

Supplementary Material

Multiple genes with potential tumor suppressive activity are present on chromosome 10q loss in neuroblastoma and are associated with poor prognosis

Ognibene M. et al.

Supplementary Genes Analysis

AGAP11

We analyzed the survival of the cohort of 498 NB patients in the SEQC-498 database in relation to the expression levels of *AGAP11* gene. Overall survival was positively associated with the gene expression (5-year OS: 71.7%, 95% CI: 65.4 – 77.0 for expression values below the median, and 85.8%, 95% CI: 80.4 – 89.8 for expression values above the median, $p < 0.001$, Supplementary Figure S1A). A clear trend was observed after splitting the data on the basis of the tertile values (5-year OS: 64.9%, 95% CI: 56.8 – 71.9 for low expression values; 83.9%, 95% CI: 76.9 – 89.0 for intermediate values; and 87.3%, 95% CI: 80.8 – 91.8 for high values, $p < 0.001$, Supplementary Figure S1B). Results from the analysis of EFS confirmed the pattern observed for OS. For instance, 5-year EFS was 56.2% (95% CI: 49.7 – 62.3) for gene expression values below the median, and 69.0% (95% CI: 62.7 – 74.5) for values above ($p = 0.002$, Supplementary Figure S1C). Splitting the data on the basis of the tertile values, 5-year EFS was 51.6% (95% CI: 43.5 – 59.0) for low expression levels, 64.7% (95% CI: 56.7 – 71.6) for intermediate levels, and 71.4% (95% CI: 63.8 – 77.8) for high values ($p < 0.001$, Supplementary Figure S1D). A statistically significant association was observed between high gene expression levels and each favorable prognostic factors (Figure 6), which included lower age at onset of disease ($p=0.030$, Supplementary Figure S2A), normal *MYCN* status ($p < 0.001$, Supplementary Figure S2B), and both localized and 4S stage ($p < 0.001$, Supplementary Figure S2C).

Multivariable regression analysis model (Supplementary Table S4) confirmed the positive association between *AGAP11* expression values and OS. Adjusted HR obtained splitting the data on the median value was 0.62 (95% CI: 0.41 – 0.95, $p = 0.025$). OS analysis performed using the tertile values as cut-offs confirmed the positive observed trend (HR = 0.49, 0.30 – 0.82 for high vs. low expression levels, and HR = 0.64, 95%CI: 0.39 – 1.0, for intermediate vs. low levels, $p = 0.003$). With regard to EFS, a quite similar pattern was observed, but differences by group were less evident and statistical significance no longer reached. Analysis of linear trend, using the original continuous gene expression value, indicated a weak protective effect both for OS and for EFS ($p = 0.072$ and 0.064 , respectively).

Results of the analysis of the *in silico* cohort of 283 NB patients in the NRC-283 database partly confirmed the positive association between *AGAP11* gene expression values and OS, but not PFS (Supplementary Figure S3). For instance, 5-year OS was 72.5% (95%CI: 63.1 – 79.9) for values above the median of gene expression and 62.2% (95%CI: 52.4 – 70.6) for values below, with a borderline statistical significance ($p = 0.067$). Splitting the data on the basis of the tertiles, OS was 75.9% (95%CI: 64.3 – 84.2) for high expression values, 64.9% (95%CI: 52.9 – 74.6) for intermediate values and 61.2% (95%CI: 48.9 – 71.4) for low values ($p = 0.029$).

Association between *AGAP11* expression levels and the major potential confounders in the NRC-283 data set showed that similar expression values were observed by age (Supplementary Figure S4A) and stage (Supplementary Figure S4C), whereas a lower expression level was associated with *MYCN* amplification ($p < 0.001$, Supplementary Figure S4B).

After correction for confounding by multivariable Cox regression analysis, the association observed between OS and *AGAP11* expression values was reduced and no longer statistically significant (HR = 0.70, splitting the data set on the median value of gene expression, 95%CI: 0.43 – 1.1, $p = 0.145$, and HR = 0.88, 95%CI: 0.52 – 1.5 and HR = 0.66, 95%CI: 0.36 – 1.2, $p = 0.199$, Supplementary Table S5). No association emerged for the PFS.

We analyzed the survival of the cohort of 786 NB patients included in the Cangelosi *et al.* data set in relation to the expression levels of *IFIT2* gene. Overall survival was 79.2% (95%CI: 74.8 – 82.9) for expression values above the median, and 66.3% (95%CI: 61.4 – 70.8) for values below the median ($p < 0.001$, Supplementary Figure S5A). The association between higher expression levels and better OS was confirmed by splitting the cohort into three groups on the tertile values of gene expression (OS = 79%, 95%CI: 73.6 – 83.5, OS = 77.5%, 95%CI: 71.9 – 82.1, and OS = 61.8%, 95%CI: 55.7 – 67.4, $p < 0.001$, Supplementary Figure S5B). A similar pattern was observed for EFS. For instance, EFS was 62.9% (95%CI: 57.9 – 67.5) above the median and 55.6% below (95%CI: 50.4 – 60.4, $p = 0.010$, Supplementary Figure S5C). Splitting the data on the tertile values the corresponding figures were: 64.5% (95%CI: 58.3 – 70.0), 62.3% (95%CI: 56.1 – 67.9), and 50.8% (95%CI: 44.4 – 56.8), $p < 0.001$ (Supplementary Figure S5D).

The association between *IFIT2* expression values and the main available potential confounders (age, *MYCN* status and stage) showed that a slight not statistically significant association was observed with age at diagnosis (Supplementary Figure S6A), while higher expression values were associated with normal *MYCN* status ($p < 0.001$, Supplementary Figure S6B) and localized and stage 4S disease ($p < 0.001$, Supplementary Figure S6C).

The association between high *IFIT2* expression levels and better OS was confirmed in multivariable analysis splitting the data on the median value (HR = 0.70, 95%CI: 0.54 – 0.92, $p = 0.010$, Supplementary Table S6). However, in the analysis stratified by tertile values, the trend was no longer evident. With regard to EFS, the association with *IFIT2* expression was reduced and no longer significant in multivariable analysis after splitting the cohort both on the median and on the tertile levels. However, a statistically significant linear trend was observed for both OS (HR = 0.87, 95%CI: 0.75 – 0.99, $p = 0.041$) and EFS (HR = 0.89, 95%CI: 0.78 – 1.0, $p = 0.048$) using the original continuous values of gene expression.

Validation analysis on the cohort of 283 NB patients in the NRC-283 database found a slightly better OS for patients with *IFIT2* expression values above the median (OS = 61.0%, 95%CI: 51.1 – 69.5, vs. 73.8%, 95%CI: 64.4 – 81.1, $p = 0.038$, Supplementary Figure S7A). This association was confirmed by splitting the data set into three groups using the tertile expression values (low levels: OS = 50.9%, 95%CI: 38.2 – 62.2; intermediate levels: 70.8%, 95%CI: 58.6 – 80.0; high levels: 78.9%, 95%CI: 68.2 – 86.4, $p = 0.009$, Supplementary Figure S7B). PFS analysis did not find a significant difference between high and low expression values by splitting the data on the median (Supplementary Figure S7C), but confirmed a positive association between *IFIT2* expression and survival stratifying the patients on the tertile values (PFS = 42.9%, 95%CI: 31.3 – 54.1 for low values, 61.6%, 95%CI: 49.5 – 71.6 for intermediate value, and 73.9%, 95%CI: 63.1 – 82.0, for high values, respectively, $p = 0.021$, Supplementary Figure S7D).

The association between *IFIT2* expression and the available potential confounders showed that higher values were observed among patients with normal *MYCN* status ($p < 0.001$, Supplementary Figure S8B), whereas expression levels were similar between different groups of age and stage at diagnosis.

Multivariable analysis via Cox regression model showed that, after adjusting for the potential effect of the available confounders, the apparent protective role of high levels of *IFIT2* gene expression was no longer observed (Supplementary Table S7).

PAPSS2

We analyzed the survival of the cohort of 786 NB patients included in the Cangelosi *et al.* data set in relation to the expression levels of *PAPSS2* gene. Overall survival was positively associated with the gene expression (OS = 81.4%, 95%CI: 77.2 – 84.9 for values above the median and OS = 64.1%, 95%CI: 59.2 – 68.6, for values below the median, $p < 0.001$, Supplementary Figure S9A). Evidence of trend emerged splitting the data on the base of the tertile values (OS = 83.6%, 95%CI: 78.5 – 87.6, 77.5%, 95%CI: 71.9 – 82.1, and 57.3%, 95%CI: 51.0 – 63.0, respectively, $p < 0.001$, Supplementary Figure S9B). A better EFS was also observed in relation with higher

gene expression levels (EFS = 64.7%, 95%CI: 59.7 – 69.2 for values above the median and 53.8%, 95%CI: 48.7 – 58.7, for values below the median, $p = 0.003$, Supplementary Figure S9C). This association was confirmed after splitting the data on the basis of the tertile of expression values (EFS = 64.5%, 95%CI: 58.3 – 70.0, 63.7%, 95%CI: 57.5 – 69.2, and 49.4%, 95%CI: 43.1 – 55.4, $p < 0.001$, Supplementary Figure S9D).

