institut Curie

LITO

université PARIS-SACLAY

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

Analyse radiomique corps-entier d'images TEP/TDM en cancérologie: projet NEMO-PET

Inserm

La science pour la santé
From science to health

27/11/2024

Projet NEMO-PET

= New prognostic metastatic phenotypes based on the analysis of whole-body PET/CT images using Artificial Intelligence.

Objectifs :

- ✓ Identifier et caractériser de **nouveaux phénotypes au stade métastatique**.
- ✓ Optimiser la **prise en charge thérapeutique** des patients.

Pourquoi ?

- ✓ **Unique stade IV** → patients métastatiques (American Joint Committee on Cancer).
- ✓ **Différents pronostics** → nombre et type d'organes affectés, degré d'invasion…

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From science to health

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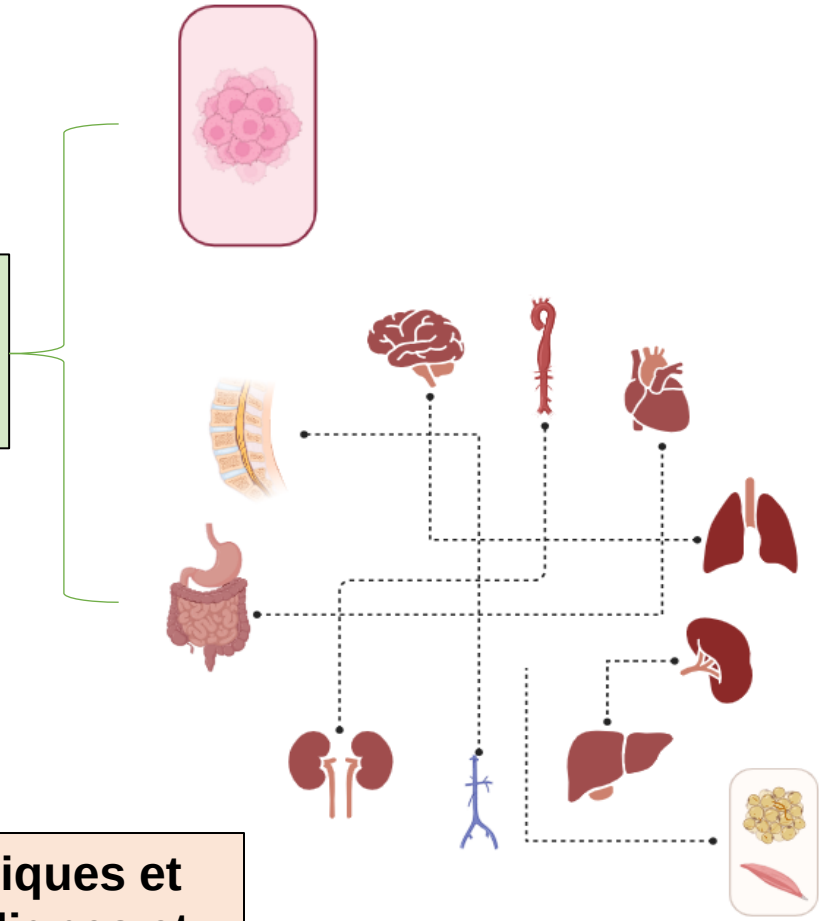
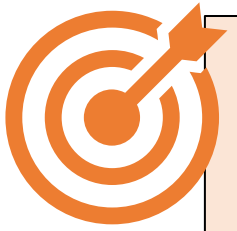
1. Contexte scientifique

Bon pronostic mais hétérogène, surtout pour les patientes métastatiques

Exploitation avancée des images corps-entier TEP/TDM au 18F-FDG

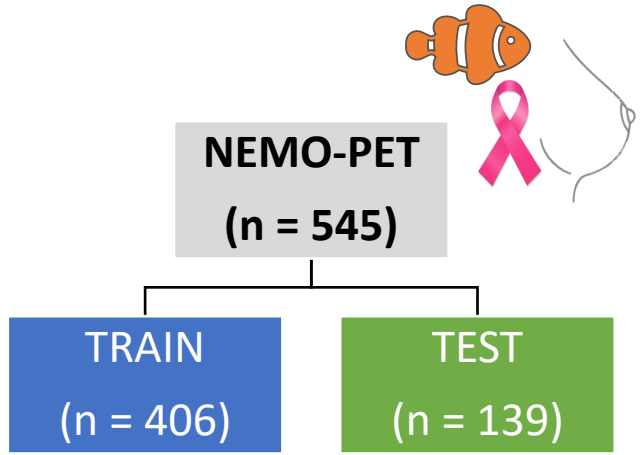


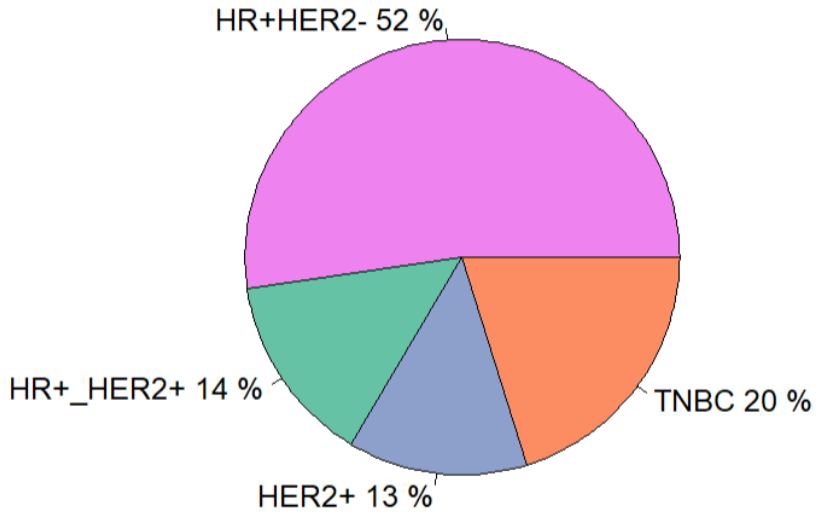


Déterminer si la combinaison des caractéristiques cliniques et radiomiques du corps entier, y compris les régions malignes et non tumorales, peut prédire la survie globale chez des patientes atteintes d'un cancer du sein métastatique.

2. Matériels & Méthodes: base de données

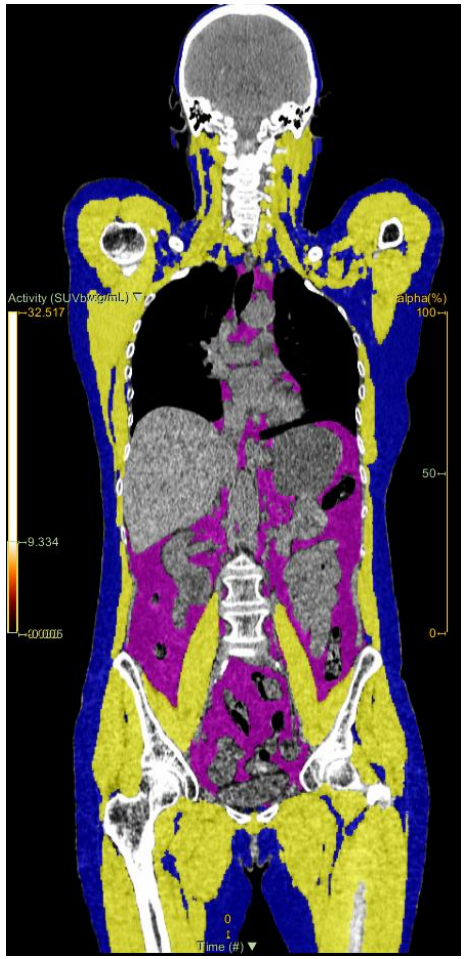
- ✓ Images TEP/TDM au 18F FDG pré-thérapeutique
- ✓ 4 sous-types moléculaires : **HR+ HER2-**, **HR+ HER2+**, **HER2+**, **TNBC**
- ✓ Suivi à 24 mois
- ✓ Séparation de la cohorte en deux groupes :
  - ✓ **Train** : patientes incluses entre **2008 et 2017**
  - ✓ **Test** : patientes incluses entre **2018 et 2019**
- ✓ Données cliniques : âge, IMC, statut HER2, expression des récepteurs hormonaux (HR)





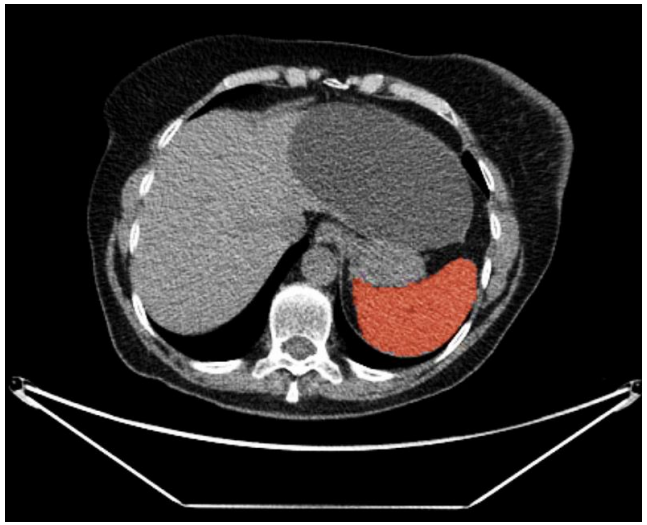
Segmentations automatiques : régions non-tumorales

TotalSegmentator (https://github.com/wasserth/TotalSegmentator)



Modèle « tissu_types » (licence) :

- ✓ Graisse sous-cutanée (bleu)
- ✓ Graisse viscérale (rose)
- ✓ Muscle squelettique (jaune)

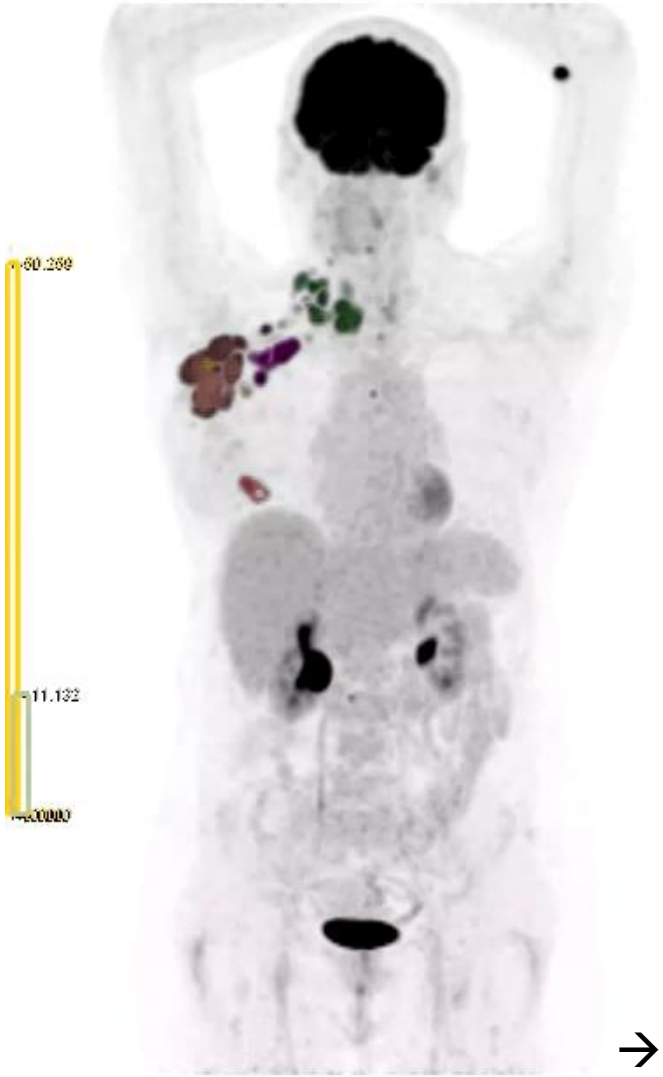


Modèle « total » :

- ✓ Rate (rouge)

Segmentations automatiques : tumeur primaire et métastases

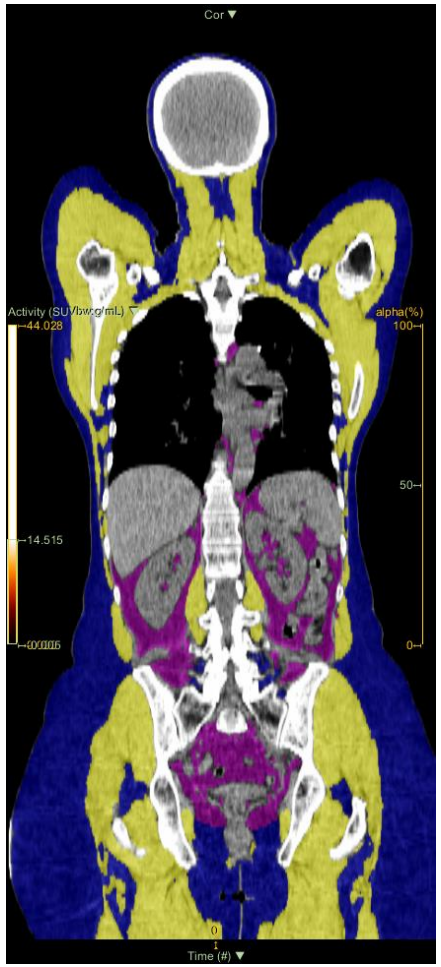
LION (https://github.com/LalithShiyam/)



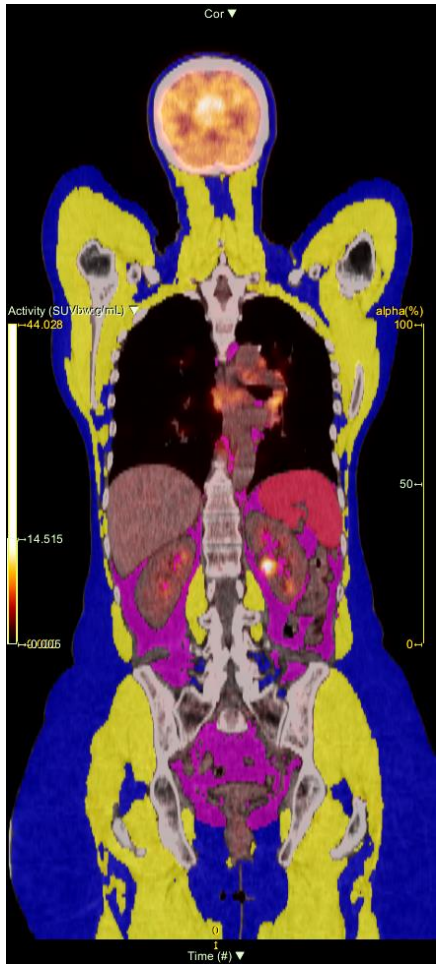
→ Seuillage à 4 SUV

Extraction des index radiomiques

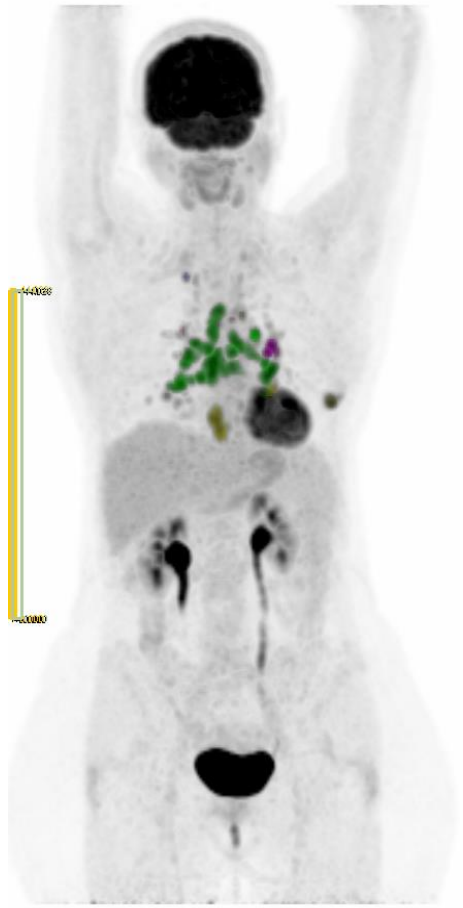
LIFEx (www.lifexsoft.org)



CT



PET/CT



PET

Index radiomiques :

- Lésions → **TMTV** & **Dmax**
- Muscles → **SULmean**, **HUmean**, **Volume**
- Rate → **SULmean**
- Graisse sous-cutanée (Fat_SC) → **SULmean**, **HUmean**, **Volume**
- Graisse viscérale (Fat_V) → **SULmean**, **HUmean**, **Volume**

Analyses statistiques

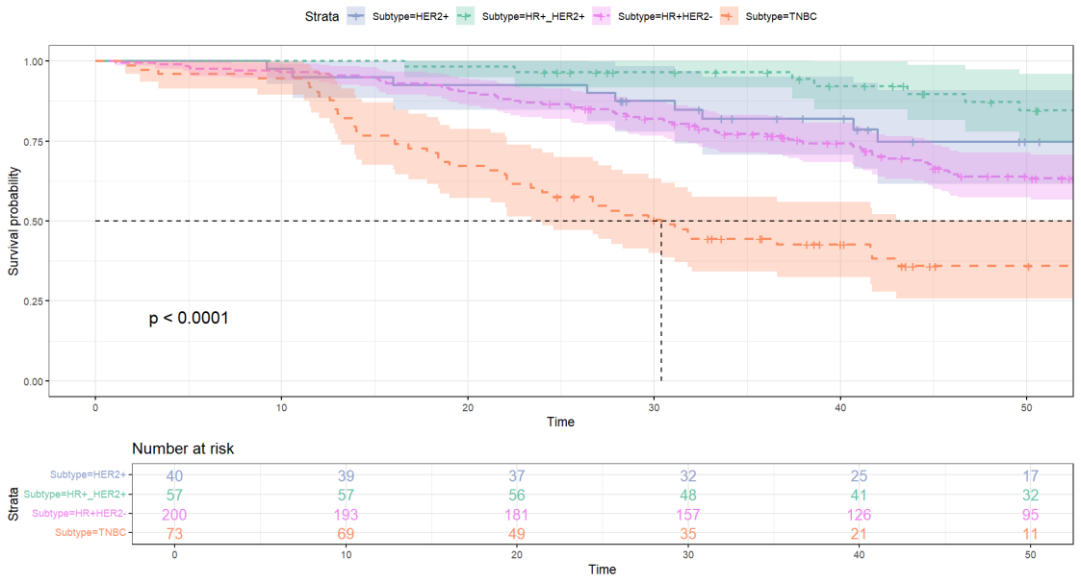
- ✓ Variables en continu
- ✓ Modèles de Cox et sélection de variables avec step AIC : **clinical**, **clinical+radiomic**, **organomic**, **clinical+radiomic+organomic**
- ✓ Prédiction d'un score de risque
- ✓ Stratification en deux et trois groupes :
  - Par la médiane et les quartiles (q1 et q3)
  - **Par les fonctions rhier et rlr (log rank)**
  - Par la courbe time ROC (index de Youden) → uniquement 2 groupes
  - Par la fonction survcutpoint (log rank) → uniquement 2 groupes
- ✓ Analyse de survie à 1 an et 2 ans : courbes de Kaplan Meier (OS)

Calcul de l’index de composition corporelle (BCi)

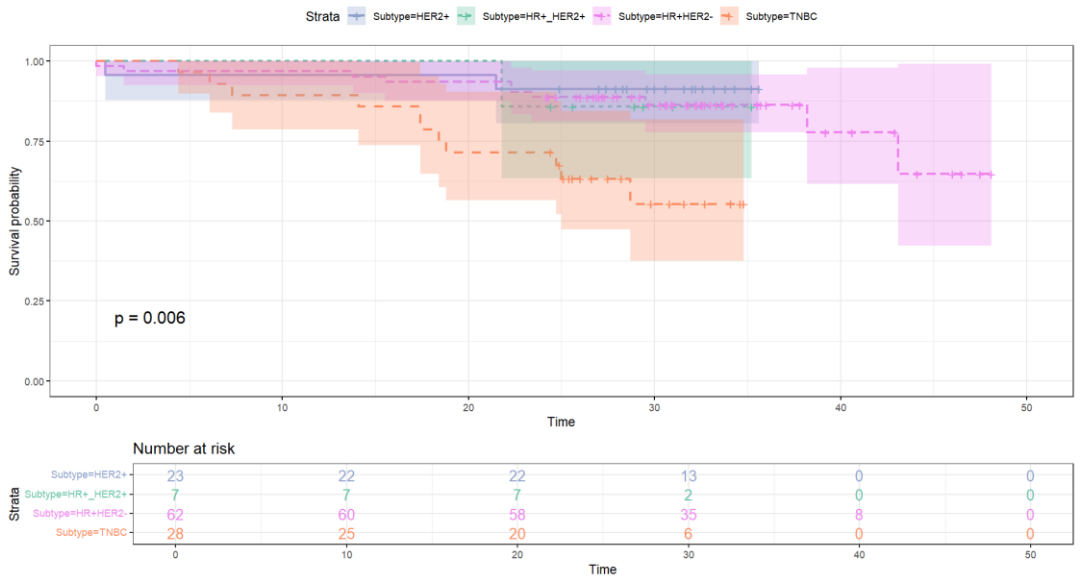
- ✓ Variables en continu
- ✓ Modèle de Cox et sélection de variables avec step AIC: **organomic (SULmean, Humean, Volumes de la graisse sous-cutanée, viscérale et des muscles)**
- ✓ Prédiction d’un score de risque

