institut Curie

LITO

université PARIS-SACLAY

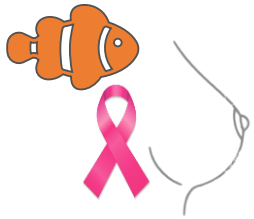
ÉCOLE DOCTORALE
Physique et ingénierie : électrons, photons, sciences du vivant (EOBE)

Abstracts EANM 2025

Inserm
La science pour la santé
From science to health

11/06/2025

Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features

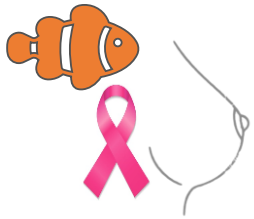


Aim/Introduction: to determine whether the combination of clinical and radiomic features from whole-body could stratify metastatic breast cancer patients according to **Progression Free Survival**.

Methodology: Database

- ✓ Baseline whole-body [18F]FDG-PET/CT images from **516** women with metastatic breast cancer before any treatment
- ✓ Four molecular subtype: TNBC, HR+ HER2-, HR+ HER2+ and HER2+
- ✓ Clinical data were retrospectively collected for all patients
- ✓ Full cohort divided into a **train** and a **test** dataset according to the date of PET/CT exam:
  - **Train**: between 2008 and 2017
  - **Test**: between 2018 and 2019

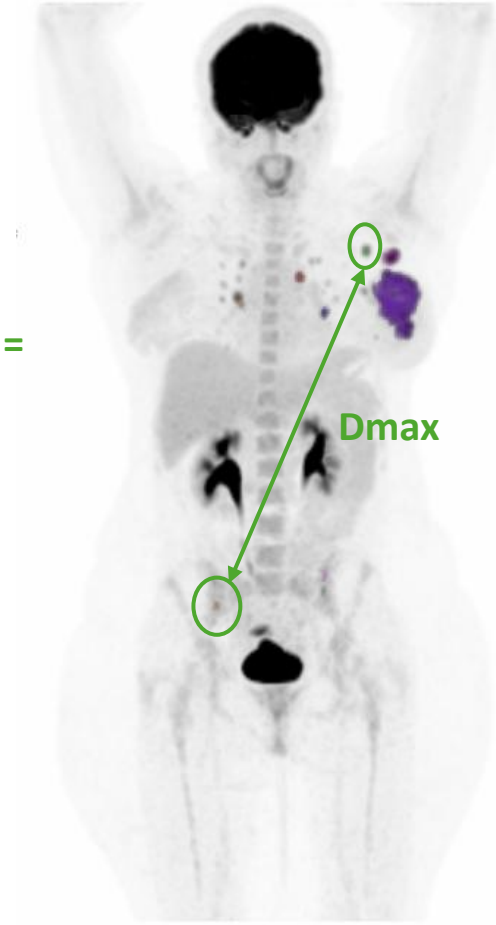
Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features



Methodology: Segmentation

1) Segmentation of primary tumor and metastasis with a threshold of 4 SUV (with LION and then corrected manually)

$\Sigma_{lesions}$ MTV = TMTV



Radiomic features – **Whole body**

→**TMTV (Total Metabolic Tumor Volume)**

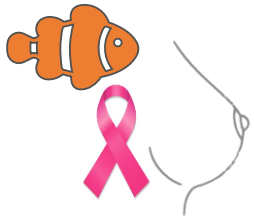
→**TSULmean**: average uptake across all tumor lesions

→**maxSULmax**: maximum uptake across all tumor lesions

→**TTLG**: product of **TSULMean** and **TMTV**

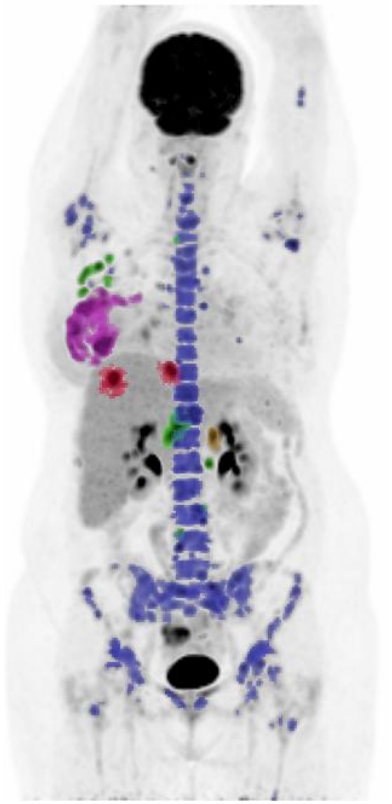
→**Dmax:** distance between the 2 most distant lesions

Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features



Methodology: Segmentation

2) Identification and annotation of primary tumor and metastatic sites

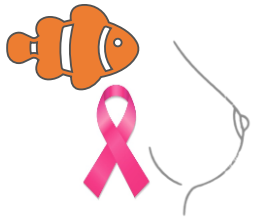


- Primary tumor
- Nodes metastasis
- Liver metastasis
- Bones metastasis
- Other metastasis
- Lung metastasis
- Pleura metastasis

Features – **TNM**

→**N-Organs**: number of organs including metastases

Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features



Methodology: Statistical analysis

- ✓ Univariate analysis based on **Cox regression:**
  - **Clinical:** Age, BMI, HR status, HER2 status
  - **Whole-body PET features:** Dmax, TMTV, TSULmean, maxSULmax, N-Organs

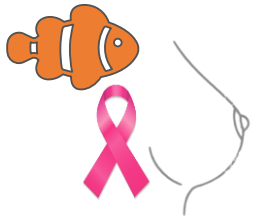
- ✓ Multivariate analysis based on **Cox regression:** features with $p<0.05$ were selected to build models combining **clinical** and **PET** features.

- ✓ For each multivariate model, a **risk score** was derived and binarized by the median in the **train** set to stratify patients in two risk groups.

- ✓ Survival analysis were performed using **Kaplan Meier** method and log-rank test

→ Application to the **test** set.

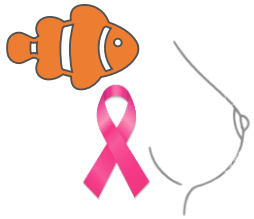
Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features



Results: Cox analysis

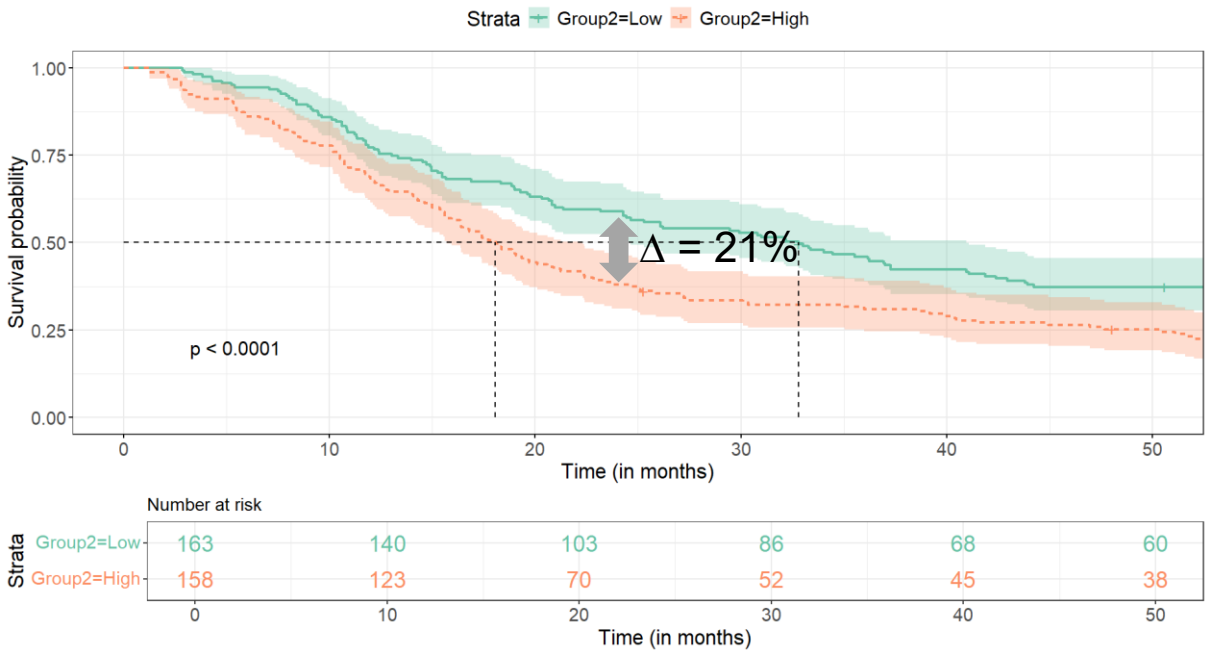
Variable	HR (95 CI)	P Value (Wald Test)
Clinical		
Age (years)	1.01 (1.00-1.02)	**0.02**
BMI (kg/m²)	1.02 (0.99-1.04)	0.16
HR status		
Positive	-	
Negative	0.80 (0.60-1.07)	0.13
HER2 status		
Positive	-	
Negative	1.90 (1.41-2.58)	**<0.001**
Whole-body PET features		
Dmax/10 (cm)	1.17 (1.11-1.24)	**<0.001**
TMTV/100 (mL)	1.08 (1.05-1.11)	**<0.001**
TSULmean	0.95 (0.87-1.05)	0.31
maxSULmax	1.01 (0.98-1.04)	0.54
N-Organs	1.36 (1.22-1.52)	**<0.001**

Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features



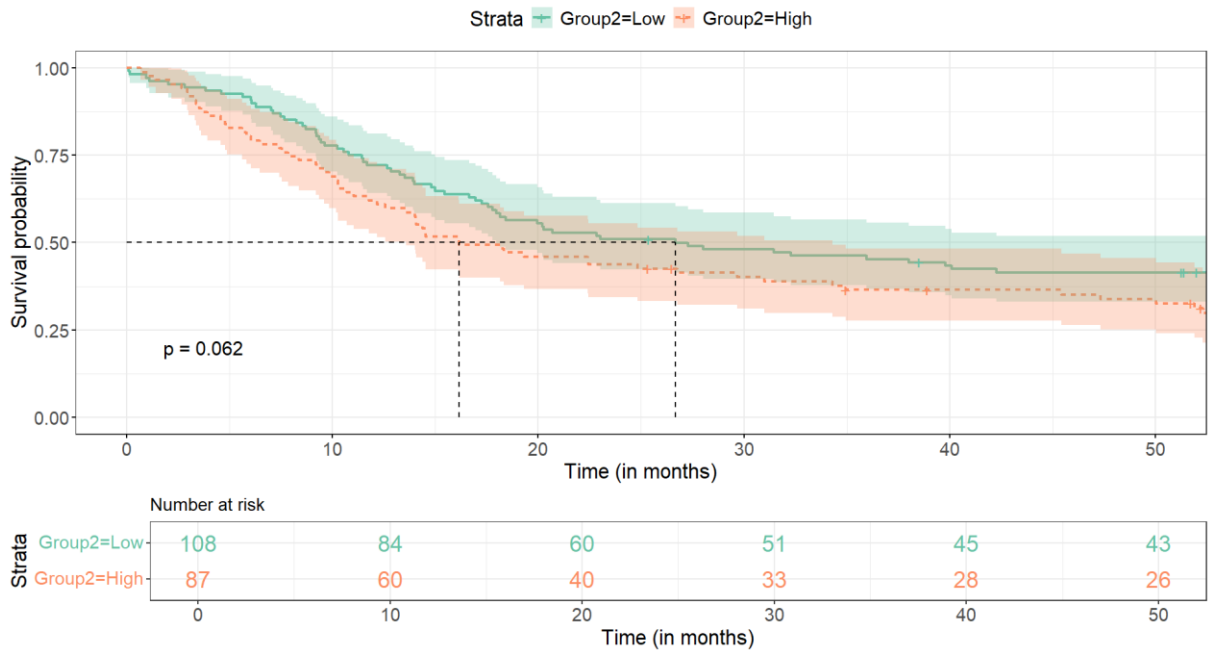
Results: Multivariate models
M1: Age + HER2 Status (Clinical)