PAPSS2 expression was associated with favorable prognostic features which included lower age at diagnosis ($p < 0.001$, Supplementary Figure S10A), normal *MYCN* status ($p < 0.001$, Supplementary Figure S10B) and localized/stage 4S disease ($p < 0.001$, Supplementary Figure S10C).

Multivariable Cox regression analysis confirmed the association between OS and *PAPSS2* expression values when the cohort was split into three groups using the tertiles values as cut-offs (HR = 0.79, 95%CI: 0.58 – 1.1, and HR = 0.67, 95%CI: 0.48 – 0.94, $p = 0.015$, Supplementary Table S8). This trend was confirmed using the original continuous variable as a predictor (HR = 0.86, 95%CI: 0.74 – 0.99, $p = 0.029$). In multivariable analysis the association between higher expression values and a better EFS was not confirmed.

A positive association between the expression of *PAPSS2* and patient survival was observed in the analysis of the NRC-283 NB cohort for both OS and PFS. For instance, OS above the median gene expression value was 74.9% (95%CI: 65.8 – 81.9) vs. 59.5% (95%CI: 49.3 – 68.2) below the median value ($p = 0.025$, Supplementary Figure S11A). A positive trend in OS was observed stratifying the data on the tertile of gene expression (55.5%, 95%CI: 42.9 – 66.3 for low values, 69.8%, 95%CI: 57.9 – 79.0 for intermediate values, and 76.6%, 95%CI: 65.4 – 84.6 for high values, respectively, $p = 0.014$, Supplementary Figure S11B). A similar pattern was observed for PFS, both stratifying on the median value (PFS = 52.3%, 95%CI: 42.8 – 61.0 and 67.8%, 95%CI: 58.4 – 75.5 for values above and below the median expression level, respectively, $p = 0.009$, Supplementary Figure S11C), and splitting the data on the tertile values (49.6%, 95%CI: 38.0 – 60.2, 63.1%, 95%CI: 51.5 – 72.7, and 67.7%, 95%CI: 56.0 – 77.0, respectively, $p = 0.015$, Supplementary Figure S11D).

The association between *PAPSS2* gene expression levels and the available potential confounders showed that higher expression values were observed in younger patients ($p = 0.001$, Supplementary Figure S12A), while no statistically significant difference was observed comparing patients with normal *MYCN* status with those with *MYCN* amplification ($p = 0.078$, Supplementary Figure S12B) and comparing different stage at diagnosis ($p = 0.078$, Supplementary Figure S12C).

The potential protective role of *PAPSS2* on patient survival, indicated by results of the univariable analysis, was not confirmed after adjustment for confounding in multivariable analysis via Cox regression model, for either OS or PFS (Supplementary Table S9).

PCGF5

We analyzed the survival of 786 NB patients included in the Cangelosi *et al.* data set in relation to the expression of *PCGF5* gene. A better OS was associated with higher expression values splitting the data both on the median (OS = 85.0%, 95%CI: 81.1 – 88.2, vs. 60.6%, 95%CI: 55.5 – 65.2, $p < 0.001$, Supplementary Figure S13A), and on the tertiles of gene expression values (OS = 87.0%, 95%CI: 82.3 – 90.6, 77.1%, 95%CI: 71.5 – 81.7, 54.2%, 95%CI: 48.0 – 60.0, $p < 0.001$, Supplementary Figure S13B). A similar pattern was observed for EFS (EFS = 70.0%, 95%CI: 65.2 – 74.3 vs. 48.3%, 95%CI: 43.2 – 53.2, splitting the data on the median value, $p < 0.001$, Supplementary Figure S13C; EFS = 70.5%, 95%CI: 64.6 – 75.6, 62.9%, 95%CI: 56.7 – 68.5, 43.8%, 95%CI: 37.6 – 49.8, splitting the data on the basis of the tertiles, $p < 0.001$, Supplementary Figure S13D).

The association between *PCGF5* expression levels and the available patients' prognostic characteristics showed that higher values were associated with a lower age at diagnosis ($p < 0.001$, Supplementary Figure S14A), normal *MYCN* status ($p < 0.001$, Supplementary Figure S14B) and localized or stage 4S disease ($p < 0.001$, Supplementary Figure S14C).

Multivariable regression analysis confirmed the positive association between survival and *PCGF5* expression (Supplementary Table S10). Splitting the data on the median value an HR = 0.56 was observed for OS (95%CI: 0.42 – 0.76, $p < 0.001$), and a clear trend emerged splitting the cohort into three groups using the tertiles (HR =

0.71, 95%CI: 0.52 – 0.97, and HR = 0.48, 95%CI: 0.33 – 0.69, $p < 0.001$). This trend was confirmed using the original expression values on a continuous scale (HR = 0.79, 95%CI: 0.66 – 0.93, $p = 0.006$). A similar pattern was observed for EFS, both splitting the data on the median value (HR = 0.67, 95%CI: 0.53 – 0.85, $p < 0.001$), and stratifying on the tertiles (HR = 0.82, 95%CI: 0.63 – 1.1, and HR = 0.66, 95%CI: 0.50 – 0.89, $p = 0.006$) and was also confirmed using the original values as a continuous predictor (HR = 0.85, 95%CI: 0.72 – 1.0, $p = 0.047$).

The association between *PCGF5* expression levels and patient survival in the validation cohort NRC-283 showed that higher values of gene expression were associated with a better survival both for OS and for EFS. In details, splitting the data on the median expression, OS was 57.2% (95%CI: 47.2 – 65.9) for low values and 77.5 (95%CI: 68.4 – 84.3) for high values ($p < 0.001$, Supplementary Figure S15A). Stratifying the cohort by the tertile values, OS was 46.7% (95%CI: 34.7 – 57.8) for low levels, 75.9% (95%CI: 64.2 – 84.2) for intermediate levels, and 79.7% (95%CI: 68.5 – 87.3) for high levels, respectively ($p < 0.001$, Supplementary Figure S15B). A quite similar pattern was observed for PFS. The corresponding figures were 53.3% (95%CI: 43.6 – 62.0) below the median, and 66.5% (95%CI: 57.2 – 74.3) above the median, respectively ($p = 0.048$, Supplementary Figure S15C). In patients with *PCGF5* expression values in the third tertile PFS was 43.6% (95%CI: 32.2 – 54.4), in the second tertile was 64.8% (95%CI: 53.0 – 74.3), and in the first tertile 71.4% (95%CI: 59.8 – 80.2, $p = 0.005$, Supplementary Figure S15D).

PCGF5 expression levels were positively associated with favorable prognostic features at diagnosis (Figure 28), including lower age ($p = 0.003$, Supplementary Figure S16A), normal *MYCN* status ($p < 0.001$, Supplementary Figure S16B) and localized or stage 4S stage ($p = 0.023$, Supplementary Figure S16C).

Results of the analysis by multivariable Cox regression model indicated that the potential protective effect observed in univariable analysis was mainly due to confounding by the main prognostic patient characteristics both for OS and for PFS (Supplementary Table S11).

NUDT9P1

We analyzed the survival of the cohort of 498 NB patients from the SEQC-498 database in relation to the expression levels of *NUDT9P1* gene. OS was positively associated with the gene expression both splitting the data on the median (OS = 90.3%, 95%CI: 85.7 – 93.5, vs. 66.7%, 95%CI: 60.1 – 72.5, $p < 0.001$, Supplementary Figure S17A), and using the tertile values as cut-offs (OS = 92.8%, 95%CI: 87.3 – 95.9, 85.8%, 95%CI: 79.2 – 90.4, 56.0%, 95%CI: 47.4 – 63.7, $p < 0.001$, Supplementary Figure S17B). A similar pattern was observed for EFS (74.9%, 95%CI: 68.9 – 79.9 vs. 49.9%, 95%CI: 43.3 – 56.2, splitting the data on the median expression value, $p < 0.001$, Supplementary Figure S17C; EFS = 77.1%, 95%CI: 69.9 – 82.7, 66.5%, 95%CI: 58.5 – 73.3, 43.3%, 95%CI: 35.4 – 51.0, splitting the data on the tertiles, $p < 0.001$, Supplementary Figure S17D).

