling test system for breast cancer prognosis.

(a) *Identification* . A gene expression profiling test system for breast cancer prognosis is a device that measures the ribonucleic acid (RNA) expression level of multiple genes and combines this information to yield a signature (pattern or classifier or index) to aid in prognosis of previously diagnosed breast cancer.

(b) *Classification* . Class II (special controls). The special control is FDA's guidance document entitled "Class II Special Controls Guidance Document: Gene Expression Profiling Test System for Breast Cancer Prognosis." See 866.1(e) for the availability of this guidance document.

[72 FR 26291, May 9, 2007]

- Part 8 [§ 866.5785](#) - Anti-Saccharomyces cerevisiae(S. cerevisiae) antibody (ASCA) test systems.
- Part 8 [§ 866.5800](#) - Seminal fluid (sperm) immunological test system.
- Part 8 [§ 866.5820](#) - Systemic lupus erythematosus immunological test system.
- Part 8 [§ 866.5860](#) - Total spinal fluid immunological test system.
- Part 8 [§ 866.5870](#) - Thyroid autoantibody immunological test system.
- Part 8 [§ 866.5880](#) - Transferrin immunological test system.
- Part 8 [§ 866.5890](#) - Inter-alphatrypsin inhibitor immunological test system.
- Part 8 [§ 866.5900](#) - Cystic fibrosis transmembrane conductance regulator (CFTR) gene mutation detection system.
- Part 8 [§ 866.5910](#) - Quality control material for cystic fibrosis nucleic acid assays.

**Subpart G--Tumor Associated Antigen immunological Test Systems**

- [§ 866.6010](#) - Tumor-associated antigen immunological test system.
- [§ 866.6020](#) - Immunomagnetic circulating cancer cell selection and enumeration system.
- [§ 866.6030](#) - AFP-L3% immunological test system.
- [§ 866.6040](#) - Gene expression profiling test system for breast cancer prognosis.
- [§ 866.6050](#) - Ovarian adnexal mass assessment score test system.

# > FDA: determining the class



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**PART 870 -- CARDIOVASCULAR DEVICES**  
Subpart D--Cardiovascular Prosthetic Devices

Sec. 870.3925 Replacement heart valve.

(a) *Identification.* A replacement heart valve is a device intended to perform the function of any of the heart's natural valves. This device includes valves constructed of prosthetic materials, biologic valves (e.g., porcine valves), or valves constructed of a combination of prosthetic and biologic materials.

(b) *Classification.* Class III (premarket approval).

<http://www.fda.gov/MedicalDevices/DeviceRegulationandGuidance/Overview/ClassifyYourDevice/ucm051530.htm>

- [§ 870.3690](#) - Pacemaker test magnet.
- [§ 870.3700](#) - Pacemaker programmers.
- [§ 870.3710](#) - Pacemaker repair or replacement material.
- [§ 870.3720](#) - Pacemaker electrode function tester.
- [§ 870.3730](#) - Pacemaker service tools.
- [§ 870.3800](#) - Annuloplasty ring.
- [§ 870.3850](#) - Carotid sinus nerve stimulator.
- [§ 870.3925](#) - Replacement heart valve.
- [§ 870.3935](#) - Prosthetic heart valve holder.
- [§ 870.3945](#) - Prosthetic heart valve sizer.



- IVD directive 98/79/EG (IVDD - *In vitro diagnostic directive*)
- Directive 90/385/EWG (e.g. implants)
- Medical Device Directive (MDD) 93/42/EWG
- All in-vitro diagnostics have to be CE-labeled

## > Example of „hitters“

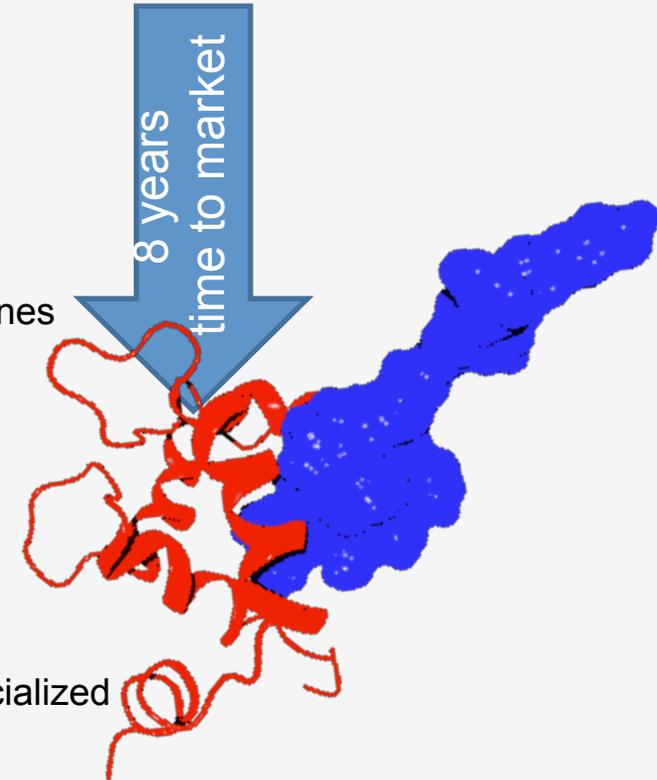


### **Troponin-I**

- 1987 first polyclonal antibodies reported
- 1992 first monoclonal antibodies reported
- 1995 first automated commercial assay
- 1997/8 acceptance comparable to CKMB
- 2001 new gold standard test for AMI per ACC/ESC Guidelines

### **BNP / NT-proBNP**

- 1995 Research activity reaches a high level
- 1997 Monoclonal antibodies available
- 2001 First commercial BNP assay available
- 2003 First commercial NT-proBNP (Bayer) assay commercialized
- 2005/6 ESC guideline; NACB/AHA guideline
- TBD Acceptance as a gold standard test for CHF



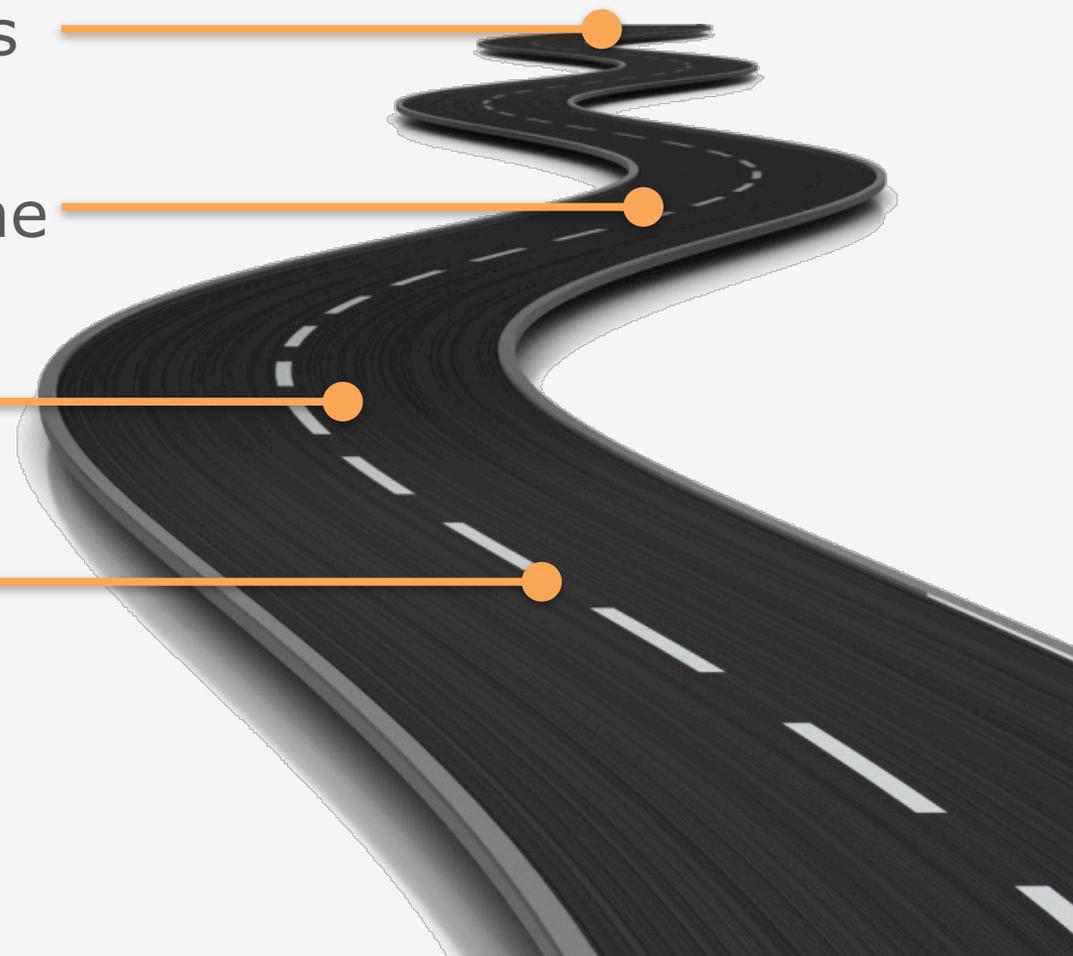


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Three paradigms:

Develop a minimal-invasive test (screening blood cells, serum, urine)

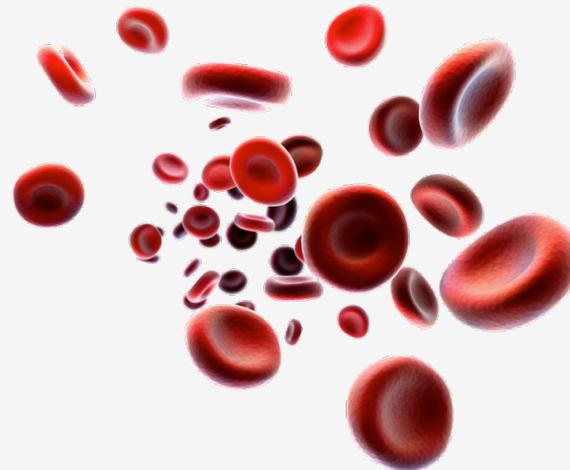
Combine the diagnostic power of many markers