TRAIN



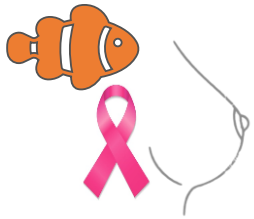
Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	59%	38%	21%

TEST



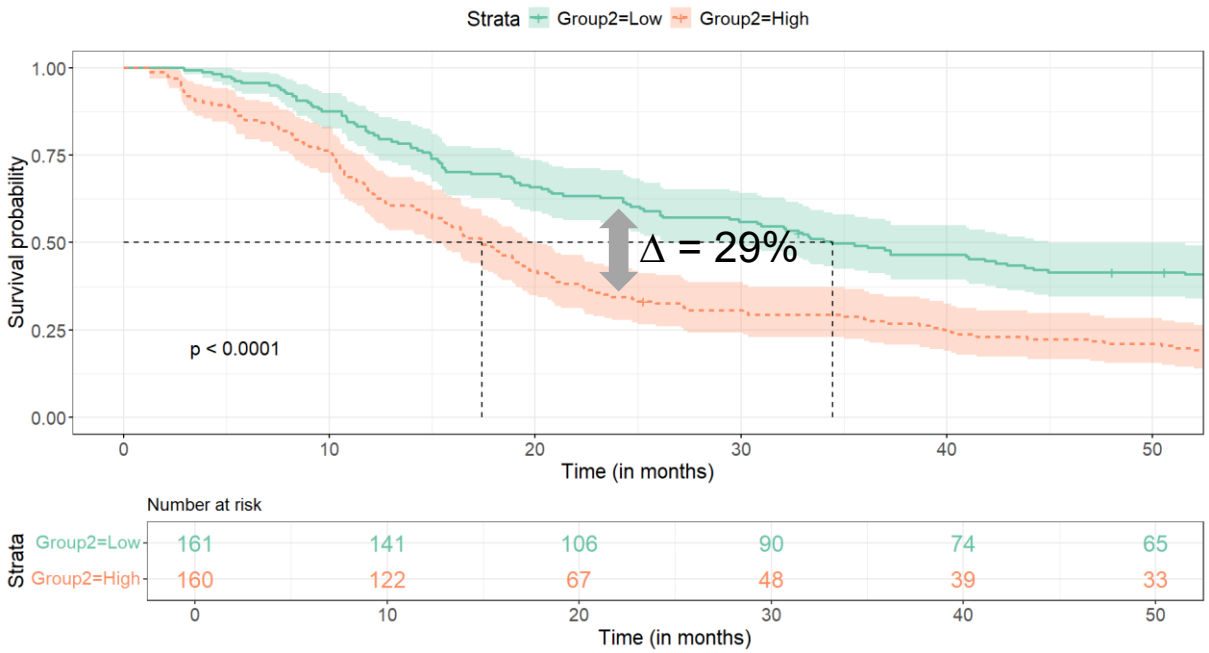
Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	51%	44%	7%

Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features



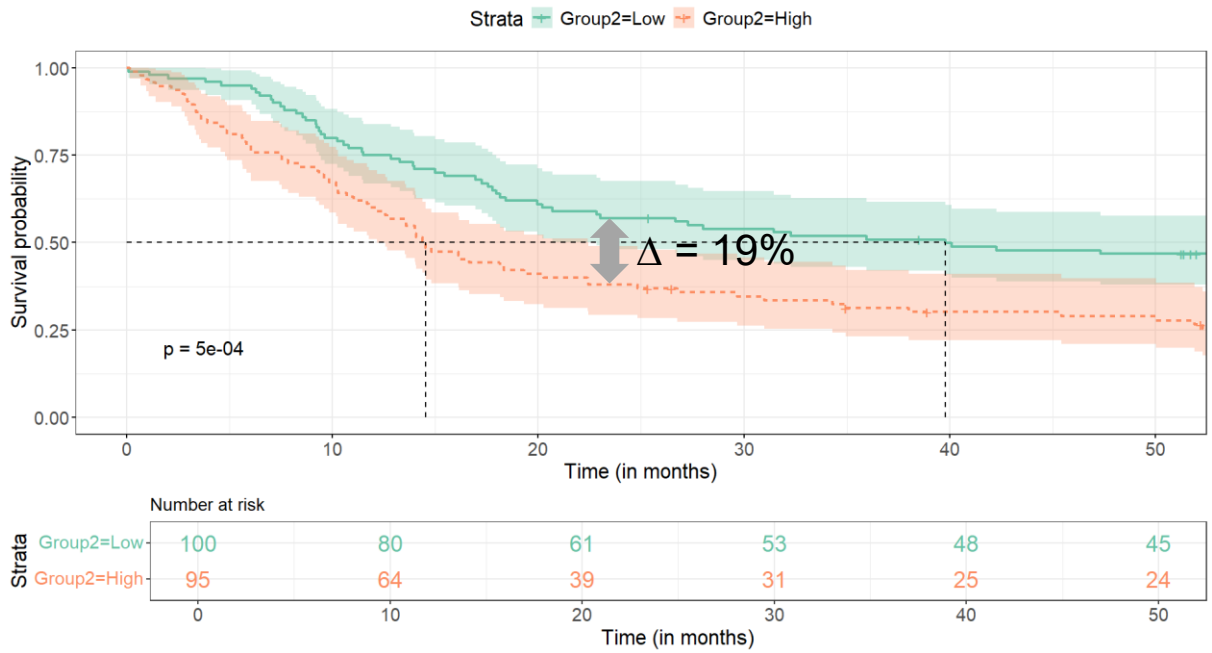
Results: Multivariate models
M2: Clinical + TMTV

TRAIN



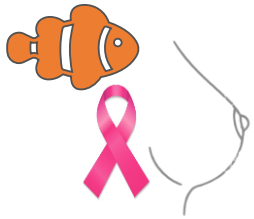
Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	63%	34%	29%

TEST



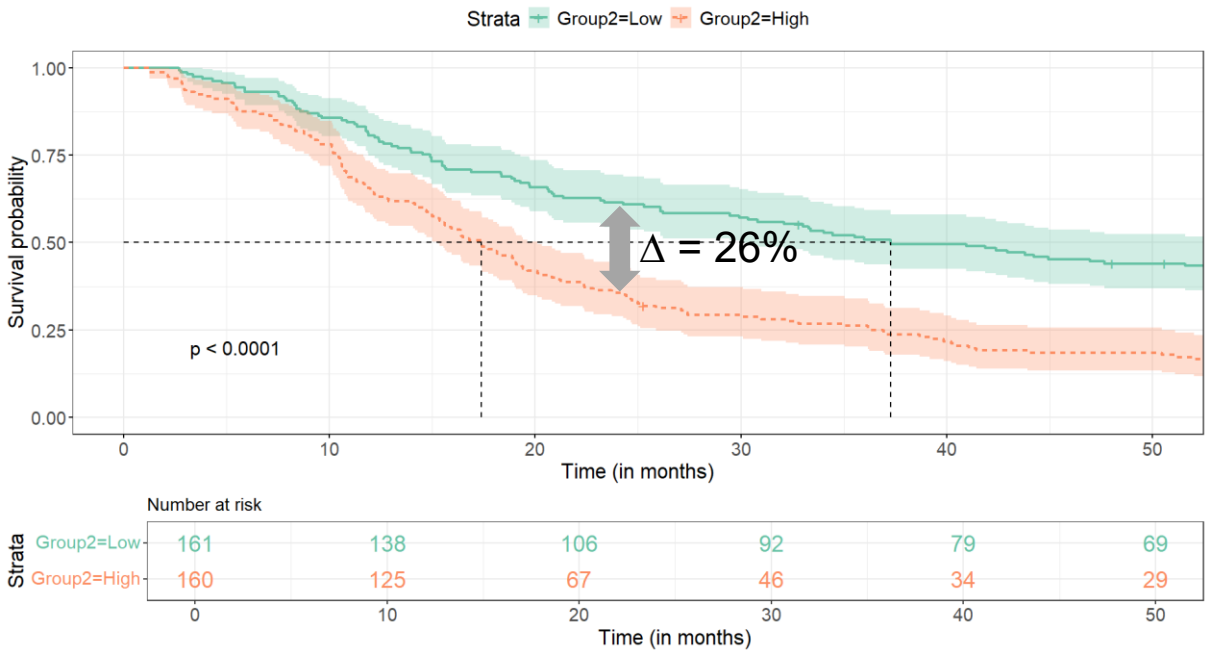
Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	57%	38%	19%

Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features



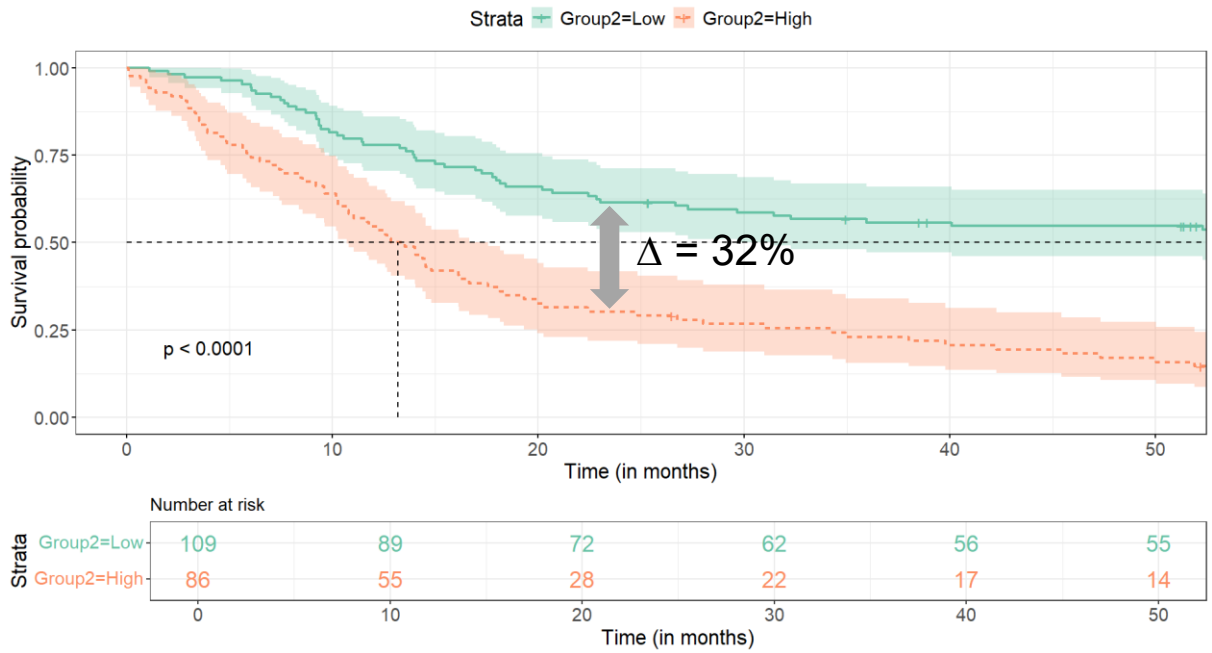
Results: Multivariate models
M3: Clinical + TMTV + Dmax