The association between *NUDT9P1* expression levels and the available patients' prognostic characteristics showed that higher values were associated with a lower age at diagnosis ($p = 0.001$, Supplementary Figure S18A), normal *MYCN* status ($p < 0.001$, Supplementary Figure S18B) and localized or stage 4S disease ($p < 0.001$, Supplementary Figure S18C).

Multivariable regression analysis confirmed the positive association between patients' survival and *NUDT9P1* expression values (Supplementary Table S12). Splitting the data on the median, an HR = 0.36 was observed for OS (95%CI: 0.23 – 0.58, $p < 0.001$). A clear trend emerged splitting the cohort into three groups using the tertiles (HR = 0.56, 95%CI: 0.34 – 0.92, and HR = 0.24, 95%CI: 0.13 – 0.44, respectively, $p < 0.001$). This trend was confirmed analyzing the original expression values on a continuous scale (HR = 0.06, 95%CI: 0.02 – 0.20, $p < 0.001$). A similar pattern was observed for EFS. Splitting the data on the median value, HR was 0.52 (95%CI: 0.38 – 0.72, $p < 0.001$). A clear trend was observed splitting the cohort on the tertile values (HR = 0.71, 95%CI: 0.49 – 1.0, and HR = 0.41, 95%CI: 0.28 – 0.62, $p < 0.001$) and was confirmed using the original values as a continuous predictor (HR = 0.19, 95%CI: 0.08 – 0.43, $p < 0.001$).

We analyzed the association between *NUDT9P1* expression levels and patient survival in the validation cohort NRC-283. For OS, higher values of gene expression were associated with a better survival both splitting the

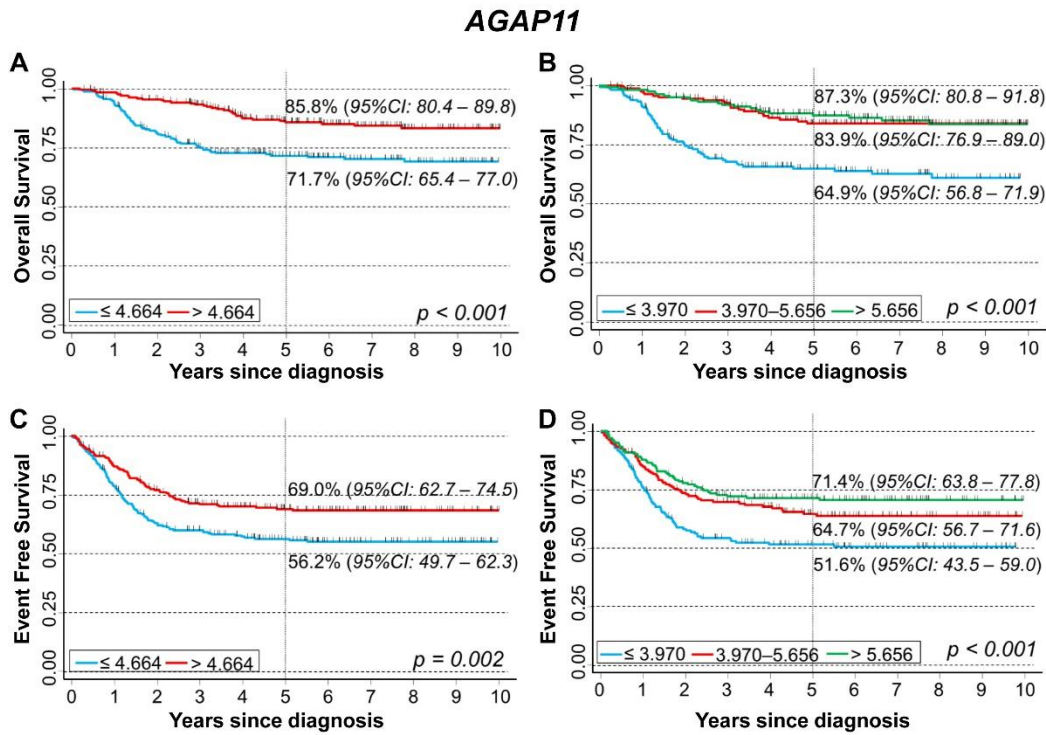
data on the median value (56.3%, 95%CI: 46.5 – 65.1, vs. 78.4%, 95%CI: 69.4 – 85.1, $p < 0.001$, Supplementary Figure S19A) and on the tertiles (49.9% 95%CI: 37.8 – 60.7 for low values, 75.6%, 95%CI: 63.9 – 83.9, for intermediate values, and 77.0%, 95%CI: 65.4 – 85.1, $p < 0.001$, Supplementary Figure S19B). With regard to PFS, results were consistent with those obtained for OS. PFS for patients with *NUDT9P1* expression levels above the median was 48.6% (95%CI: 39.2 – 57.4) vs. 71.4% (95%CI: 62.2 – 78.7) for patients with values above ($p < 0.001$, Supplementary Figure S19C). Stratifying the cohort on the tertile values PFS was 42.5%, 95%CI: 31.2 – 53.4) for low values, 65.3% (95%CI: 53.5 – 74.8) for intermediate values, and 72.3% (95%CI: 60.9 – 80.9) for high values, respectively ($p < 0.001$, Supplementary Figure S19D).

NUDT9P1 expression was associated with favorable patient characteristics at diagnosis. Higher values were observed for younger patients ($p = 0.036$, Supplementary Figure S20A), with normal *MYCN* status ($p < 0.001$, Supplementary Figure S20B), and localized stage or stage 4S ($p = 0.001$, Supplementary Figure S20C).

Correcting for confounding in multivariable Cox regression analysis, the association between high levels of *NUDT9P1* expression values observed in univariable analysis was reduced and no longer statistically significant (Supplementary Table S13) for both OS and PFS.