Investigate different diseases to understand the specificity of the profiles



**Toward the blood-borne miRNome of human diseases**

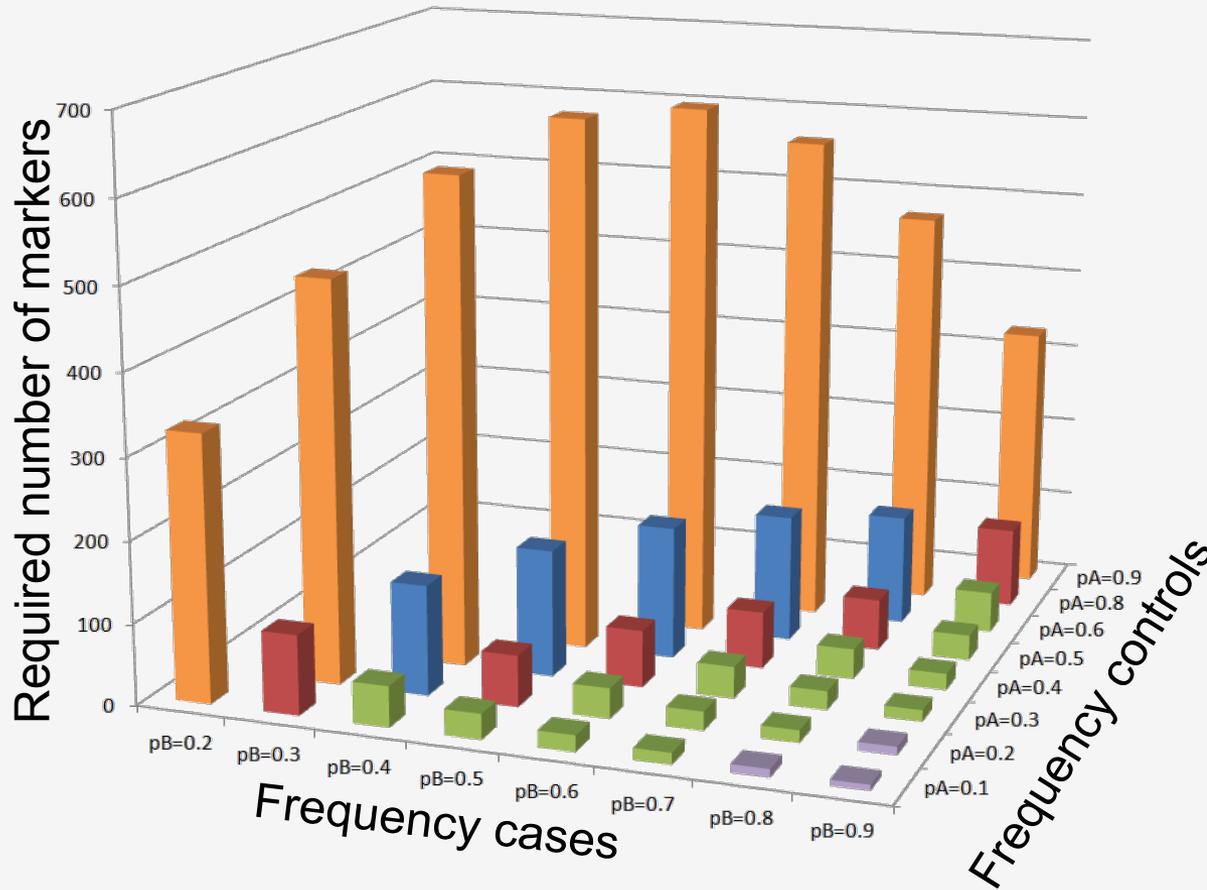
Andreas Keller<sup>1,2,21</sup>, Petra Leidinger<sup>2,21</sup>,  
Andrea Bauer<sup>3</sup>, Abdou ElSharawy<sup>4</sup>, Jan Haas<sup>5</sup>,  
Christina Backes<sup>2</sup>, Anke Wendschlag<sup>6</sup>, Nathalia Giese<sup>7</sup>,  
Christine Tjaden<sup>7</sup>, Katja Ott<sup>7</sup>, Jens Werner<sup>7</sup>,  
Thilo Hackert<sup>1</sup>, Klemens Ruprecht<sup>8</sup>, Hanno Huwer<sup>9</sup>,  
Junko Huebers<sup>10</sup>, Gunnar Jacobs<sup>4</sup>, Philip Rosenstiel<sup>4</sup>,  
Henrik Dommisch<sup>11</sup>, Arne Schaefer<sup>4</sup>,  
Joachim Müller-Quernheim<sup>12</sup>, Bernd Wullich<sup>13</sup>,  
Bastian Keck<sup>13</sup>, Norbert Graf<sup>14</sup>, Joerg Reichrath<sup>15</sup>,  
Britta Vogel<sup>6</sup>, Almut Nebel<sup>4</sup>, Sven U Jager<sup>16</sup>,  
Peer Staehler<sup>6</sup>, Ioannis Amarantos<sup>6</sup>, Valesca Boisguerin<sup>6</sup>,  
Cord Staehler<sup>6</sup>, Markus Beier<sup>6</sup>, Matthias Scheffler<sup>6</sup>,  
Markus W Büchler<sup>7</sup>, Joerg Wischhusen<sup>17,18</sup>,  
Sebastian F M Haeussler<sup>17</sup>, Johannes Dietl<sup>17</sup>,  
Sylvia Hofmann<sup>1</sup>, Hans-Peter Lenhof<sup>19</sup>,  
Stefan Schreiber<sup>20</sup>, Hugo A Katus<sup>9</sup>, Wolfgang Rothbauer<sup>9</sup>,  
Benjamin Meder<sup>2</sup>, Joerg D Hohenseil<sup>2</sup>, Andre Franke<sup>4,21</sup> &  
Eckart Meese<sup>2,21</sup>



> Why do we need more than one marker



## The advantage of marker sets



Required number of independent biomarkers to achieve specificity and sensitivity of 99%.



- > miRNAs
- > Potentially disruptive biomarkers



## Structure

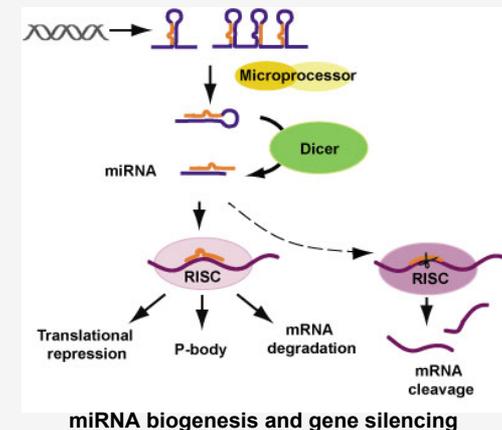
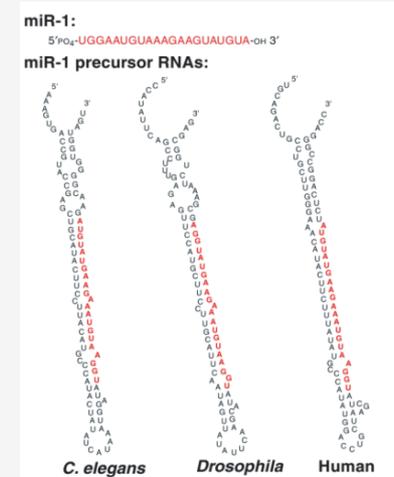
- Small non-coding RNAs (17-23 nucleotides length)
- Very stable and conserved across organisms
- Per ~120 base precursor molecule transcribed from the genome usually two mature forms are build and exported from nucleus, -3p and -5p

## Biology

- > 20,000 miRNAs in >100 species are known
- For *h. sapiens* > 2,200 are annotated
- These build 0.0002% of the human genome
- ... while regulating > 70% of genes and majority of biochemical pathways

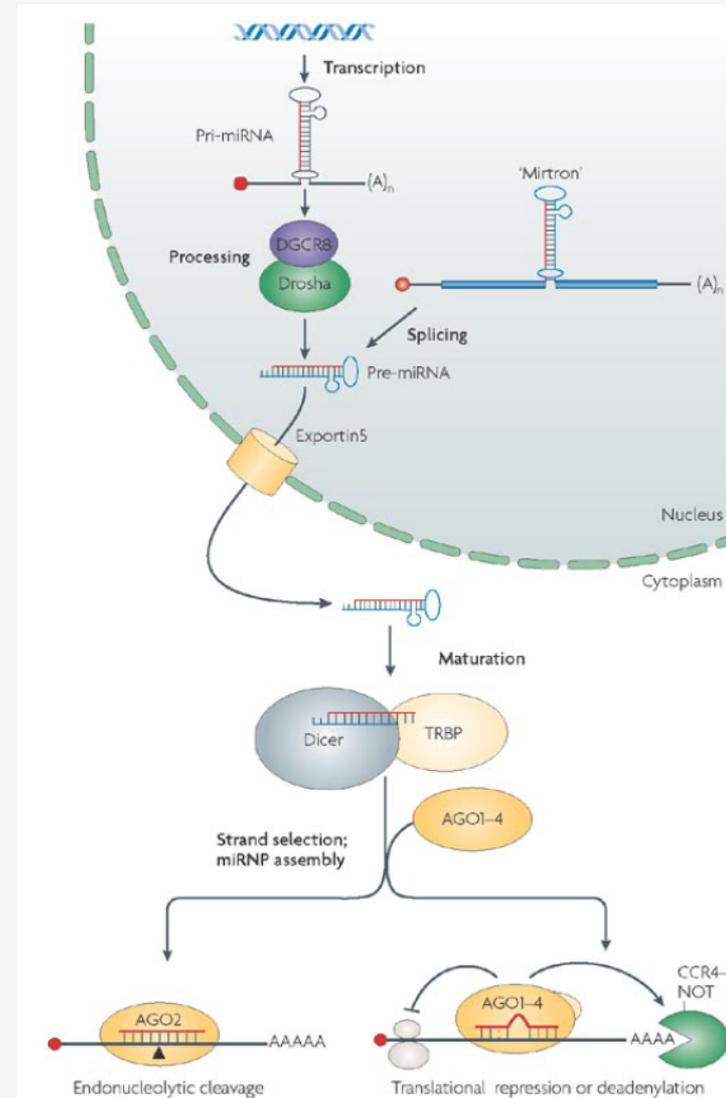
## Potential

- Are expressed specifically in tissues and body fluids
- Have demonstrated a wide potential as diagnostic biomarkers





- Transcription of the pre-miRNAs is done via the RNA-Polymerase II
- The pre-miRNAs can contain multiple miRNA sequences in their hairpin structure
- The typical hairpin-structure is due to two symmetrical strands.
- Additional characteristics are a 5'-cap and a 3'-poly-A tail.
- The pre-miRNAs are exported from the nucleus to the cytoplasm via Exportin5
- DICER splices out the loop-structures of the pre-miRNA.
- Result is the mature miRNA



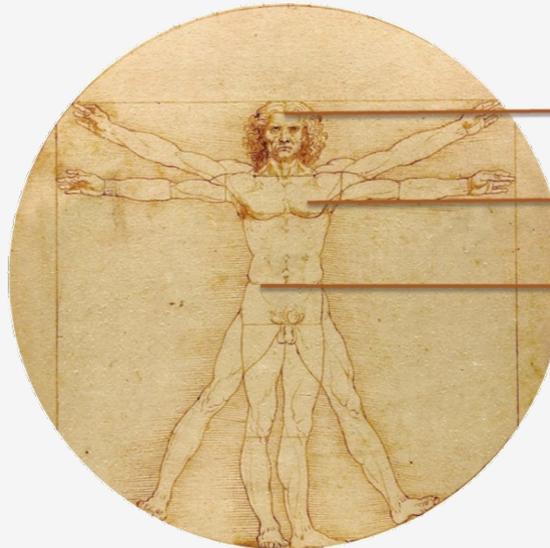
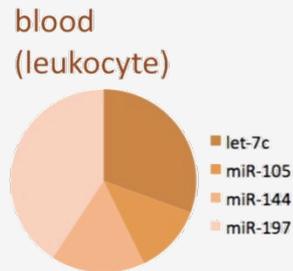


- miRNAs are often very similar to each other (see let-7 family as example)
- it is however, especially in the light of multiplex assays, important to distinguish between these miRNAs
- standard hybridization assays, e.g., may show a high degree of so-called „cross-hybridization“ introducing noise to the multiplex profiles