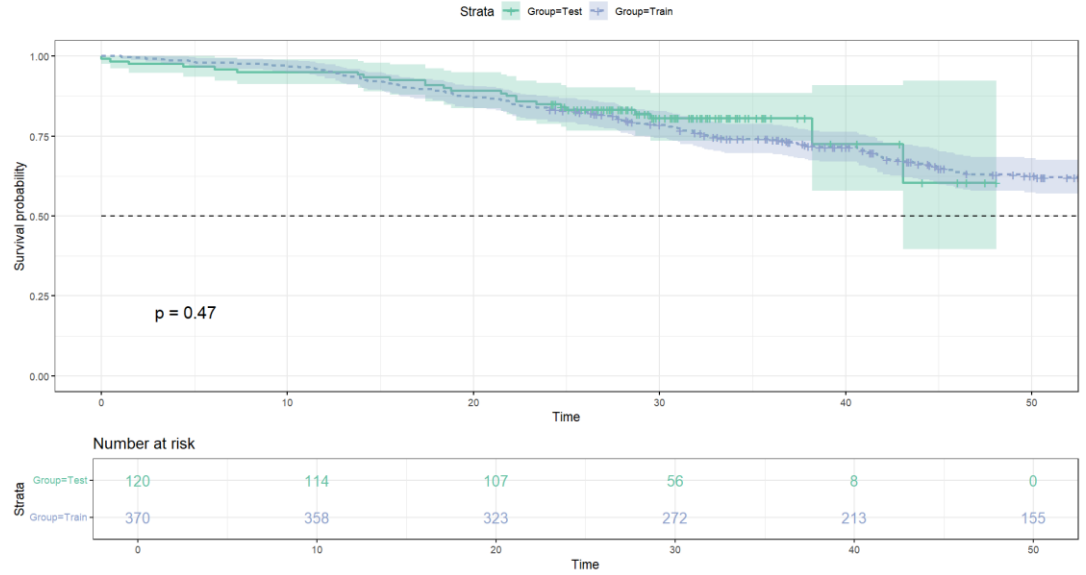
3. Résultats

TRAIN (n=370)

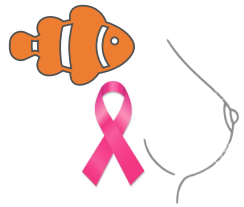


TEST (n=120)





Caractéristiques patientes



	Train (n = 370)	Test (n = 120)	p (Wilcoxon test)
Age (year)	53 ± 13	52 ± 13	0.52
BMI (kg/m²)	25.9 ± 5.2	25.8 ± 5.6	0.47
HER2			0.89
Positive	97 (26%)	30 (25%)	
Negative	273 (74%)	90 (75%)	
HR			**0.02**
Positive	257 (69%)	69 (58%)	
Negative	113 (31%)	51 (42%)	
Dmax (cm)	33 ± 22	34 ± 24	0.85
TMTV (mL)	110 ± 291	120 ± 252	0.57
SULmean Fat SC	0.27 ± 0.06	0.27 ± 0.05	0.38
SULmean Fat V	0.64 ± 0.16	0.65 ± 0.13	0.19
SULmean Skeletal muscles	0.52 ± 0.09	0.53 ± 0.08	0.11
SULmean Spleen	1.18 ± 0.25	1.22 ± 0.22	**0.05**
HUmean Fat SC	-91.6 ± 7.3	-91.3 ± 7.2	0.52
HUmean Fat V	-71.2 ± 13.8	-71.1 ± 12.1	0.72
HUmean Skeletal muscles	34.1 ± 7.9	33.6 ± 7.3	0.46
Volume Fat SC (mL)	21 297 ± 8629	22 329 ± 9394	0.37
Volume Fat V (mL)	2290 ± 1658	2888 ± 1446	0.85
Volume Skeletal muscles (mL)	13 624 ± 2300	14 172 ± 2559	**0.04**

mean ± sd
mean (%)

Quantitative data: Wilcoxon test
Qualitative data: chi² test

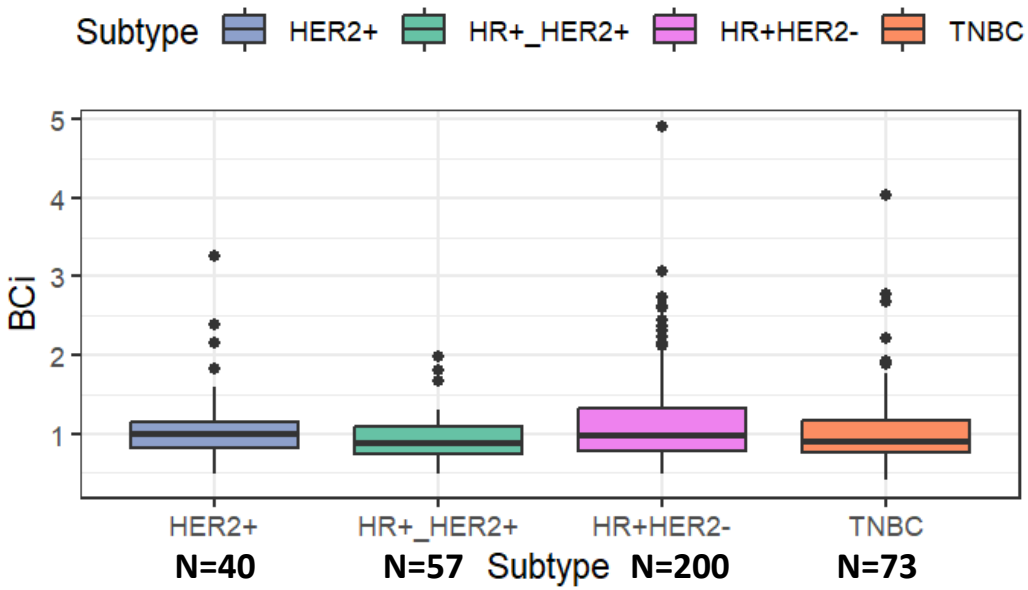
Index de composition corporelle (BCi*) : Train-Test

**BCi basé sur: Volume Fat SC & V, SULmean Muscles, HUmean Fat SC & Muscles*

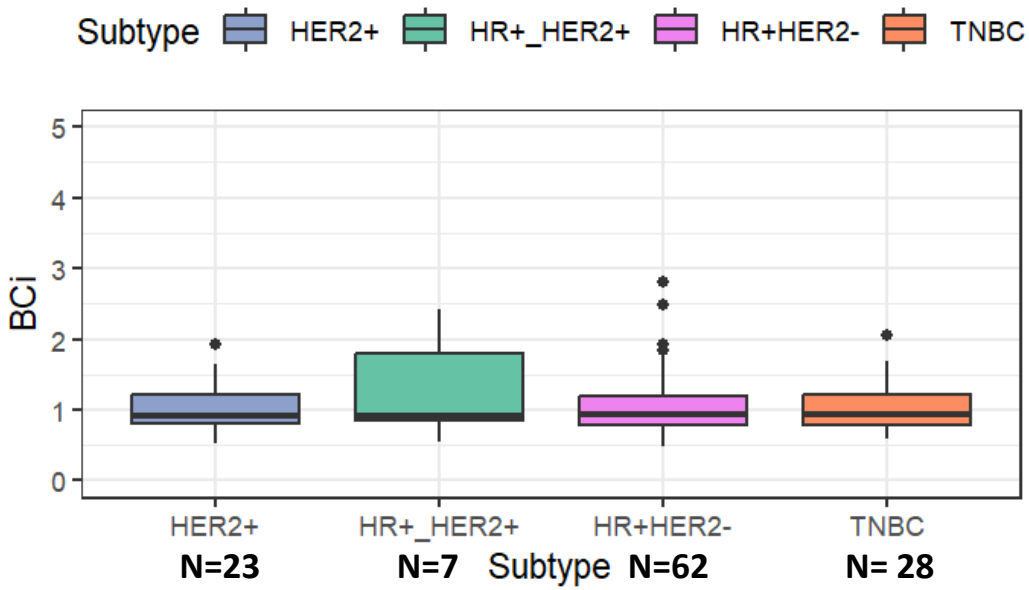
	min	q1	median	mean	q3	max
Train	0.40	**0.76**	**0.94**	**1.09**	**1.24**	4.90
Test	0.49	**0.80**	**0.93**	**1.07**	**1.21**	2.81

p = 0.85

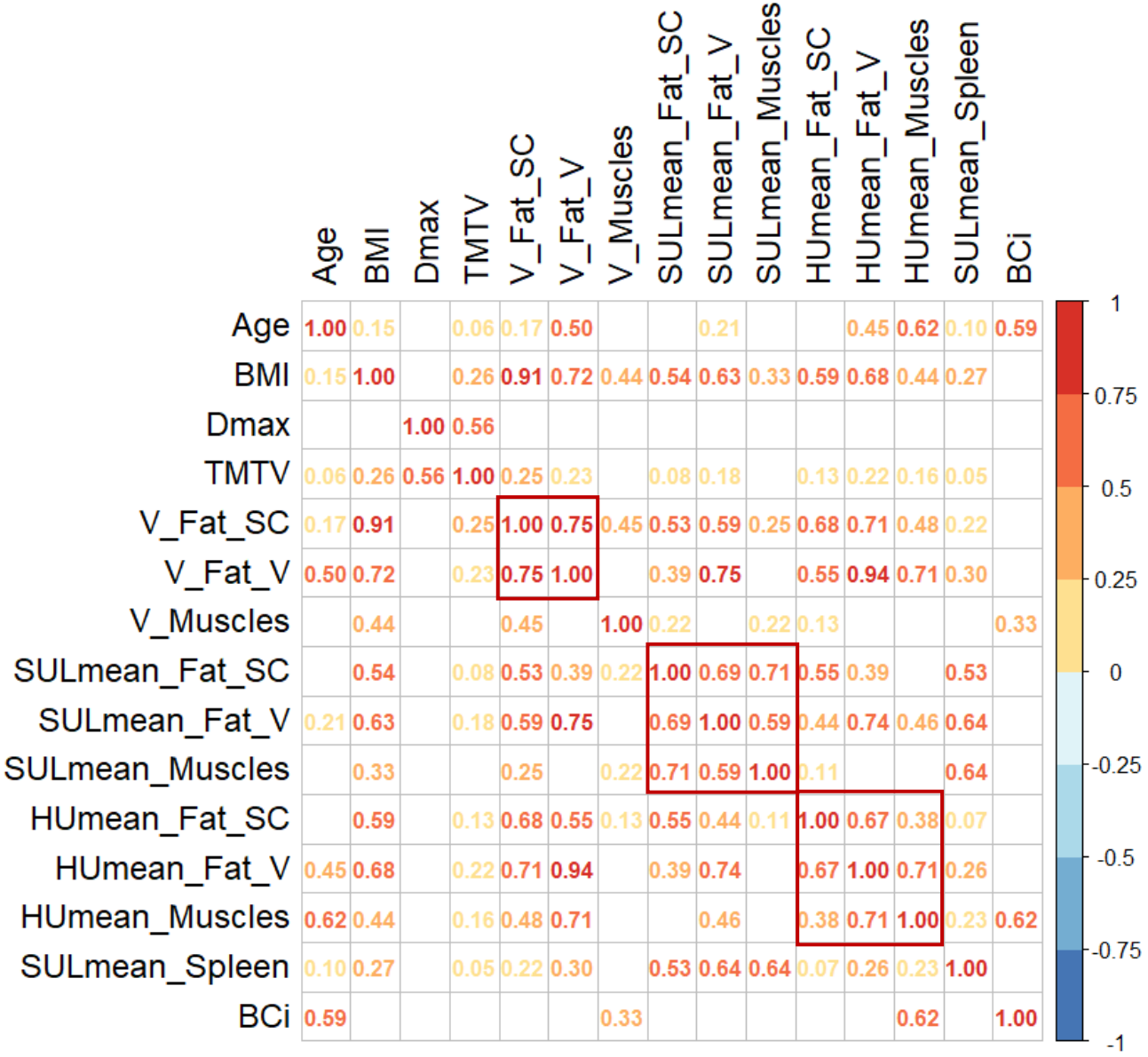
Train



Test



Corrélation de Spearman



	Age	BMI	Dmax	TMTV	V_Fat_SC	V_Fat_V	V_Muscles	SULmean_Fat_SC	SULmean_Fat_V	SULmean_Muscles	HUmean_Fat_SC	HUmean_Fat_V	HUmean_Muscles	SULmean_Spleen	BCi
Age	1.00	0.15		0.06	0.17	0.50			0.21			0.45	0.62	0.10	0.59
BMI	0.15	1.00		0.26	0.91	0.72	0.44	0.54	0.63	0.33	0.59	0.68	0.44	0.27	
Dmax			1.00	0.56											
TMTV	0.06	0.26	0.56	1.00	0.25	0.23		0.08	0.18		0.13	0.22	0.16	0.05	
V_Fat_SC	0.17	0.91		0.25	1.00	0.75	0.45	0.53	0.59	0.25	0.68	0.71	0.48	0.22	
V_Fat_V	0.50	0.72		0.23	0.75	1.00		0.39	0.75		0.55	0.94	0.71	0.30	
V_Muscles		0.44			0.45		1.00	0.22		0.22	0.13				0.33
SULmean_Fat_SC		0.54		0.08	0.53	0.39	0.22	1.00	0.69	0.71	0.55	0.39		0.53	
SULmean_Fat_V	0.21	0.63		0.18	0.59	0.75		0.69	1.00	0.59	0.44	0.74	0.46	0.64	
SULmean_Muscles		0.33			0.25		0.22	0.71	0.59	1.00	0.11			0.64	
HUmean_Fat_SC		0.59		0.13	0.68	0.55	0.13	0.55	0.44	0.11	1.00	0.67	0.38	0.07	
HUmean_Fat_V	0.45	0.68		0.22	0.71	0.94		0.39	0.74		0.67	1.00	0.71	0.26	
HUmean_Muscles	0.62	0.44		0.16	0.48	0.71			0.46		0.38	0.71	1.00	0.23	0.62
SULmean_Spleen	0.10	0.27		0.05	0.22	0.30		0.53	0.64	0.64	0.07	0.26	0.23	1.00	
BCi	0.59						0.33						0.62		1.00

**BCi basé sur: Volume Fat SC & V, SULmean Muscles, HUmean Fat SC & Muscles*

BMI corrélé à :
- Volume Fat SC (rS = 0.91)
- Volume Fat V (rS = 0.72)

TMTV & Dmax : rS = 0.56

Index de composition corporelle (BCi) corrélé à :
- HUmean muscles (rS = 0.62)
- Age (rS = 0.59)
- Volume muscles (rS = 0.33)

HUmean muscles corrélé à :
- Volume Fat V (rS = 0.71)
- HUmean Fat V (rS = 0.71)
- Age (rS = 0.62)

BCi corrélé à:
- HUmean muscles (rS = 0.62)
- Age (rS = 0.59)

Analyses multivariées – TRAIN – Clinical – COX

ENTREE

- **HR**: POSITIVE vs **NEGATIVE**
- **HER2**: POSITIVE vs **NEGATIVE**
- **Age**
- BMI

SORTIE (STEP AIC)

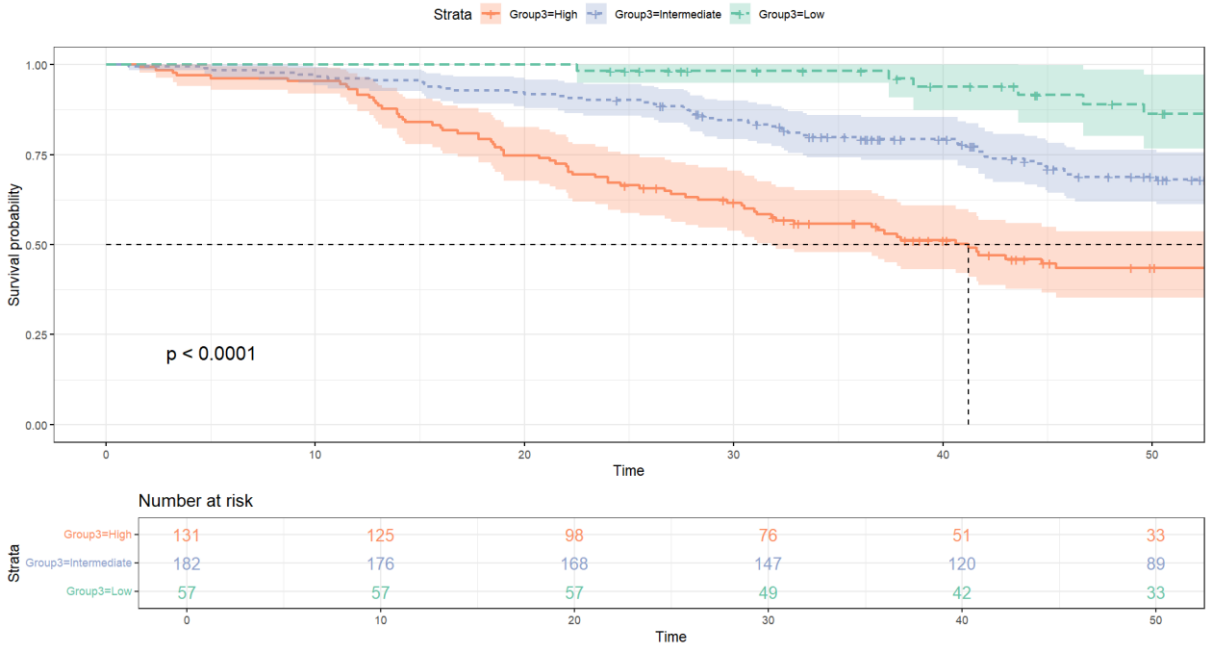
```
coxph(formula = Surv(Time, Status) ~ HR + HER2 + Age, data = model_train)

  n= 370, number of events= 157

              coef exp(coef)  se(coef)      z Pr(>|z|)
HRPOS    -0.794557  0.451781  0.172552 -4.605 4.13e-06 ***
HER2POS -1.219588  0.295352  0.250809 -4.863 1.16e-06 ***
Age      0.017532  1.017687  0.005998  2.923  0.00347 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

         exp(coef) exp(-coef) lower .95 upper .95
HRPOS       0.4518     2.2135    0.3221    0.6336
HER2POS     0.2954     3.3858    0.1807    0.4829
Age         1.0177     0.9826    1.0058    1.0297

Concordance= 0.688  (se = 0.021 )
Likelihood ratio test= 53.82  on 3 df,   p=1e-11
Wald test            = 47.87  on 3 df,   p=2e-10
Score (logrank) test = 49.68  on 3 df,   p=9e-11
```

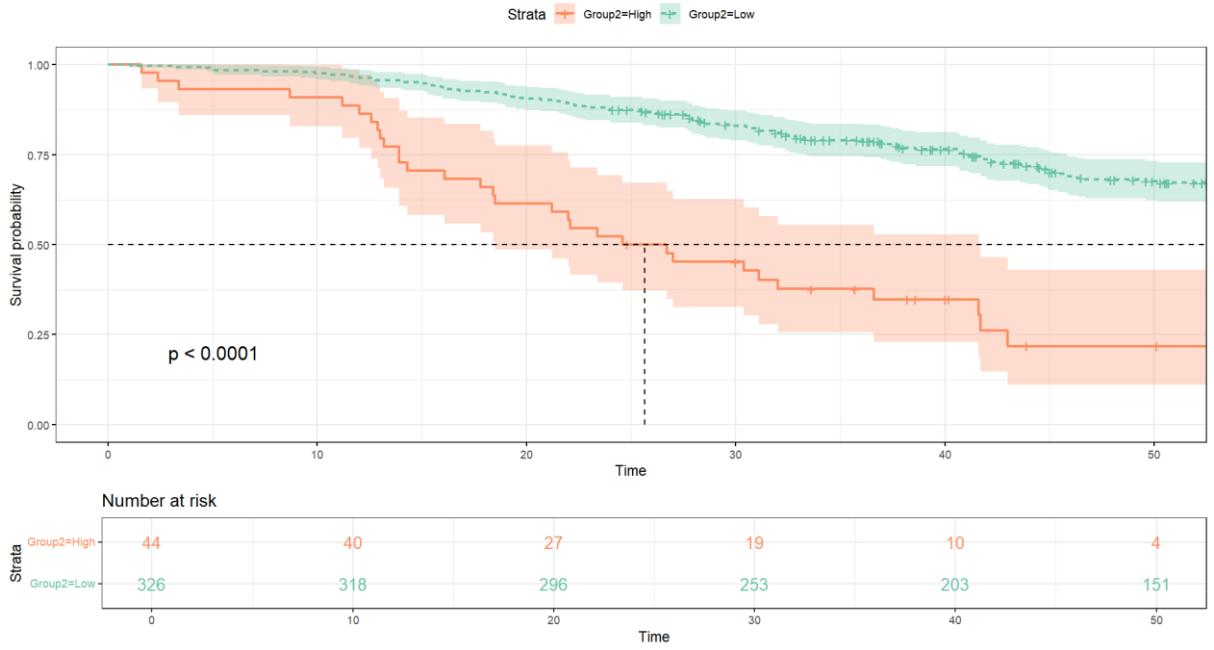
Poor OS:

- Low values
- High values

Analyses multivariées – TRAIN – Clinical – OS

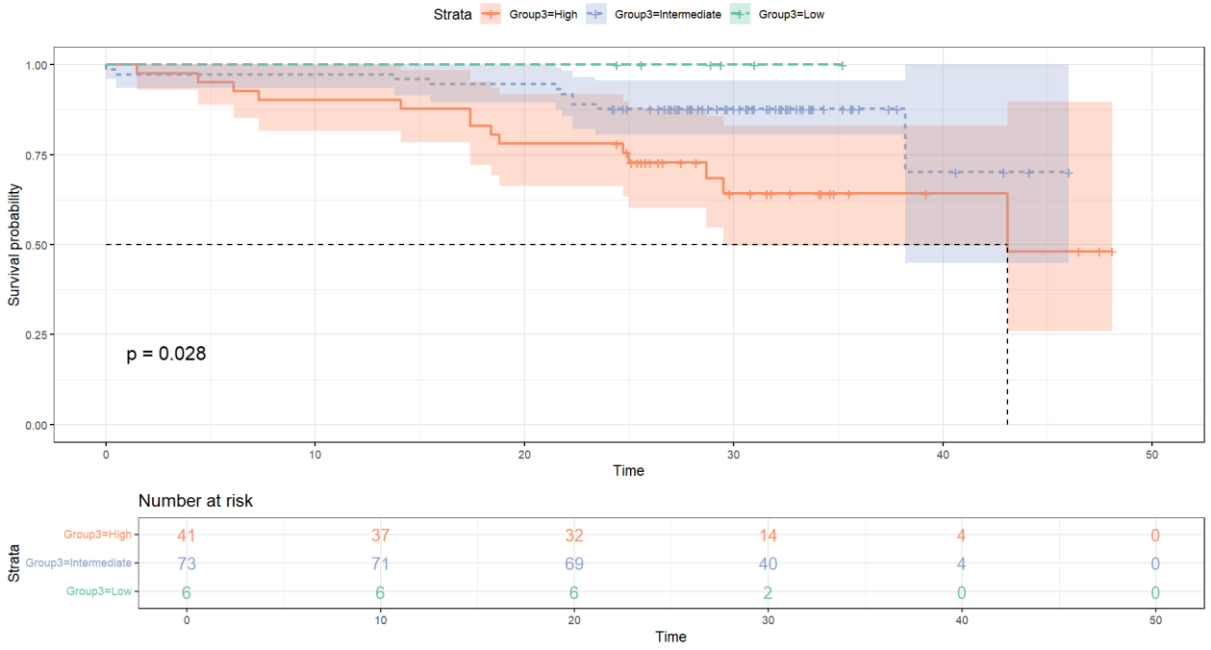
→ Groupes déterminés avec les fonctions rhier et rlr (log rank), **ns = 45**

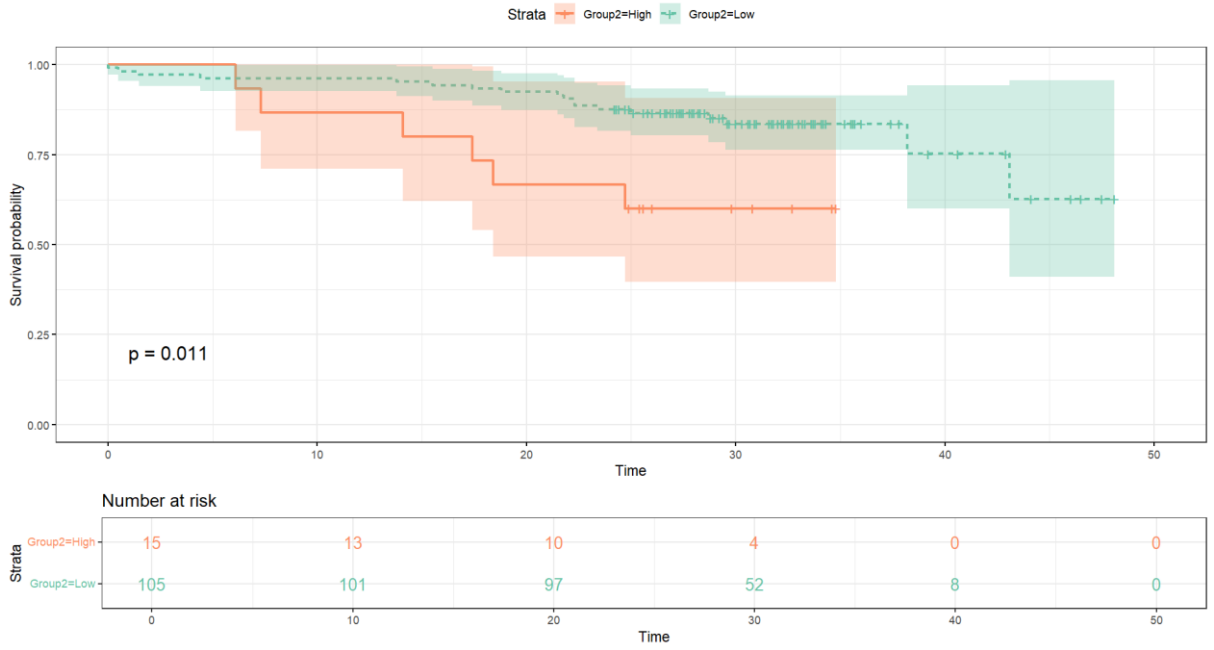




Analyses statistiques : analyses multivariées – TEST – Clinical – OS

→ Groupes déterminés avec les fonctions rhier et rlr (log rank)





Analyses multivariées – TRAIN – RADIOMIC – COX

ENTREE

- TMTV
- DMAX

SORTIE (STEP AIC)

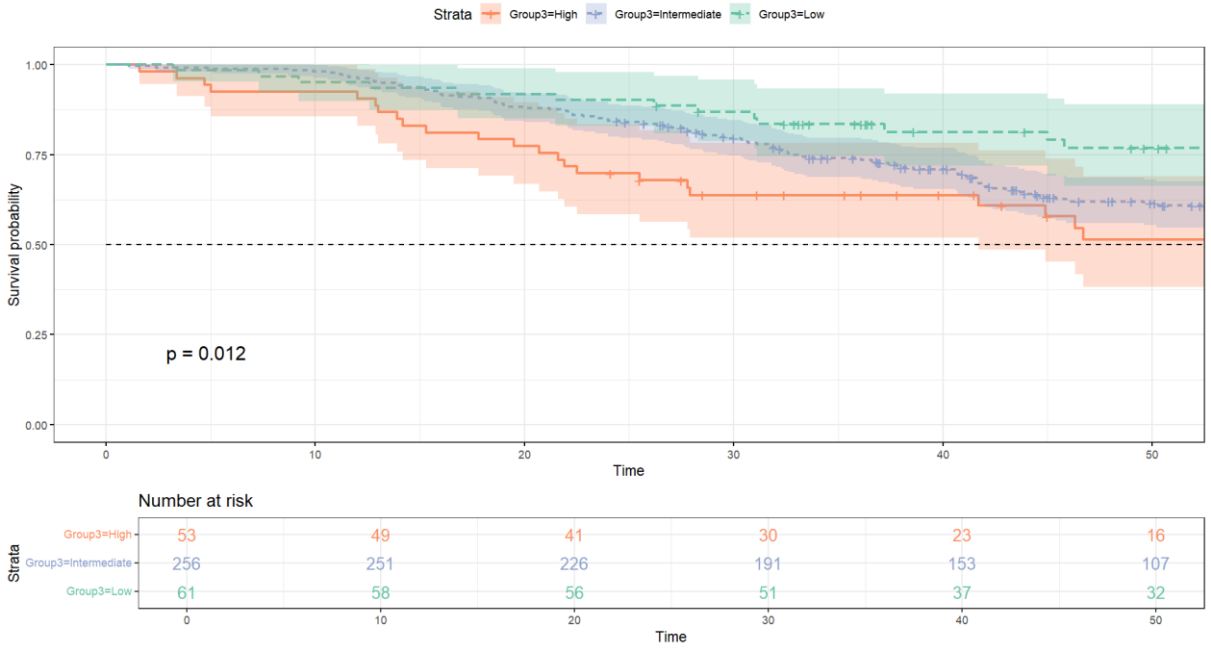
```
coxph(formula = Surv(Time, Status) ~ Dmax, data = model_train)

  n= 370, number of events= 157

         coef exp(coef) se(coef)    z Pr(>|z|)
Dmax 0.006582  1.006604 0.003617 1.82   0.0688 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

     exp(coef) exp(-coef) lower .95 upper .95
Dmax     1.007     0.9934    0.9995     1.014

Concordance= 0.554  (se = 0.025 )
Likelihood ratio test= 3.26  on 1 df,   p=0.07
Wald test            = 3.31  on 1 df,   p=0.07
Score (logrank) test = 3.32  on 1 df,   p=0.07
```

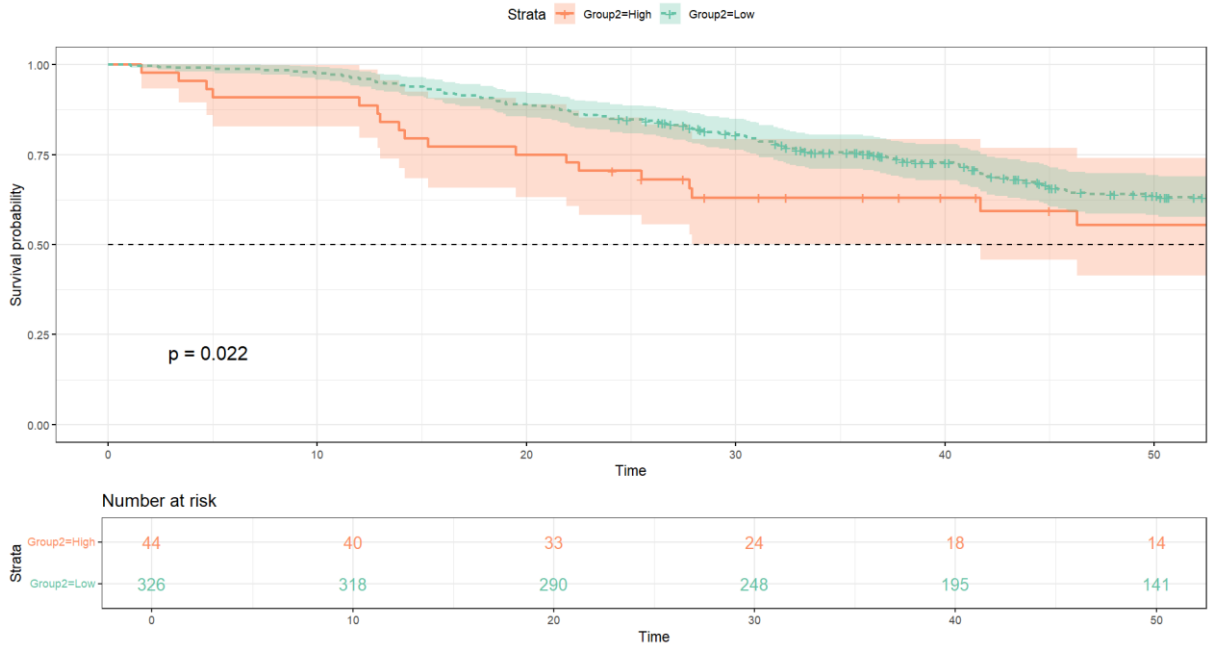
Poor OS:

- Low values
- High values

Analyses multivariées – TRAIN – RADIOMIC – OS

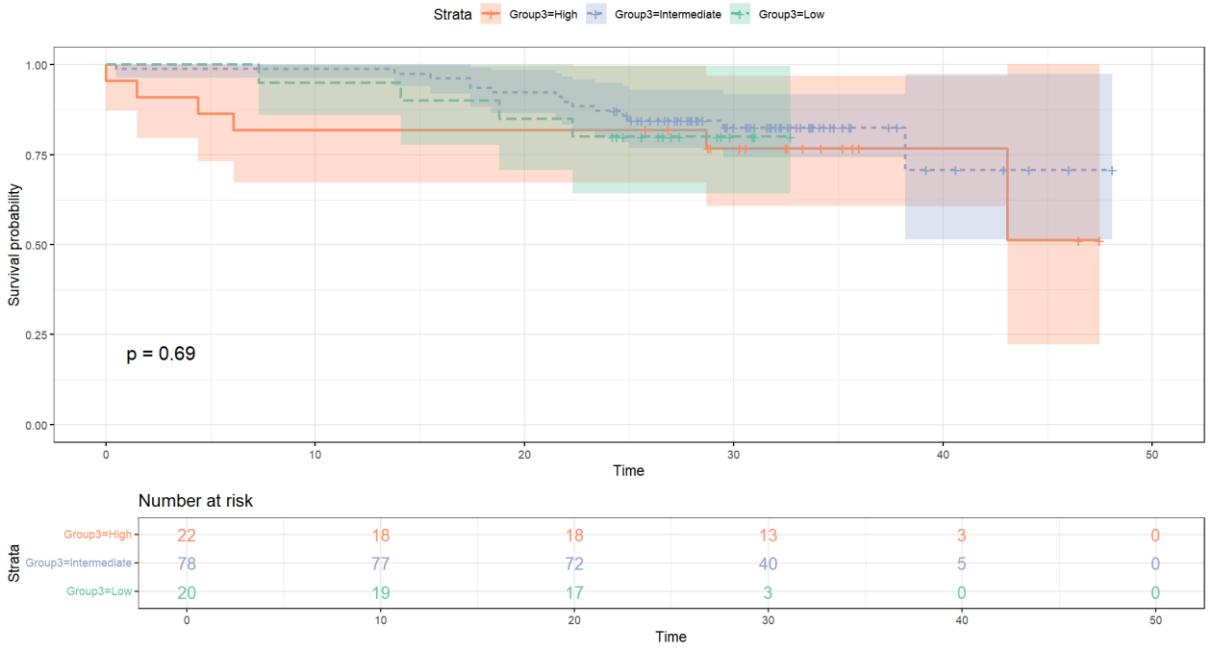
→ Groupes déterminés avec les fonctions rhier et rlr (log rank), **ns = 45**

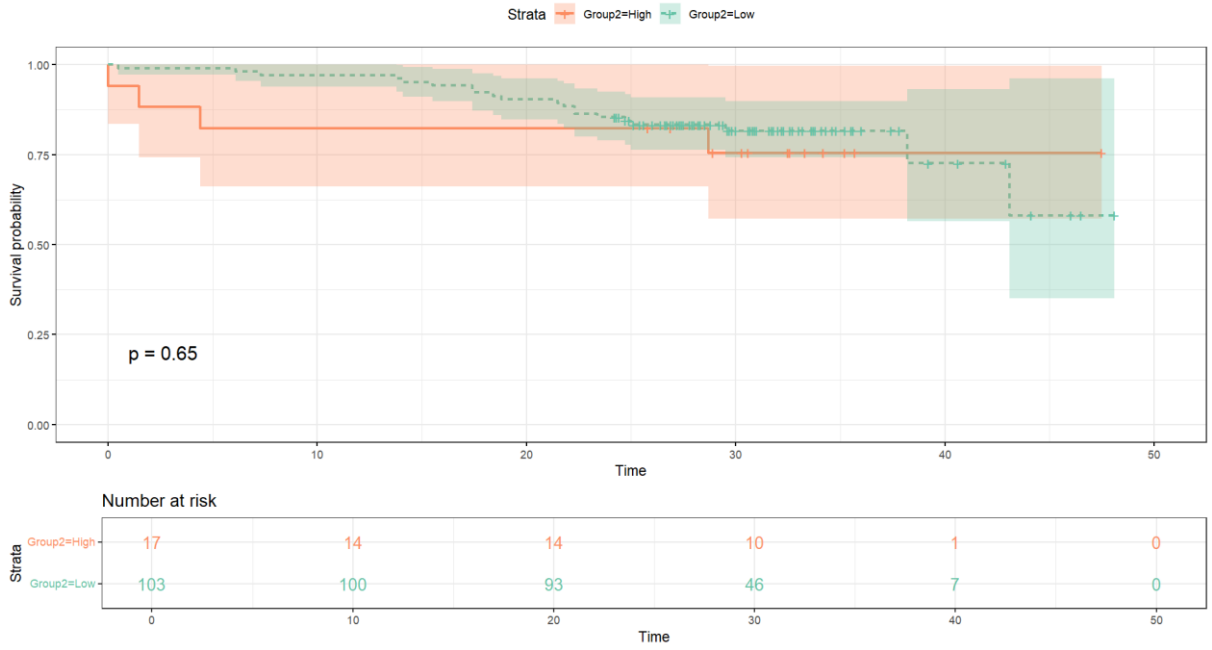




Analyses multivariées – TEST – RADIOMIC – OS

→ Groupes déterminés avec les fonctions rhier et rlr (log rank)





Analyses multivariées – TRAIN – CLIN+RADIOMIC – COX

ENTREE

- **HR**: POSITIVE vs **NEGATIVE**
- **HER2**: POSITIVE vs **NEGATIVE**
- **Age**
- BMI
- **TMTV**
- **Dmax**

SORTIE (STEP AIC)

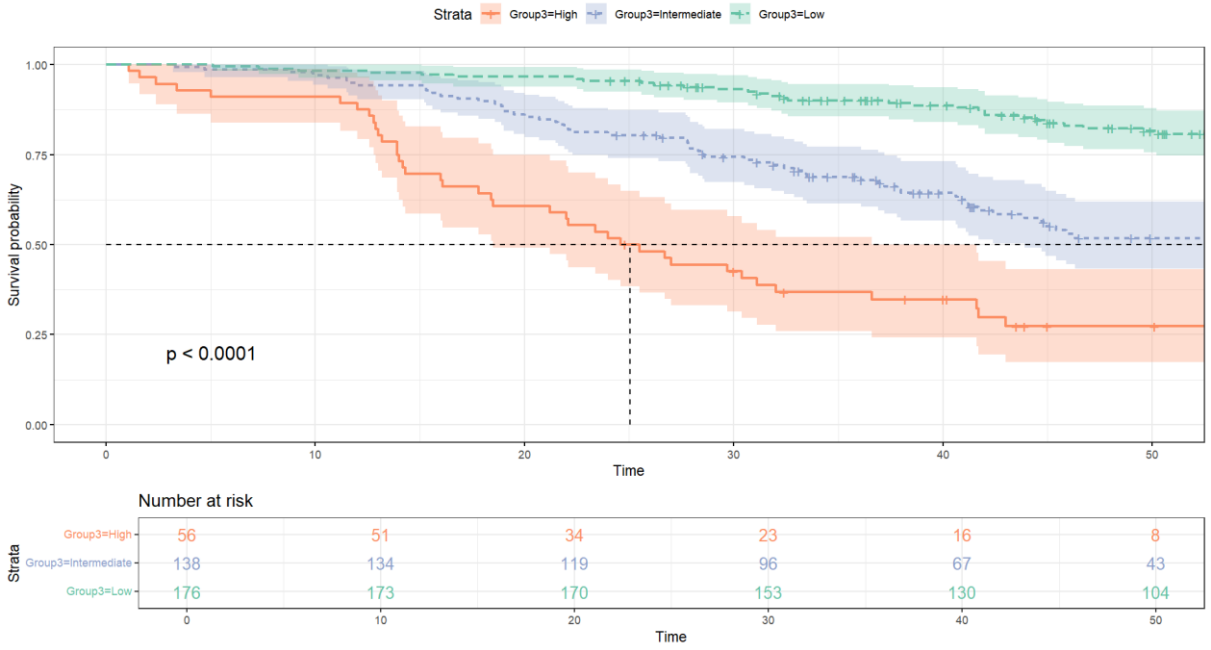
```
coxph(formula = Surv(Time, Status) ~ HR + HER2 + Age + Dmax +
    TMTV, data = model_train)

  n= 370, number of events= 157

              coef  exp(coef)   se(coef)      z Pr(>|z|)
HRPOS    -0.9992110  0.3681698  0.1894015 -5.276 1.32e-07 ***
HER2POS -1.3587082  0.2569925  0.2580770 -5.265 1.40e-07 ***
Age       0.0177550  1.0179136  0.0060761  2.922  0.00348 **
Dmax      0.0115021  1.0115685  0.0041809  2.751  0.00594 **
TMTV      0.0004408  1.0004409  0.0002635  1.673  0.09429 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

         exp(coef) exp(-coef) lower .95 upper .95
HRPOS       0.3682     2.7161    0.2540    0.5337
HER2POS     0.2570     3.8912    0.1550    0.4262
Age         1.0179     0.9824    1.0059    1.0301
Dmax        1.0116     0.9886    1.0033    1.0199
TMTV        1.0004     0.9996    0.9999    1.0010

Concordance= 0.71  (se = 0.021 )
Likelihood ratio test= 68.98  on 5 df,   p=2e-13
Wald test            = 60.61  on 5 df,   p=9e-12
Score (logrank) test = 63.75  on 5 df,   p=2e-12
```