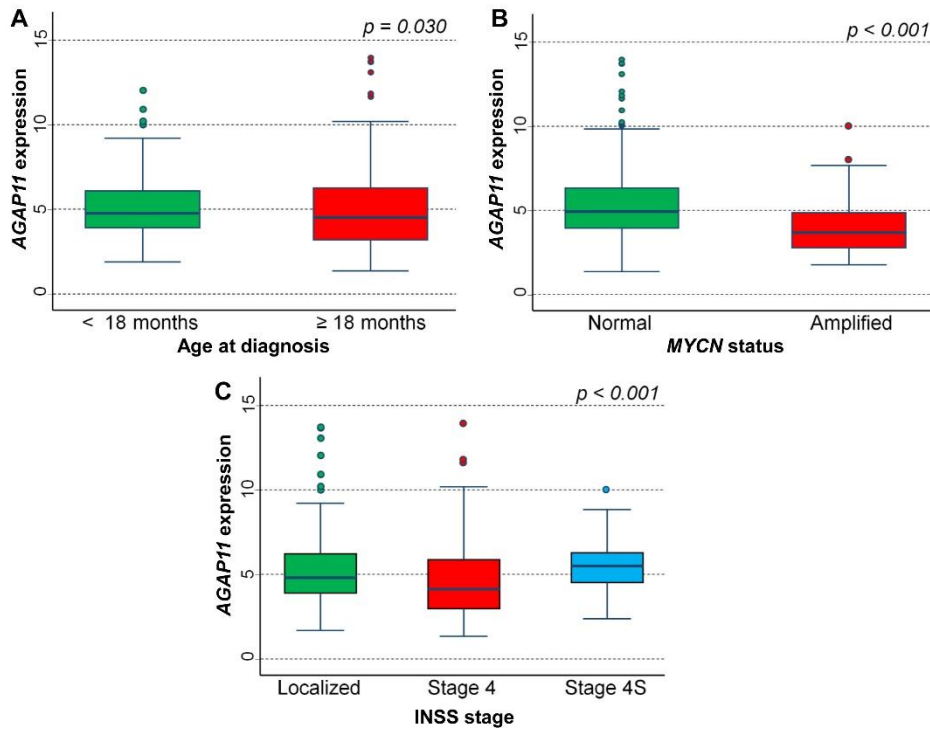
Supplementary Figures

Supplementary Figure S1



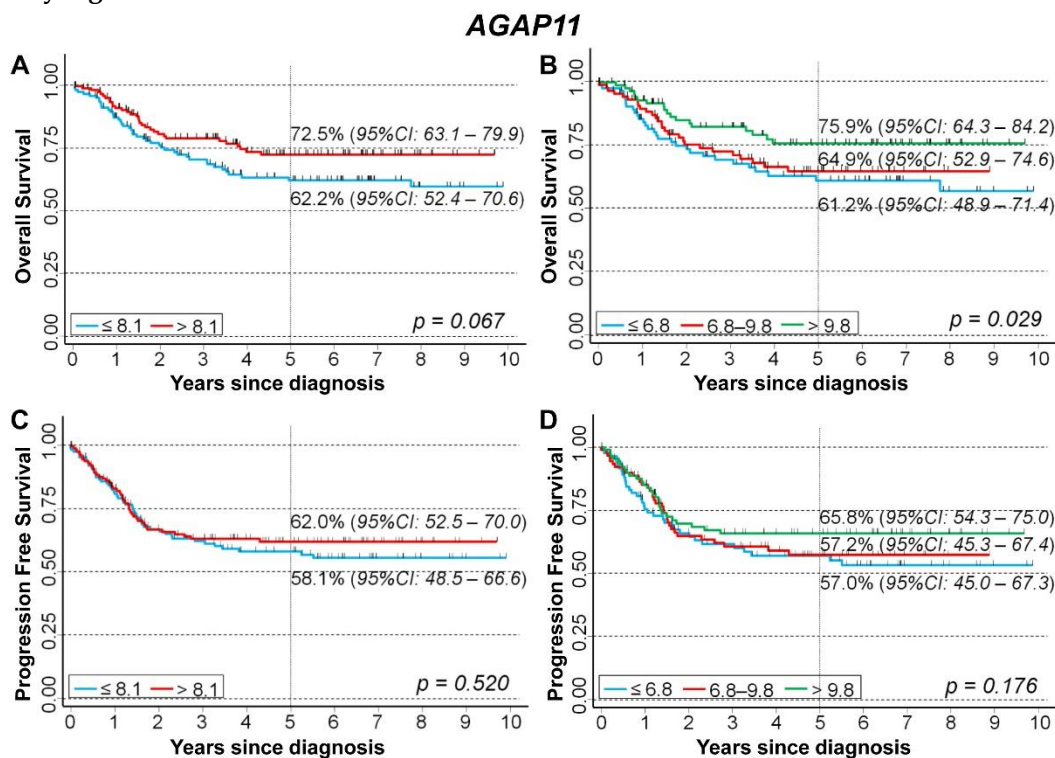
Survival analyses of 498 NB patients using the SEQC-498 dataset for *AGAP11* gene expression. Overall survival, cut-off on the median (A) or tertile (B) expression value; Event free survival, cut-off on the median (C) or tertile (D) expression value. Five-year survival estimates and the related 95% CI are shown

Supplementary Figure S2



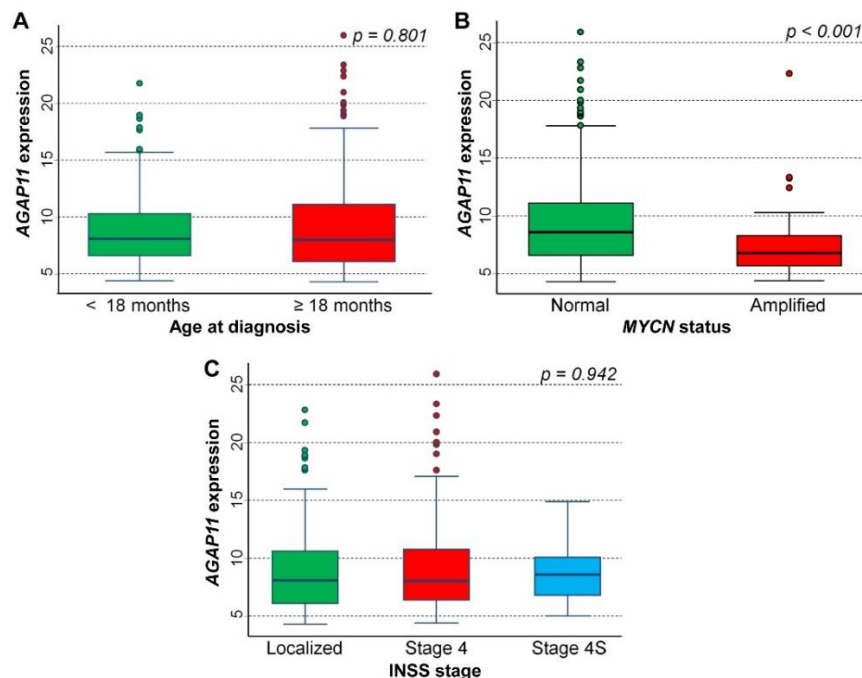
Association between *AGAP11* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 498 neuroblastoma patients in the SEQC-498 data set. (A) Age; (B) MYCN status; (C) INSS stage.

Supplementary Figure S3



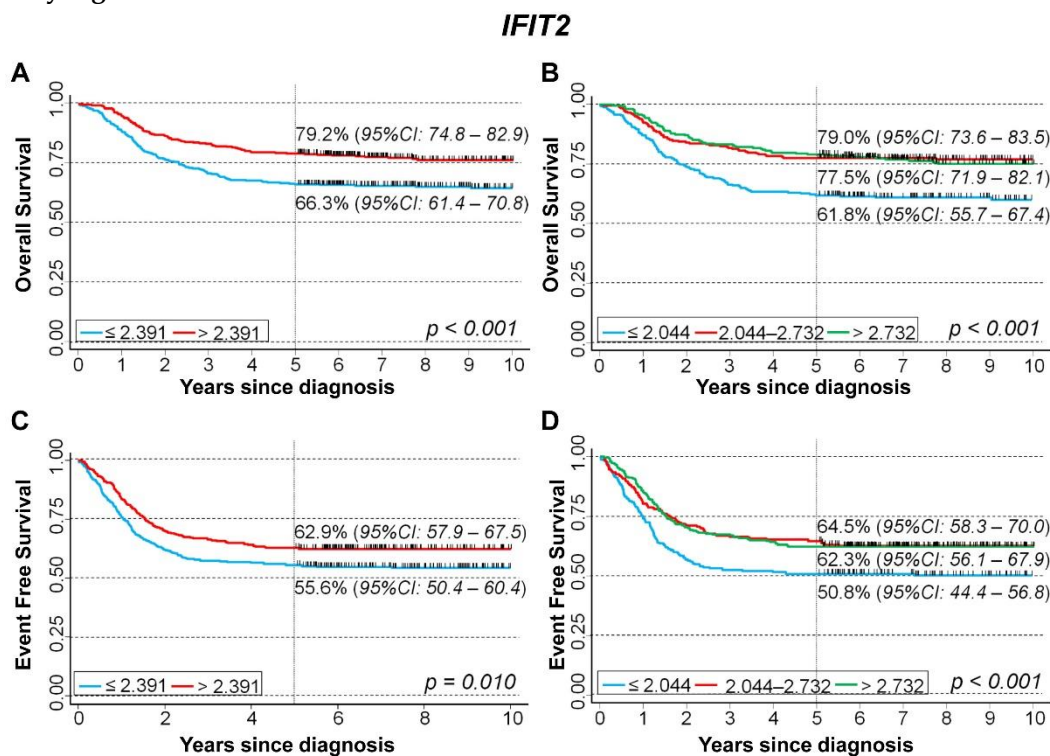
Survival analysis of 283 NB patients using the NRC-283 dataset for *AGAP11* gene expression. Overall survival, cut-off on the median (A) or tertile (B) expression value; Progression free survival, cut-off based on the median (C) or tertile (D) expression value. Five-year survival estimates and their related 95% CI are shown.

Supplementary Figure S4



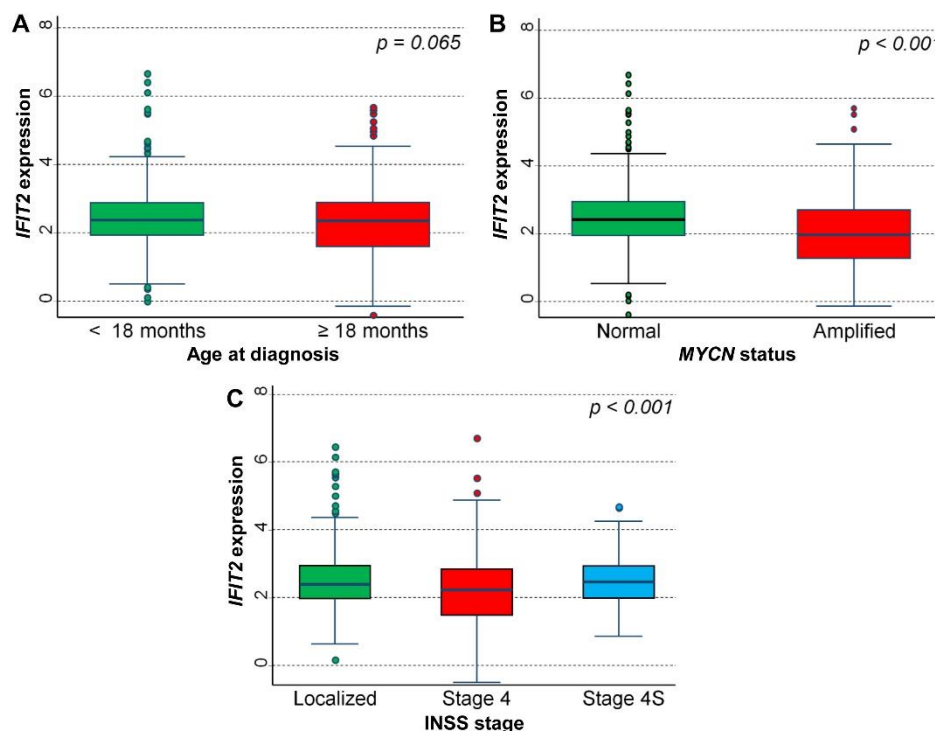
Association between *AGAP11* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 283 neuroblastoma patients in the NRC-283 data set. (A) Age; (B) *MYCN* status; (C) INSS stage.

