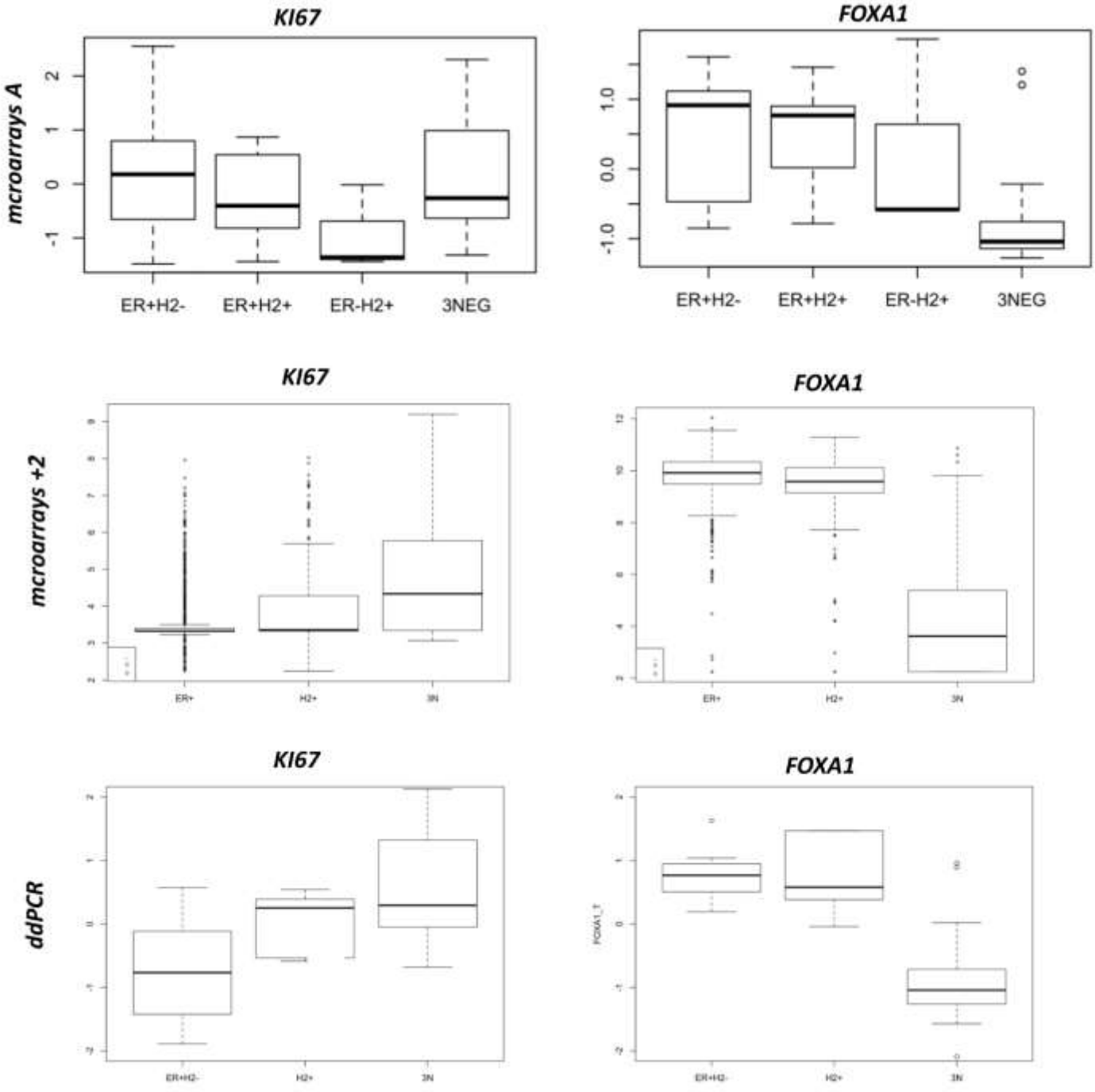
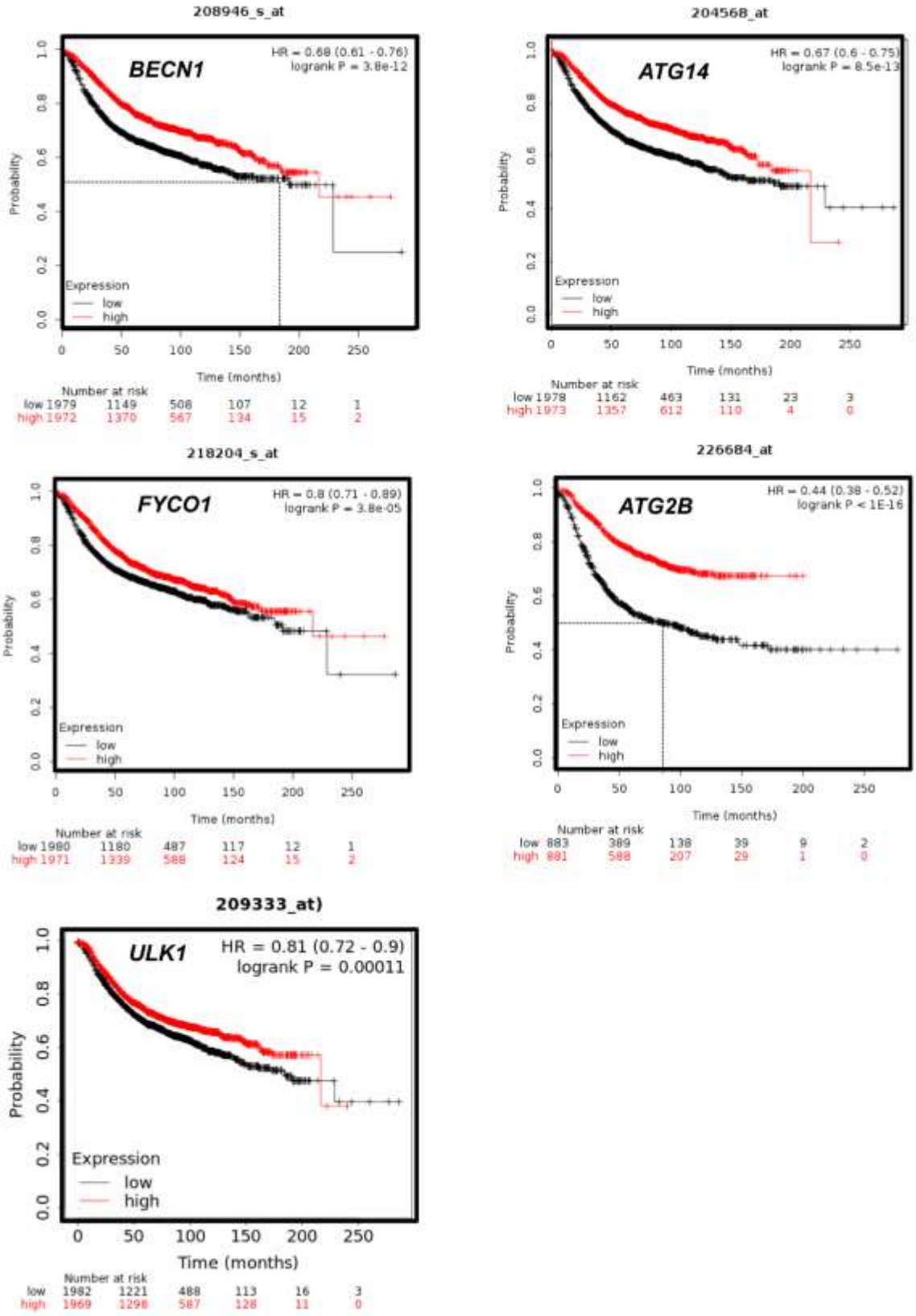
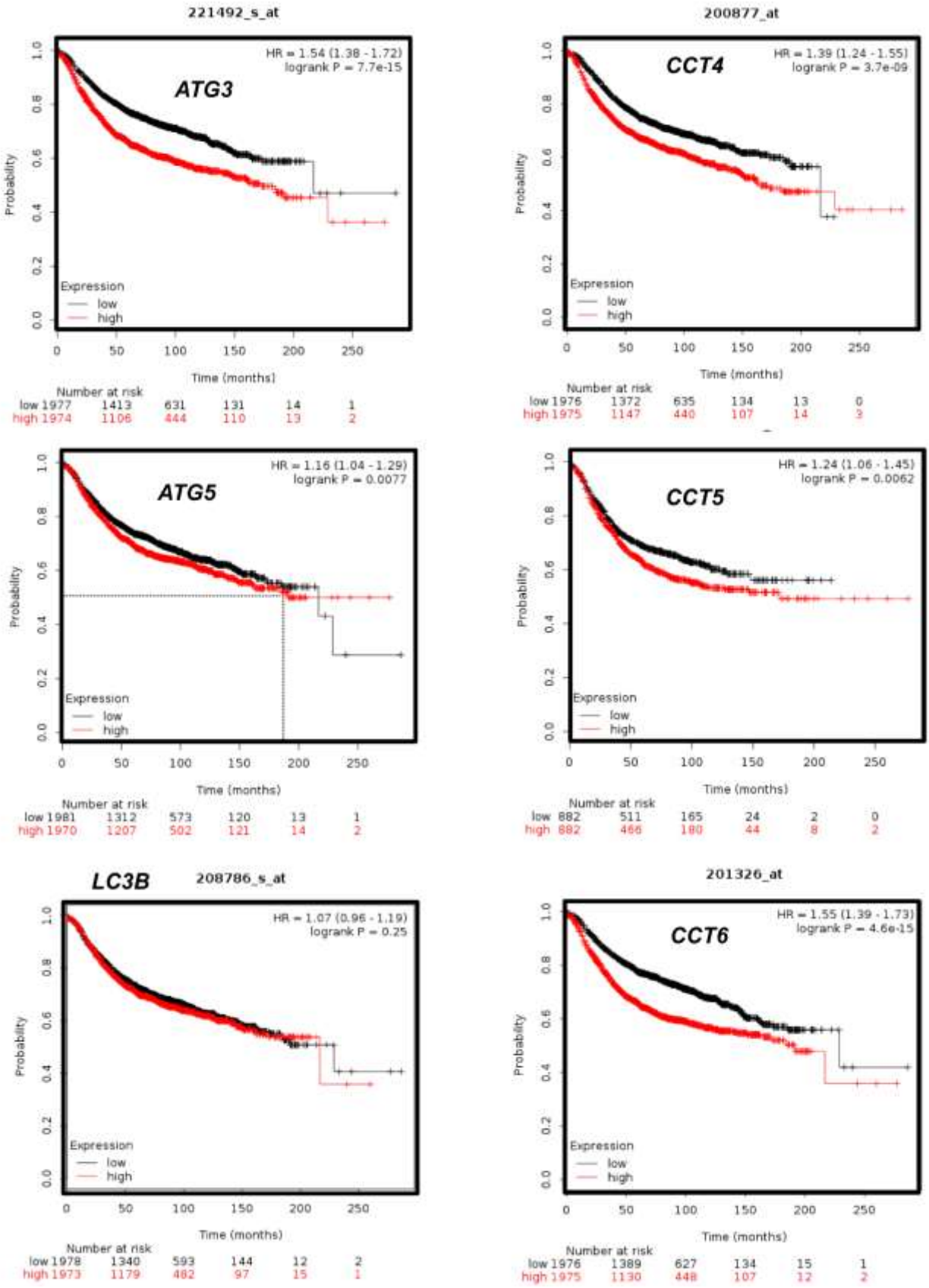
Autophagy is associated with a robust specific transcriptional signature in breast