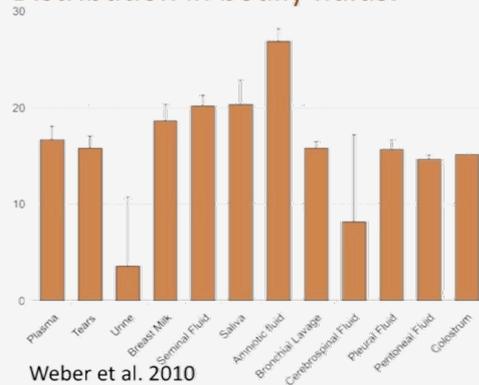
Multiple alignment

```
let-7b UGAGGUAGUAGGUUGUGUGGUU
let-7c UGAGGUAGUAGGUUGUAUGGUU
let-7d AGAGGUAGUAGGUUGCAUAGUU
let-7e UGAGGUAGGAGGUUGUAUAGUU
let-7a UGAGGUAGUAGGUUGUAUAGUU
let-7f UGAGGUAGUAGAUUGUAUAGUU
let-7g UGAGGUAGUAGUUUGUACAGUU
let-7i UGAGGUAGUAGUUUGUGCUGUU
      ***** ** ***   ***
```

# > Uniqueness per tissue



Distribution in bodily fluids:

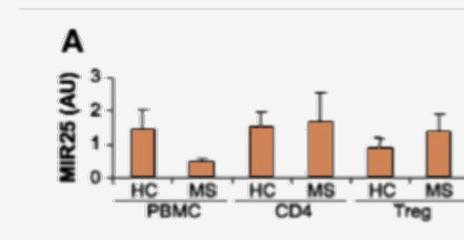


Communication via Exosomes

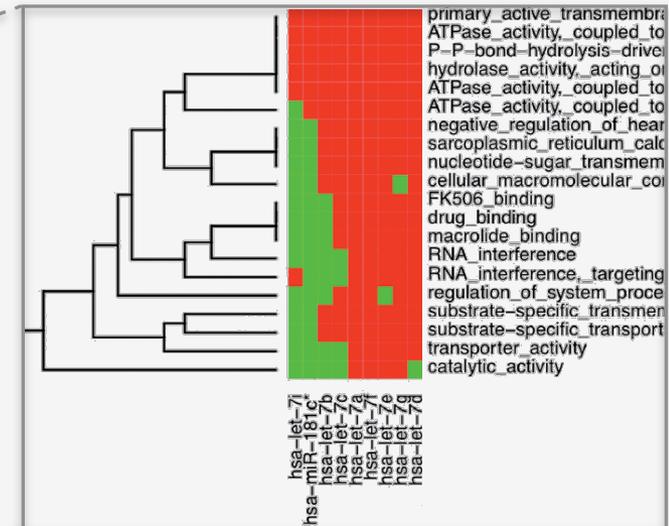
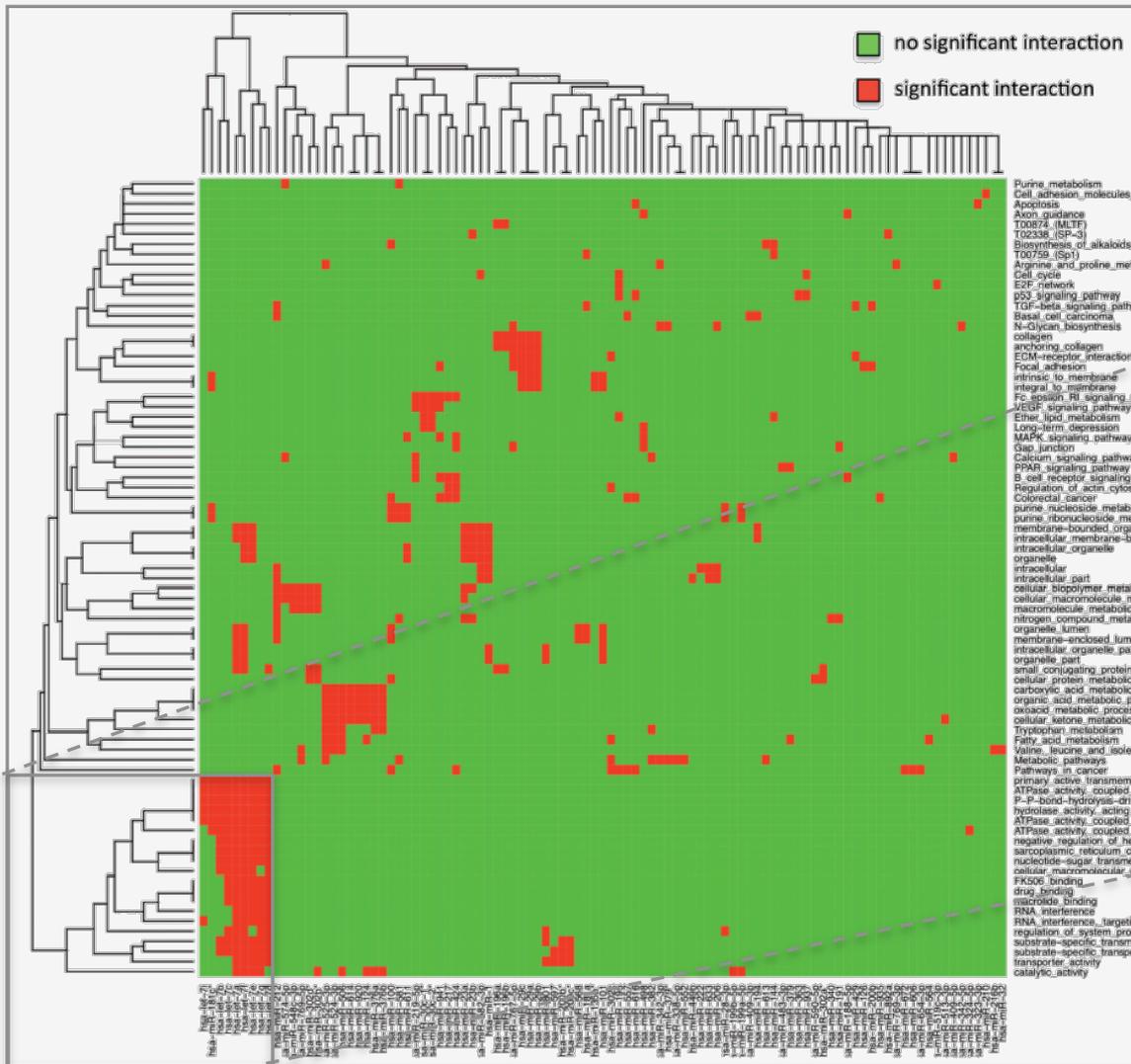


Zomer et al. 2010

PBMC versus T regulatory cells



# > miRNAs regulate pathways





- > **Version 2.0**
- > of the whole miRNome project



## Cohort

Category	ICD10	# Samples
<b>Normal</b>		203
<b>long-lived individuals (lli)</b>		15
<b>tumor of stomach</b>	C16	13
<b>colon cancer</b>	C18	29
<b>lung cancer</b>	C24	73
<b>pancreatic cancer ducatal</b>	C25	45
<b>Melanoma</b>	C43	35
<b>breast cancer</b>	C50	48
<b>ovarian cancer</b>	C56	24
<b>prostate cancer</b>	C61	65
<b>wilms tumor</b>	C64	124
<b>renal cancer</b>	C65	20
<b>Glioma</b>	C71	20
<b>Sarcoidosis</b>	D86.0	45
<b>multiple sclerosis</b>	G35	23
<b>acute myocardial infarction</b>	I21.3	62
<b>dilatative cardiomyopathie</b>	I42	33
<b>COPD</b>	J40-47	47
<b>Peridontitis</b>	K05.4	18
<b>crohn's disease</b>	K50	62
<b>Colitis</b>	K51	46
<b>Pancreatitis</b>	K85	37
<b>Psoriasis</b>	L40	43
<b>benign prostate hyperplasia</b>	N40	35
<b>pre-eclampsia</b>	O14	16
<b>Others</b>		133

## Key characteristics

1,314 samples screened using microarray technology

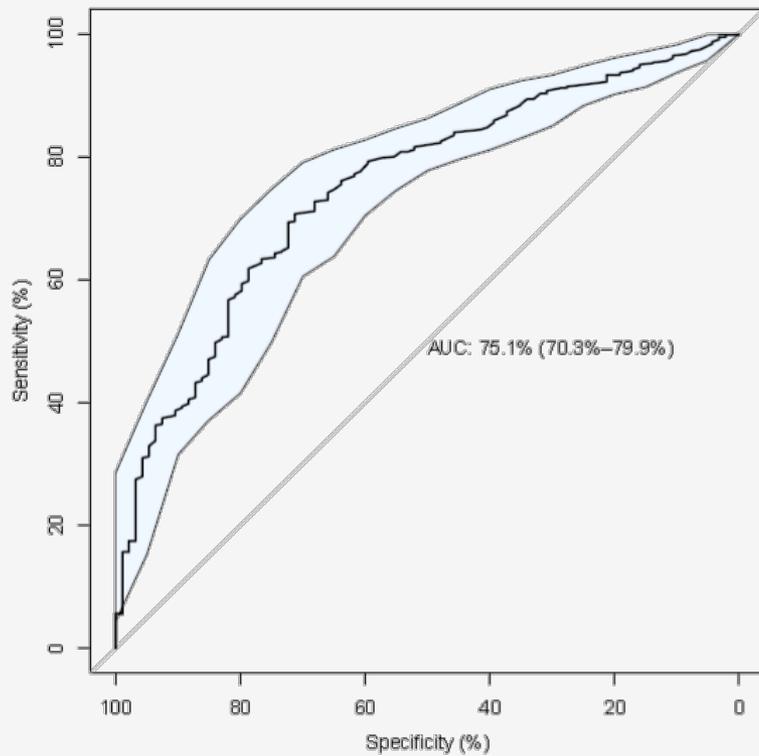
863 miRNAs (miRBase 16) screened

On average 10 replicates per miRNA measured

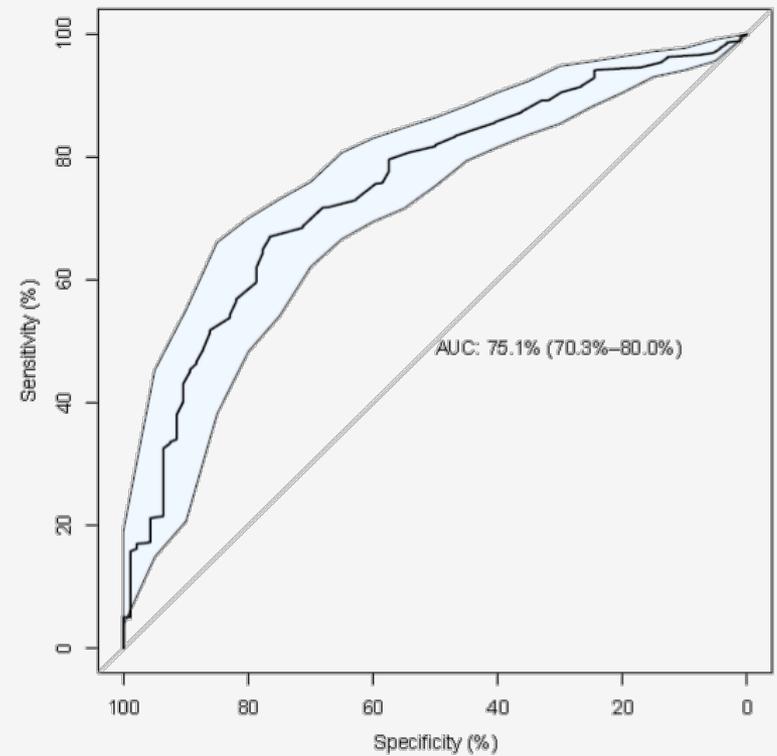
Corresponds to  $\approx 12$  million single measurements

Unsupervised and supervised analysis carried out.