Supplementary Figure S5



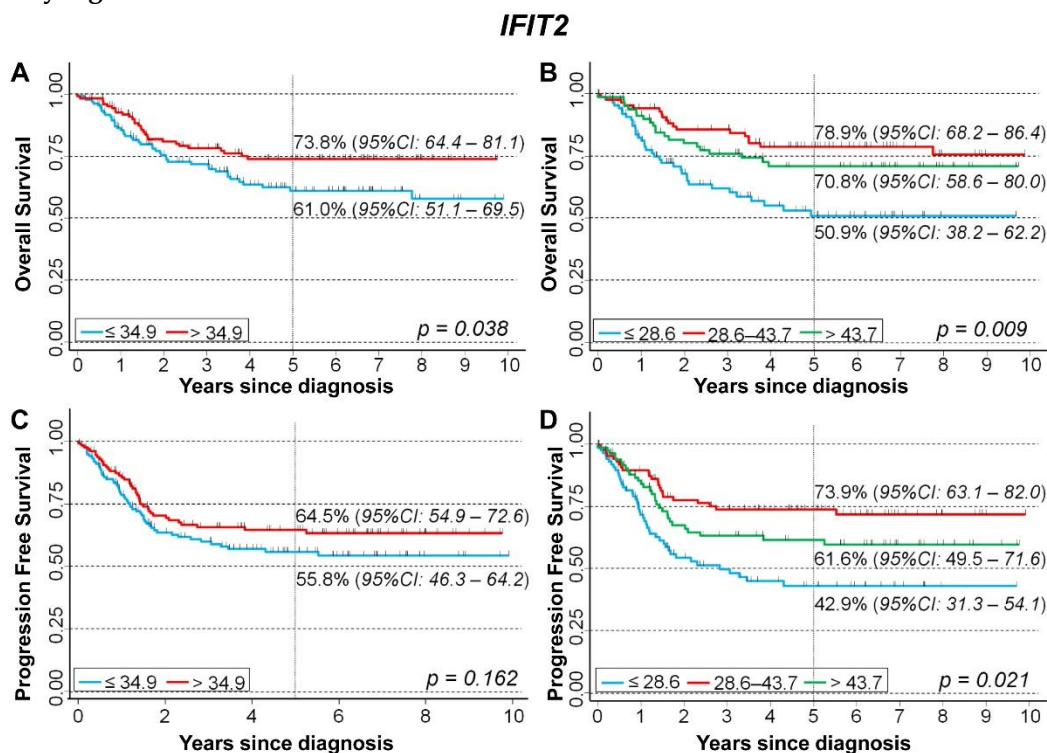
Survival analyses of 786 NB patients using the Cangelosi et al. dataset for *IFIT2* gene expression. Overall survival, cut-off on the median (A) or tertile (B) expression value; Event free survival, cut-off on the median (C) or tertile (D) expression value. Five-year survival estimates and their related 95% CI are shown.

Supplementary Figure S6



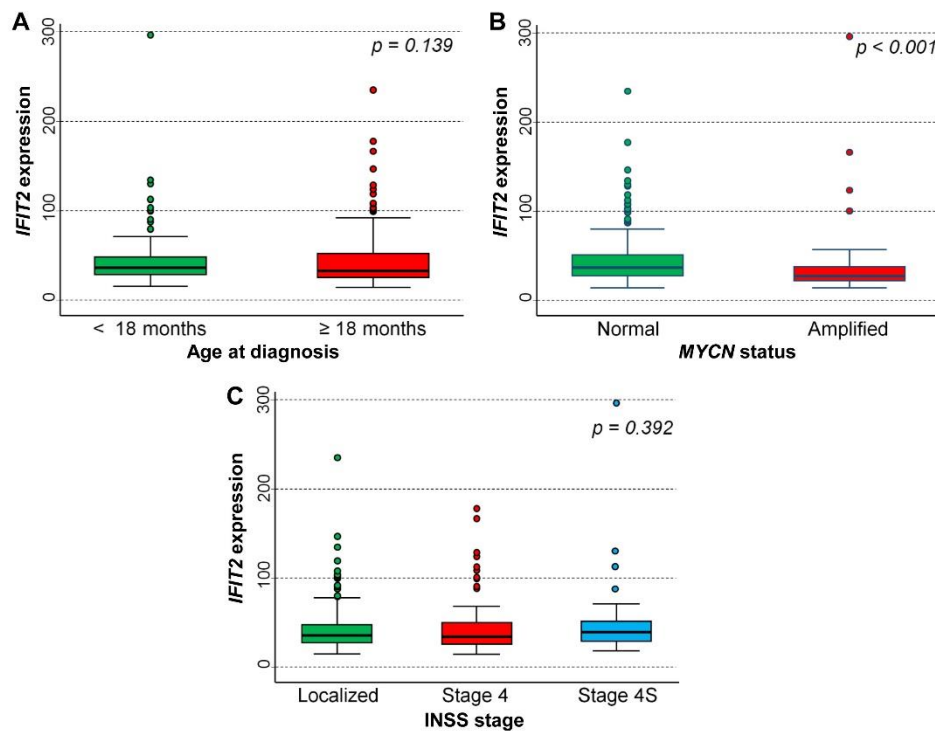
Association between *IFIT2* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 786 neuroblastoma patients in the data set of Cangelosi *et al.* (A) Age; (B) MYCN status; (C) INSS stage.

Supplementary Figure S7



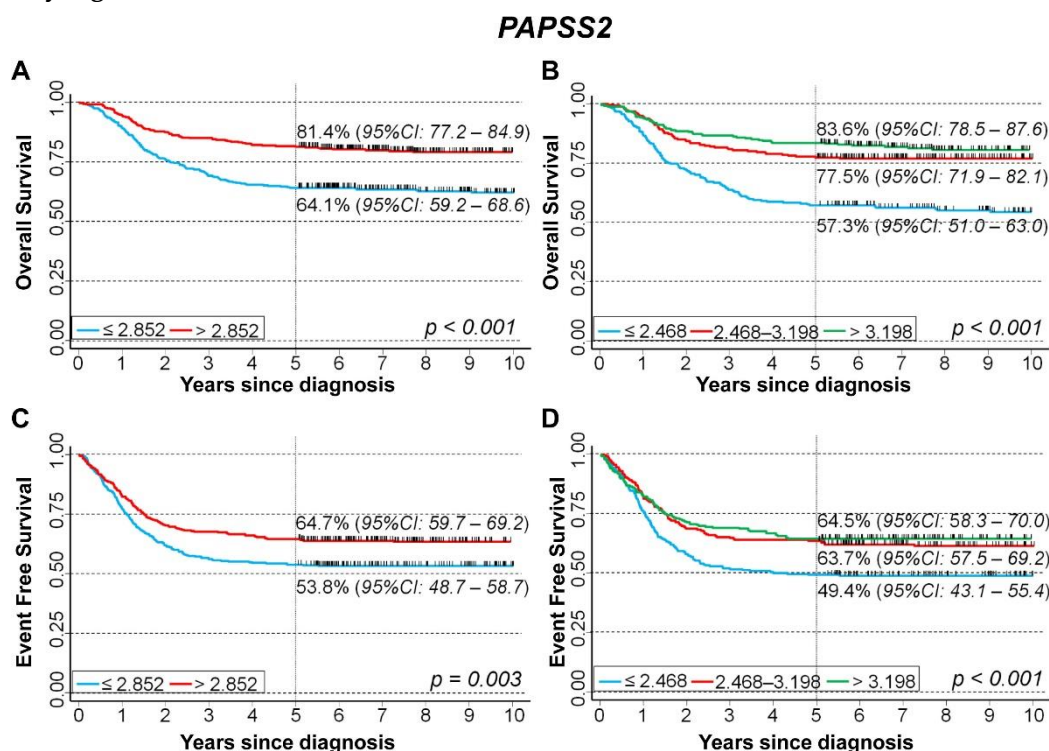
Survival analyses of 283 NB patients using the NRC-283 dataset for *IFIT2* gene expression. Overall survival, cut-off on the median (A) or tertile (B) expression value; Progression free survival, cut-off on the median (C) or tertile (D) expression value. Five-year survival estimates and their related 95% CI are shown.