cancer subtypes – Grandvallet et al



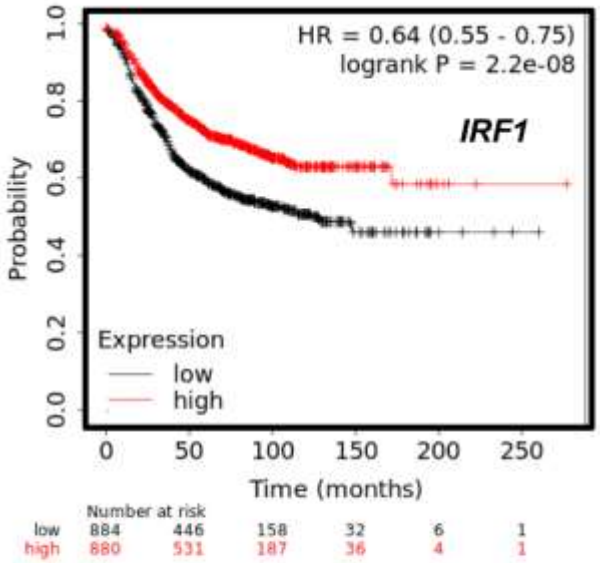
Supplementary Figure 1: Confirmation of BC subgroups classification using ddPCR. ***KI67*** **and** ***FOXA1*** **expressions