Classification is carried out as 10-fold cross validation radial basis function SVM with stepwise forward subset selection together with non-parametric permutation tests



miR-144\*, diseases vs. control

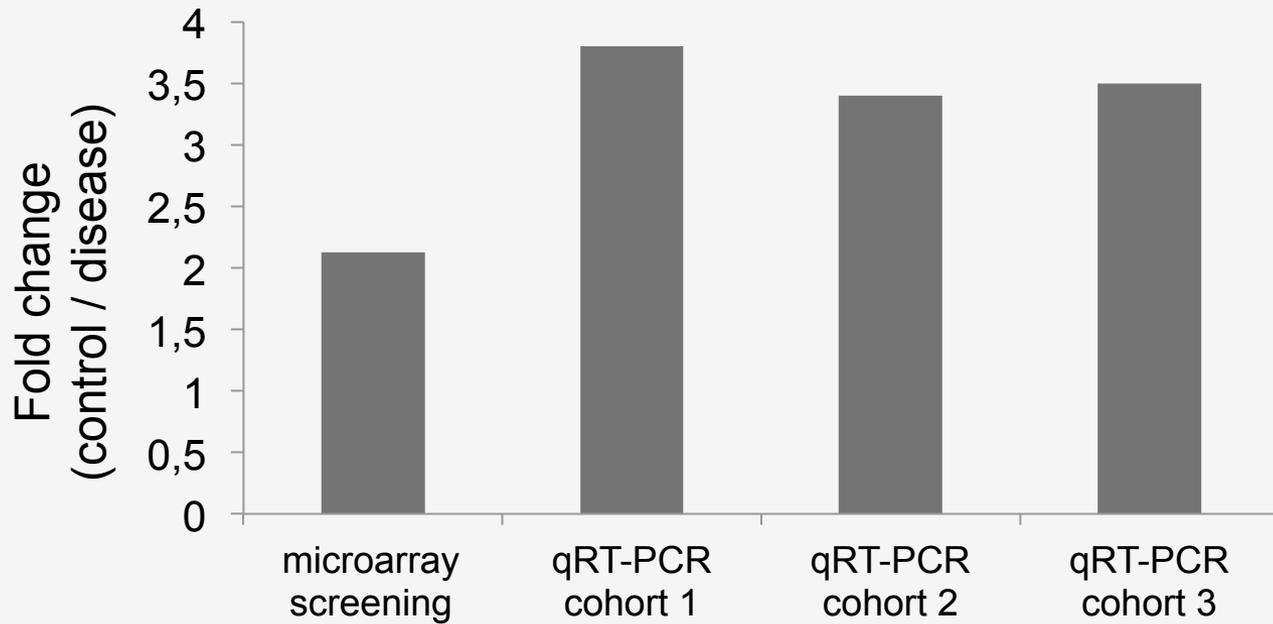


miR-144\*, cancer vs. control

- > miR-144\* qRT-PCR validation
- > 3 cohorts > 300 samples



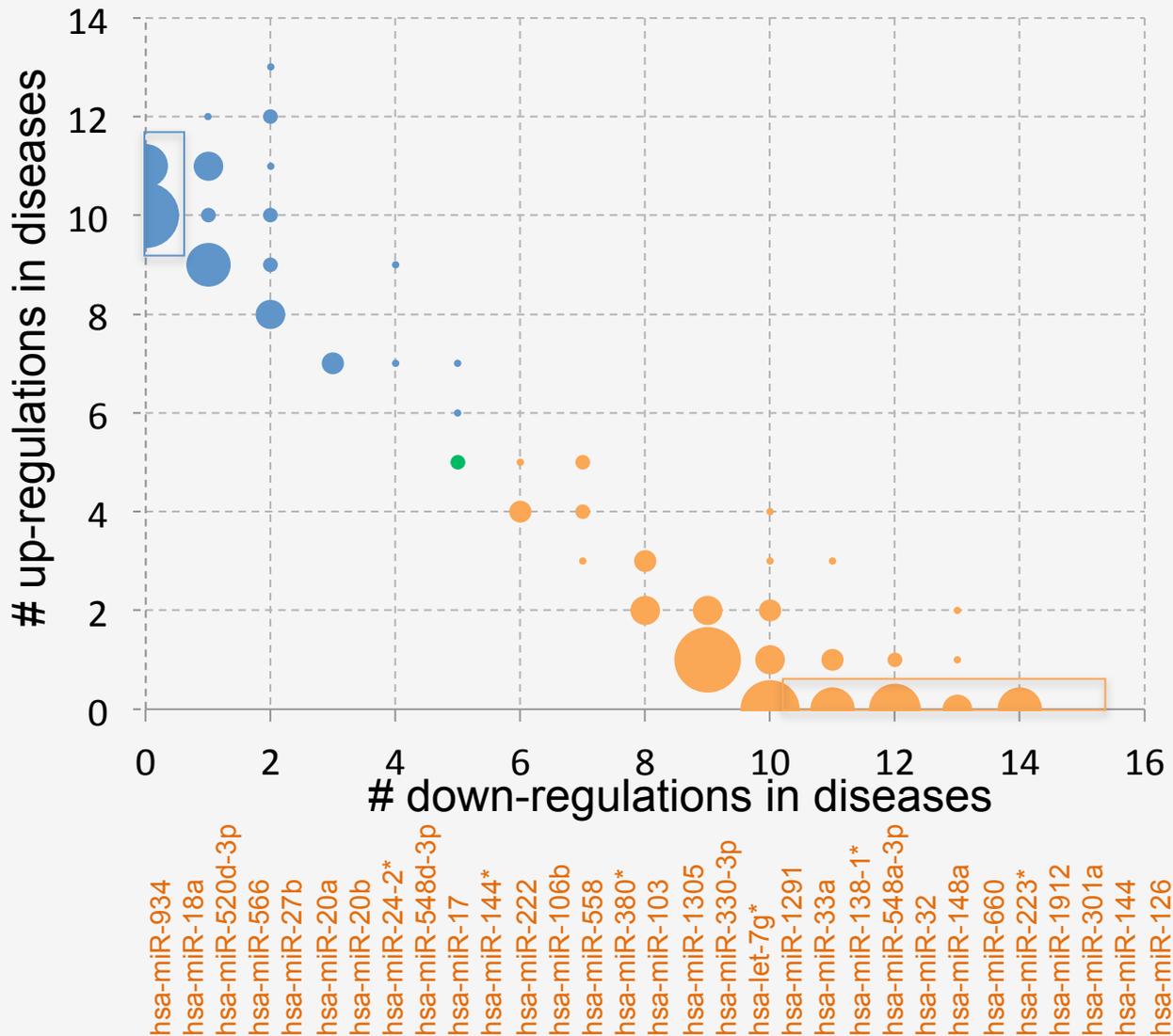
Constant down-regulation in all cohorts



> Single markers are not specific

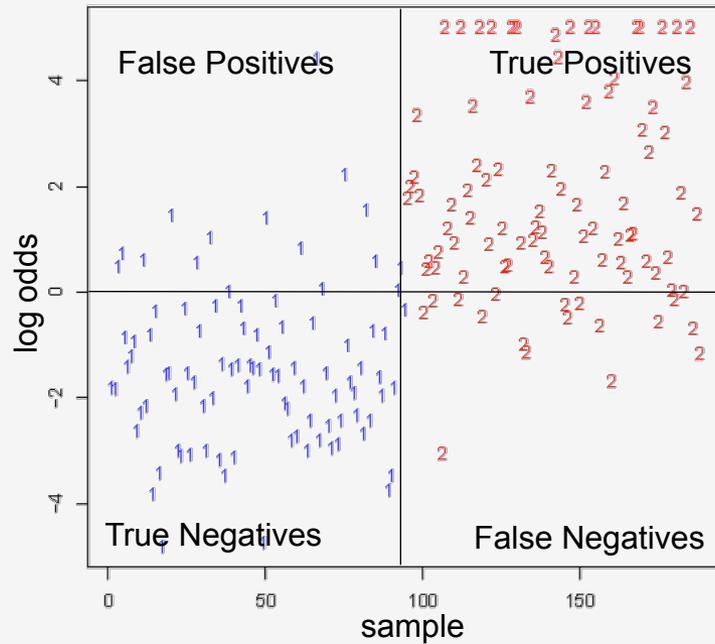


- hsa-miR-1246
- hsa-miR-223
- hsa-let-7e\*
- hsa-miR-1303
- hsa-miR-25\*
- hsa-miR-491-5p
- hsa-miR-885-5p
- hsa-miR-539
- hsa-miR-194\*
- hsa-miR-658
- hsa-miR-145
- hsa-miR-130b\*
- hsa-miR-499-5p
- hsa-miR-484
- hsa-miR-126\*