Supplementary Figure S8



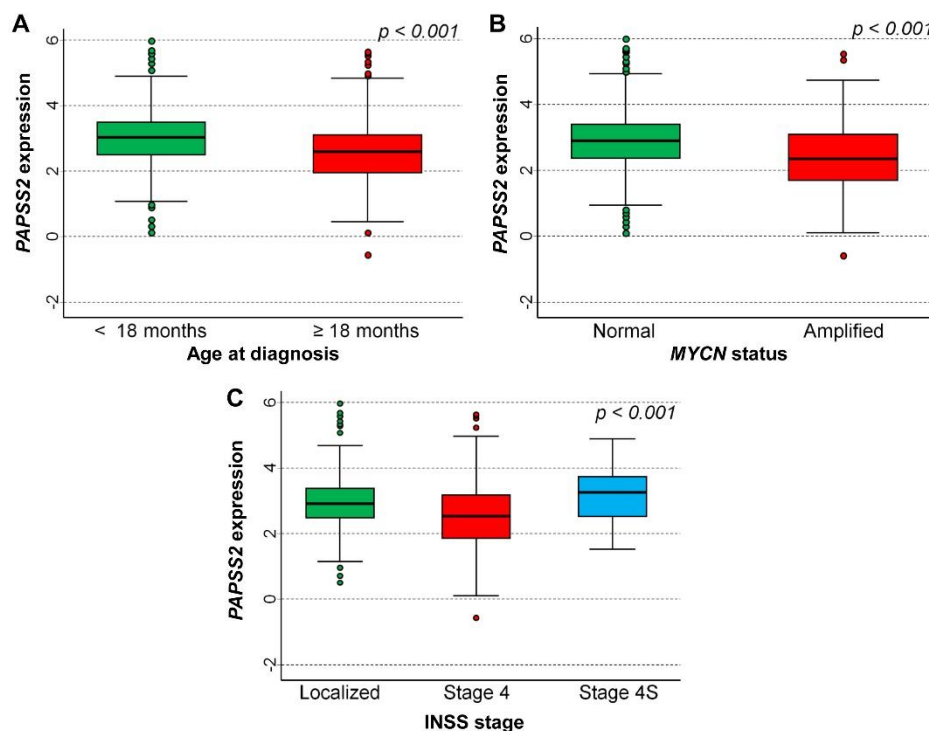
Association between *IFIT2* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 283 NB patients in the NRC-283 data set. (A) Age; (B) *MYCN* status; (C) INSS stage.

Supplementary Figure S9



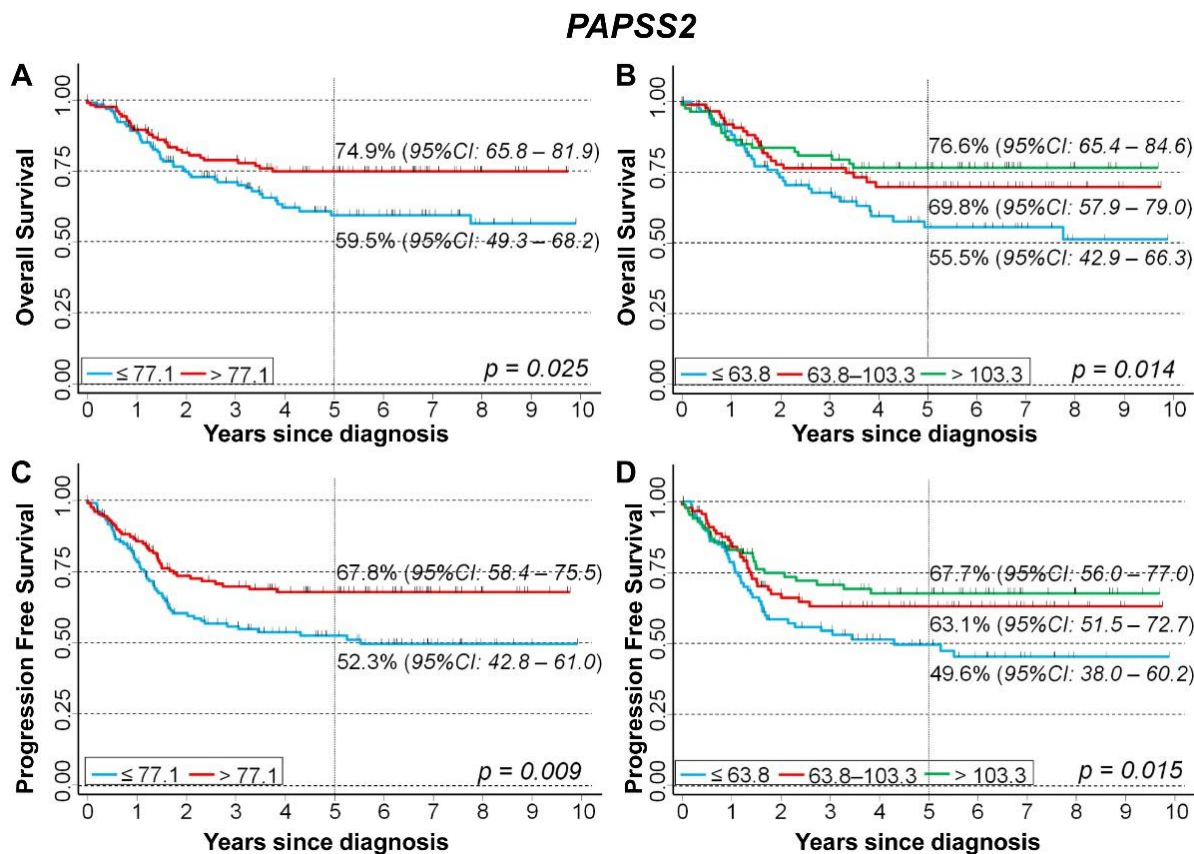
Survival analyses of 786 NB patients using the Cangelosi et al. dataset for *PAPSS2* gene expression. Overall survival, cut-off on the median (A) or tertile (B) expression value; Event free survival, cut-off on the median (C) or tertile (D) expression value. Five-year survival estimates and their related 95% CI are shown.

Supplementary Figure S10



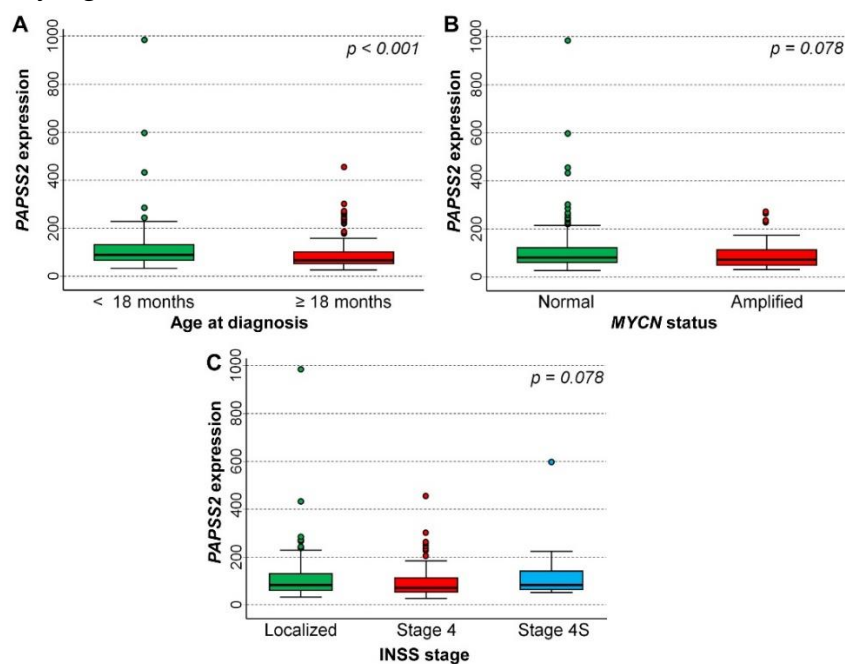
Association between *PAPSS2* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 786 neuroblastoma patients in the data set of Cangelosi *et al.* (A) Age; (B) *MYCN* status; (C) INSS stage.