were quantified using HG-U133 plus2, microarrays "A" or ddPCR.**

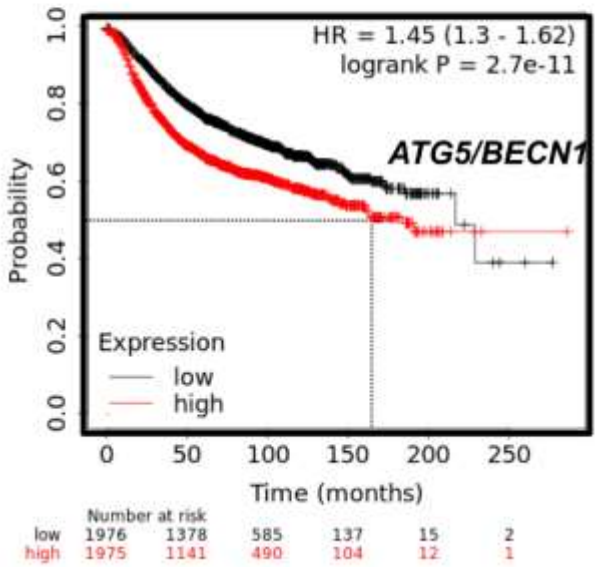


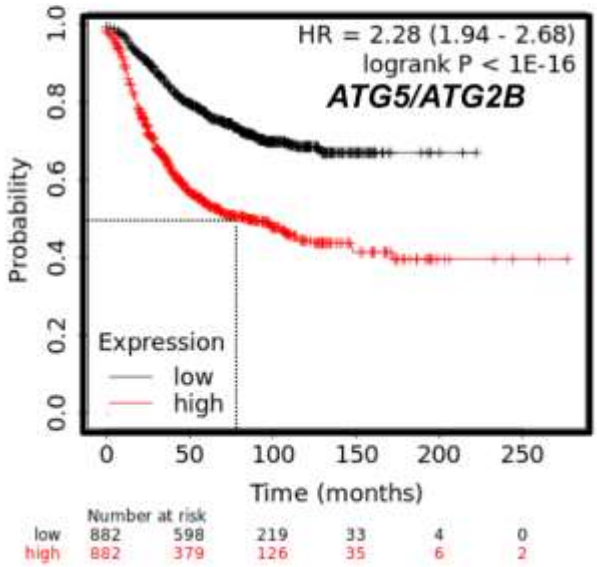
Supplementary Figure 2: A high expression of *ATG2B, BECN1, ATG14* or *FYCO1* is associated with a good prognosis. Kaplan Meier data analysis confirmed a significant better prognosis for BC patients presenting a high expression of *ATG2B, BECN1*, *ATG14* or *FYCO1*.