TRAIN



Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	62%	36%	26%

TEST



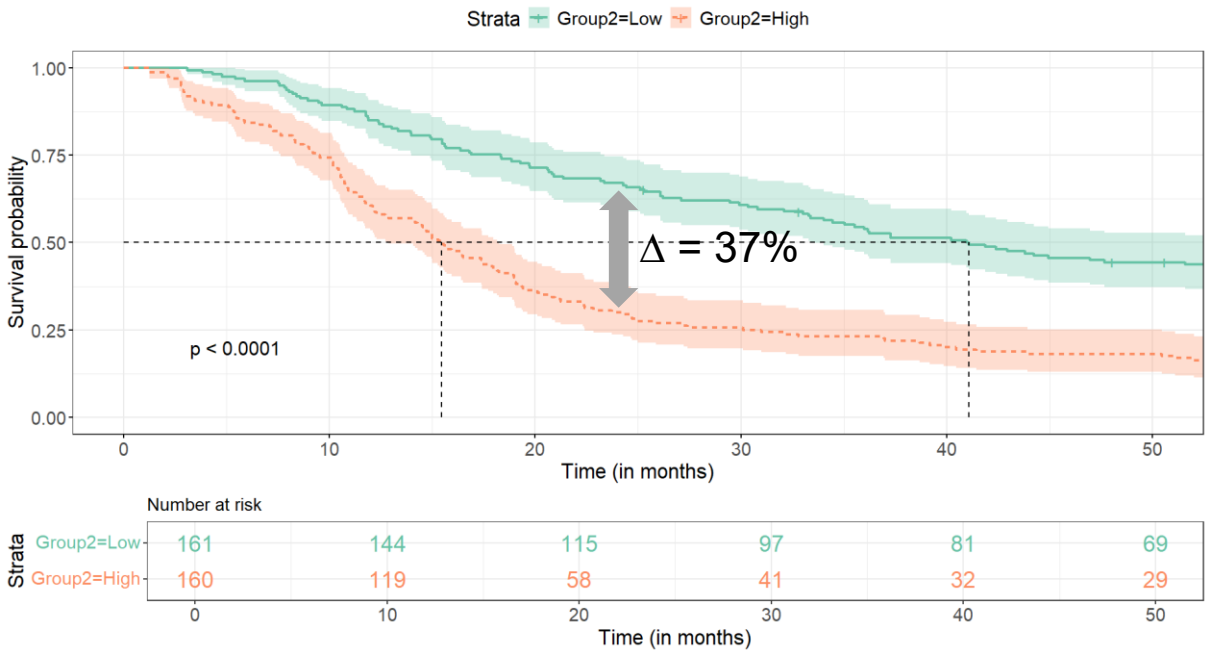
Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	62%	30%	32%

Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features

Results: Multivariate models

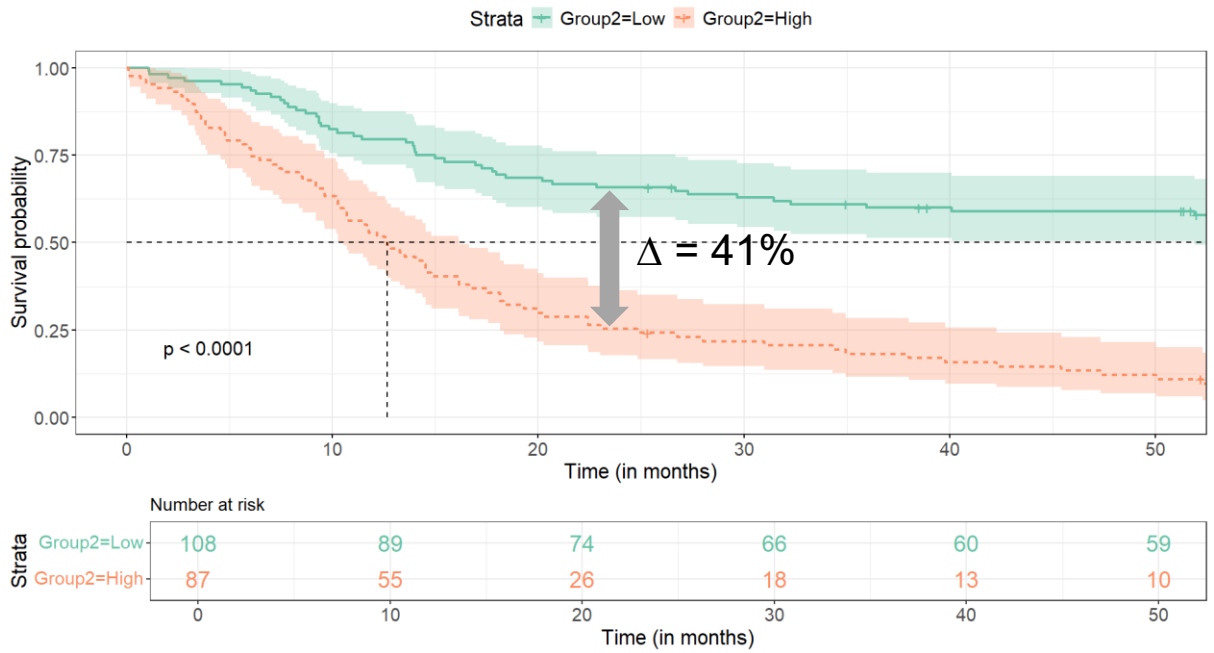
M4: Clinical + TMTV + Dmax + N-Organs

TRAIN



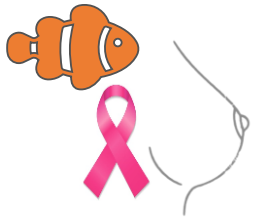
Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	67%	30%	37%

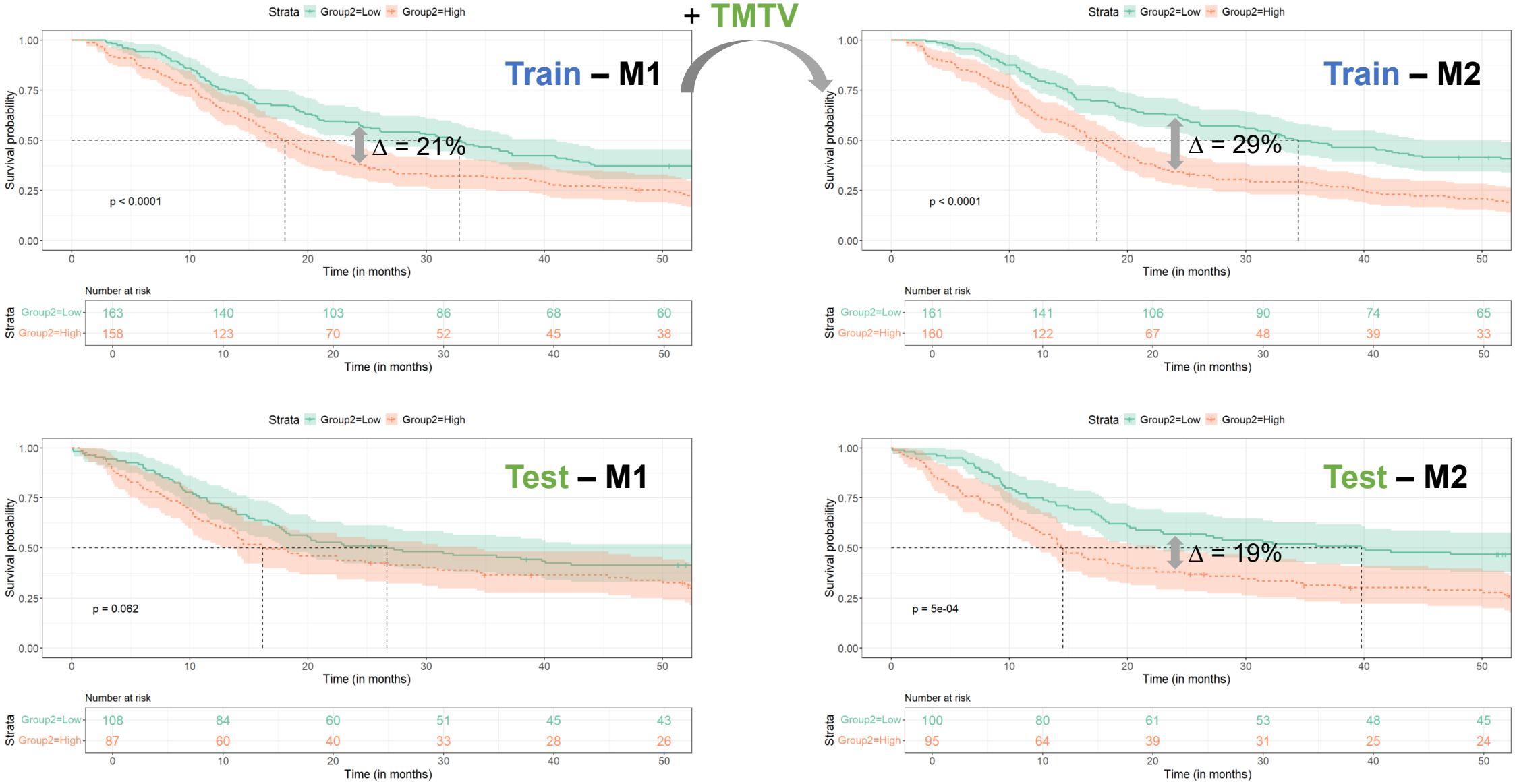
TEST



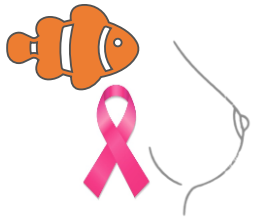
Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	66%	25%	41%

Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features

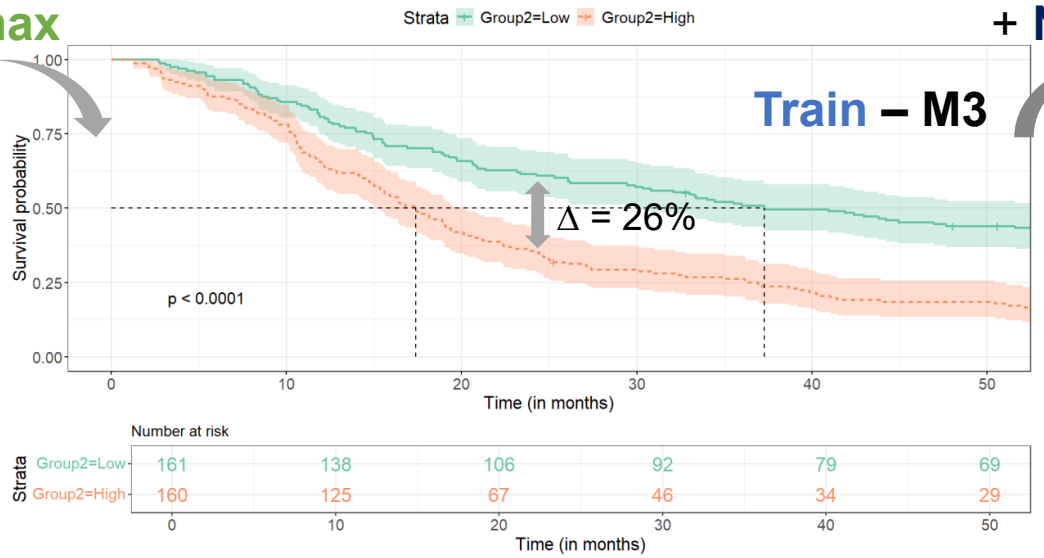




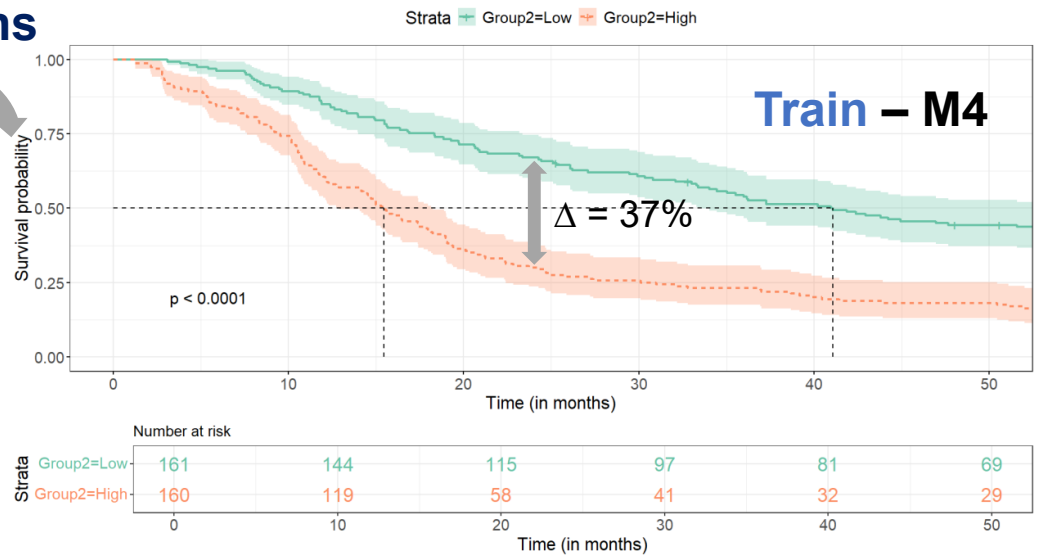
Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features