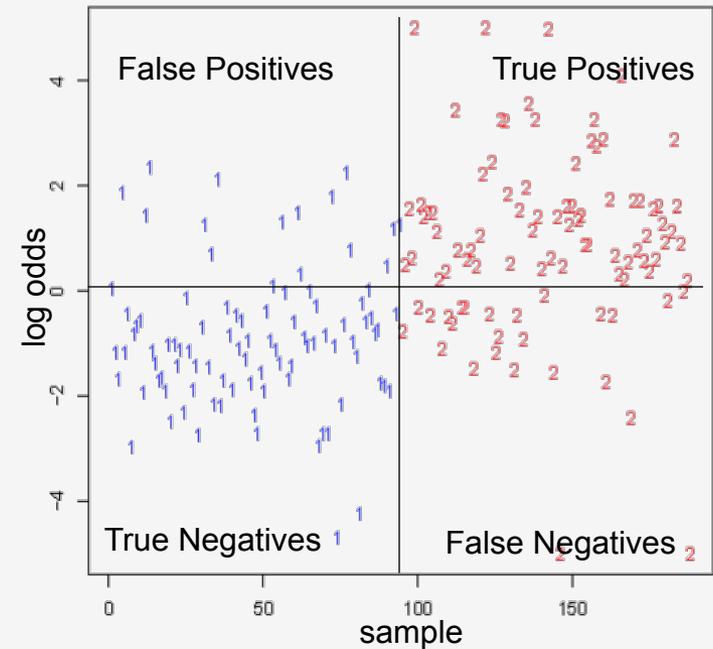


diseases vs. controls

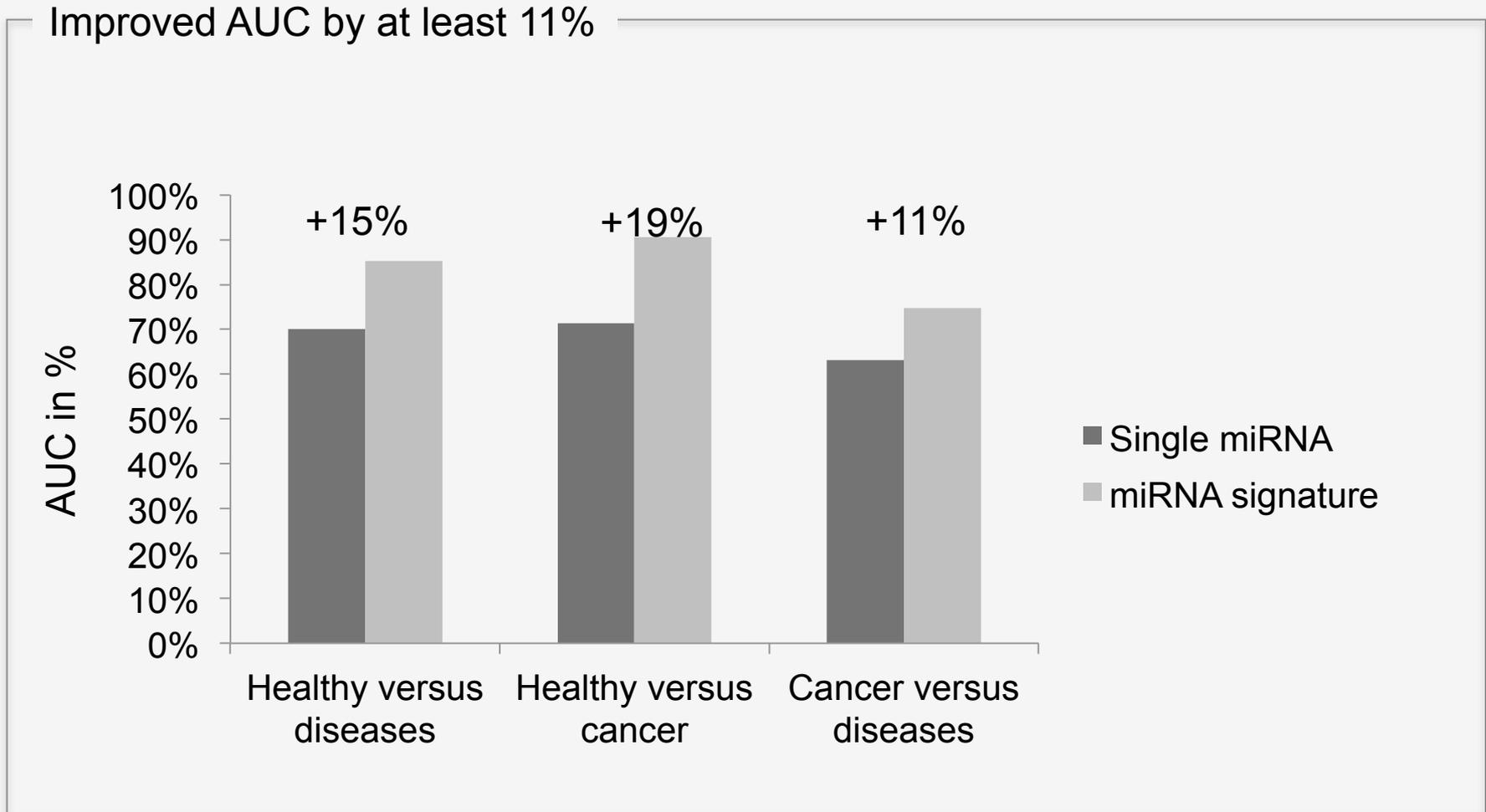


Accuracy 78%  
 Specificity 81%  
 Sensitivity 75%

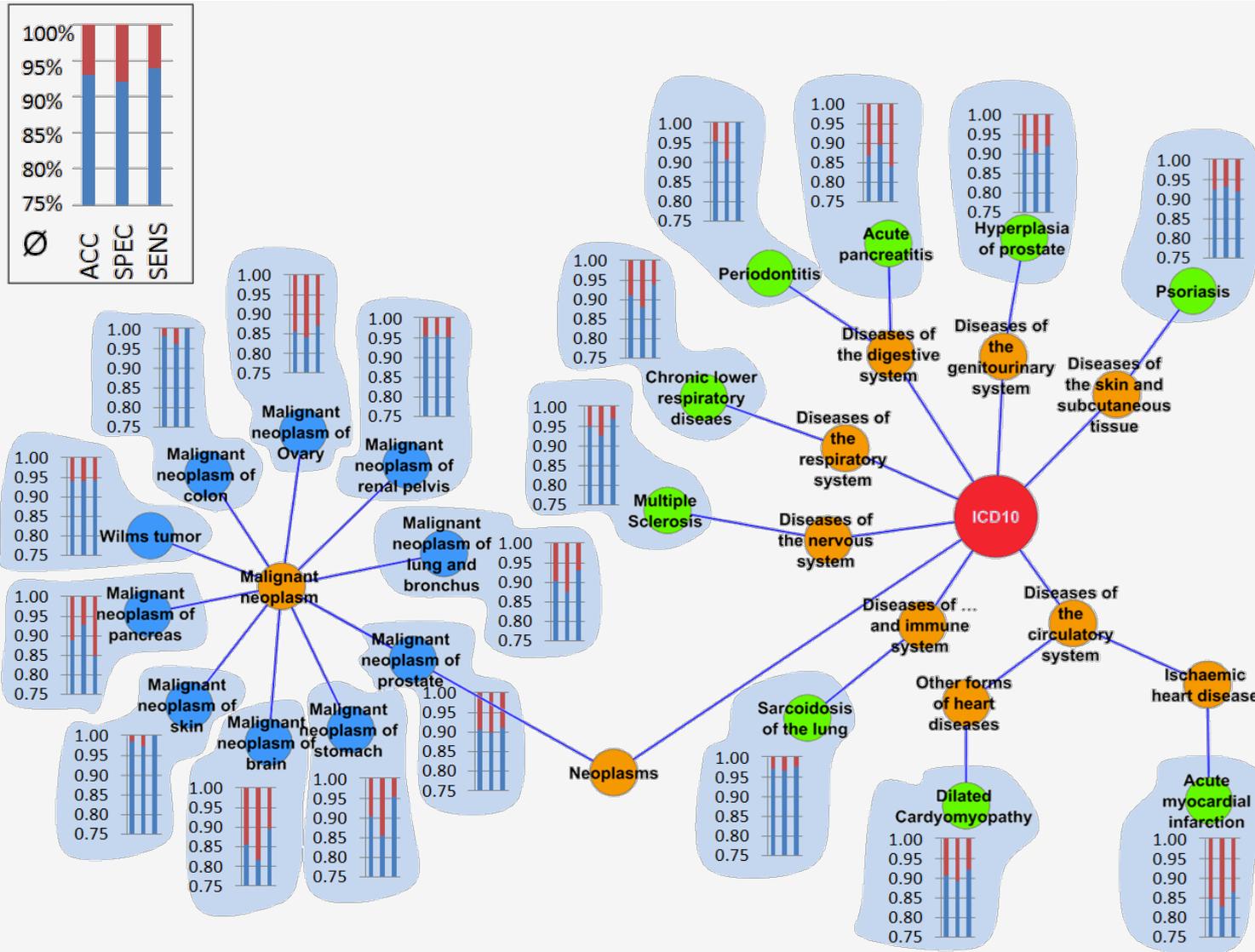
Cancer



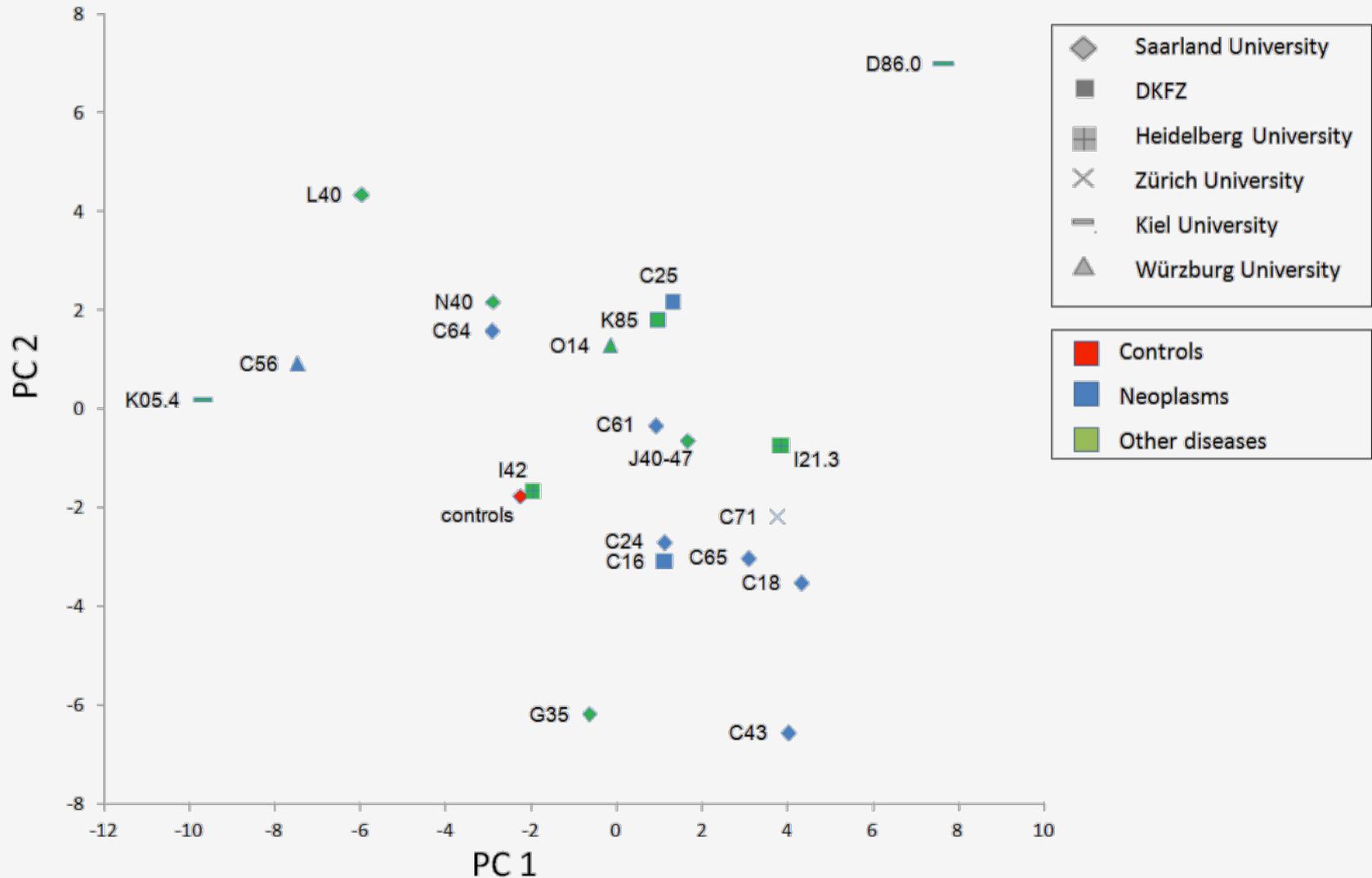
Accuracy 82%  
 Specificity 81%  
 Sensitivity 83%