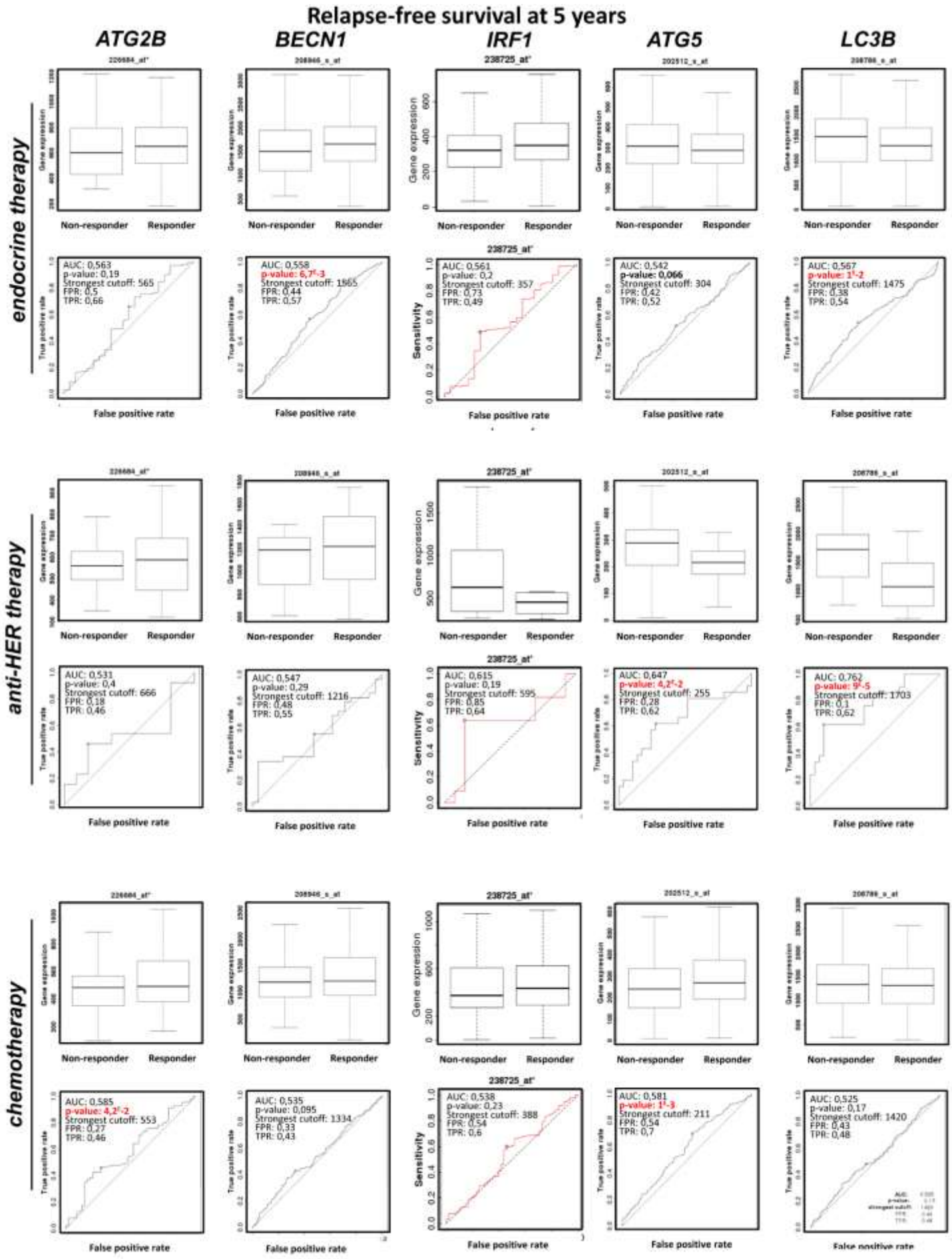
Supplementary Figure 3: A high expression of *ATG5, ATG3, LC3B, CCT4, CCT5* or *CCT6* is associated with a poor prognosis. Kaplan Meier data analysis confirmed a significant worst prognosis for BC patients presenting a high expression of *ATG5*, *ATG3*, *CCT4*, *CCT5* or *CCT6*.