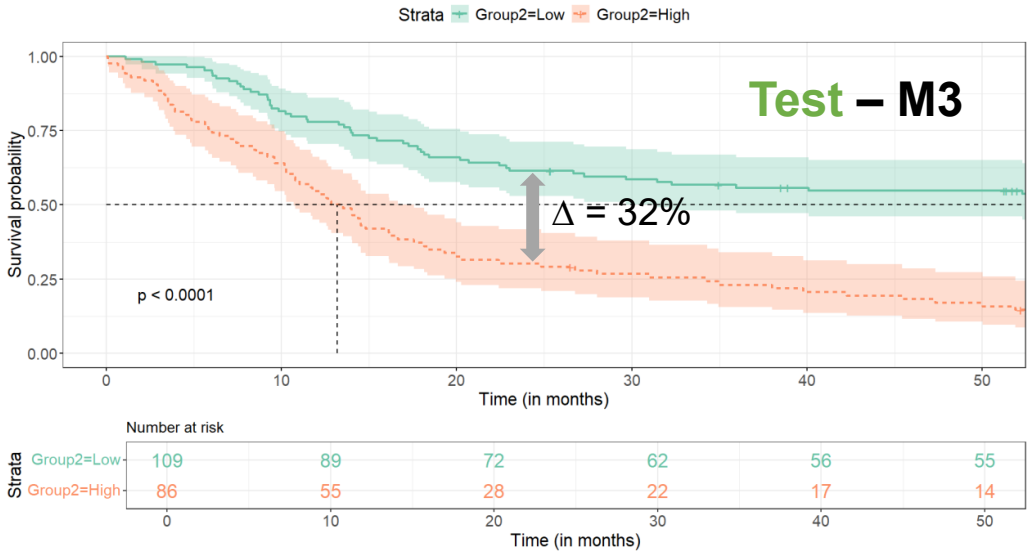


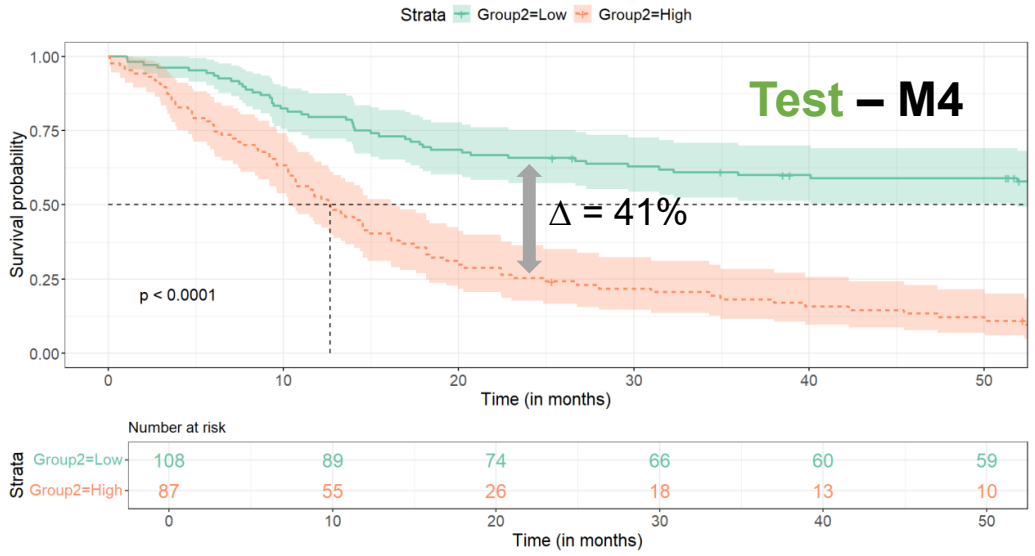
+ Dmax



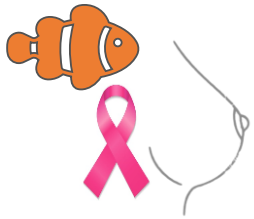
+ N-Organs







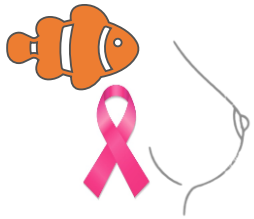
Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features



Results: Summary

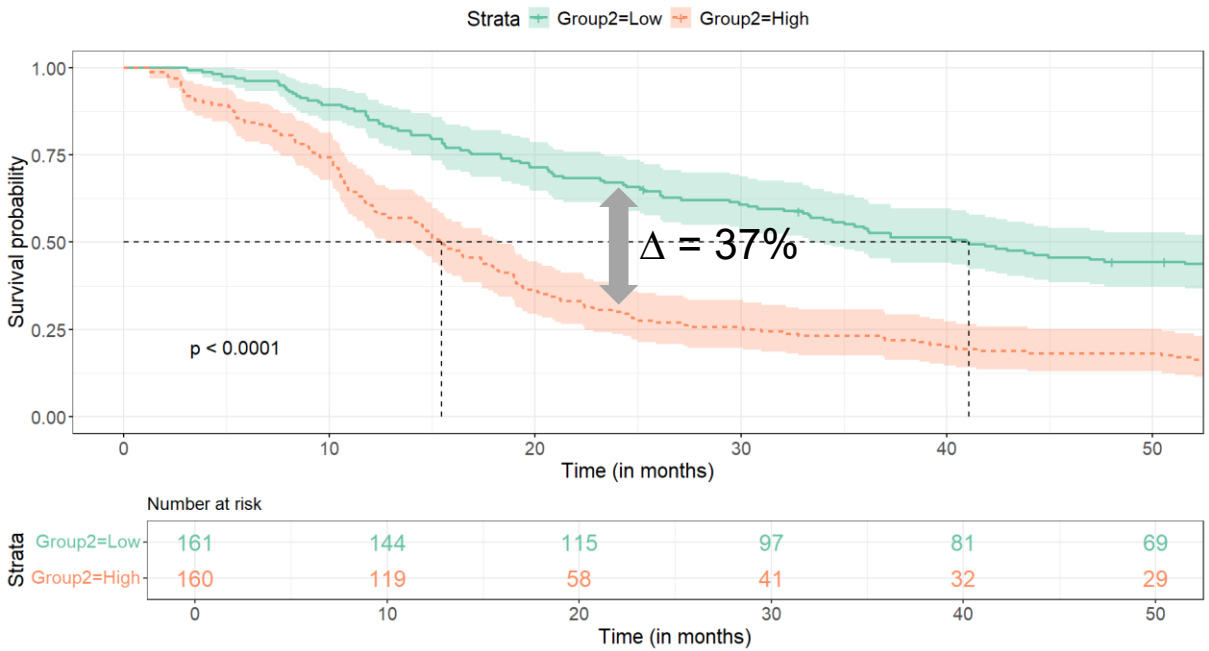
Multivariate models	HR (95 CI)	P Value (Wald Test)	ANOVA (χ^2 test, vs. previous model)	Δ2y-PFS-Discovery set (high vs. low-risk)	Δ2y-PFS-Test set (high vs. low-risk)
M1: Age + HER2 Status (Clinical)	1.98 (1.51-2.60)	<0.001	-	21%	7%
M2: Clinical + TMTV	1.23 (1.16-1.31)	<0.001	**<0.001**	29%	19%
M3: Clinical + TMTV + Dmax	1.39 (1.28-1.51)	<0.001	**<0.001**	26%	32%
M4: Clinical + TMTV + Dmax + N-Organs	1.43 (1.31-1.55)	<0.001	**0.01**	**37%**	**41%**

Refining prognostic models in metastatic breast cancer patients using whole-body radiomic features



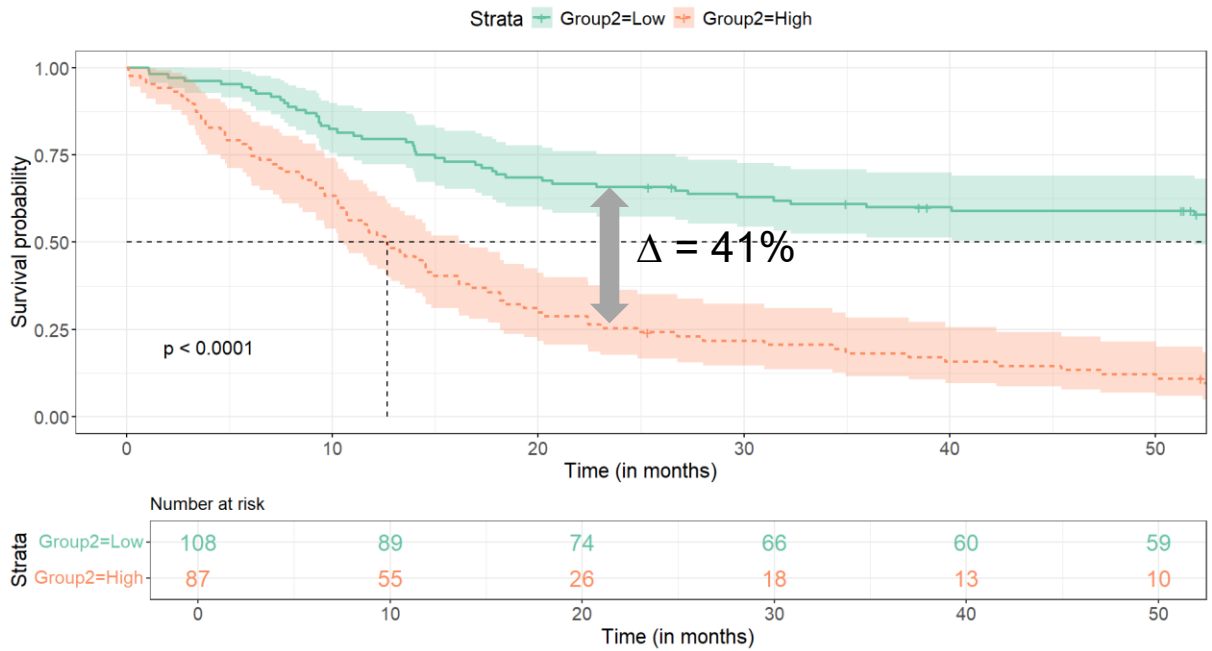
Conclusion: In addition to clinical data, TMTV, Dmax and the number of involved organs further improve patient stratification in metastatic breast cancer and could therefore enhance patient management.

TRAIN



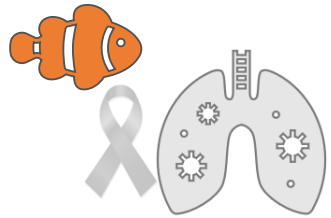
Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	67%	30%	37%

TEST



Progression-Free-Survival	Low risk	High risk	Δ
24 months – PFS	66%	25%	41%

Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients



Aim/Introduction: Whole-body PET/CT images associated with automated segmentation tools offer new opportunities to investigate inter-organ metabolic connections. Doing so, we identified an unexpected relationship between brain FDG uptake and overall survival (OS) in metastatic Non-Small Cell Lung Cancer (NSCLC) patients that we thoroughly investigated in this study.