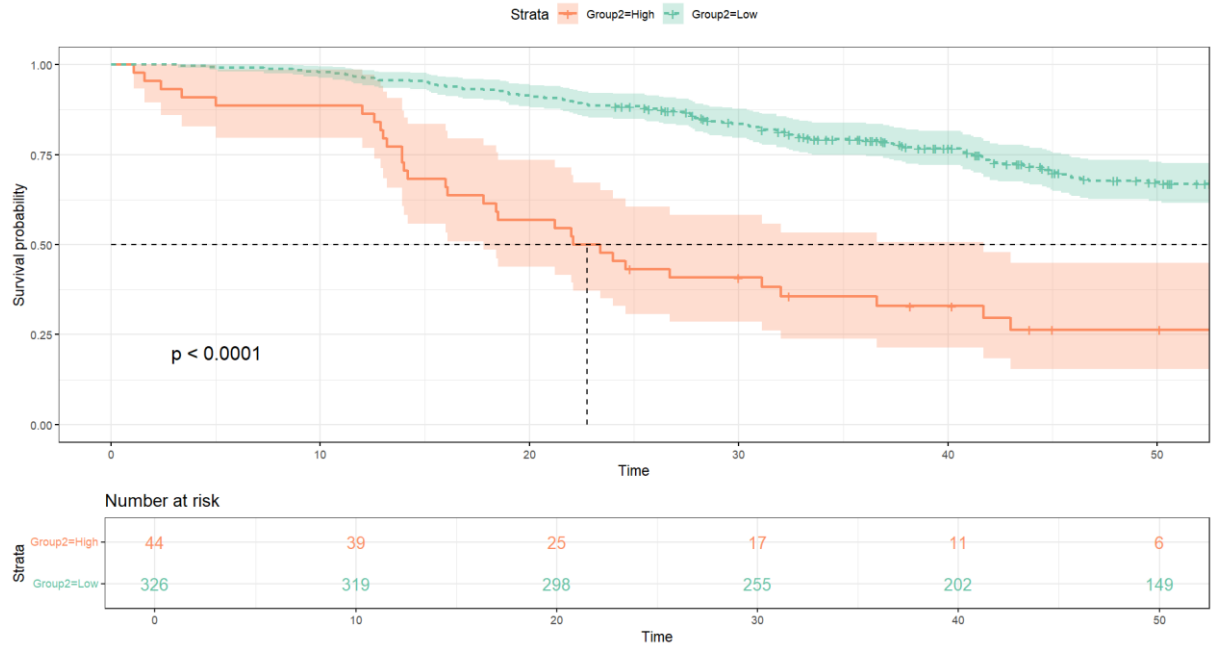
Poor OS:

- Low values
- High values

Analyses multivariées – TRAIN – CLIN+RADIOMIC – OS

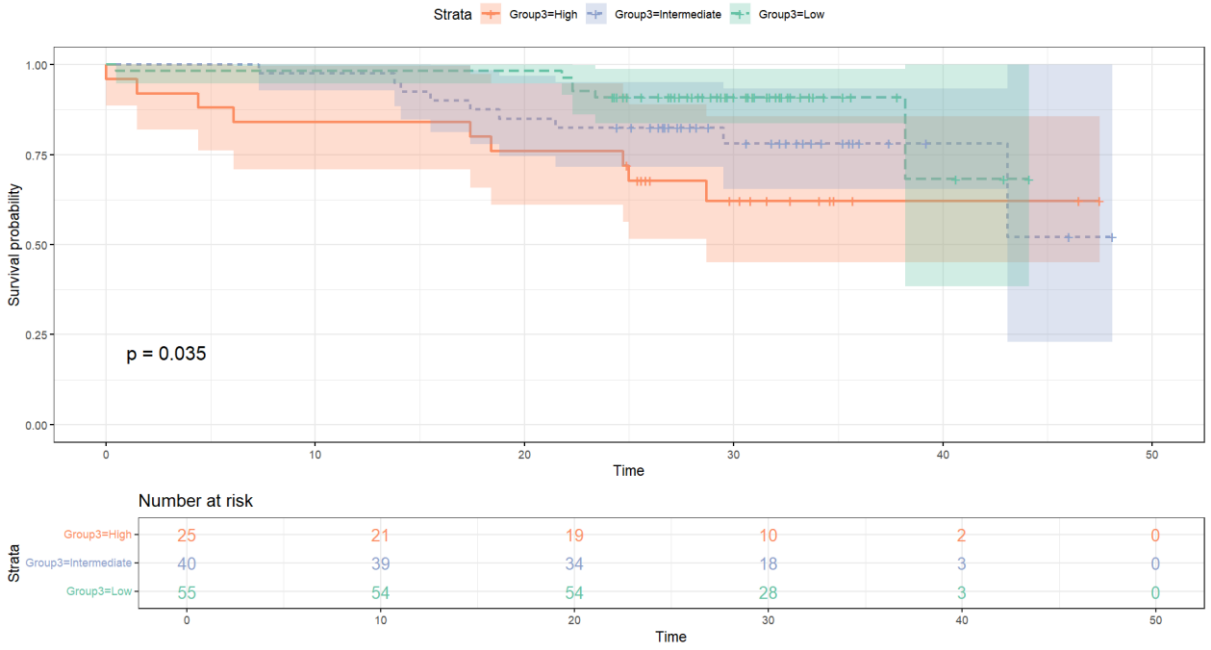
→ Groupes déterminés avec les fonctions rhier et rlr (log rank), **ns = 45**

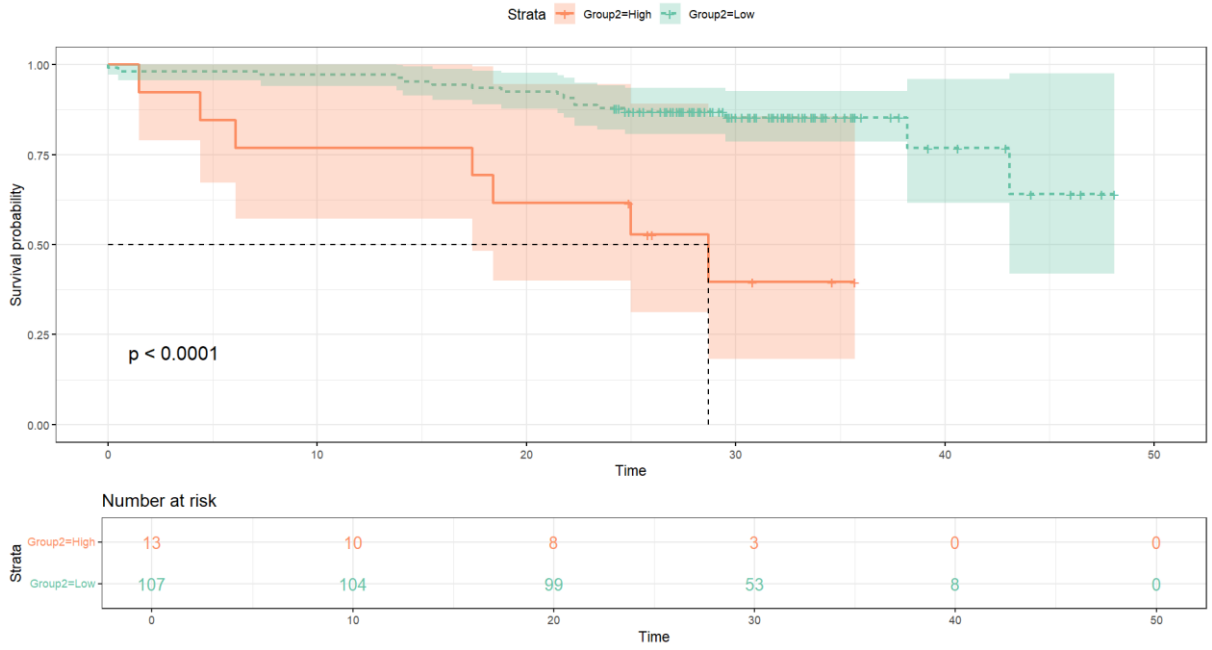




Analyses multivariées – TEST – CLIN+RADIOMIC – OS

→ Groupes déterminés avec les fonctions rhier et rlr (log rank)





Analyses multivariées – TRAIN – BCi (Body Composition index) – COX

ENTREE

- V Fat SC
- V Fat V
- V Muscles
- SULmean Fat SC
- SULmean Fat V
- SULmean Muscles
- HUmean Fat SC
- HUmean Fat V
- HUmean Muscles

SORTIE

```
coxph(formula = Surv(Time, Status) ~ V_Fat_SC + V_Fat_V + SULmean_Muscles +
    HUmean_Fat_SC + HUmean_Muscles, data = model_train)

  n= 370, number of events= 157

                    coef  exp(coef)   se(coef)      z Pr(>|z|)
V_Fat_SC       -2.314e-05  1.000e+00  1.559e-05 -1.484   0.1377
V_Fat_V         1.821e-04  1.000e+00  8.511e-05  2.140   0.0324 *
SULmean_Muscles 1.276e+00  3.584e+00  8.321e-01  1.534   0.1250
HUmean_Fat_SC   2.838e-02  1.029e+00  1.182e-02  2.402   0.0163 *
HUmean_Muscles -2.669e-02  9.737e-01  1.392e-02 -1.917   0.0552 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

                exp(coef) exp(-coef) lower .95 upper .95
V_Fat_SC           1.0000     1.0000    0.9999     1.000
V_Fat_V            1.0002     0.9998    1.0000     1.000
SULmean_Muscles    3.5837     0.2790    0.7016    18.305
HUmean_Fat_SC      1.0288     0.9720    1.0052     1.053
HUmean_Muscles     0.9737     1.0270    0.9475     1.001

Concordance= 0.6  (se = 0.024 )
Likelihood ratio test= 25.08  on 5 df,   p=1e-04
Wald test            = 27.48  on 5 df,   p=5e-05
Score (logrank) test = 27.76  on 5 df,   p=4e-05
```

Poor OS:

- Low values
- High values

Analyses multivariées – TRAIN – BCi (Body Composition index) – COX

ENTREE

- BCi
- SULmean Spleen

SORTIE

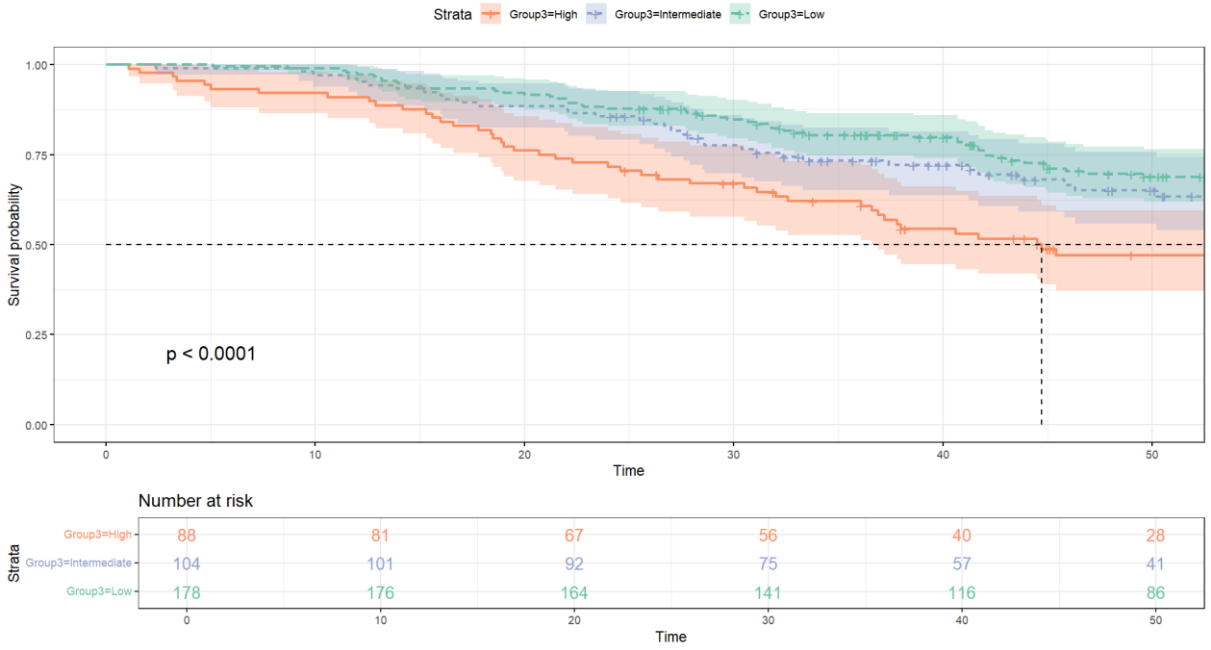
```
coxph(formula = Surv(Time, Status) ~ BCi, data = model_train)

  n= 370, number of events= 157

       coef exp(coef) se(coef)     z Pr(>|z|)
BCi 0.6187    1.8565   0.1067 5.799 6.67e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

    exp(coef) exp(-coef) lower .95 upper .95
BCi     1.856     0.5386     1.506     2.288

Concordance= 0.6  (se = 0.024 )
Likelihood ratio test= 23.9  on 1 df,   p=1e-06
Wald test            = 33.63  on 1 df,   p=7e-09
Score (logrank) test = 33.52  on 1 df,   p=7e-09
```

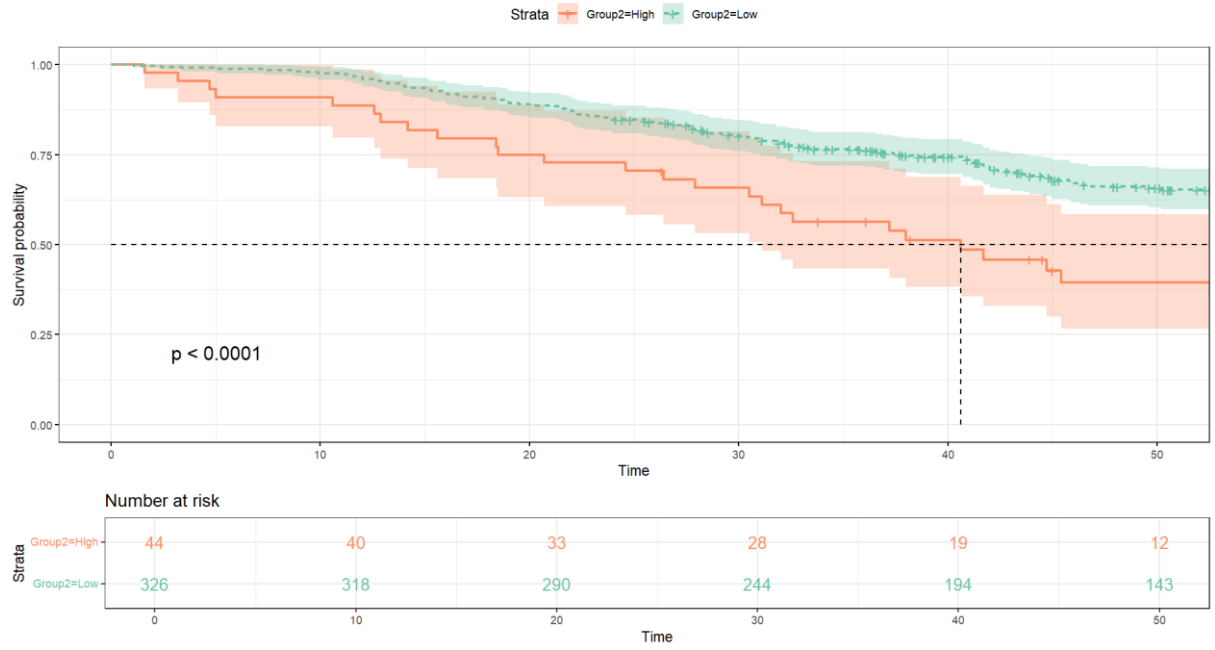
Poor OS:

- Low values
- High values

Analyses multivariées – TRAIN – BCi (Body Composition index) – OS

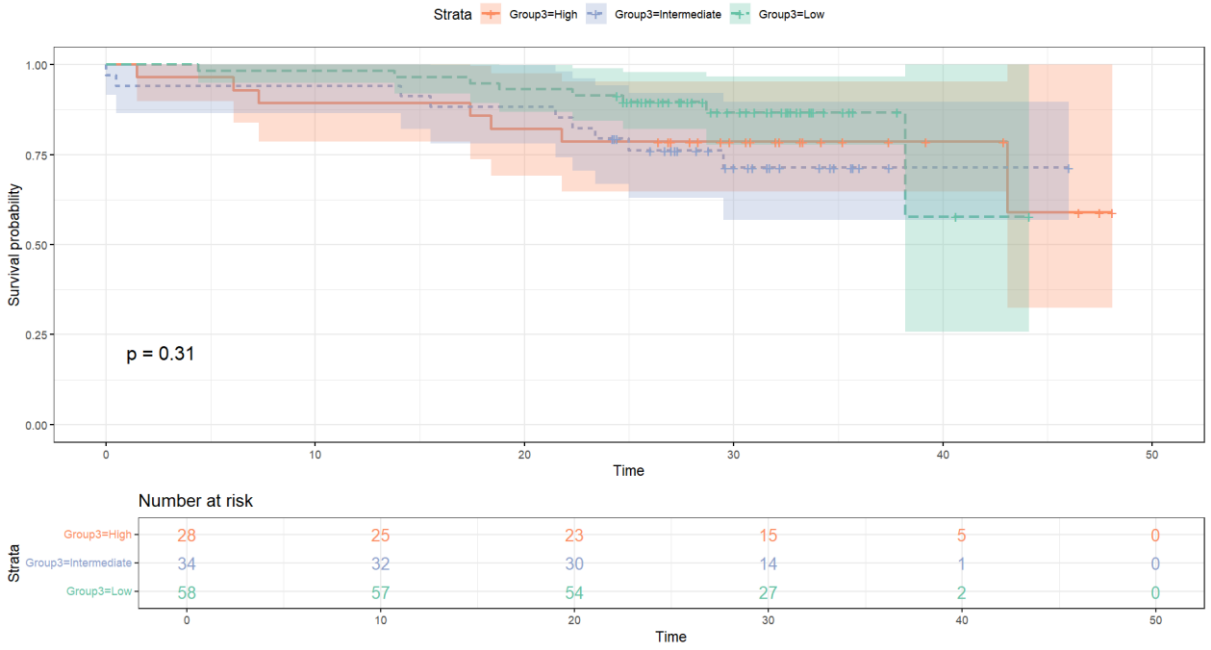
→ Groupes déterminés avec les fonctions rhier et rlr (log rank), **ns = 45**