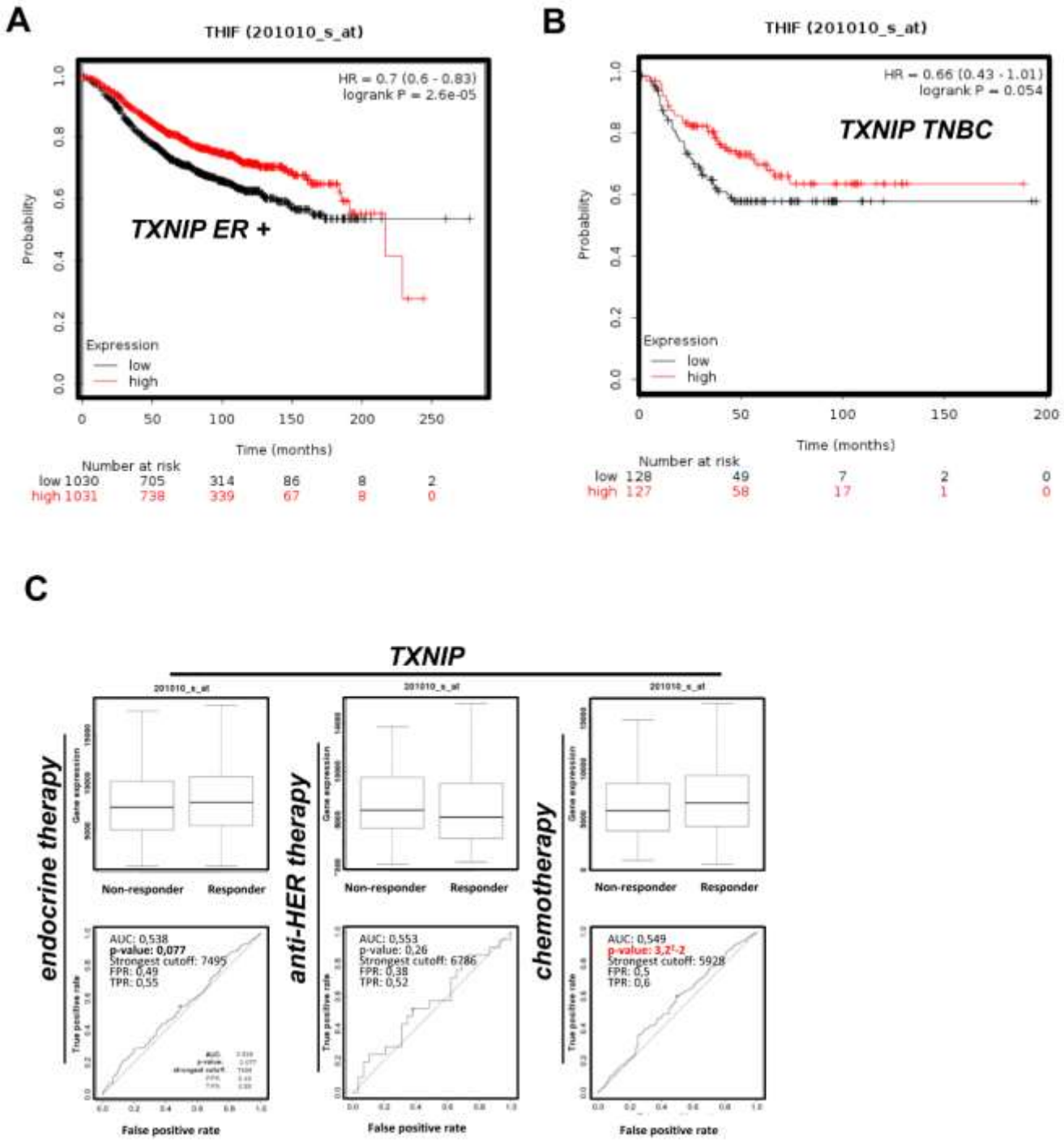




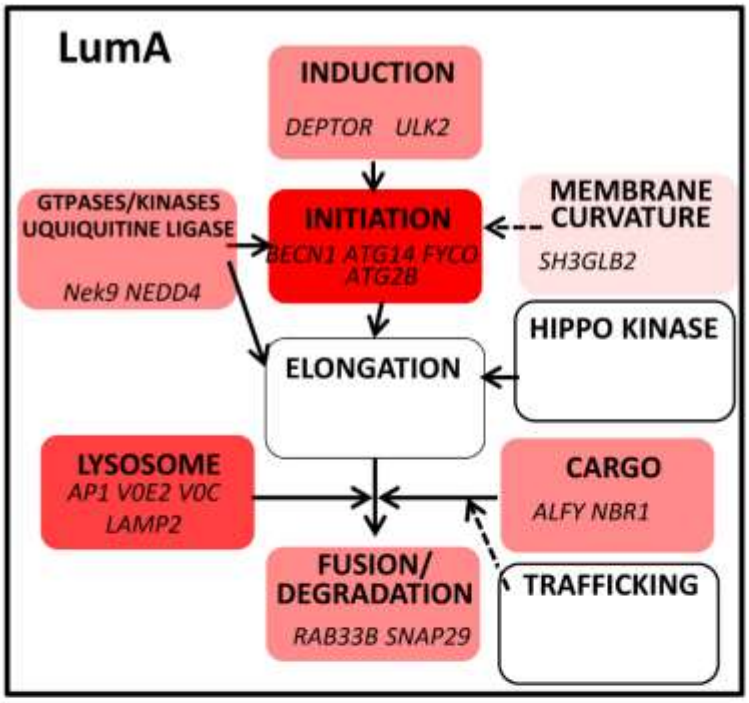
Supplementary Figure 4: A high *ATG5/BECN1* and *ATG5/ATG2B* expression ratio is associated with a poor prognosis.


Relapse-free survival at 5 years
ATG2B
BECN1
IRF1
ATG5
LC3B
endocrine therapy
anti-HER therapy
chemotherapy
Non-responder
Responder
Gene expression
Sensitivity
False positive rate
AUC: 0,563
p-value: 0,19
Strongest cutoff: 565
FPR: 0,5
TPR: 0,66
AUC: 0,558
p-value: 6,7E-3
Strongest cutoff: 1865
FPR: 0,44
TPR: 0,57
AUC: 0,561
p-value: 0,2
Strongest cutoff: 357
FPR: 0,73
TPR: 0,49
AUC: 0,542
p-value: 0,066
Strongest cutoff: 304
FPR: 0,42
TPR: 0,52
AUC: 0,567
p-value: 1E-2
Strongest cutoff: 1475
FPR: 0,38
TPR: 0,54
AUC: 0,531
p-value: 0,4
Strongest cutoff: 666
FPR: 0,18
TPR: 0,46
AUC: 0,547
p-value: 0,29
Strongest cutoff: 1216
FPR: 0,48
TPR: 0,55
AUC: 0,615
p-value: 0,19
Strongest cutoff: 595
FPR: 0,85
TPR: 0,64
AUC: 0,647
p-value: 4,2E-2
Strongest cutoff: 255
FPR: 0,28
TPR: 0,62
AUC: 0,762
p-value: 9E-5
Strongest cutoff: 1703
FPR: 0,1
TPR: 0,62
AUC: 0,585
p-value: 4,2E-2
Strongest cutoff: 553