# > Classification for all diseases



- > Principal Component Analysis
- > Weak clustering of Neoplasms

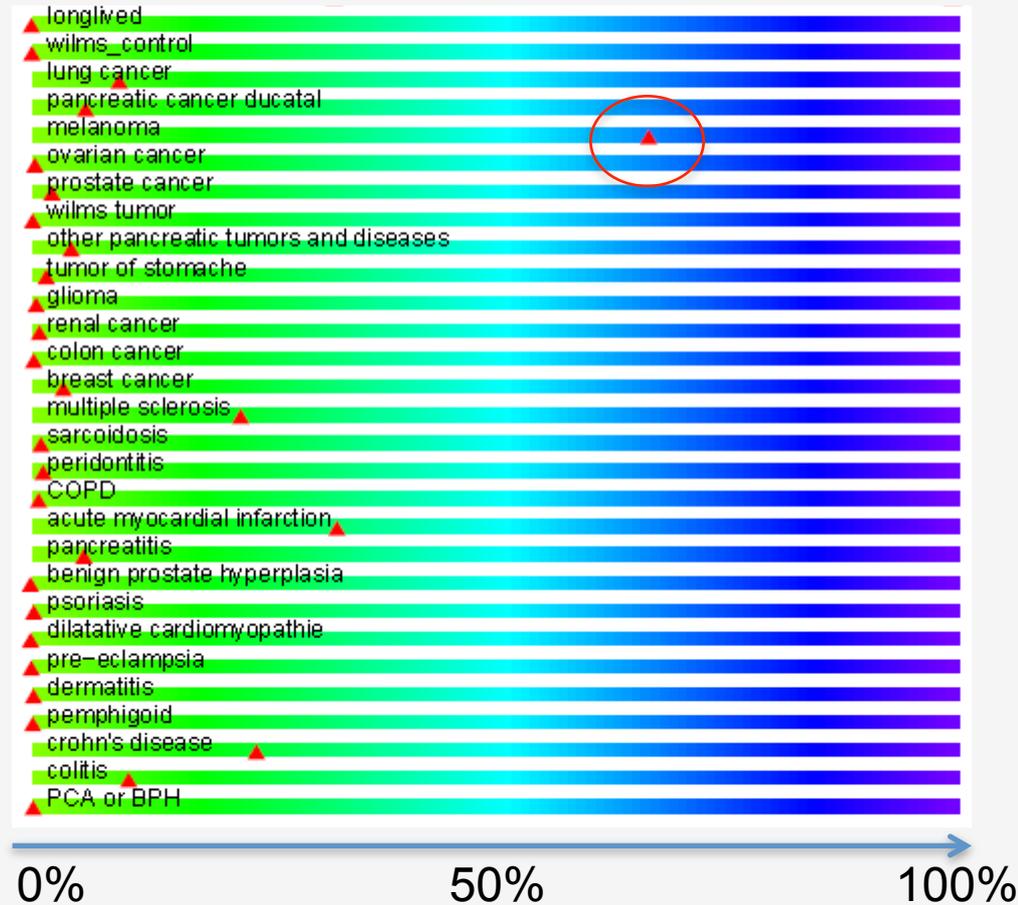


> Disease Probability Plot (DPP)



- ▶ For each patient  $i$  and each disease  $j$  we compute the probability that the patient is positive for this disease as  $p_{(i,j)}$  relying on the distance from the SVM hyperplane
- ▶ For each patient the disease with highest probability is selected OR
- ▶ Alternatively all diseases with probability above a selected threshold
- ▶ The hit rate of the "best" disease was 48%

DPP for one melanoma patient



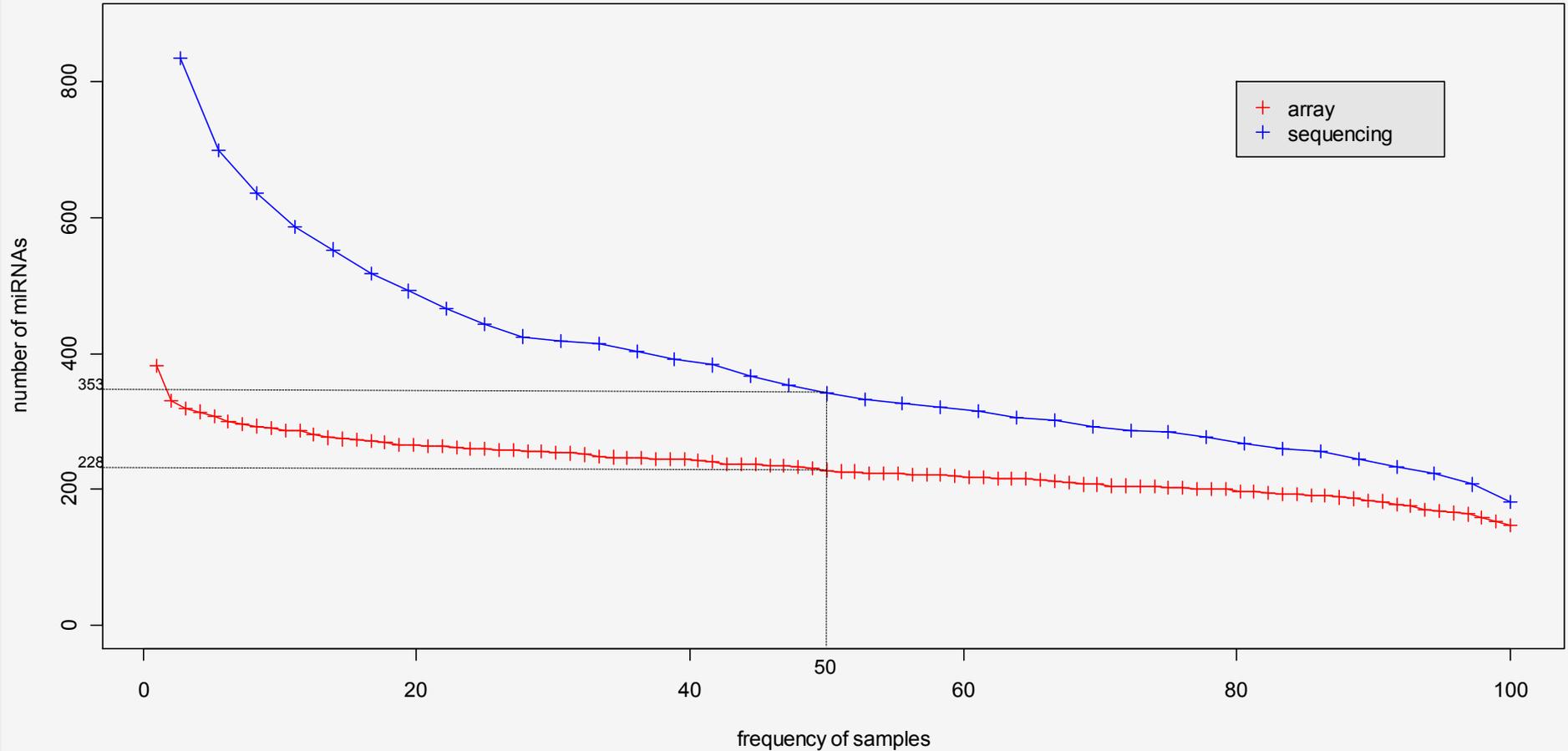
Keller et al, in preparation



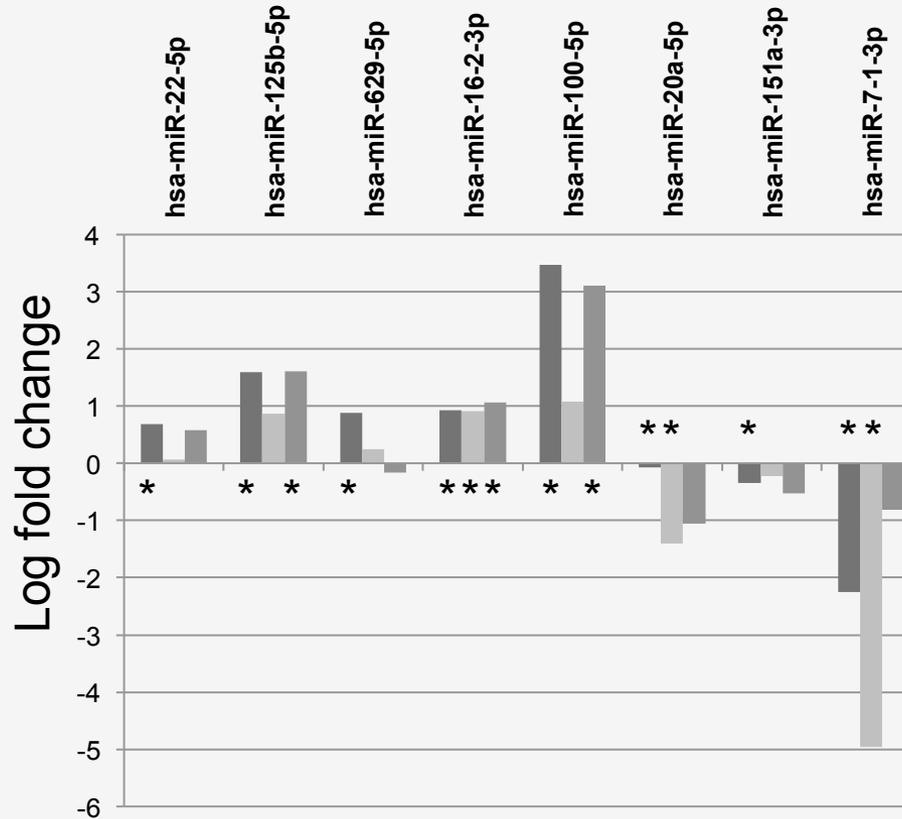
## Five advantages of NGS

- NGS offers to screen for all known miRNAs at once
  - NGS enables the detection of novel miRNAs
  - NGS allows for detecting SNPs in miRNAs
  - NGS enables ultra-high throughput screening
  - NGS is more sensitive
- We screened about 1,000 patients using NGS

- > Application Multiple Sclerosis
- > Microarray, NGS, qRT-PCR on the same cohort



- > 8-miRNA signature
- > to differentiate between MS and control



- > Application Alzheimer
- > 12 miRNA signature



Sample group	Number	Age (mean ± SD)	Sex (female/male)	MMSE (mean ± SD)	cohort size NGS	cohort size RT-qPCR
Alzheimer disease	106	72.7 (10.4)	53/53	18.9 (3.4)	48	94
healthy control	22	67.1 (7.5)	11/11	29.3 (1.2)	22	21
mild cognitive impairment	18	73.9 (6.2)	9/9	25.3 (1.4)	-	18
multiple sclerosis	16	32.3 (10.7)	12/4	not available	-	16
Parkinson disease	9	69.7 (9.0)	1/8	25.2 (4.2)	-	9
major depression	15	45.2 (9.1)	0/15	not available	-	15
bipolar disorder	15	41.9 (13.7)	14/1	29.5 (1.6)	-	15
schizophrenia	14	41.7 (7.9)	1/13	26.1 (4.3)	-	14