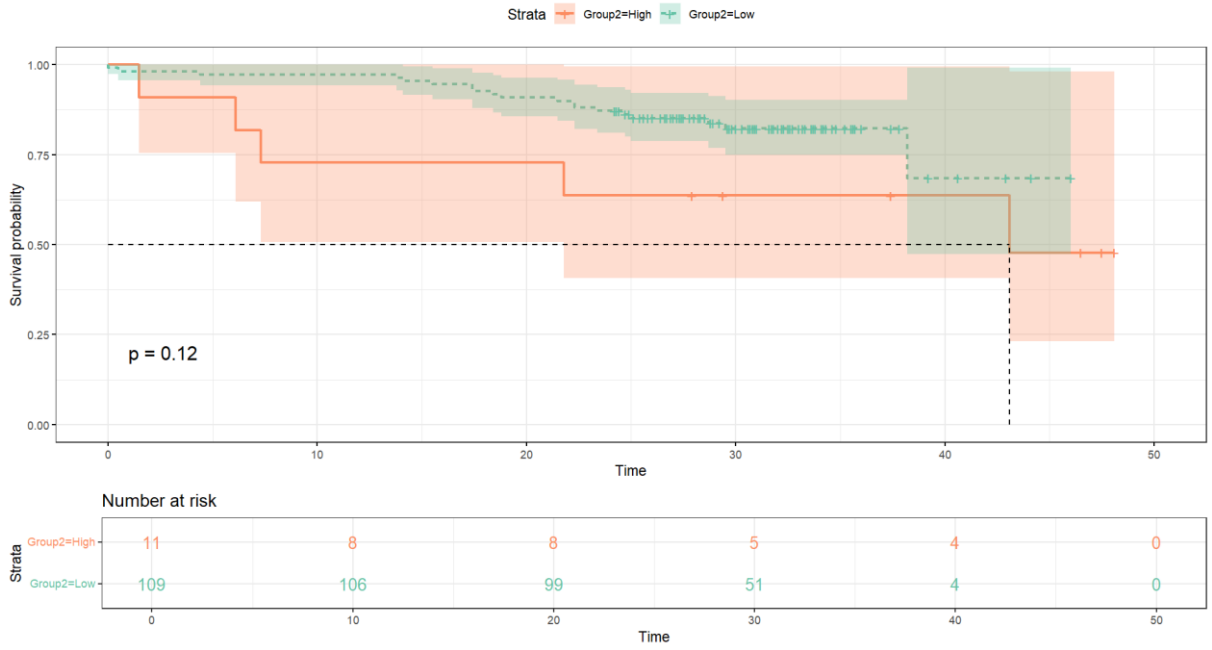




Analyses multivariées – TEST – BCi (Body Composition index) – OS

→ Groupes déterminés avec les fonctions rhier et rlr (log rank)





Analyses multivariées – TRAIN – CLIN+RADIOMIC+ORGANOMIC (BCI) – COX

ENTREE

- **HR**: POSITIVE vs NEGATIVE
- **HER2**: POSITIVE vs NEGATIVE
- Age
- BMI
- TMTV
- Dmax
- Bci
- SULmean Spleen

SORTIE

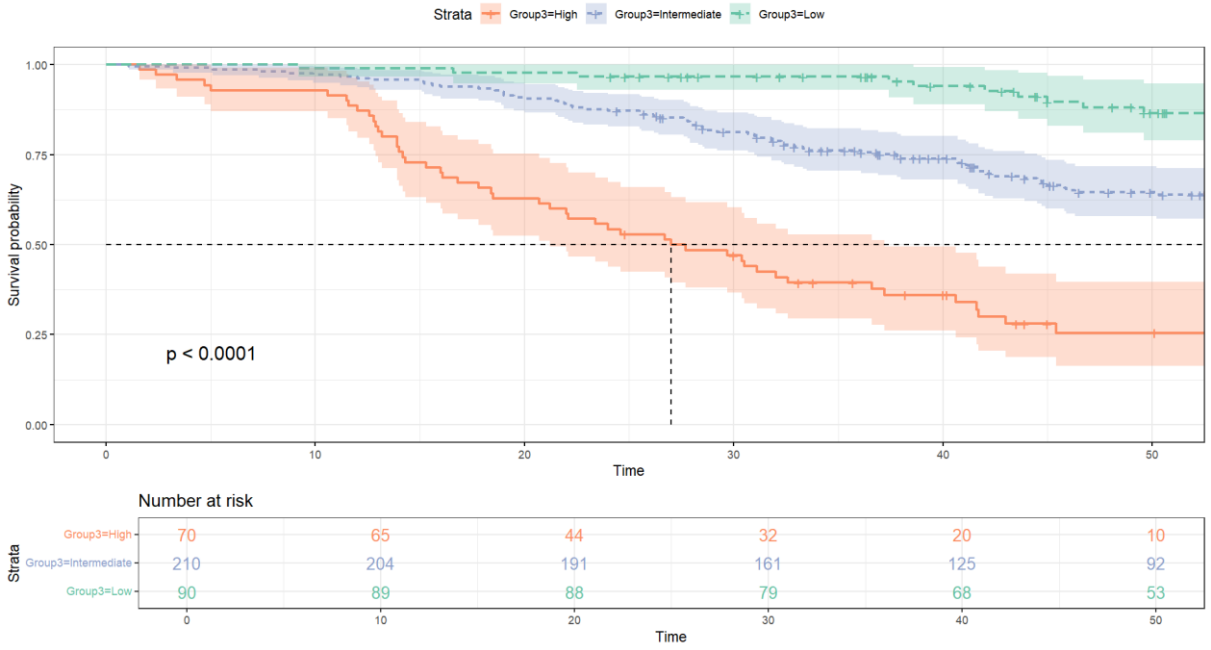
```
coxph(formula = Surv(Time, Status) ~ HR + HER2 + Dmax + BCi,
    data = model_train)

  n= 370, number of events= 157

              coef exp(coef)  se(coef)      z Pr(>|z|)
HRPOS    -1.099719  0.332965  0.192762 -5.705 1.16e-08 ***
HER2POS -1.332100  0.263923  0.253511 -5.255 1.48e-07 ***
Dmax     0.012619  1.012699  0.003823  3.301 0.000964 ***
BCi      0.606227  1.833500  0.116231  5.216 1.83e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

         exp(coef) exp(-coef) lower .95 upper .95
HRPOS       0.3330     3.0033    0.2282    0.4858
HER2POS     0.2639     3.7890    0.1606    0.4338
Dmax        1.0127     0.9875    1.0051    1.0203
BCi         1.8335     0.5454    1.4600    2.3026

Concordance= 0.716  (se = 0.021 )
Likelihood ratio test= 79.09  on 4 df,   p=3e-16
Wald test            = 74.32  on 4 df,   p=3e-15
Score (logrank) test = 79.97  on 4 df,   p=<2e-16
```

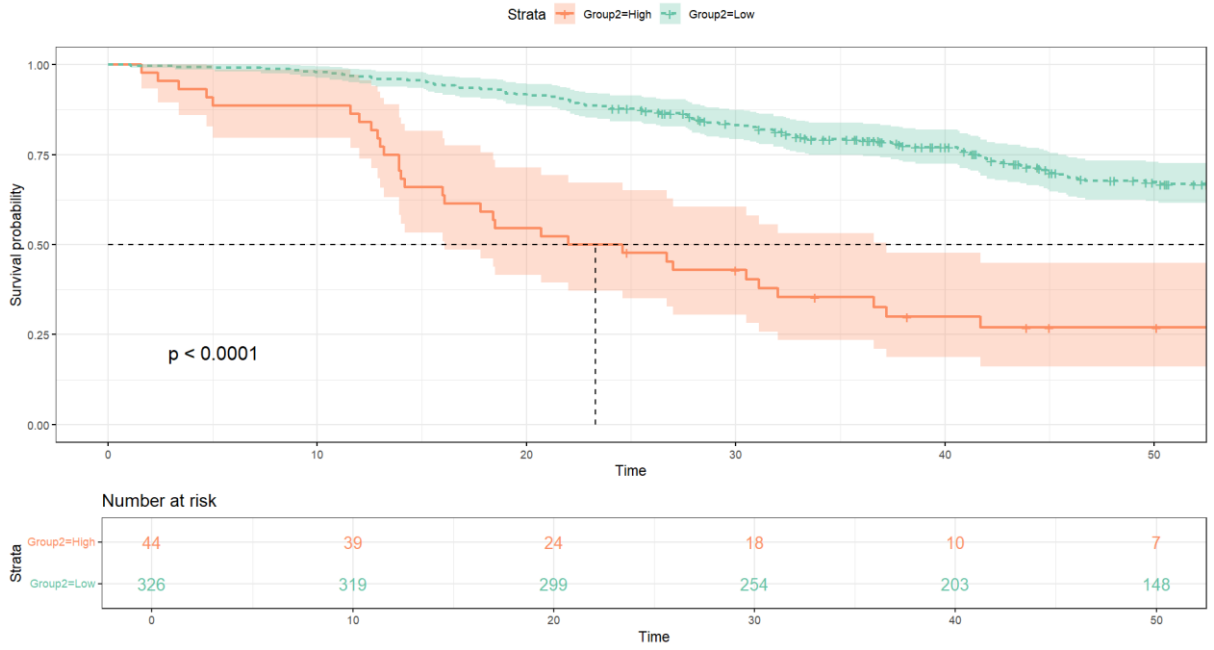
Poor OS:

- Low values
- High values

Analyses multivariées – TRAIN – CLIN+RADIOMIC+ORGANOMIC (BCI) – OS

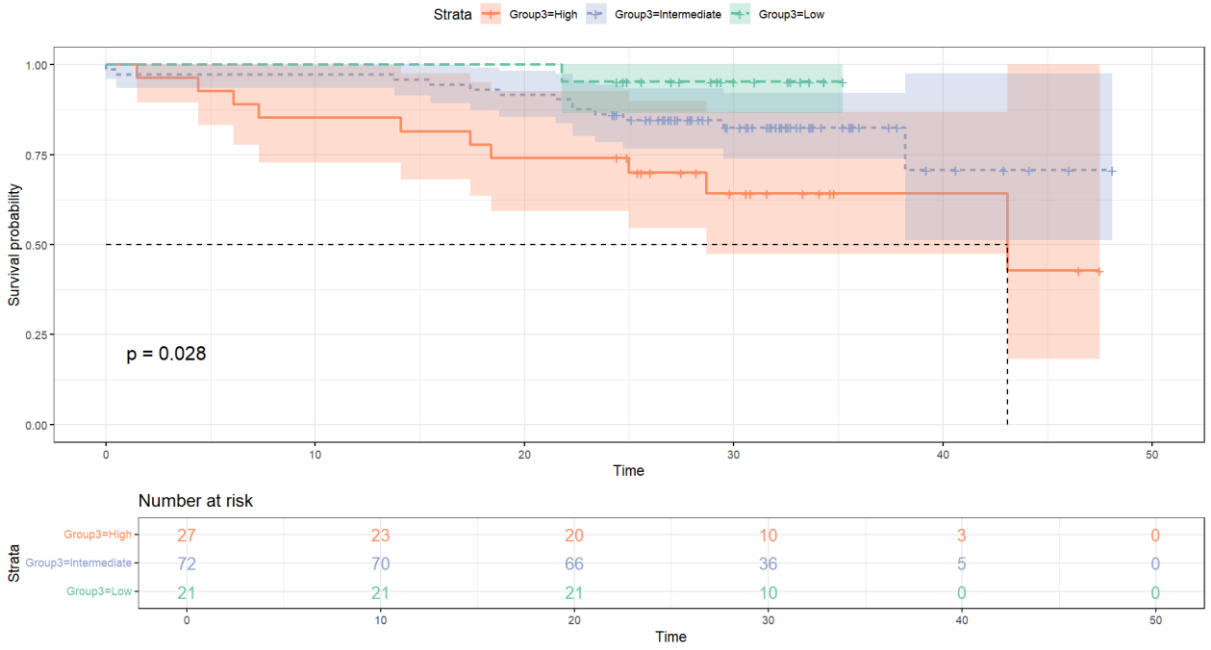
→ Groupes déterminés avec les fonctions rhier et rlr (log rank), **ns = 45**

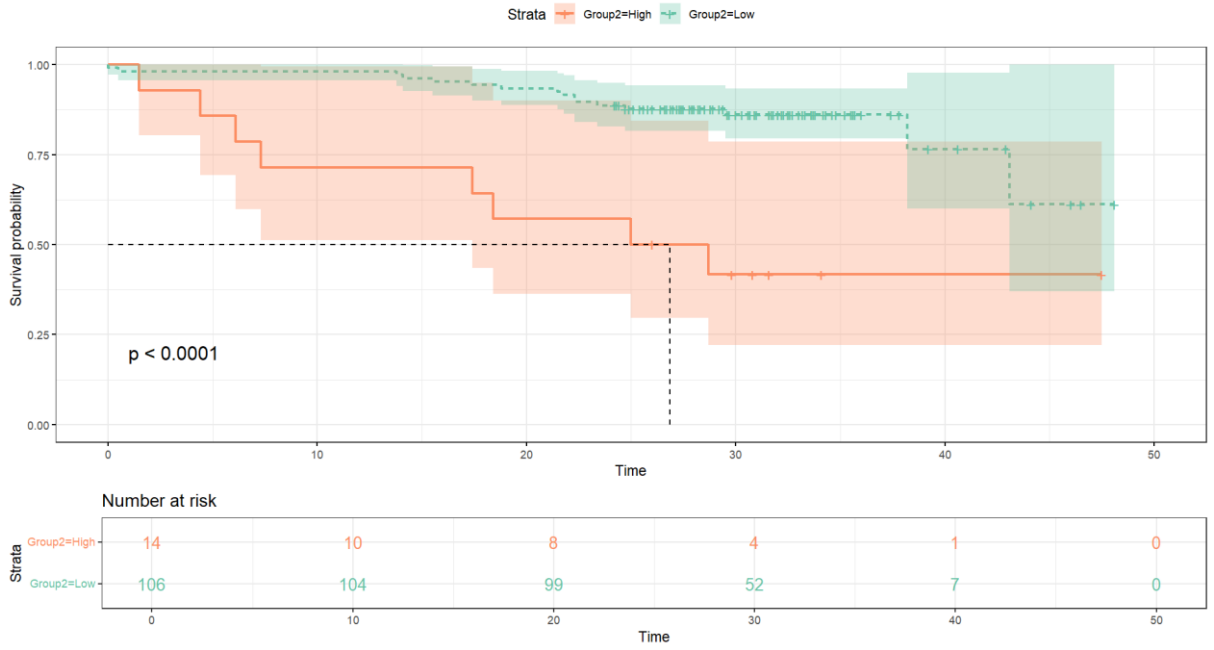




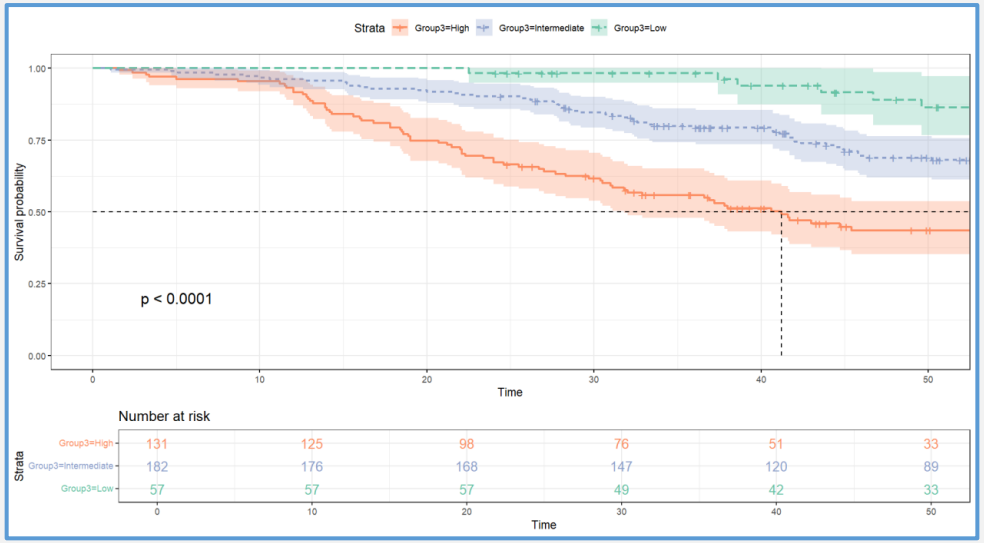
Analyses multivariées – TEST – CLIN+RADIOMIC+ORGANOMIC (BCI) – OS

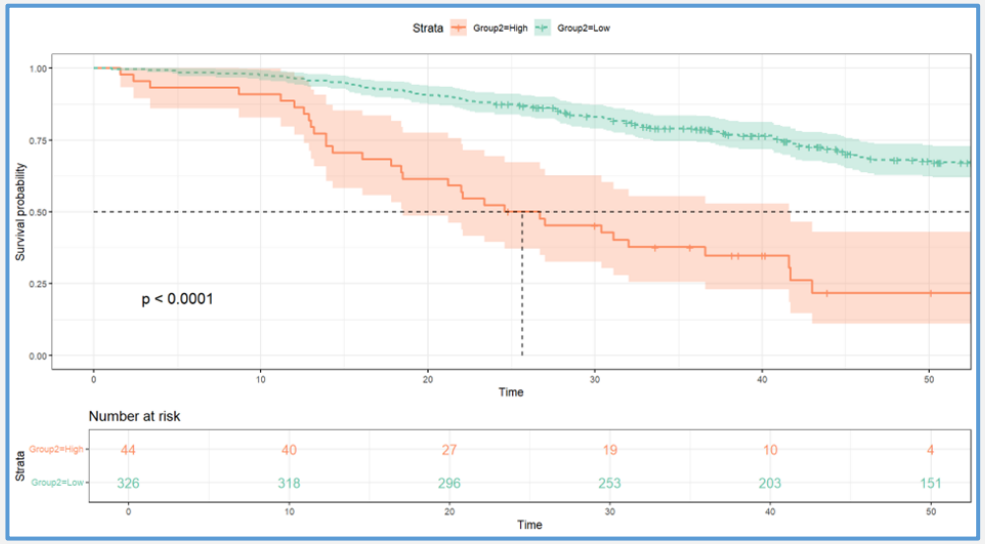
→ Groupes déterminés avec les fonctions rhier et rlr (log rank)



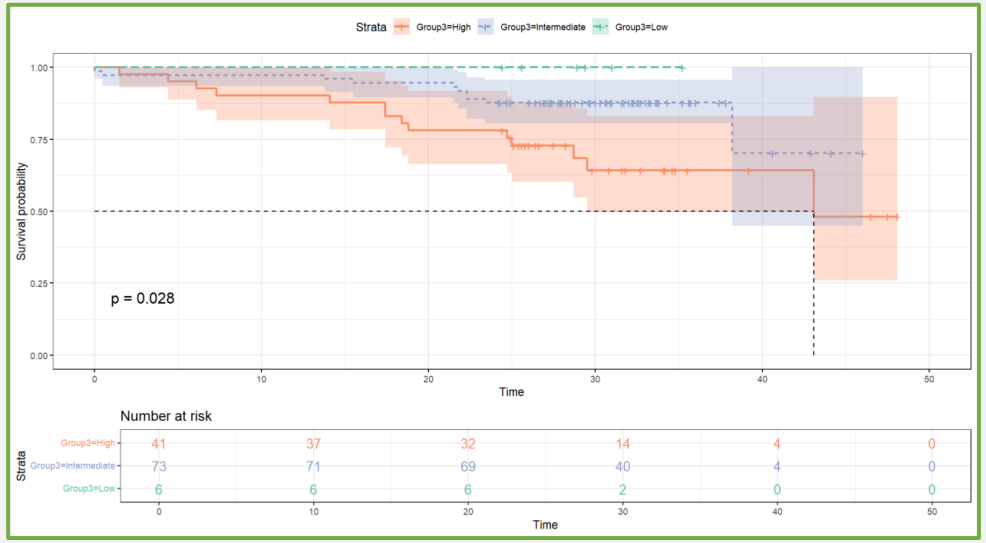


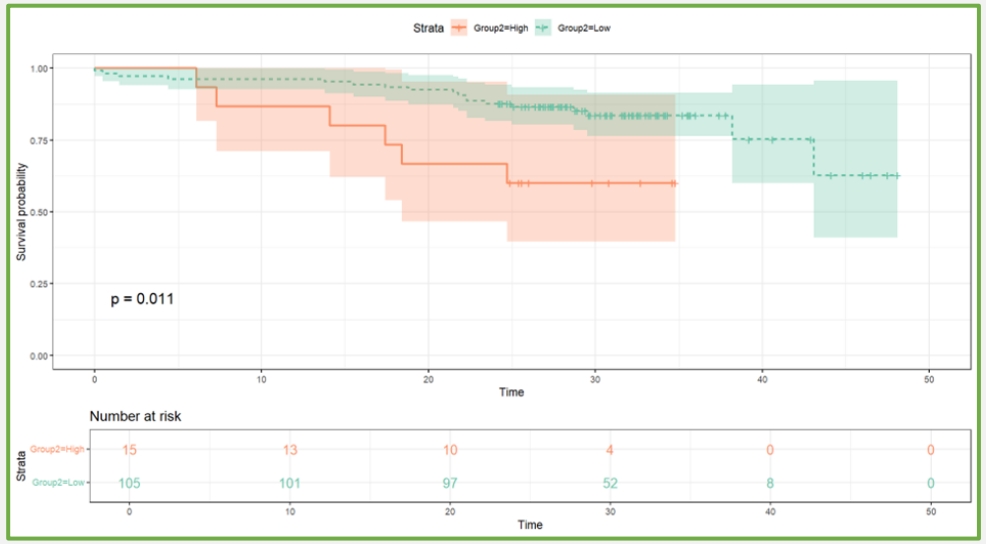
Train





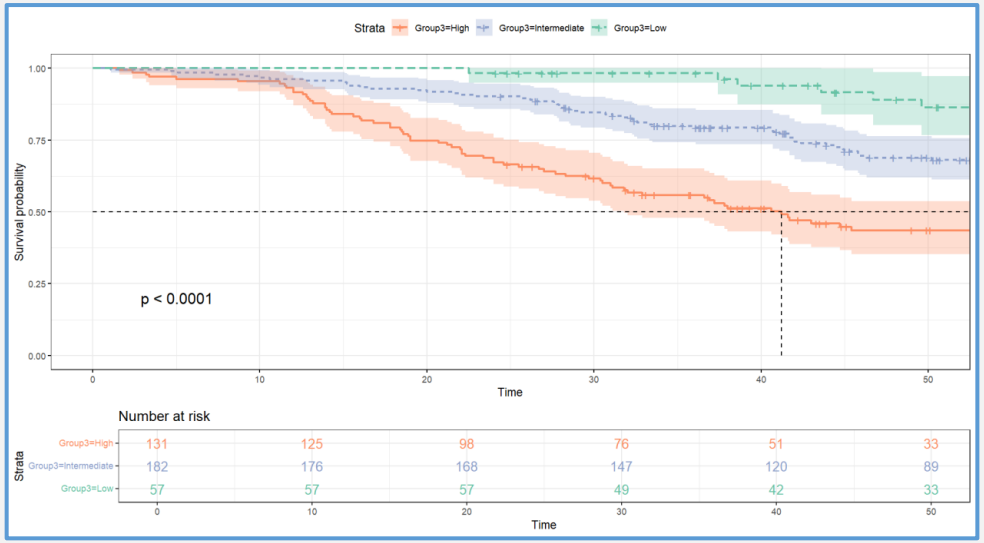
Test





(fonctions rhier et rlr)