Supplementary Figure S11



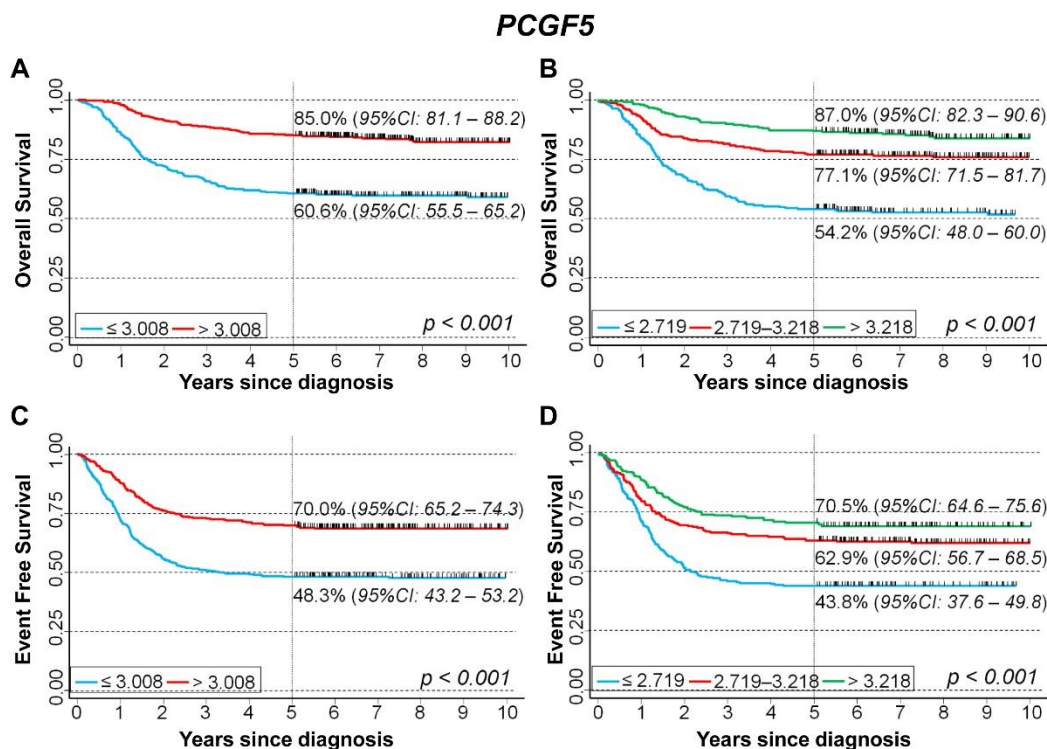
Survival analyses of 283 NB patients using the NRC-283 dataset for *PAPSS2* gene expression. Overall survival, cut-off on the median (A) or tertile (B) expression value; Progression free survival, cut-off on the median (C) or tertile (D) expression value. Five-year survival estimates and their related 95% CI are shown.

Supplementary Figure S12



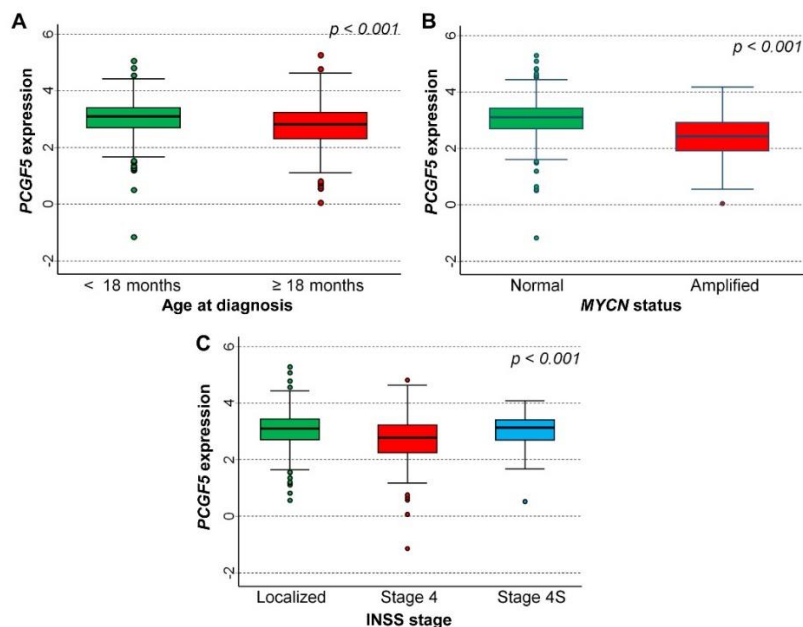
Association between *PAPSS2* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 498 neuroblastoma patients in the SEQC-498 data set. (A) Age; (B) *MYCN* status; (C) INSS stage.

Supplementary Figure S13



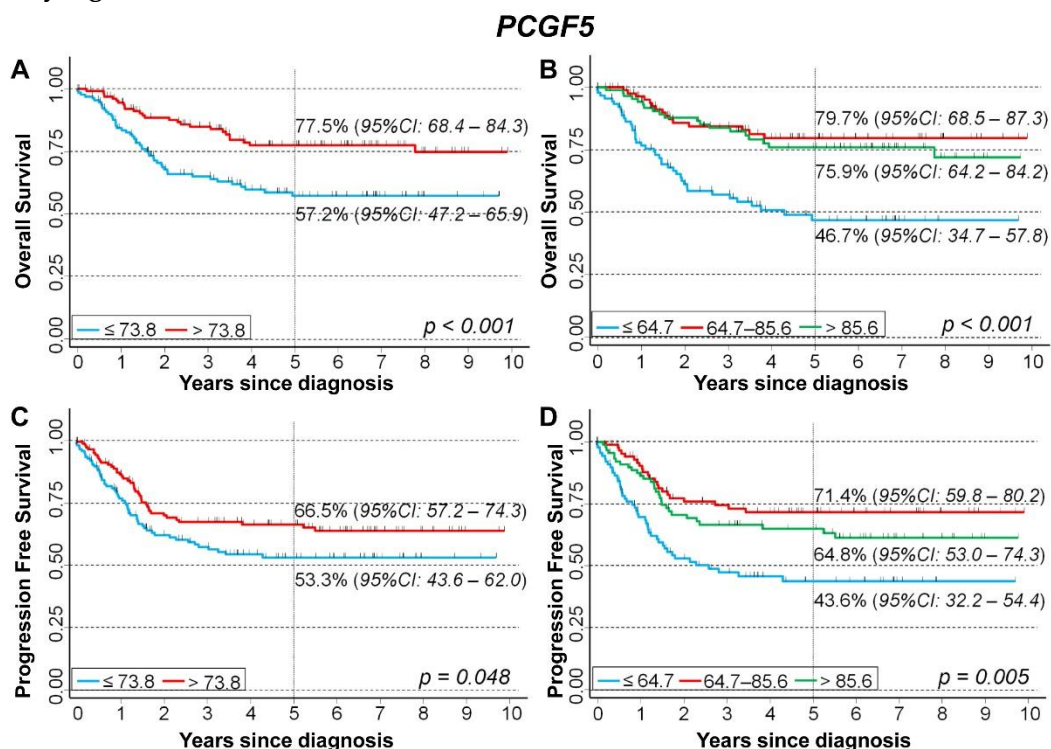
Survival analyses of 786 NB patients using the Cangelosi et al. dataset for *PCGF5* gene expression. Overall survival, cut-off on the median (A) or tertile (B) expression value; Event free survival, cut-off on the median (C) or tertile (D) expression value. Five-year survival estimates and their related 95% CI are shown.

Supplementary Figure S14



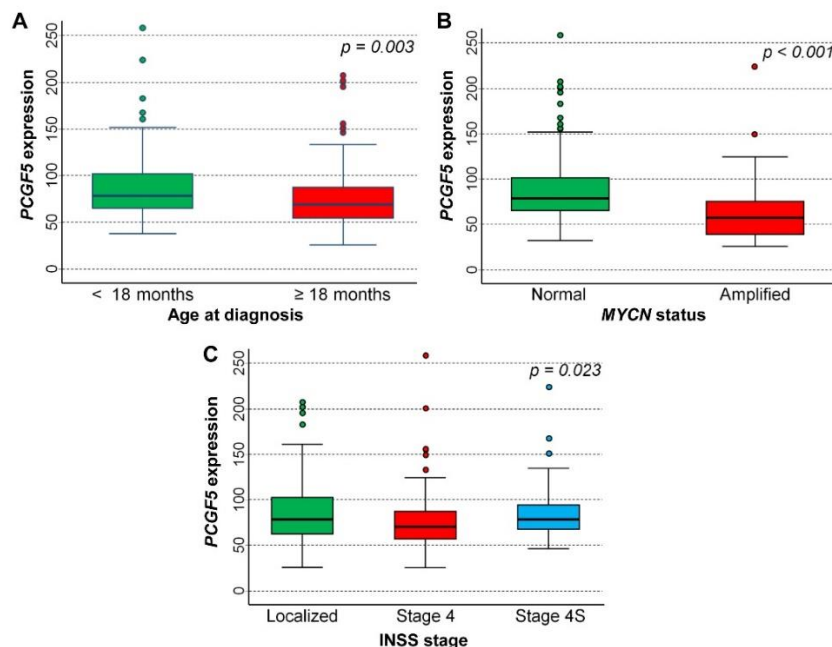
Association between *PCGF5* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 786 neuroblastoma patients in the data set of Cangelosi *et al.* (A) Age; (B) *MYCN* status; (C) INSS stage.