Research

Highly accessed

Open Access

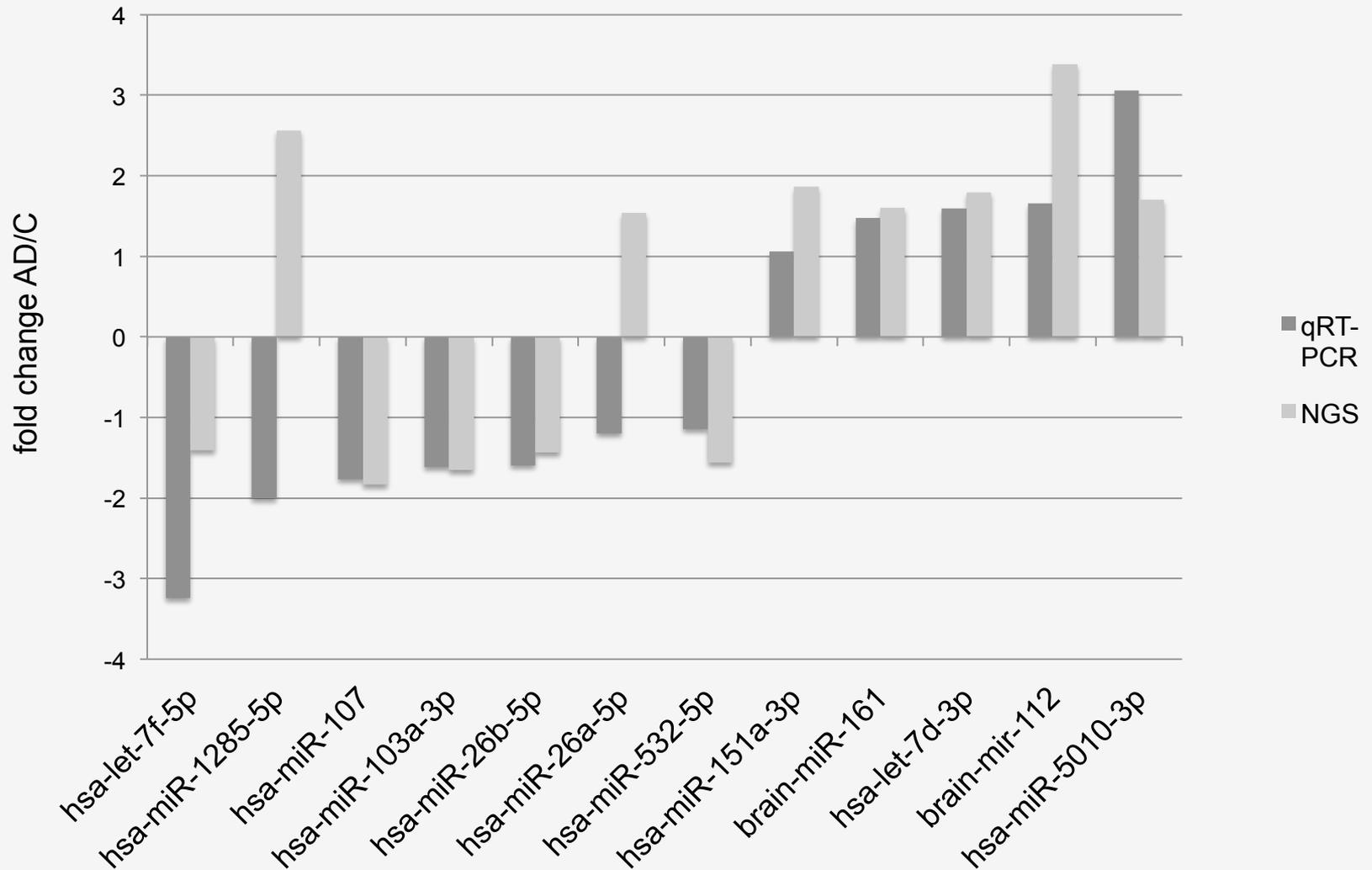
**A blood based 12-miRNA signature of Alzheimer disease patients**

Petra Leidinger, Christina Backes, Stephanie Deutscher, Katja Schmitt, Sabine C Muller, Karen Frese, Jan Haas, Klemens Ruprecht, Friedemann Paul, Cord Stahler, Christoph JG Lang, Benjamin Meder, Tamas Bartfai, Eckart Meese and Andreas Keller