Train

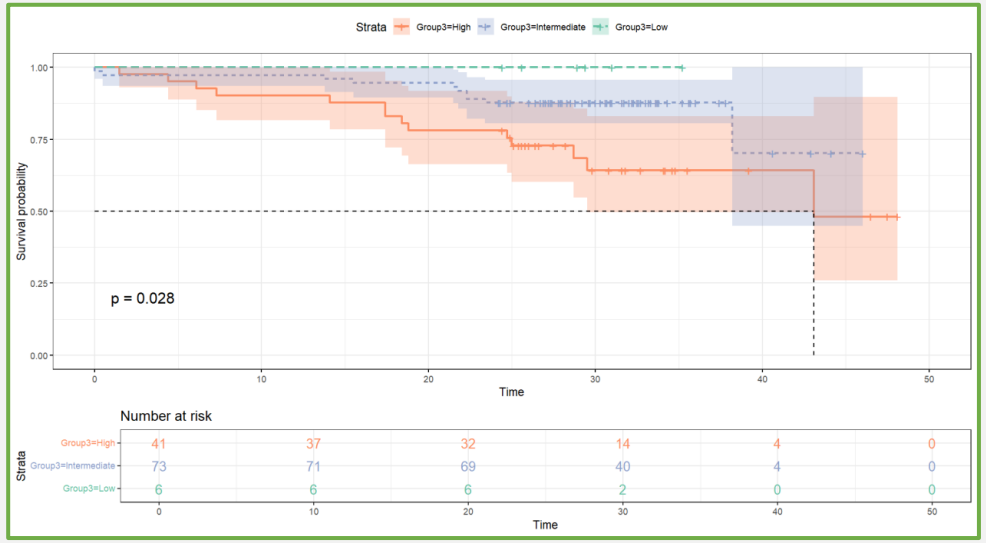


Survival	Low risk	Intermediate risk	High risk
1y - OS	100%	96%	92%
2y - OS	98%	90%	67%

Subtype	Low risk	Intermediate risk	High risk
TNBC (n=73)	0	0	73
HR+ HER2- (n=200)	0	142	58
HR+ HER2+ (n=57)	56	1	0
HER2+ (n=40)	1	39	0

- ➔ Toutes les TNBC sont **high risk**
- ➔ Les HR+HER2- sont partagées entre **intermediate** et **high risk**
- ➔ Quasi toutes les HR+ HER2+ sont **low risk**
- ➔ Quasi toutes les HER2+ sont **intermediate risk**

Test

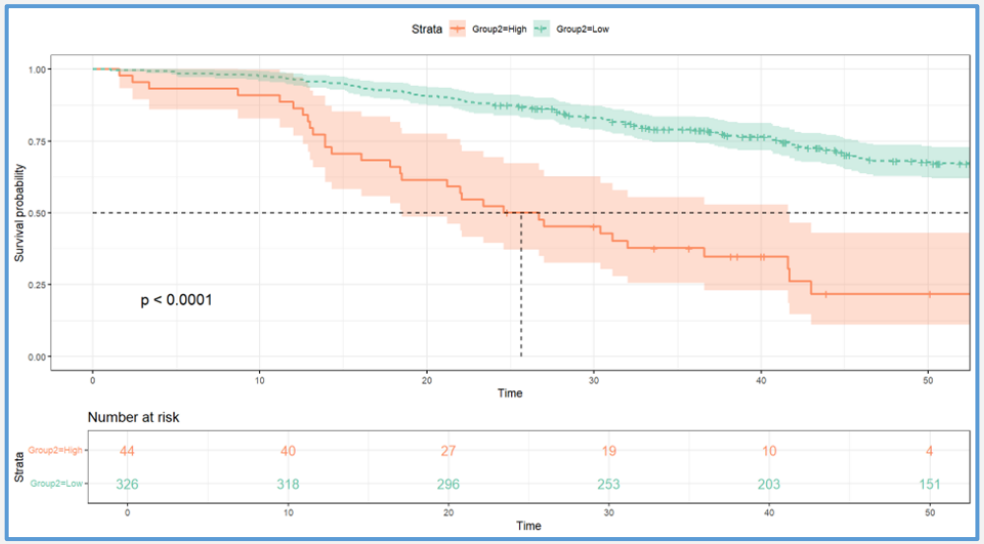


Survival	Low risk	Intermediate risk	High risk
1y - OS	100%	97%	90%
2y - OS	100%	88%	78%

Subtype	Low risk	Intermediate risk	High risk
TNBC (n=28)	0	0	28
HR+ HER2- (n=62)	0	49	13
HR+ HER2+ (n=7)	6	1	0
HER2+ (n=23)	0	23	0

- ➔ Toutes les TNBC sont **high risk**
- ➔ Les HR+HER2- sont partagées entre **intermediate** et **high risk**
- ➔ Quasi toutes les HR+ HER2+ sont **low risk**
- ➔ Toutes les HER2+ sont **intermediate risk**

Train

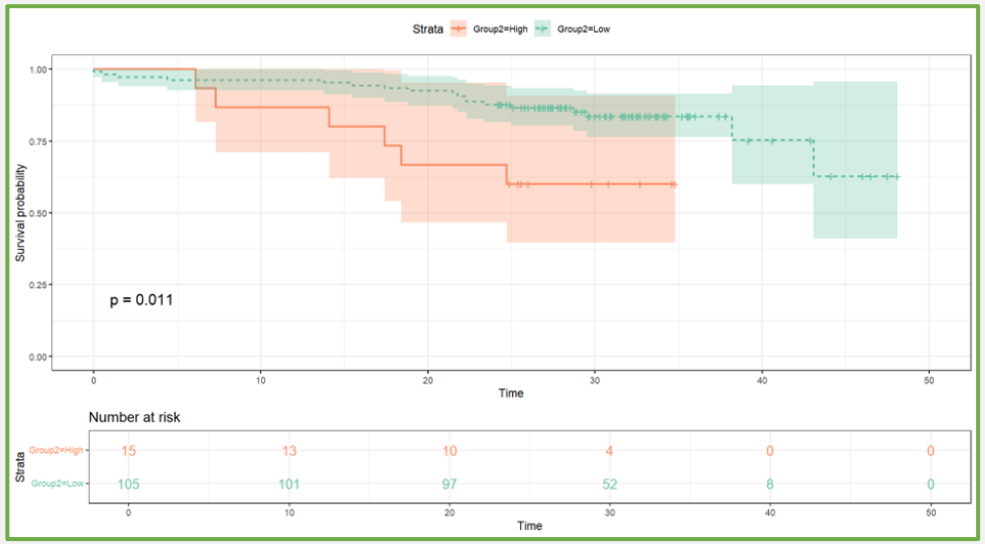


Survival	Low risk	High risk	Δ
1y - OS	96%	86%	10%
2y - OS	87%	52%	35%

Subtype	Low risk	High risk
TNBC (n=73)	29	44
HR+ HER2- (n=200)	200	0
HR+ HER2+ (n=57)	57	0
HER2+ (n=40)	40	0

➔ Tous les **high risk** sont des TNBC

Test



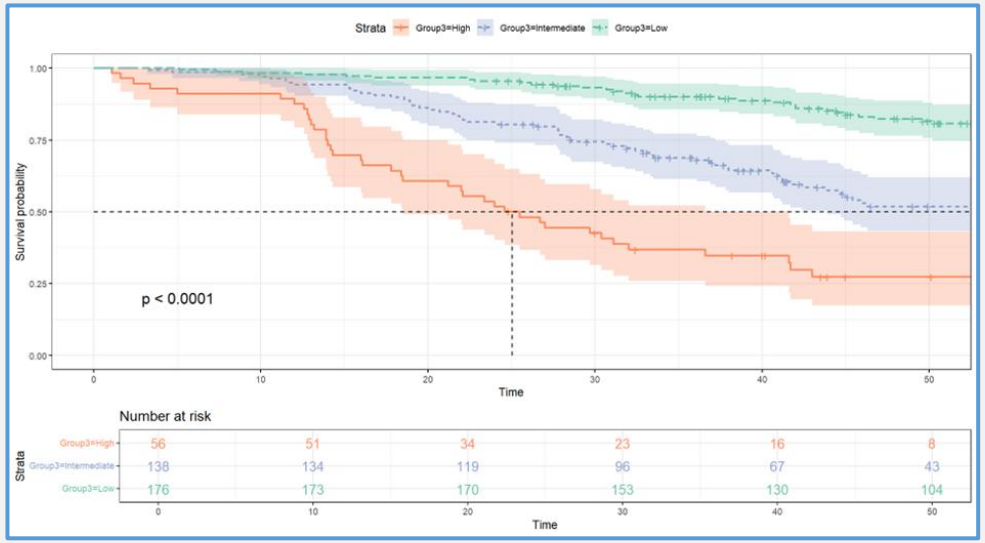
Survival	Low risk	High risk	Δ
1y - OS	96%	87%	9%
2y - OS	88%	67%	21%

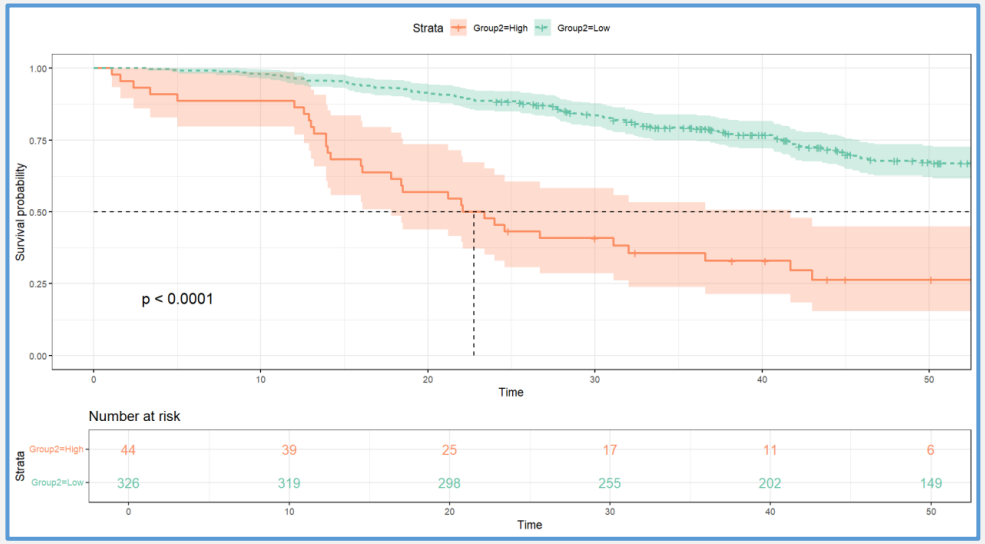
Subtype	Low risk	High risk
TNBC (n=28)	13	15
HR+ HER2- (n=62)	62	0
HR+ HER2+ (n=7)	7	0
HER2+ (n=23)	23	0

➔ Tous les **high risk** sont des TNBC

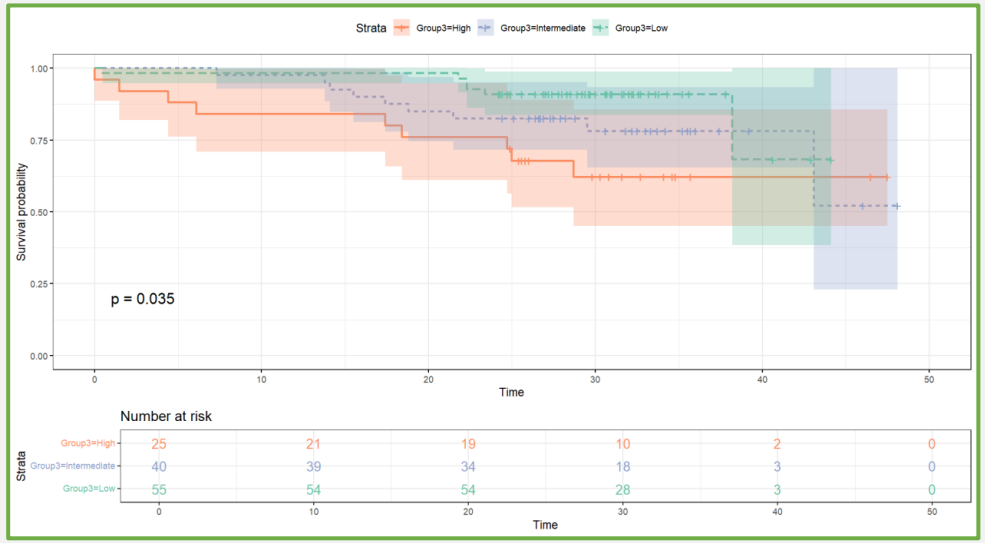
CLINICAL+RADIOMIC

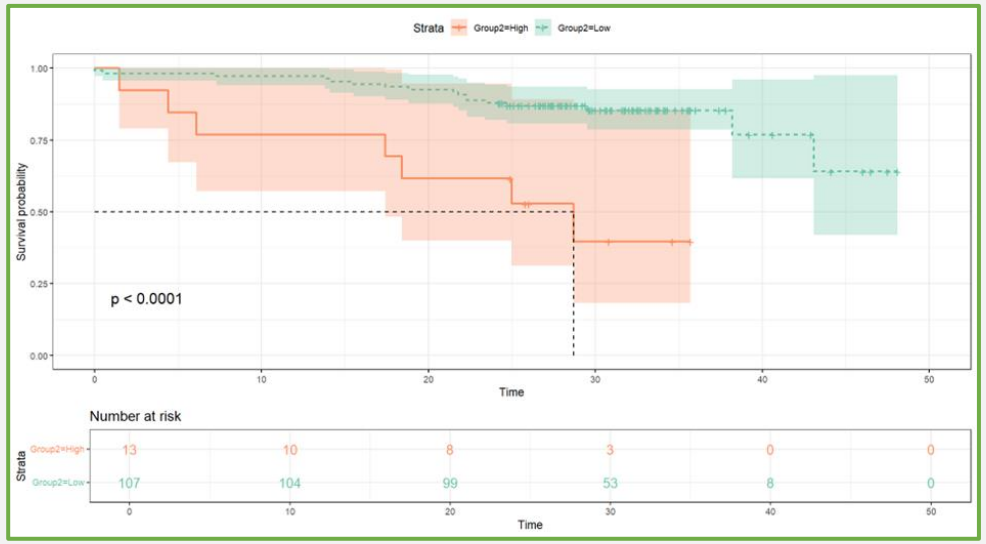
Train





Test

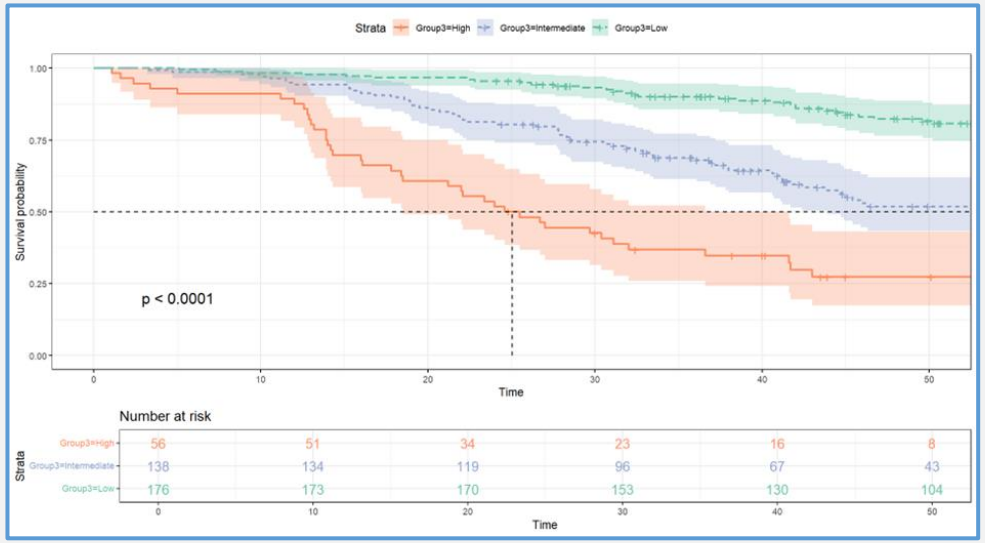




(fonctions rhier et rlr)

CLINICAL+RADIOMIC

Train

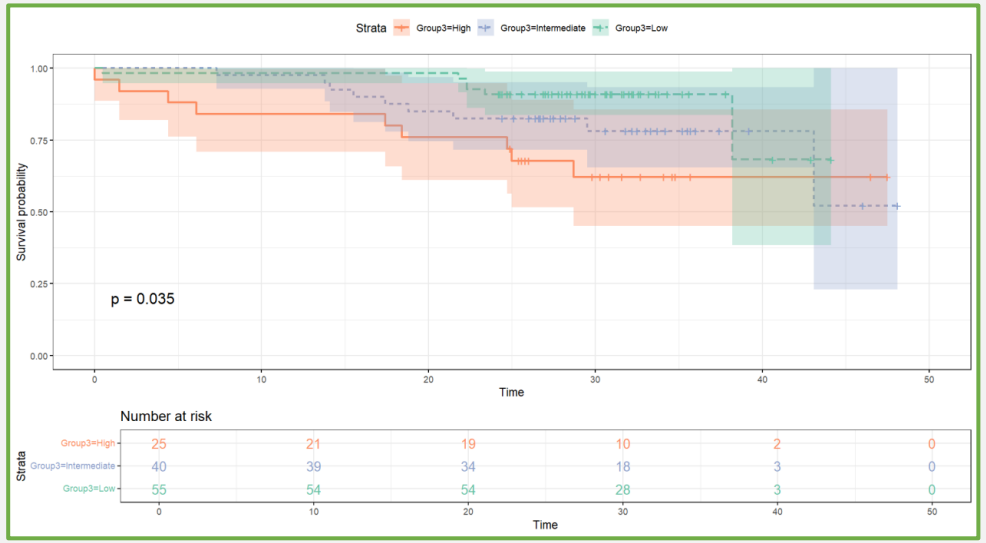


Survival	Low risk	Intermediate risk	High risk
1y - OS	98%	94%	88%
2y - OS	96%	80%	52%

Subtype	Low risk	Intermediate risk	High risk
TNBC (n=73)	0	27	46
HR+ HER2- (n=200)	87	104	9
HR+ HER2+ (n=57)	57	0	0
HER2+ (n=40)	32	7	1

- ➔ Toutes le TNBC ne sont PAS **high risk** (≠clinical)
- ➔ On identifie une HER2+ **high risk** (≠clinical)
- ➔ Les HR+HER2- sont partagées entre dans les **3 groupes de risque** (≠clinical)
- ➔ Toutes les HER2+ ne sont pas **intermediate risk** (≠clinical)