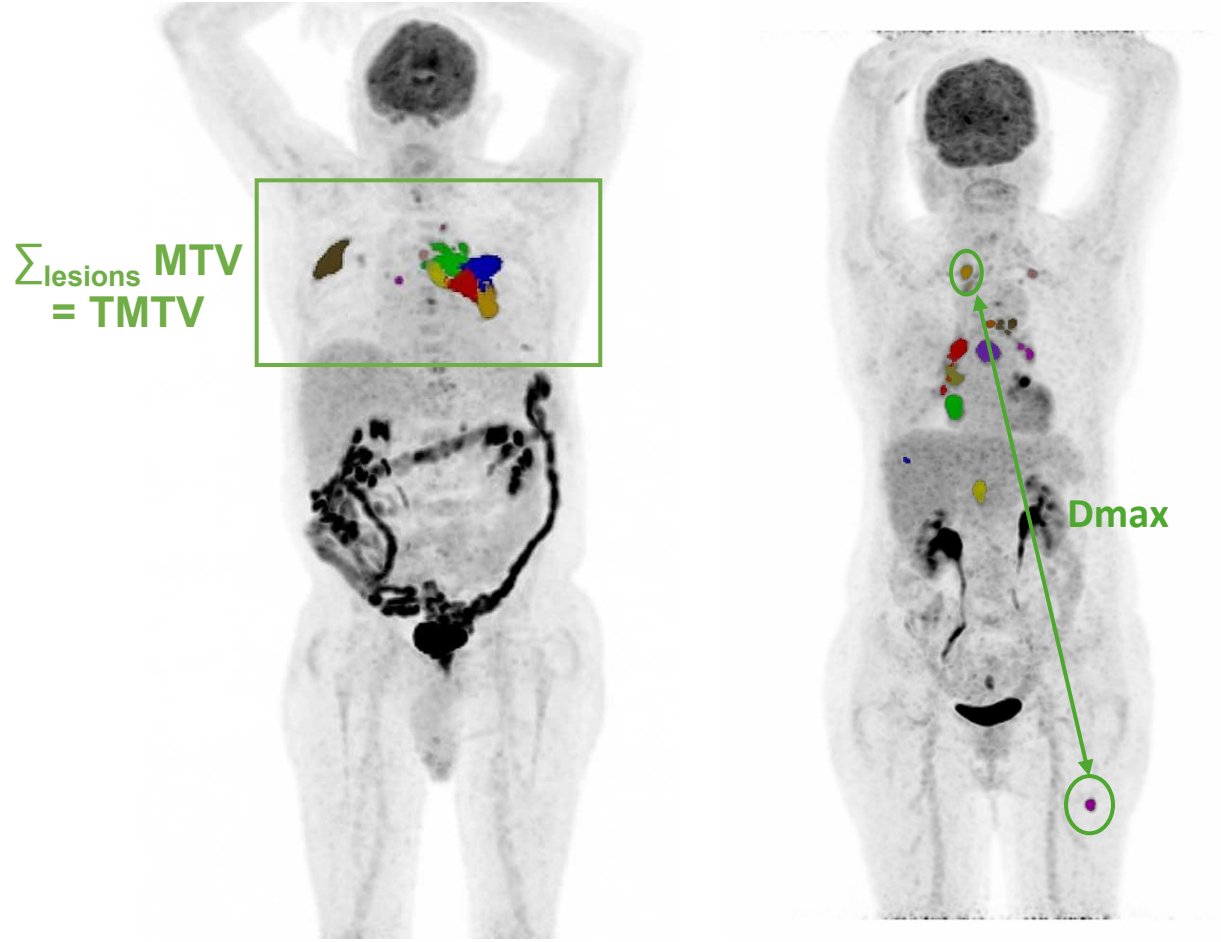
Methodology: Database

- ✓ Baseline whole-body [18F]FDG-PET/CT images from **380** metastatic NSCLC patients before any treatment
- ✓ Clinical and biological data were retrospectively collected for all patients
- ✓ Full cohort divided into a **train** and a **test** dataset according to the date of PET/CT exam:
  - **Train**: between 2010 and 2019
  - **Test**: between 2020 and 2023

Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

Methodology: Segmentation

1) Segmentation of primary tumor and metastasis with a threshold of 4 SUV using LION



Radiomic features – **Whole body**

→**TMTV (Total Metabolic Tumor Volume)**

→**TSUVmean**: average uptake across all tumor lesions

→**maxSUVmax**: maximum uptake across all tumor lesions

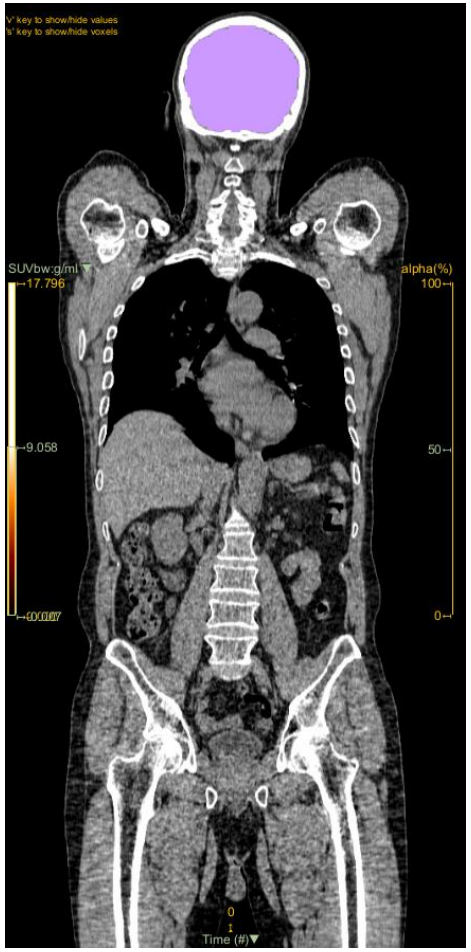
→**TTLG**: product of **TSUVMean** and **TMTV**

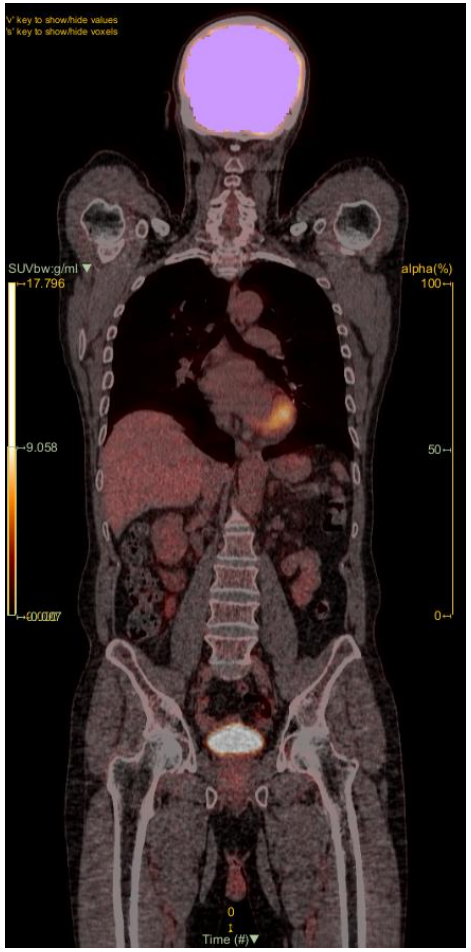
→**Dmax:** distance between the 2 most distant lesions

Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

Methodology: Segmentation

2) Segmentation of the brain with TotalSegmentator

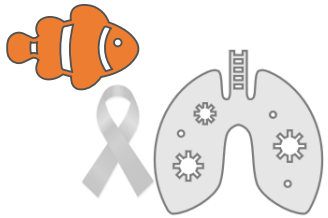




Radiomic features – Whole brain

→$SUVmean_{brain}$: average FDG uptake value over the brain region

Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients



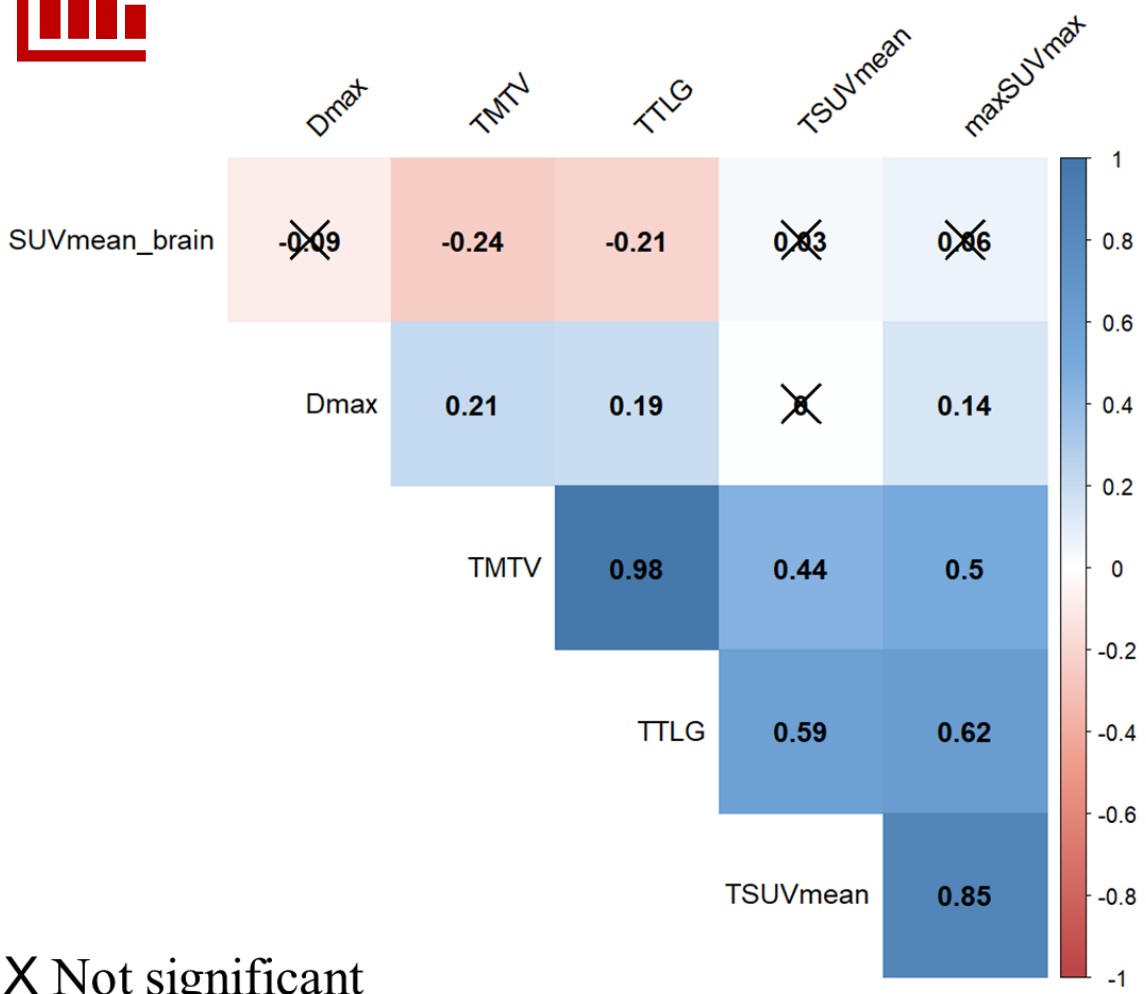
Methodology: Statistical analysis

- ✓ Univariate analysis based on **Cox regression**
- ✓ Multivariate analysis based on **Cox regression:** features with $p<0.05$ were included in a Cox multivariable model without (Model1) and with $SUVmean_{brain}$ (Model2)
- ✓ For each multivariate model, a **risk score** was derived and binarized by the median in the **train** set to stratify patients in two risk groups
- ✓ Survival analysis were performed using **Kaplan Meier** method and log-rank test
- ✓ The relationship between $SUVmean_{brain}$ and clinical/imaging features was investigated using **Spearman coefficients** (rS) and **Wilcoxon test**.

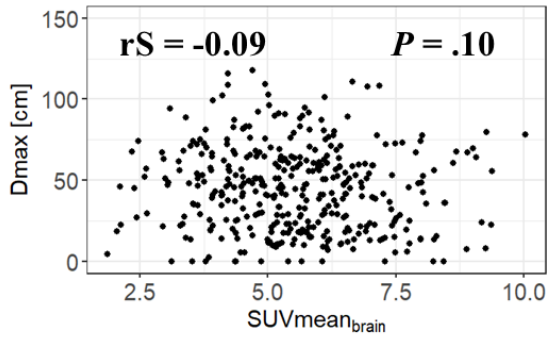
→ Application to the **test** set.