FPR: 0,27
TPR: 0,46
AUC: 0,535
p-value: 0,095
Strongest cutoff: 1334
FPR: 0,33
TPR: 0,43
AUC: 0,538
p-value: 0,23
Strongest cutoff: 388
FPR: 0,54
TPR: 0,6
AUC: 0,581
p-value: 1E-3
Strongest cutoff: 211
FPR: 0,54
TPR: 0,7
AUC: 0,525
p-value: 0,17
Strongest cutoff: 1420
FPR: 0,43
TPR: 0,48

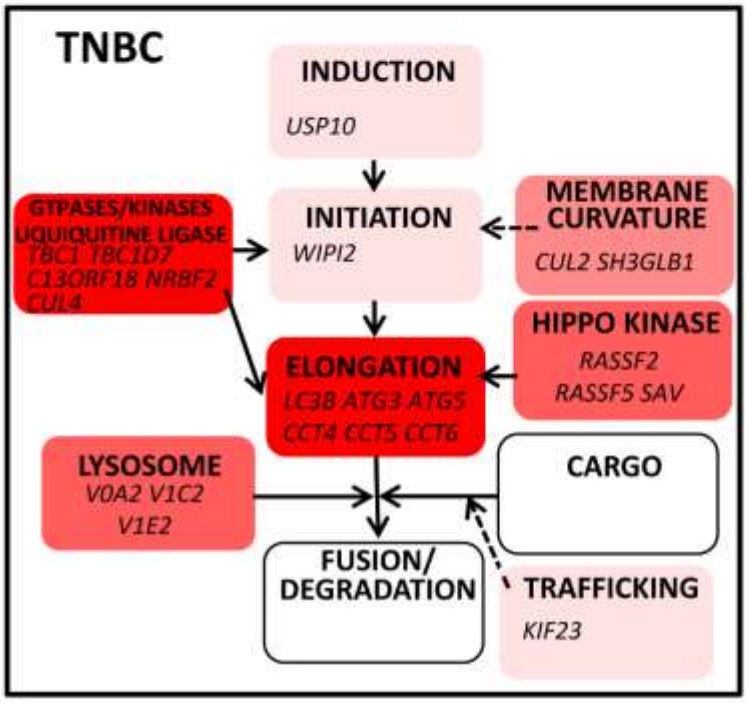
Supplementary Figure 5: The expression of *ATG2B, BECN1, ATG5, LC3B* and *ATG3* can be used to establish the prognosis of relapse-free survival at 5 years following anti-cancer therapies. ROC Plotter database showed: *i)* the association of a high expression of *BECN1* with a higher response to endocrine therapy; *ii)* an inverse correlation between a high expression of *ATG5* to response to endocrine therapy and to anti-HER therapy and a correlation to response to chemotherapy; *iii)* an inverse correlation between the expression of *LC3B* to endocrine and anti-HER therapy responses.



Supplementary Figure 6: The expression of *TXNIP1* is a marker of good prognosis in BC patients, independently of BC subgroups. A: ER patients presented a higher *TXNIP* expression compared to TNBC patients. **B-C**: Kaplan Meier data analysis demonstrated that a high *TXNIP* expression remained associated with a good prognosis in both ER+ patients and TNBC patients. **D**: ROC Plotter database showed that the *TXNIP* expression was associated with a good response to any chemotherapy.



Chi-square 17,54; 9
P=0,04



Supplementary Figure 7: The genes involved in the different steps of autophagy are differentially expressed between LumA and TNBC. The 50 genes with the highest differential expression presented in the heatmap of Figure 1 were classified according to the different autophagy steps, meaning induction, GTPases/kinases/ ubiquitine ligase, initiation, membrane curvature, hippo kinase, elongation, lysosome, cargo, fusion/degradation and trafficking, for LumA **A**. or TNBC **B**. patients. Colors (from white = 0 gene in the category to brilliant red ≥ 4 genes in the category) indicates the proportions of genes mostly expressed in the category. Chi-square confirmed a differential distribution in activated categories between LumA and TNBC tumors.