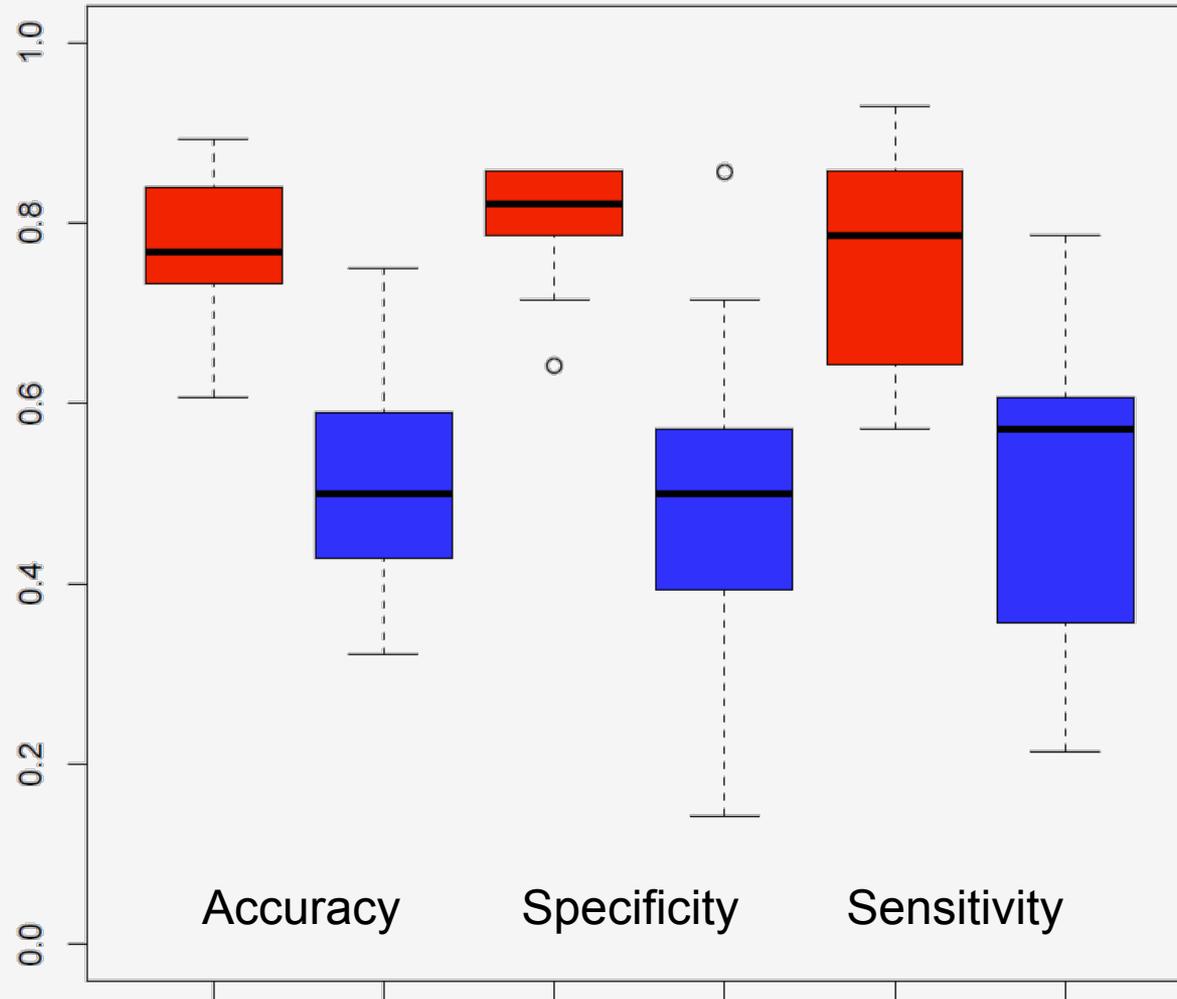
Genome Biology 2013, 14:R78

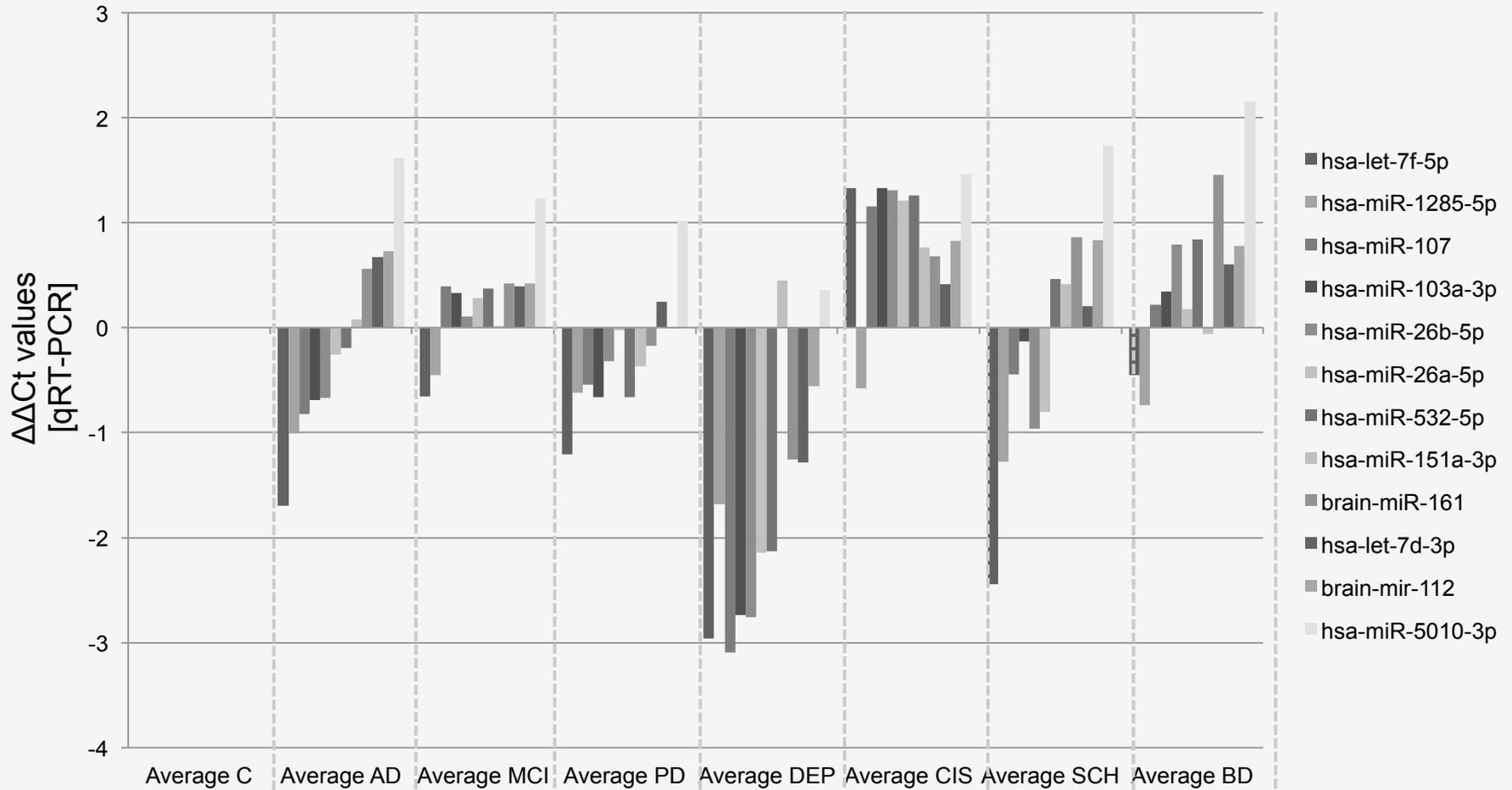
doi:10.1186/gb-2013-14-7-r78

- > Alzheimer vs. Controls
- > NGS vs. qRT-PCR



- > Classification AD vs. controls
- > Highly specific test

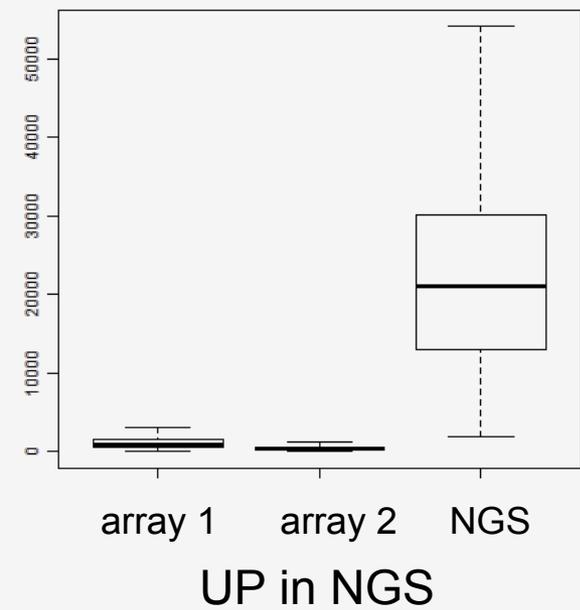
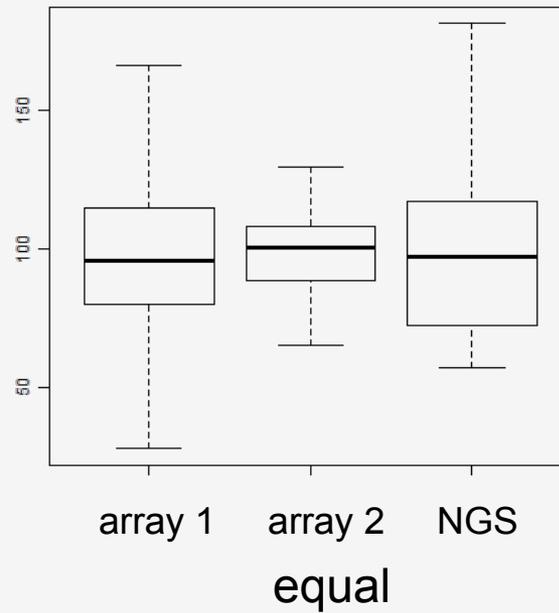
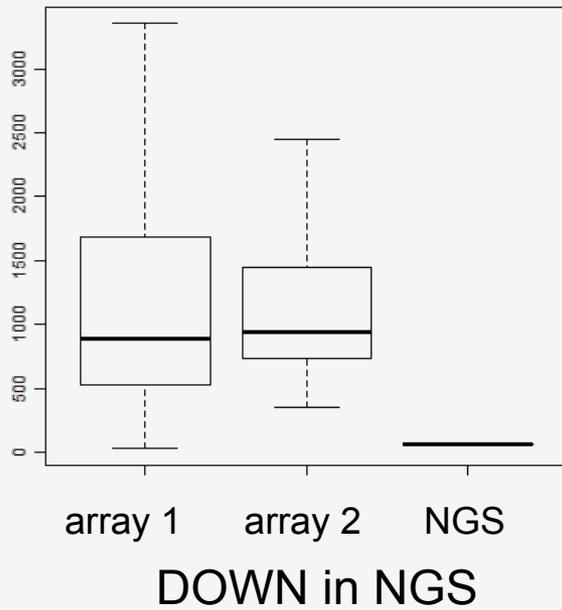




- > Potential pitfalls
- > Systemic bias



## Technological bias

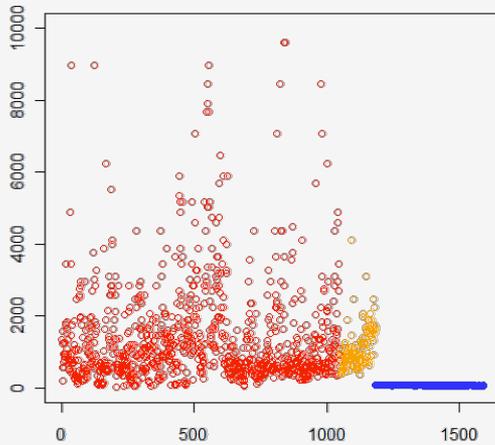


The technological bias leads to results that can't be reproduced by qRT-PCR technically, causing avoidable cost and precious biological material.

- > Potential pitfalls
- > Systemic bias

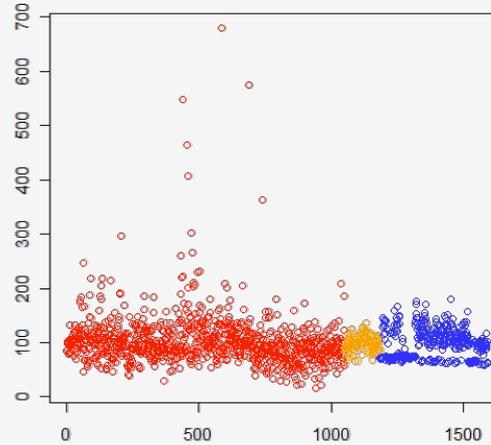


## Technological bias



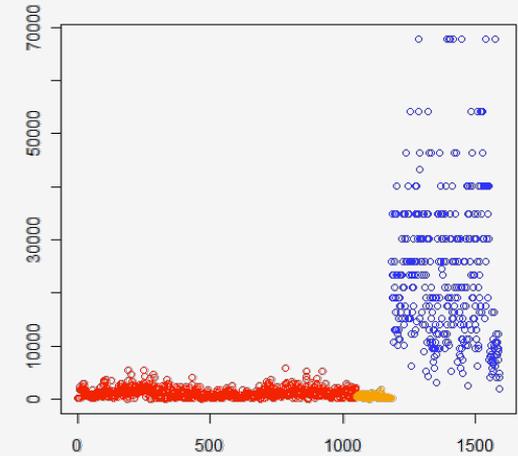
array 1      array 2    NGS

DOWN in NGS



array 1      array 2    NGS

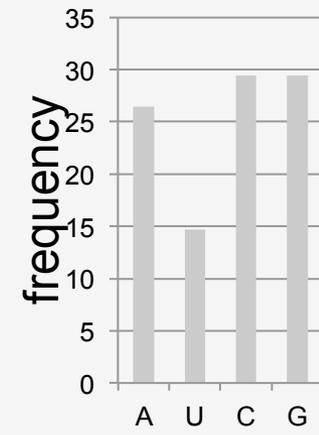
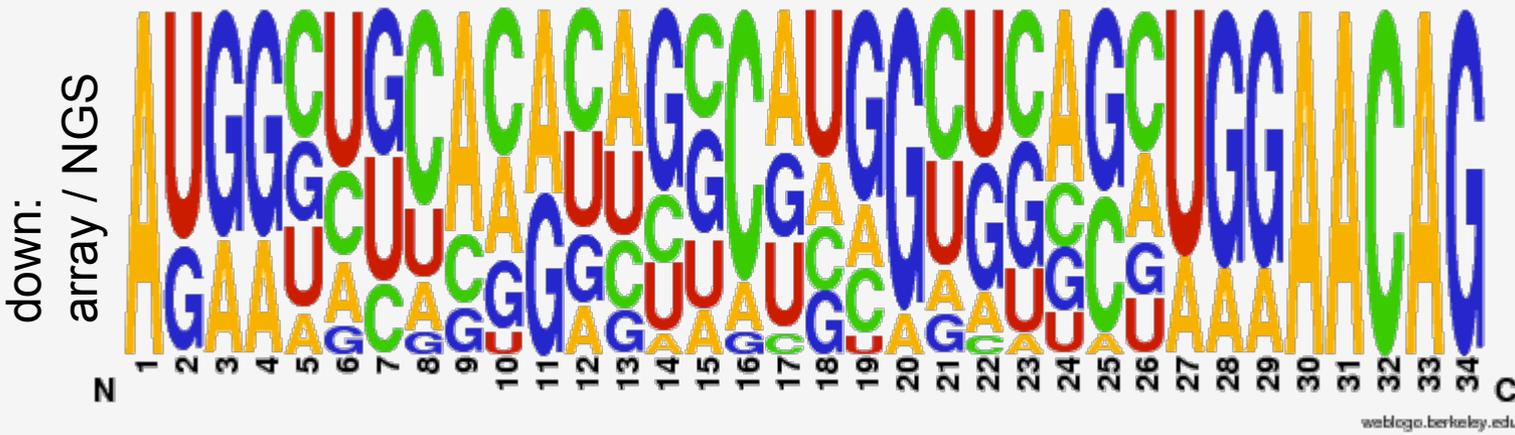
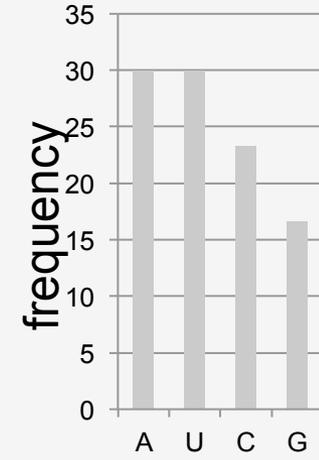
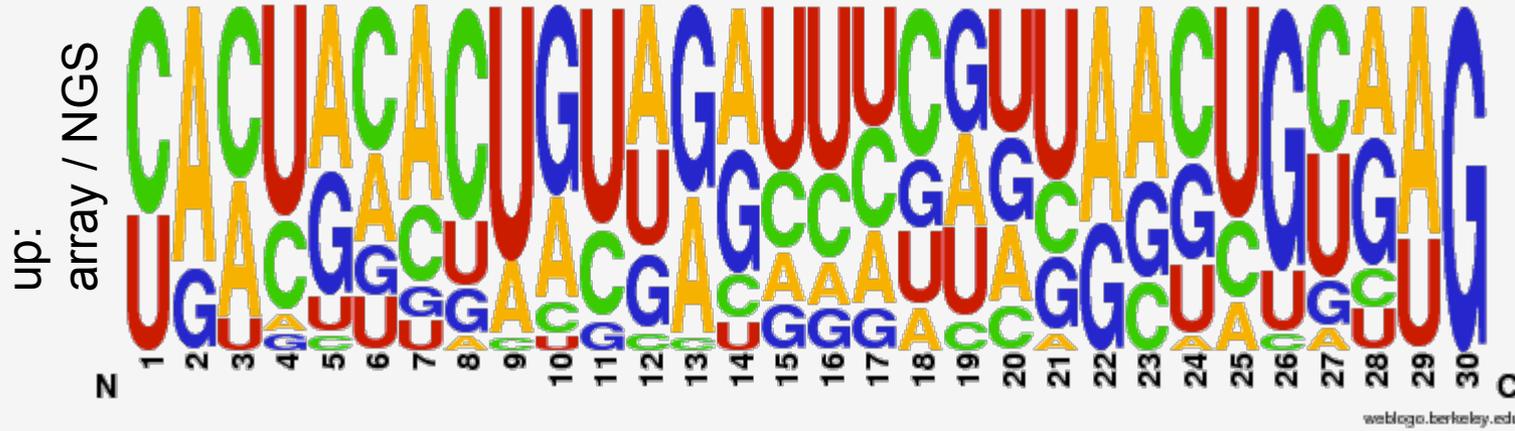
equal



array 1      array 2    NGS

UP in NGS

The technological bias leads to results that can't be reproduced by qRT-PCR technically, causing avoidable cost and precious biological material.





## Concept

For many miRNAs array, NGS and qRT-PCR data are available. Use them to train three statistical models.

For new studies use

- a) NGS data & sequence OR
- b) Array data & sequence OR
- c) NGS & Array data & sequence OR
- d) sequence

in order to predict whether effects come from technical bias or biological effects

## Training & prediction

$$f(s, a) = x \quad a \in R^n$$

$$f(s, b) = x \quad b \in R^m$$

$$f(s, a, b) = x \quad x \in \{0,1\}$$

$$f(s) = x \quad s \in \{0,1\}^k$$

In Silicio prediction of PCR validation (isiPCR validation)

## Result for case a)

Special problems in this case:

- a) Very old samples of bad quality and severely affected sequencing quality
- b) Only small amount of samples available

➔ No trial and error validation possible

miRNA	Predicted performance	performance
miR-x	Green	Green
miR-x	Green	Green
miR-x	Green	Red
miR-x	Green	Green
zns-miR-x	Green	Green
zns-miR-x	Green	Green
zns-miR-x	Green	Red

Validation of 8 of 10 markers despite weak quality



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für Bildung  
und Forschung



**DFG** Deutsche  
Forschungsgemeinschaft

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**SIEMENS**



> Selected references

> Focus: minimally-invasive miRNA biomarkers



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