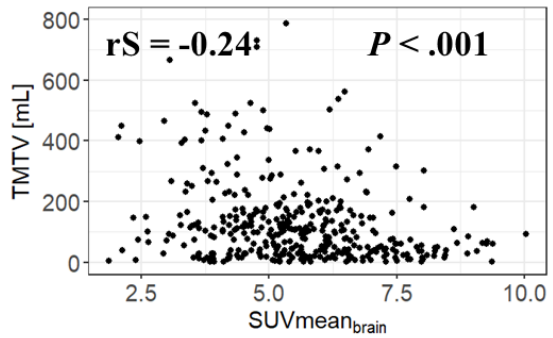
Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

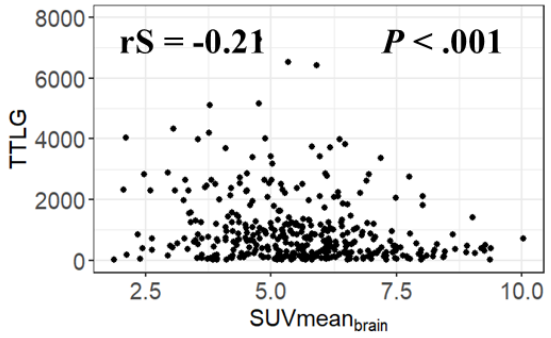
Results: Selection of radiomic features

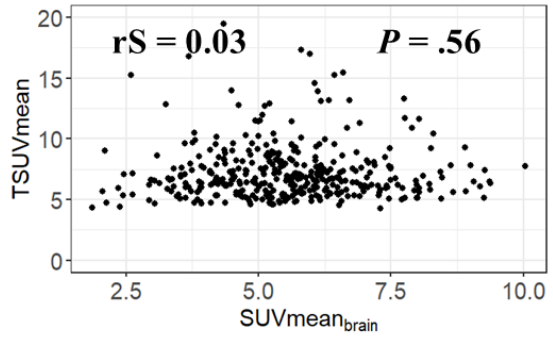


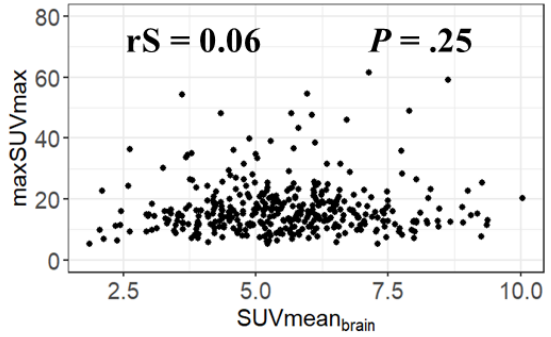
X Not significant



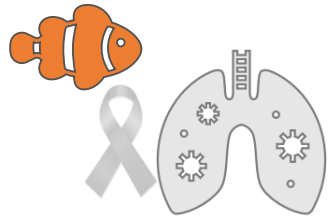








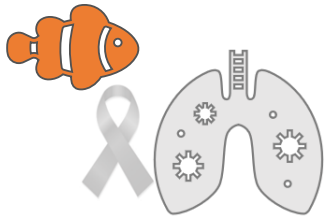
Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients



Results: Cox analysis

	Univariable analysis	
Variable	HR	*P* Value
Age (years)	1.01 (1.00-1.02)	.08
BMI (kg/m²)	0.99 (0.95-1.03)	.56
Performance Status		
0-1	**-**	
≥2	**2.20 (1.60-3.03)**	**< .001**
Sex		
Female	-	
Male	1.19 (0.90-1.57)	.21
Smoking history		
Never	**-**	
Current or Former	**1.63 (1.10-2.42)**	**.01**
Dmax/10	**1.07 (1.02-1.13)**	**.009**
TMTV/100	**1.12 (1.06-1.19)**	**< .001**
TSUVmean	1.05 (0.99-1.12)	.11
maxSUVmax	1.00 (1.00-1.01)	.06
$SUVmean_{brain}$	**0.83 (0.76-0.92)**	**< .001**

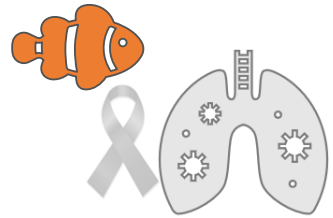
Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients



Results: Cox analysis

	Univariable analysis		Model 1*	
Variable	HR	*P* Value	HR	*P* Value
Age (years)	1.01 (1.00-1.02)	.08		
BMI (kg/m²)	0.99 (0.95-1.03)	.56		
Performance Status				
0-1	**-**		-	
≥2	**2.20 (1.60-3.03)**	**< .001**	**2.04 (1.47-2.82)**	**< .001**
Sex				
Female	-			
Male	1.19 (0.90-1.57)	.21		
Smoking history				
Never	-		-	
Current or Former	**1.63 (1.10-2.42)**	**.01**	**1.58 (1.06-2.35)**	**.03**
Dmax/10	**1.07 (1.02-1.13)**	**.009**	1.05 (0.99-1.10)	.10
TMTV/100	**1.12 (1.06-1.19)**	**< .001**	**1.06 (1.06-1.19)**	**< .001**
TSUVmean	1.05 (0.99-1.12)	.11		
maxSUVmax	1.00 (1.00-1.01)	.06		
$SUVmean_{brain}$	**0.83 (0.76-0.92)**	**< .001**		

Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients



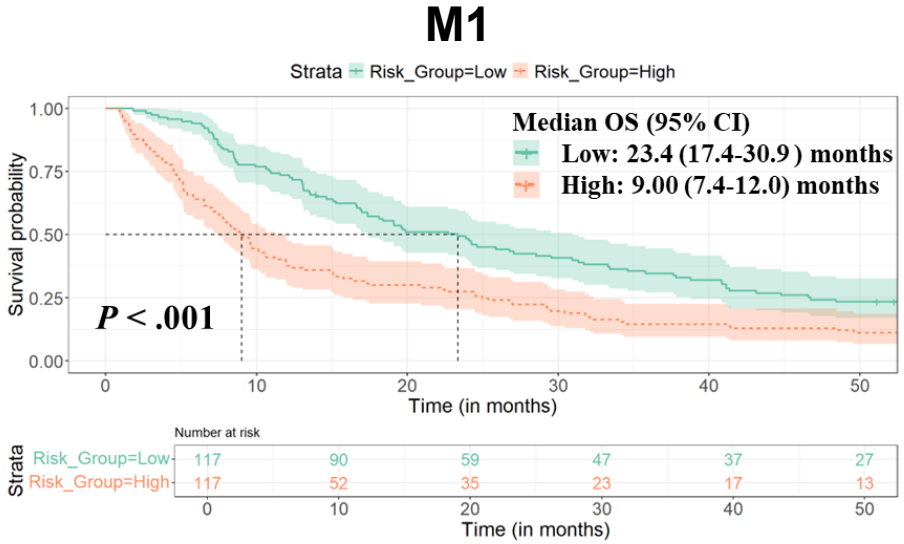
Results: Cox analysis

	Univariable analysis		Model 1*		Model 2†	
Variable	HR	*P* Value	HR	*P* Value	HR	*P* Value
Age (years)	1.01 (1.00-1.02)	.08				
BMI (kg/m²)	0.99 (0.95-1.03)	.56				
Performance Status						
0-1	**-**		-		-	
≥2	**2.20 (1.60-3.03)**	**< .001**	**2.04 (1.47-2.82)**	**< .001**	**1.98 (1.43-2.74)**	**< .001**
Sex						
Female	-					
Male	1.19 (0.90-1.57)	.21				
Smoking history						
Never	-		-		-	
Current or Former	**1.63 (1.10-2.42)**	**.01**	**1.58 (1.06-2.35)**	**.03**	1.40 (0.93-2.12)	.11
Dmax/10	**1.07 (1.02-1.13)**	**.009**	1.05 (0.99-1.10)	.10	1.04 (0.99-1.10)	.13
TMTV/100	**1.12 (1.06-1.19)**	**< .001**	**1.06 (1.06-1.19)**	**< .001**	**1.11 (1.04-1.17)**	**< .001**
TSUVmean	1.05 (0.99-1.12)	.11				
maxSUVmax	1.00 (1.00-1.01)	.06				
$SUVmean_{brain}$	**0.83 (0.76-0.92)**	**< .001**			**0.88 (0.80-0.98)**	**.02**

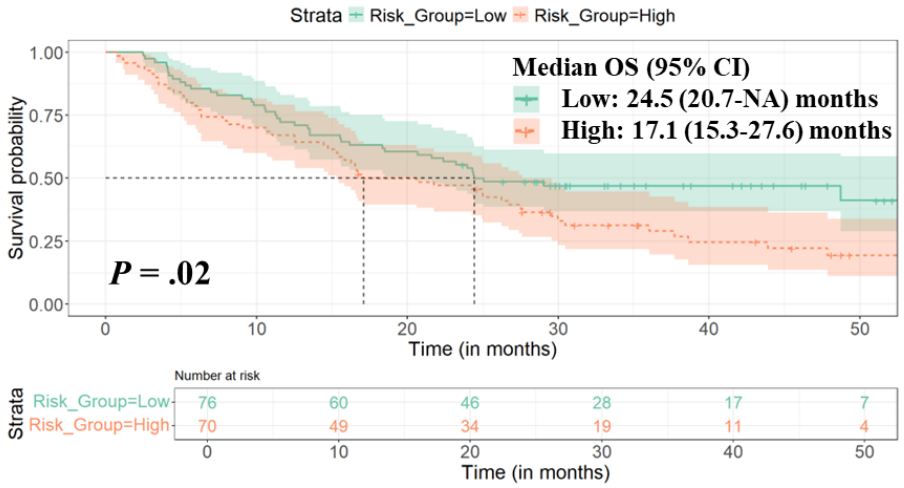
Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

Results:

TRAIN



TEST

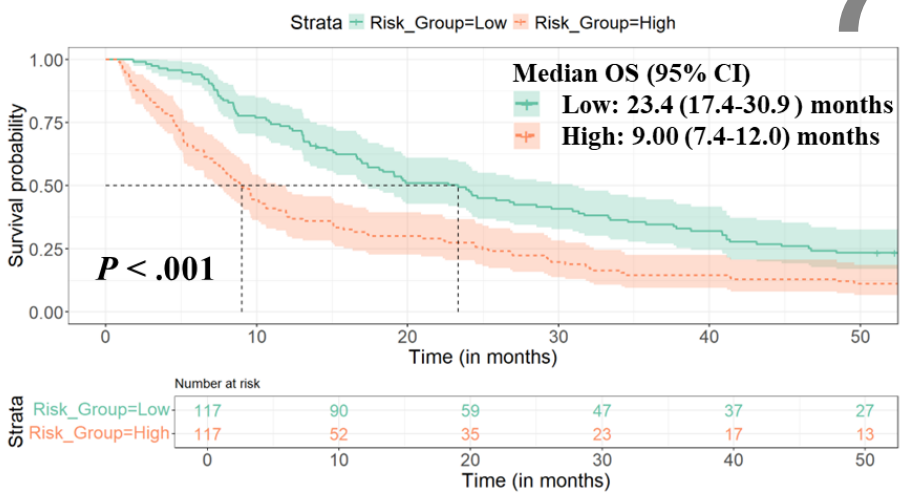


Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

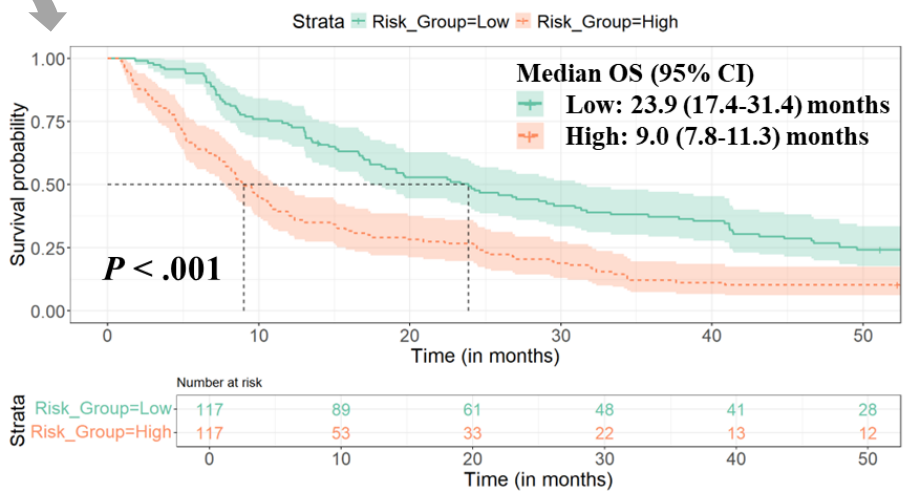
Results:

+ $SUVmean_{brain}$

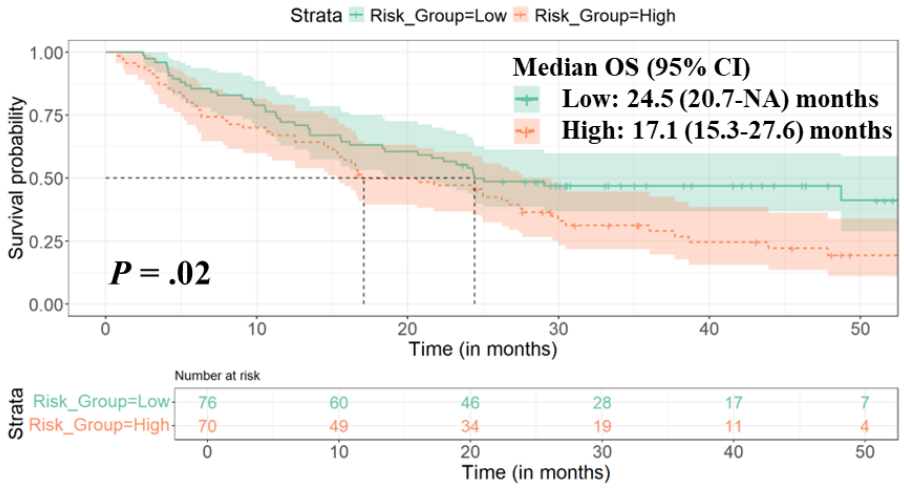
M1

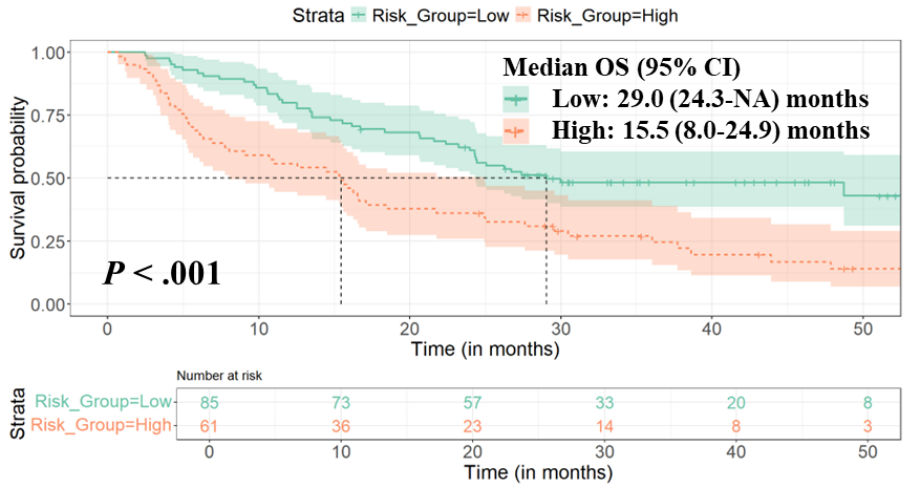


M2



TRAIN

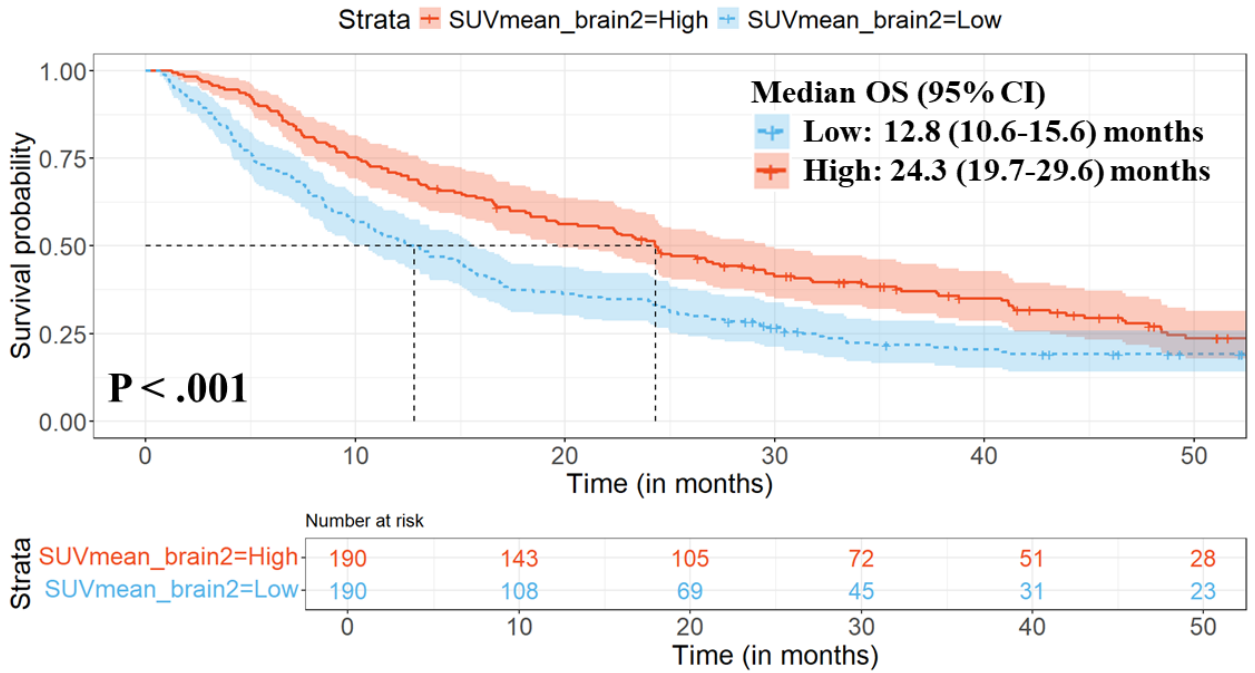


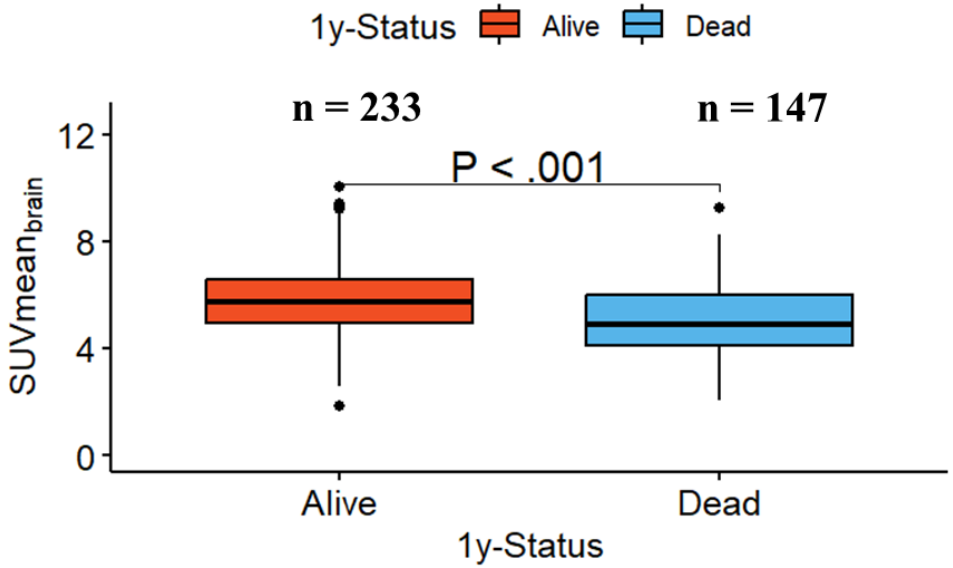


TEST

Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

Results: Relationship between $SUVmean_{brain}$ and overall survival in metastatic NSCLC patients.



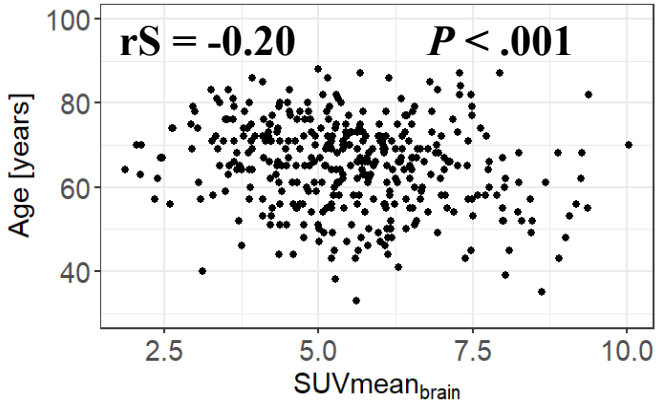


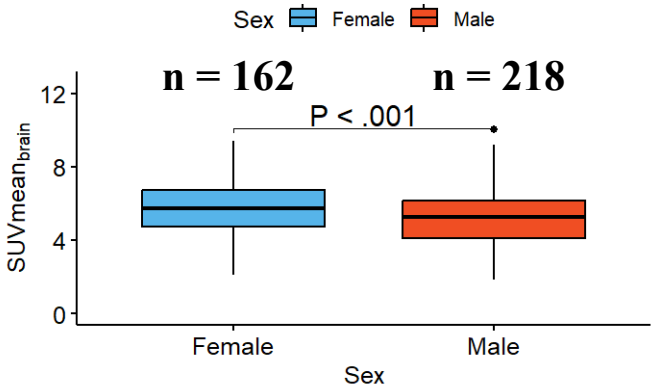
→ Kaplan Meier curves for NSCLC patients in the full cohort (n = 380) stratified into risk groups by the median of the $SUVmean_{brain}$ (median = 5.45).

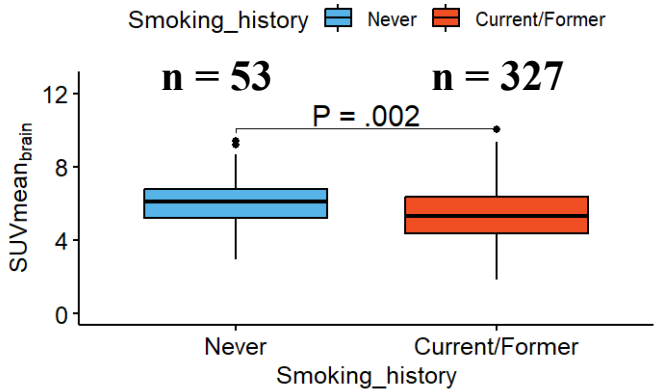
→ Boxplot representation of $SUVmean_{brain}$ according to the 1-year vital status in the full cohort.

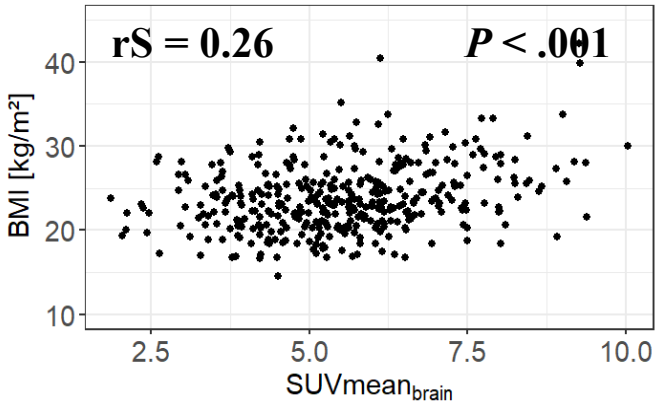
Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

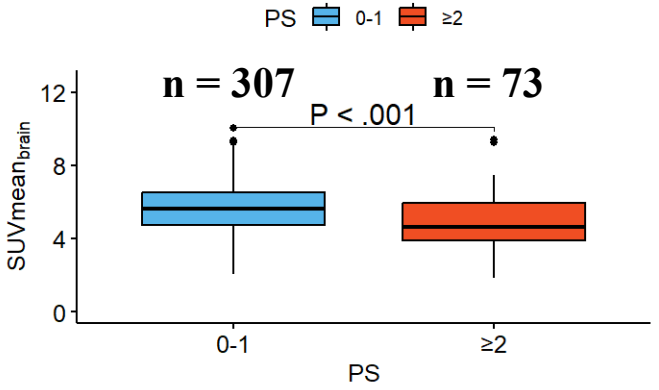
Results: Relationship between $SUVmean_{brain}$ and **clinical**