Test



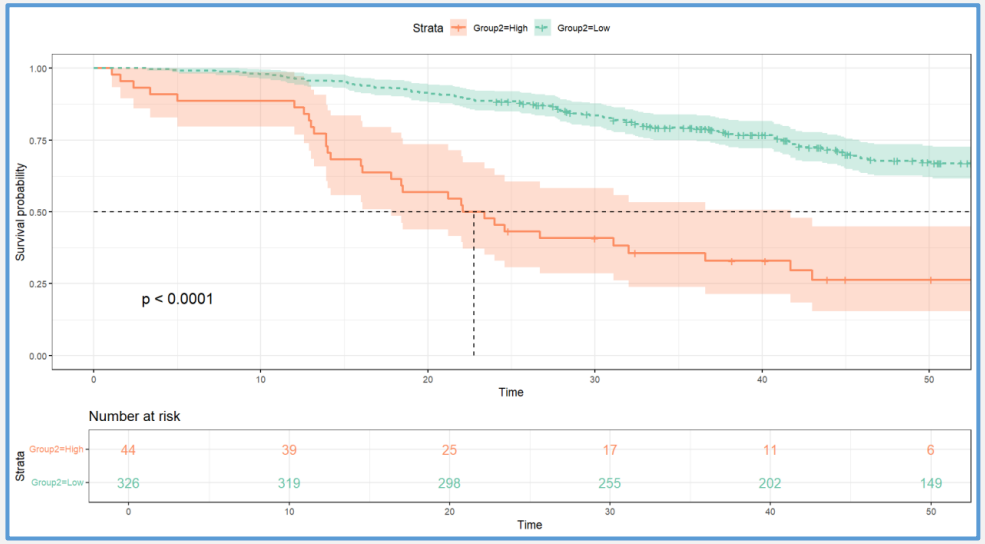
Survival	Low risk	Intermediate risk	High risk
1y - OS	98%	98%	84%
2y - OS	91%	83%	76%

Subtype	Low risk	Intermediate risk	High risk
TNBC (n=28)	0	10	18
HR+ HER2- (n=62)	28	27	7
HR+ HER2+ (n=7)	7	0	0
HER2+ (n=23)	20	3	0

- ➔ Toutes les TNBC ne sont PAS **high risk** (≠clinical)
- ➔ Les HR+HER2- sont partagées entre dans les **3 groupes de risque** (≠clinical)
- ➔ Toutes les HER2+ ne sont pas **intermediate risk** (≠clinical)

CLINICAL+RADIOMIC

Train

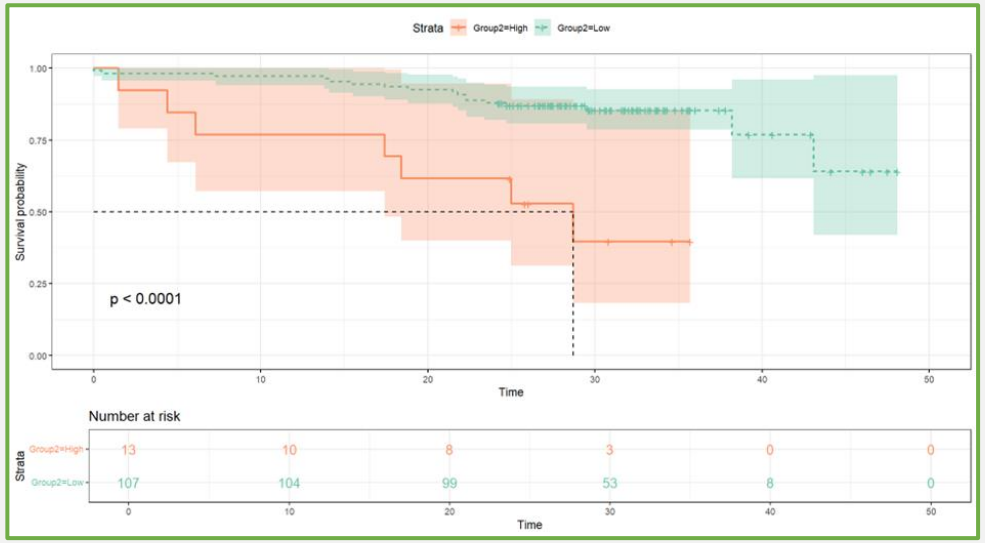


Survival	Low risk	High risk	Δ
1y - OS	96%	86%	10%
2y - OS	88%	46%	42%

Subtype	Low risk	High risk
TNBC (n=73)	37	36
HR+ HER2- (n=200)	193	7
HR+ HER2+ (n=57)	57	0
HER2+ (n=40)	39	1

➔ Tous les **high risk** ne sont PAS des TNBC (≠clinical)

Test



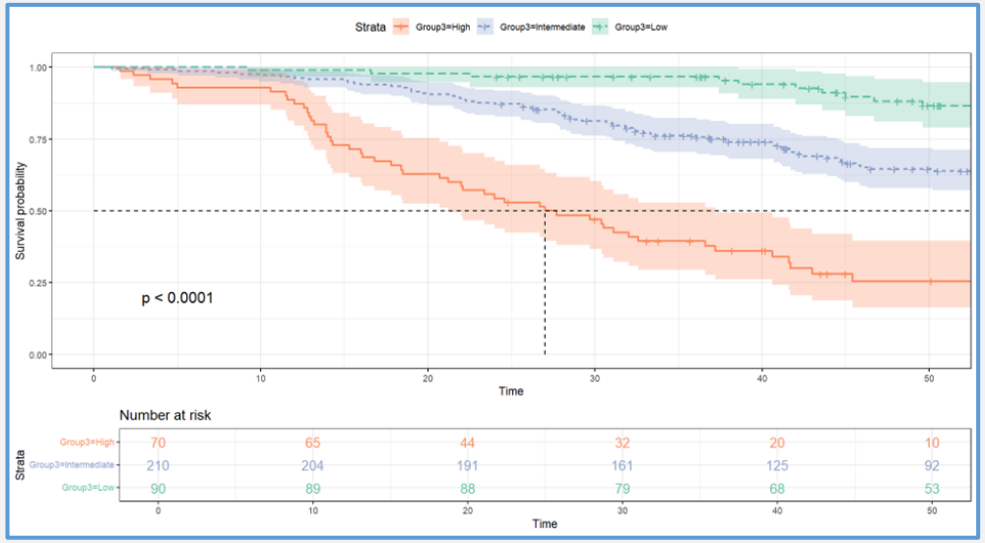
Survival	Low risk	High risk	Δ
1y - OS	97%	77%	20%
2y - OS	88%	62%	26%

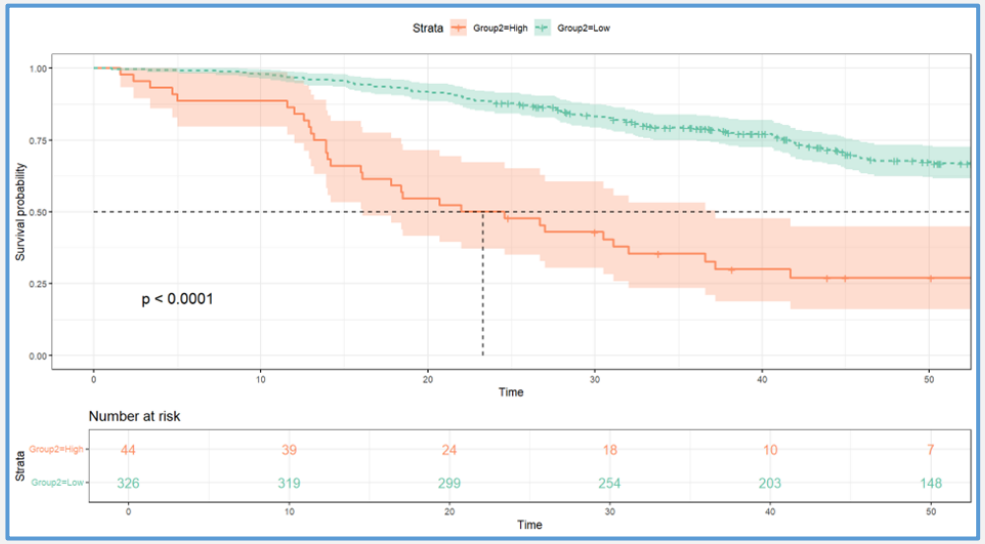
Subtype	Low risk	High risk
TNBC (n=28)	18	10
HR+ HER2- (n=62)	59	3
HR+ HER2+ (n=7)	7	0
HER2+ (n=23)	23	0

➔ Tous les **high risk** ne sont PAS des TNBC (≠clinical)

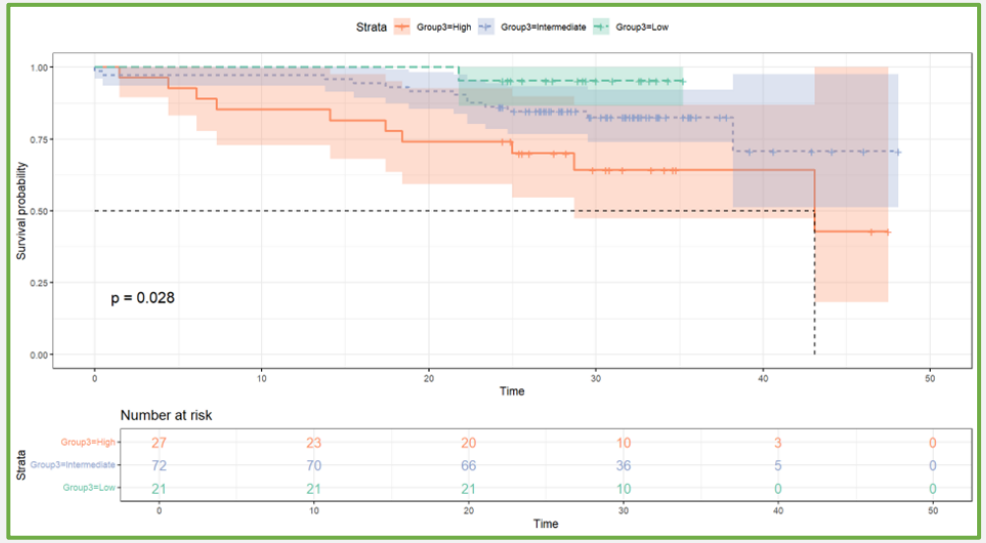
CLINICAL+RADIOMIC+BCi

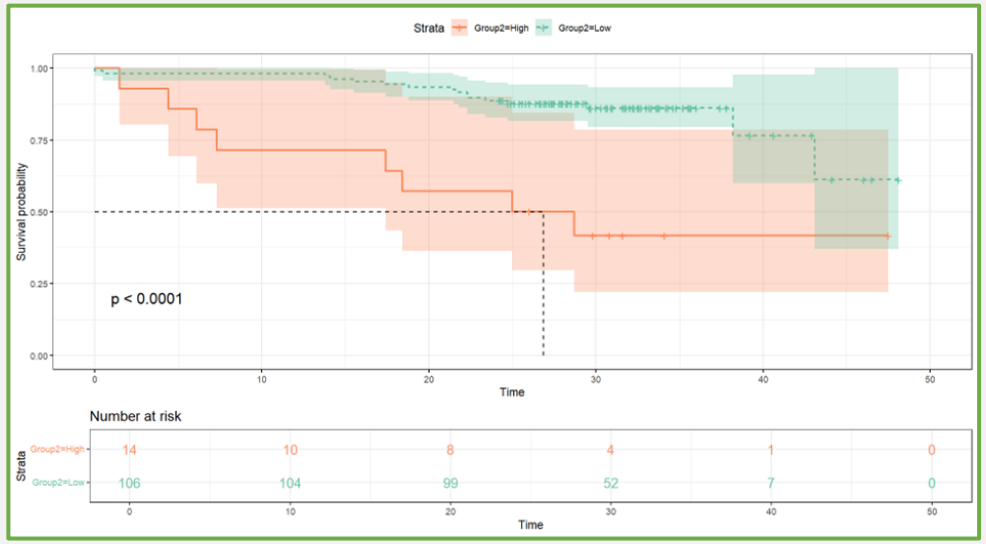
Train





Test

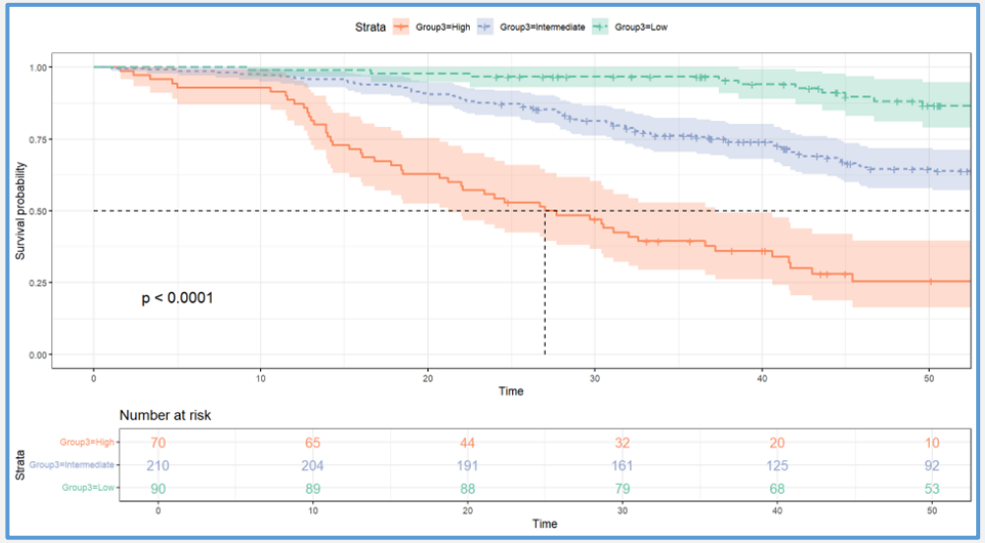




(fonctions rhier et rlr)

CLINICAL+RADIOMIC+BCi

Train

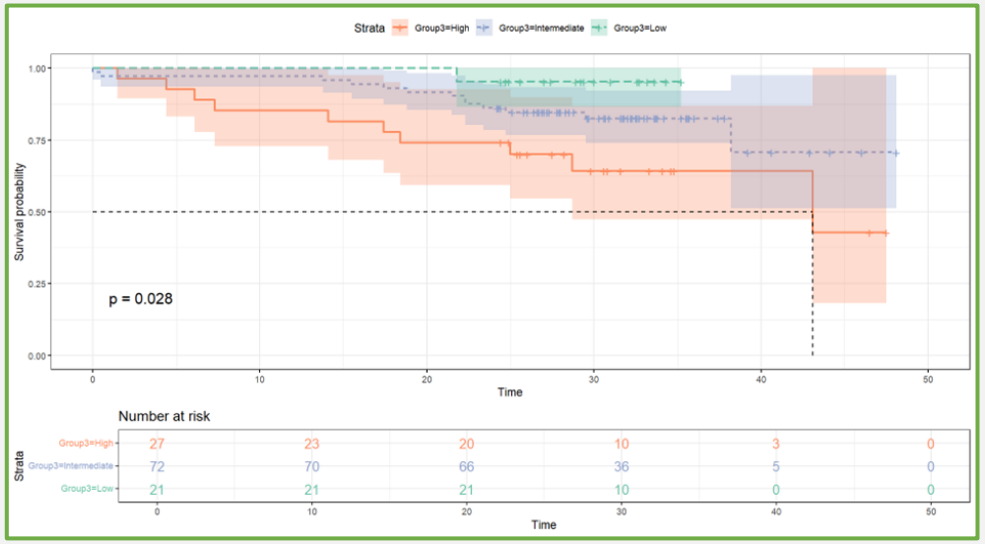


Survival	Low risk	Intermediate risk	High risk
1y - OS	99%	96%	87%
2y - OS	97%	87%	54%

Subtype	Low risk	Intermediate risk	High risk
TNBC (n=73)	0	22	51
HR+ HER2- (n=200)	20	163	17
HR+ HER2+ (n=57)	57	0	0
HER2+ (n=40)	13	25	2

- ➔ Toutes le TNBC ne sont PAS **high risk** (≠clinical)
- ➔ On identifie deux HER2+ **high risk** (≠clinical)
- ➔ Les HR+HER2- sont partagées entre dans les **3 groupes de risque** (≠clinical)
- ➔ Toutes les HER2+ ne sont pas **intermediate risk** (≠clinical)

Test



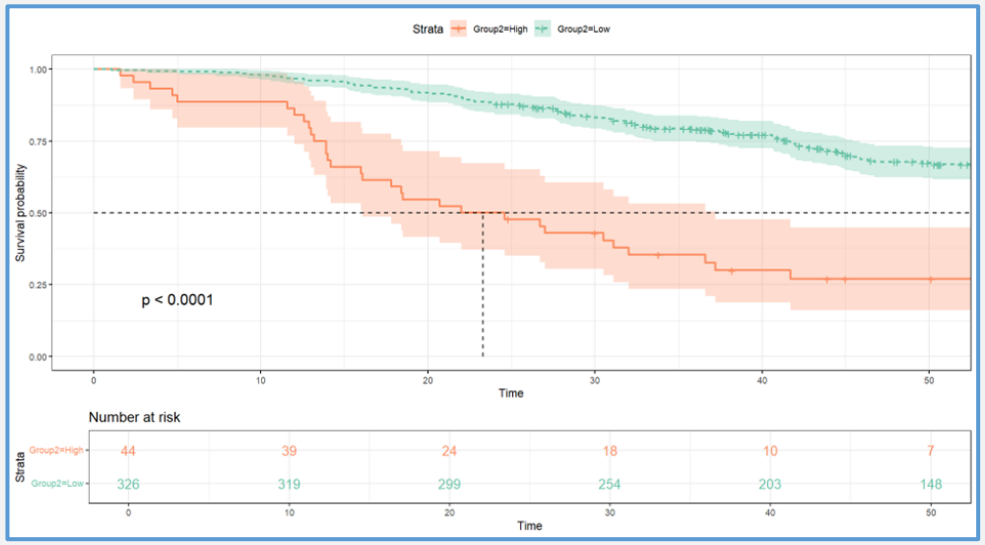
Survival	Low risk	Intermediate risk	High risk
1y - OS	100%	97%	85%
2y - OS	95%	86%	74%

Subtype	Low risk	Intermediate risk	High risk
TNBC (n=28)	0	7	21
HR+ HER2- (n=62)	6	50	6
HR+ HER2+ (n=7)	7	0	0
HER2+ (n=23)	8	15	0

- ➔ Toutes les TNBC ne sont PAS **high risk** (≠clinical)
- ➔ Les HR+HER2- sont partagées entre dans les **3 groupes de risque** (≠clinical)
- ➔ Toutes les HER2+ ne sont pas **intermediate risk** (≠clinical)

CLINICAL+RADIOMIC+BCi

Train



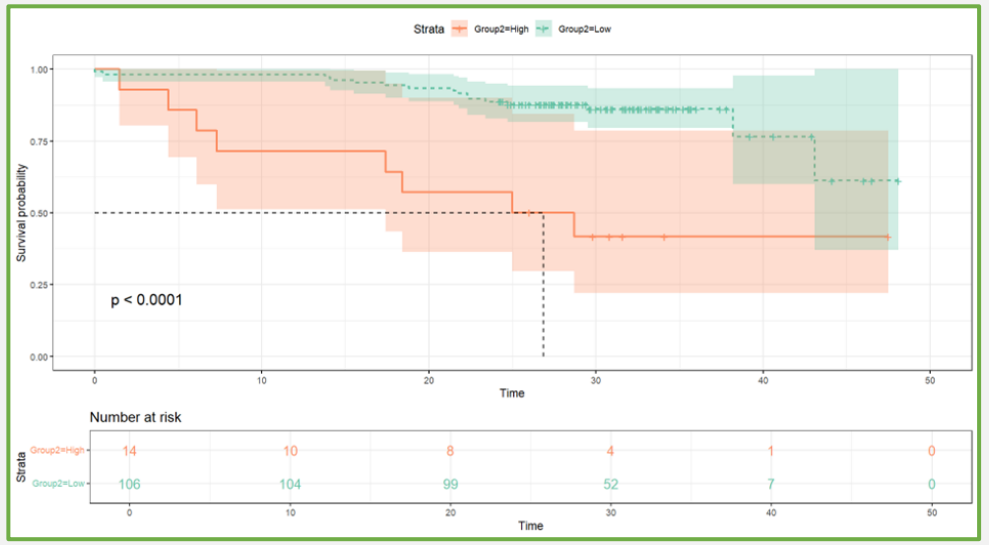
Survival	Low risk	High risk	Δ
1y - OS	94%	84%	10%
2y - OS	84%	50%	34%