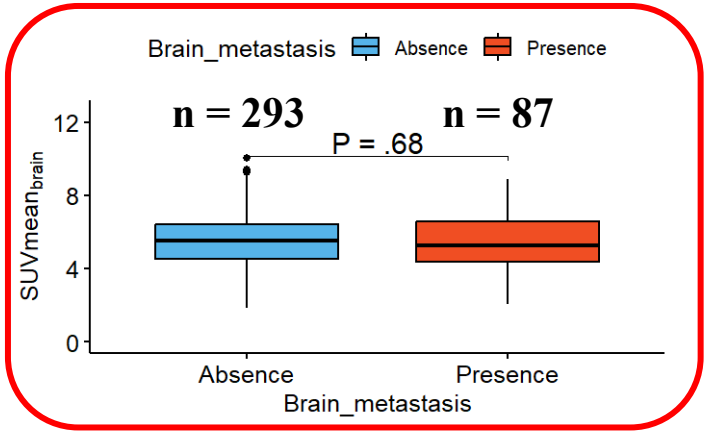








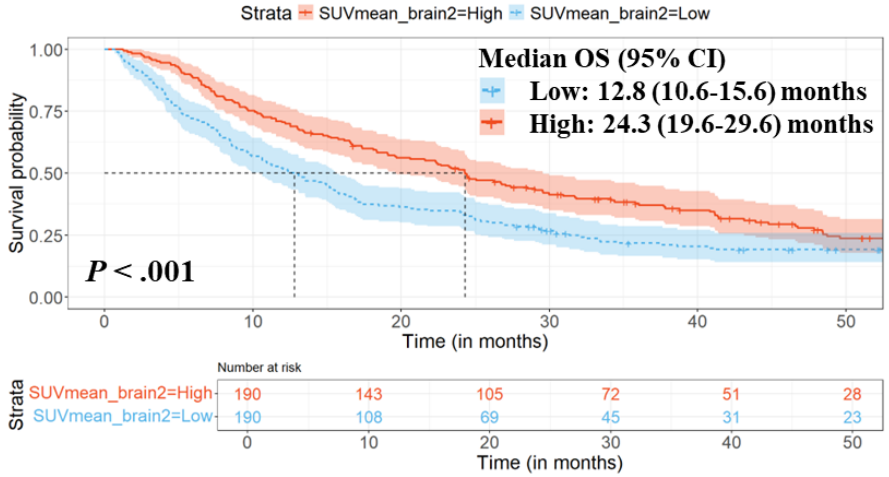


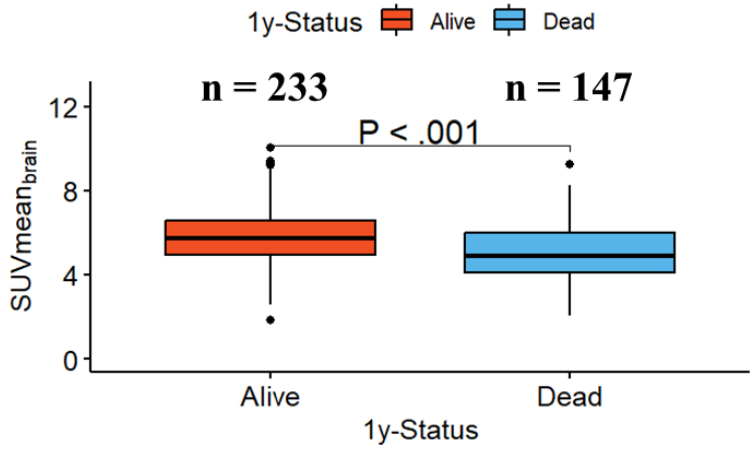


Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

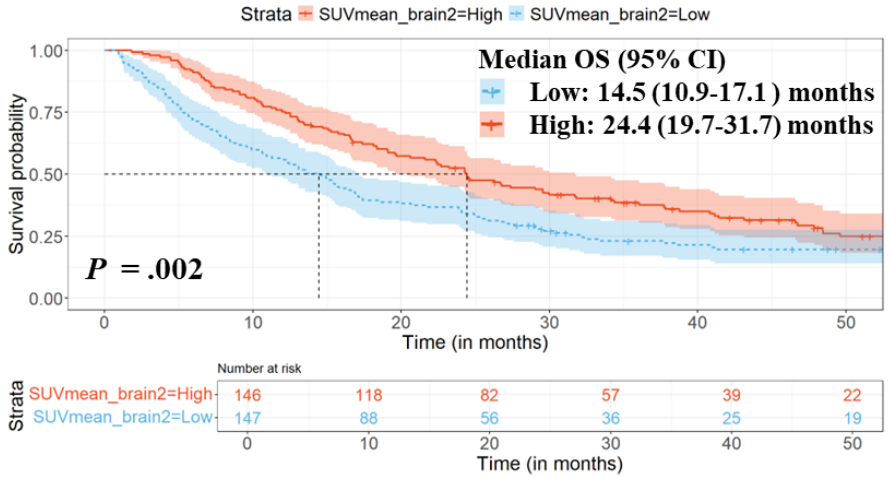
Results: Relationship between $SUVmean_{brain}$ and brain metastasis

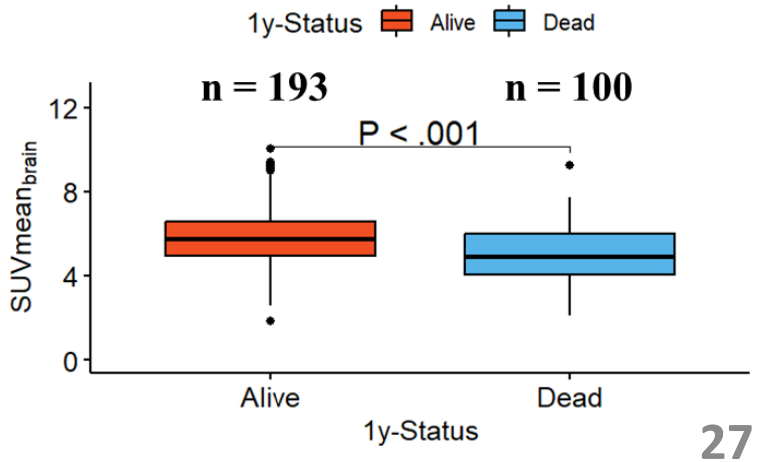
$SUVmean_{brain}$ corrected (median = 5.46)





$SUVmean_{brain}$ measured in patients <u>without brain metastasis</u> (median = 5.52)

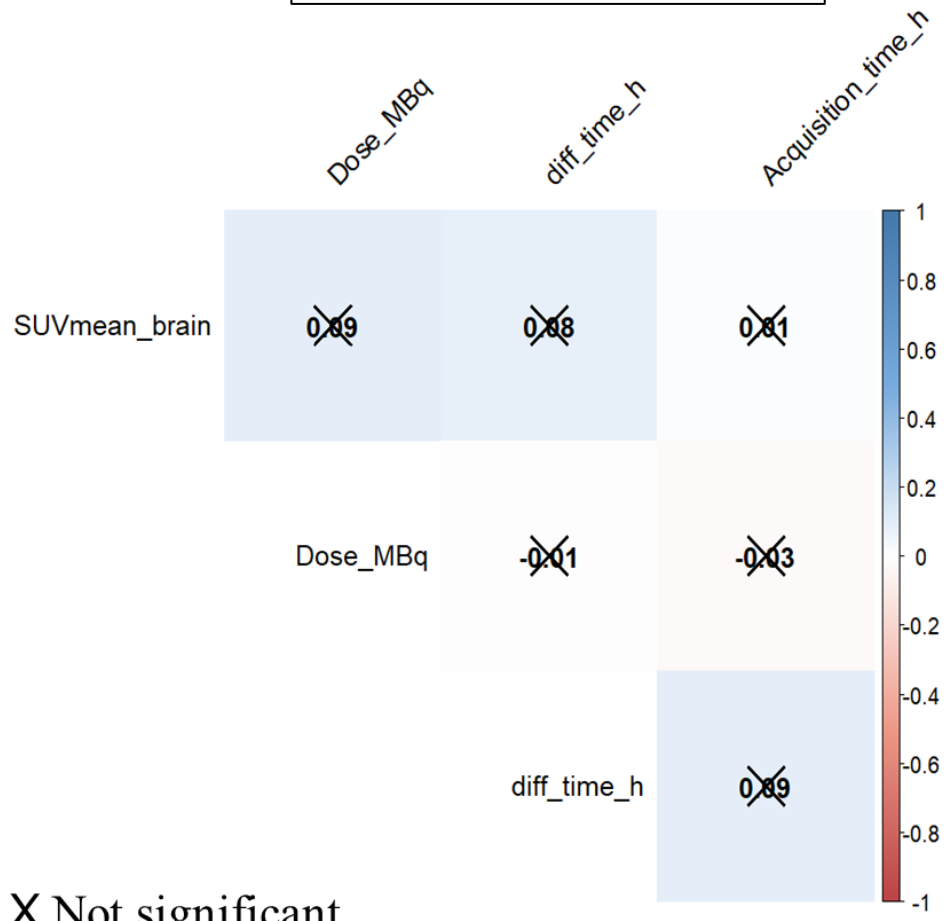




Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

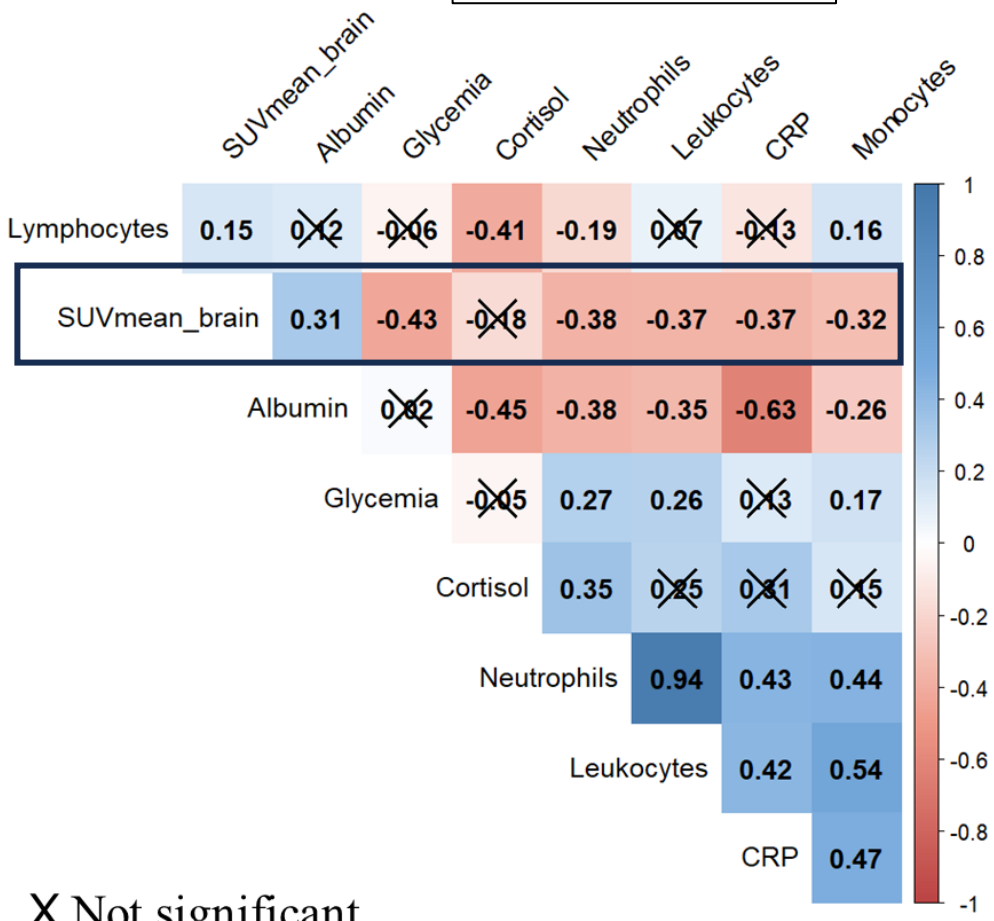
Results: Correlation analysis between $SUVmean_{brain}$, technical parameters and biological data

Technical parameters



X Not significant

Biological data



X Not significant

Prognostic value of cerebral metabolic activity in metastatic Non-Small Cell Lung Cancer (NSCLC) patients

Conclusion: $SUVmean_{brain}$ was an **independent prognostic factor** in metastatic NSCLC patients. Low-cerebral metabolism might be associated with immune response and systemic inflammation, which warrants further evaluation.