Subtype	Low risk	High risk
TNBC (n=73)	41	32
HR+ HER2- (n=200)	188	12
HR+ HER2+ (n=57)	57	0
HER2+ (n=40)	40	0

➔ Toutes les **high risk** ne sont PAS <u>que</u> des TNBC (≠clinical)

➔ Toutes les patients HER2+ sont low risk (≠clin+radiomic)

Test



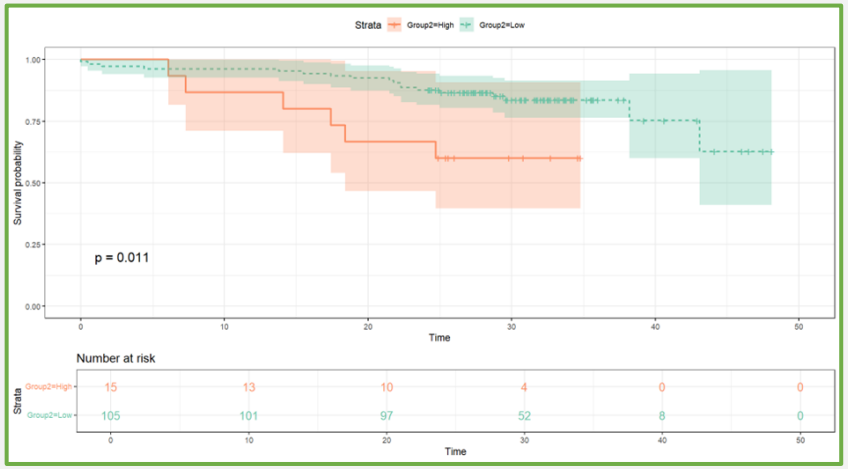
Survival	Low risk	High risk	Δ
1y - OS	98%	71%	27%
2y - OS	89%	57%	32%

Subtype	Low risk	High risk
TNBC (n=28)	16	12
HR+ HER2- (n=62)	60	2
HR+ HER2+ (n=7)	7	0
HER2+ (n=23)	23	0

-> Toutes les **high risk** ne sont PAS <u>que</u> des TNBC (≠clinical)

TEST (n=120)

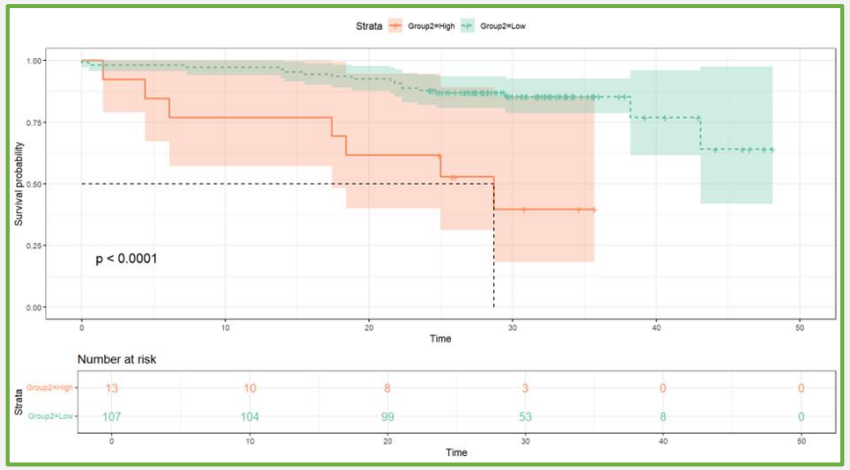
CLINICAL



Survival	Low risk	High risk	Δ
1y - OS	96%	87%	9%
2y - OS	88%	67%	21%

Subtype	Low risk	High risk
TNBC (n=28)	13	15
HR+ HER2- (n=62)	62	0
HR+ HER2+ (n=7)	7	0
HER2+ (n=23)	23	0

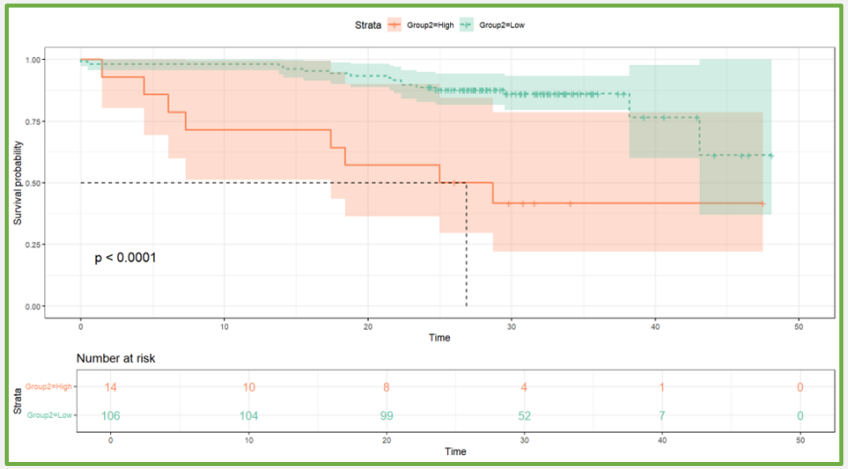
CLINICAL+RADIOMIC



Survival	Low risk	High risk	Δ
1y - OS	97%	77%	20%
2y - OS	88%	62%	26%

Subtype	Low risk	High risk
TNBC (n=28)	18	10
HR+ HER2- (n=62)	59	3
HR+ HER2+ (n=7)	7	0
HER2+ (n=23)	23	0

CLINICAL+RADIOMIC+BCi

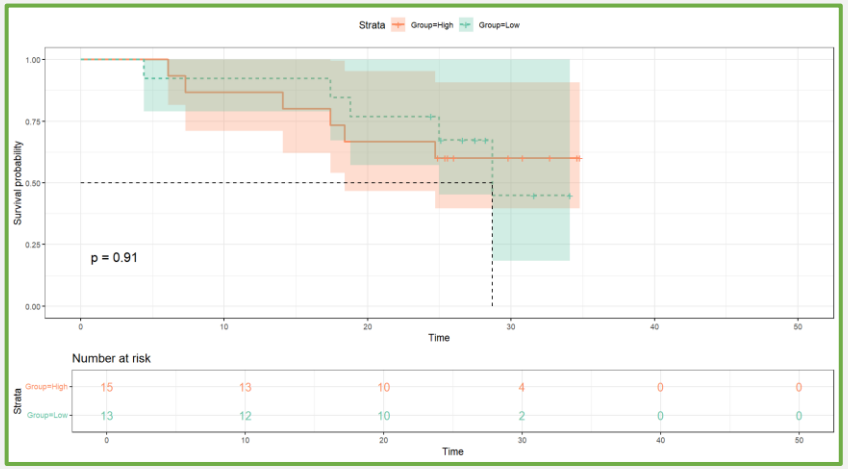


Survival	Low risk	High risk	Δ
1y - OS	**98%**	**71%**	**27%**
2y - OS	**89%**	**57%**	**32%**

Subtype	Low risk	High risk
TNBC (n=28)	16	12
HR+ HER2- (n=62)	60	2
HR+ HER2+ (n=7)	7	0
HER2+ (n=23)	23	0

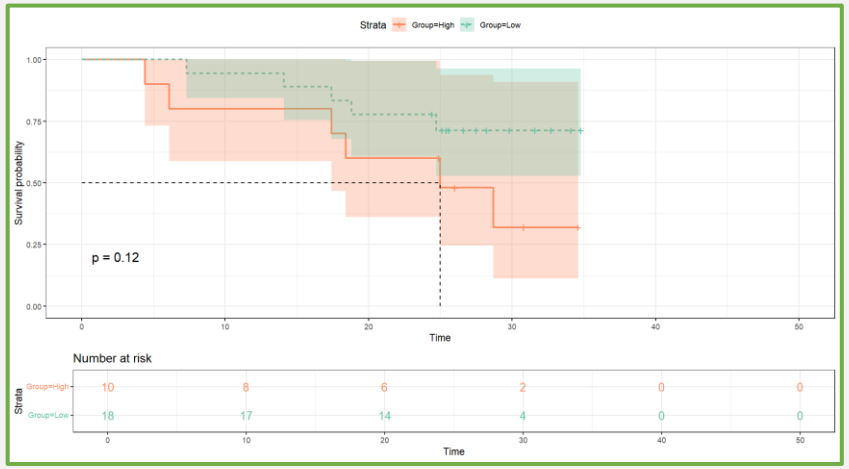
TEST_TNBC (n=28)

CLINICAL



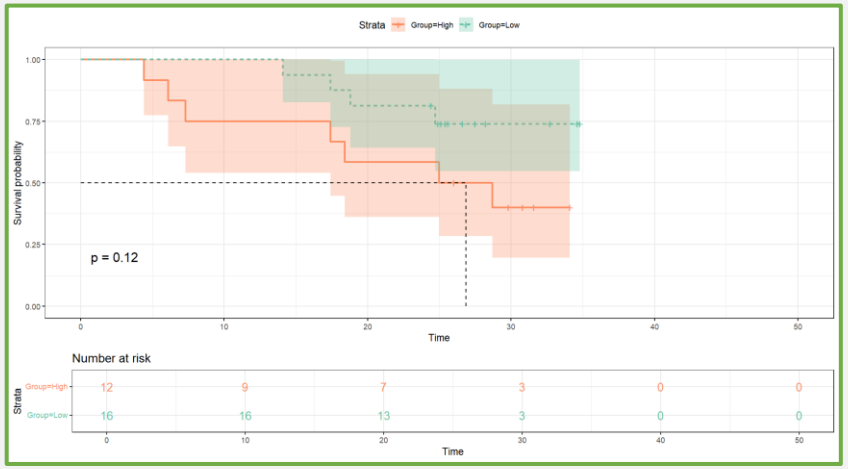
Survival	Low risk	High risk	Δ
1y - OS	92%	87%	5%
2y - OS	77%	67%	10%

CLINICAL+RADIOMIC



Survival	Low risk	High risk	Δ
1y - OS	94%	80%	14%
2y - OS	78%	60%	18%

CLINICAL+RADIOMIC+BCi

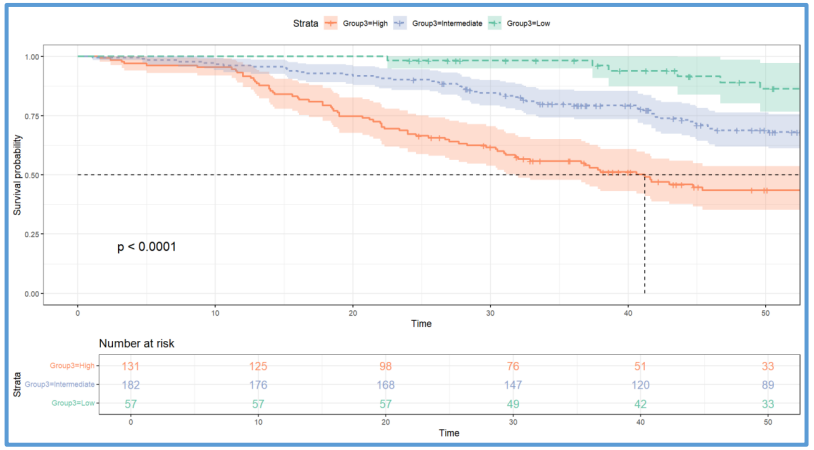


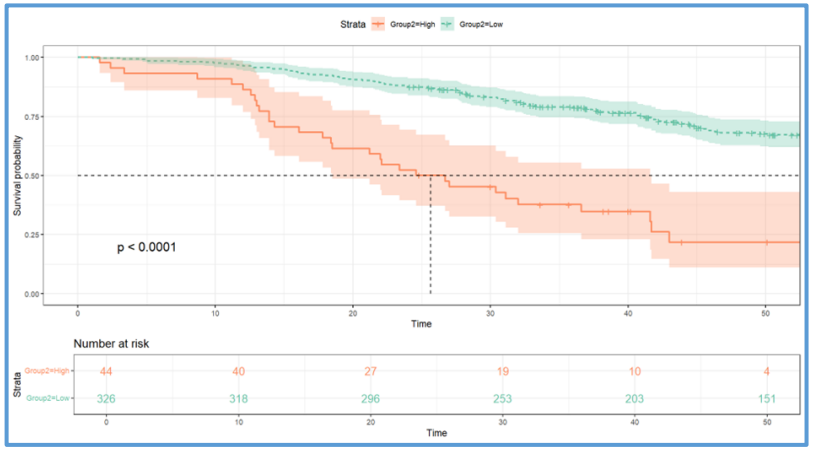
Survival	Low risk	High risk	Δ
1y - OS	100%	75%	**25%**
2y - OS	81%	58%	**23%**

4. Conclusions

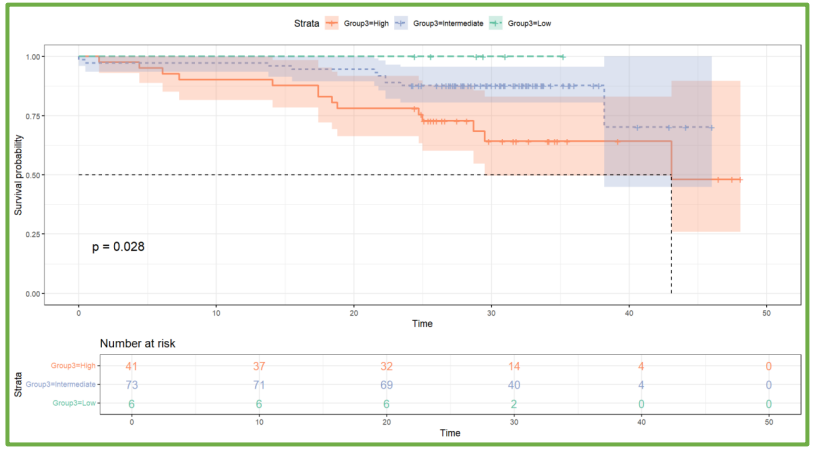
✓ Le modèle clinique est capable d'identifier plusieurs groupes de risque à partir de l'âge, le statut HER2 et l'expression des récepteurs hormonaux.

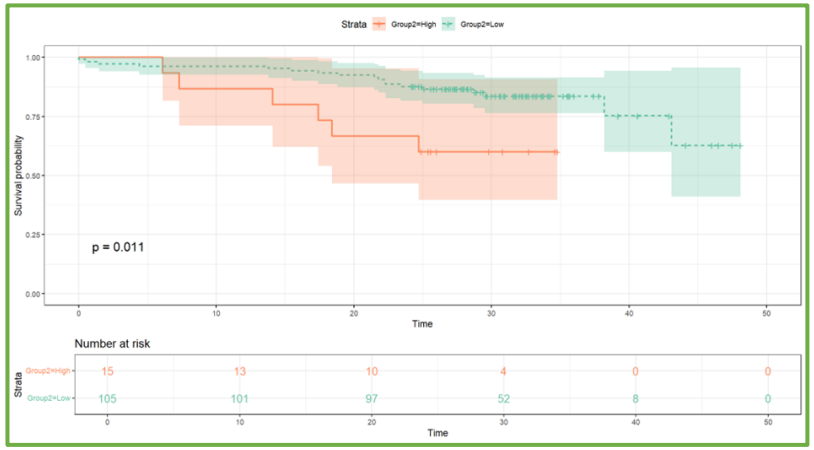
Train





Test

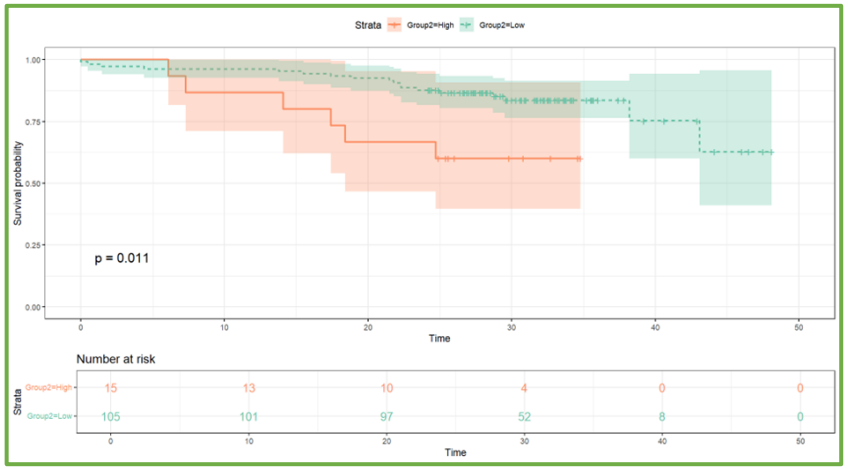




4. Conclusions

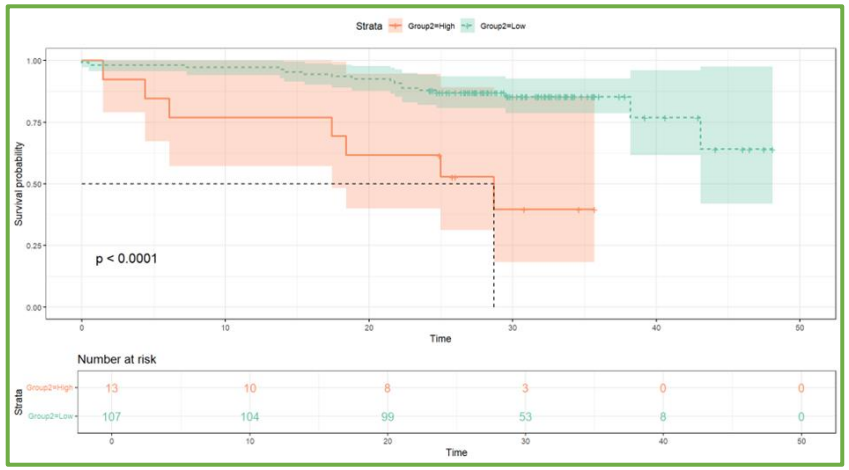
✓ L'ajout des informations **radiomiques** et **organomiques** a permis d'obtenir une meilleure stratification des patientes TNBC en identifiant des patientes de bons et mauvais pronostics.

CLINICAL



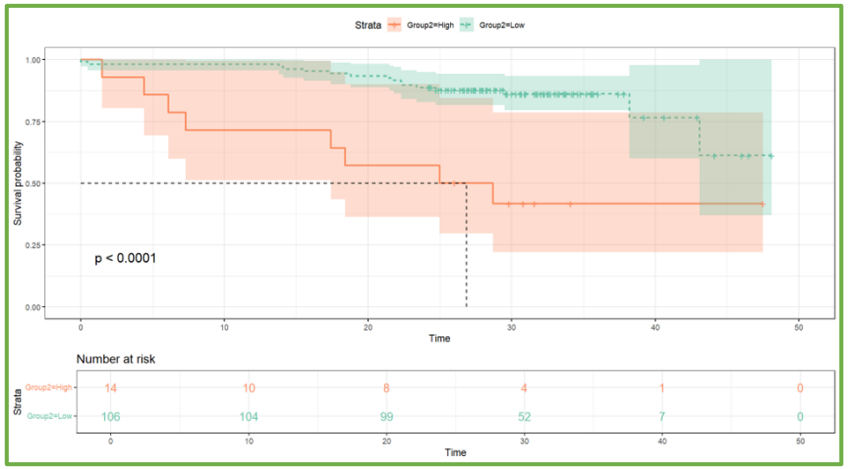
Subtype	Low risk	High risk
TNBC (n=28)	**13**	**15**
HR+ HER2- (n=62)	**62**	0
HR+ HER2+ (n=7)	7	0
HER2+ (n=23)	23	0

CLINICAL+RADIOMIC



Subtype	Low risk	High risk
TNBC (n=28)	**18**	**10**
HR+ HER2- (n=62)	**59**	**3**
HR+ HER2+ (n=7)	7	0
HER2+ (n=23)	23	0

CLINICAL+RADIOMIC+BCi



Subtype	Low risk	High risk
TNBC (n=28)	**16**	**12**
HR+ HER2- (n=62)	**60**	**2**
HR+ HER2+ (n=7)	7	0
HER2+ (n=23)	23	0

5. Perspectives

- ✓ Ajouter des nouvelles patientes dans la base **Test**
- ✓ Essayer de s'affranchir de l'effet « sous-type » en :
  - Créant un modèle **sans les variables histologiques** HR et HER2
  - Créant un modèle **TMTV & Dmax** pour chaque sous-type afin d'identifier et regrouper les patientes **mauvais**/**bon** pronostic quelque soit le sous-type
- ✓ Développer un modèle de classification pronostique à 24 mois
- ✓ Développer un modèle capable de stratifier les patientes HR+_HER2- en 3 groupes de risque en fonction de l'OS
- ✓ …