Supplementary Figure S15



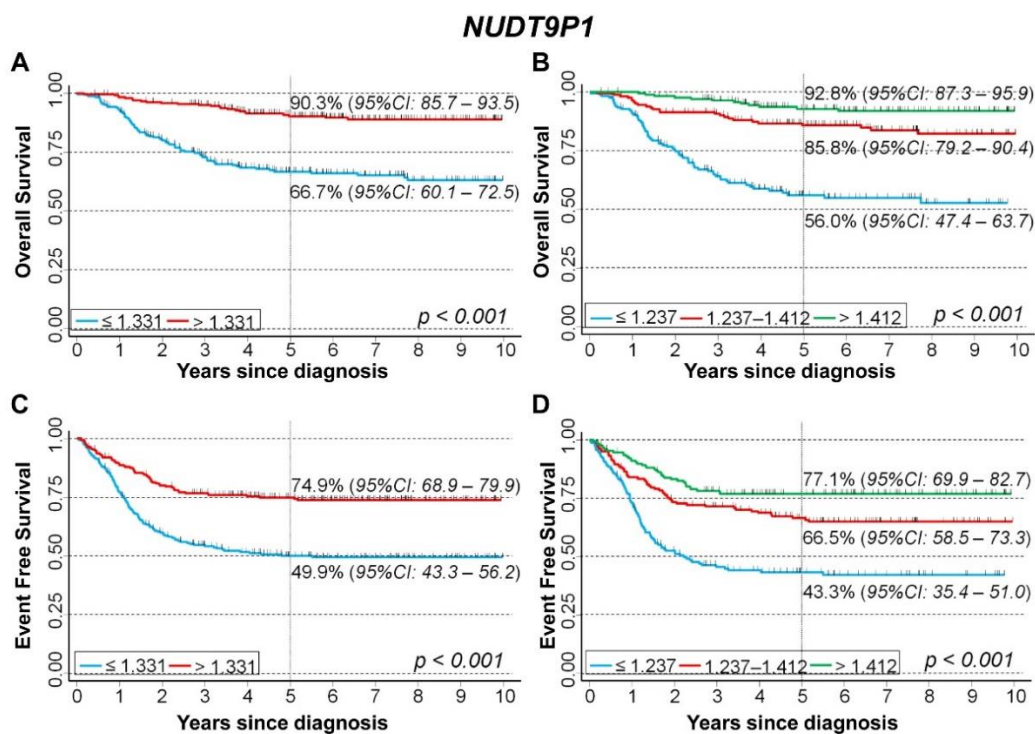
Survival analyses of 283 NB patients using the NRC-283 dataset for *PCGF5* gene expression. Overall survival, cut-off on the median (A) or tertile (B) expression value; Progression free survival, cut-off on the median (C) or tertile (D) expression value. Five-year survival estimates and their related 95% CI are shown.

Supplementary Figure S16



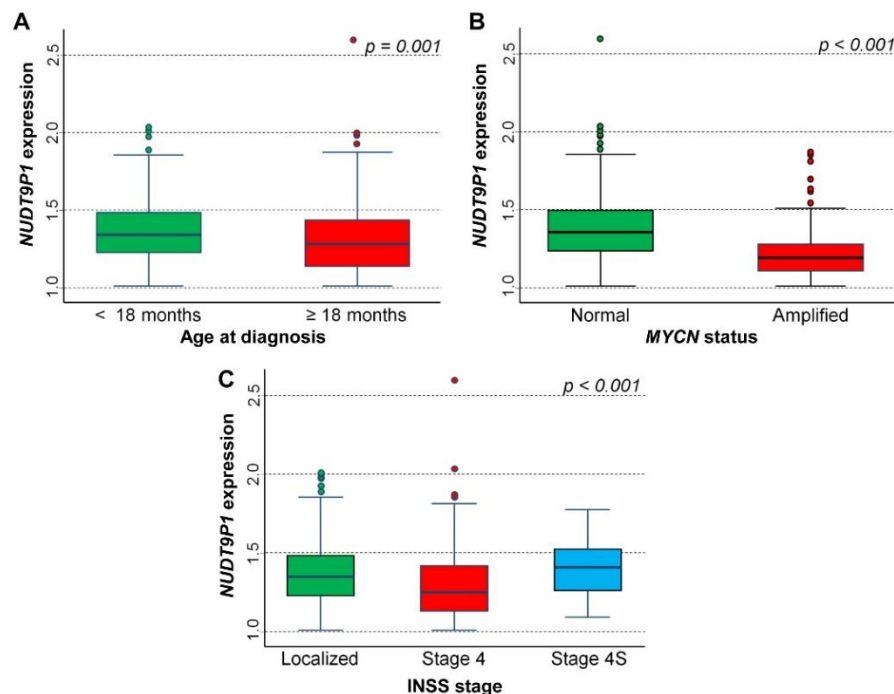
Association between *PCGF5* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 498 neuroblastoma patients in the SEQC-498 data set. (A) Age; (B) *MYCN* status; (C) INSS stage.

Supplementary Figure S17



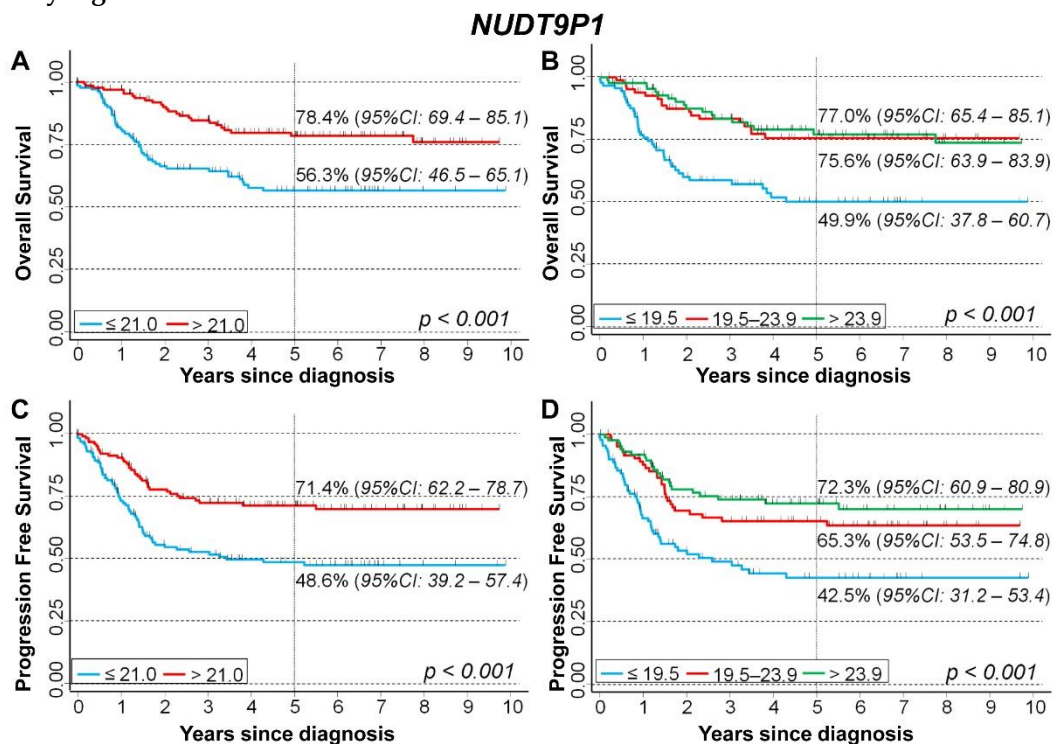
Survival analyses of 498 NB patients using the SEQC-498 data set for *NUDT9P1* gene expression Overall survival, cut-off on the median (A) or tertile (B) expression value; Event free survival, cut-off on the median (C) or tertile (D) expression value. Five-year survival estimates and their related 95% CI are shown.

Supplementary Figure S18



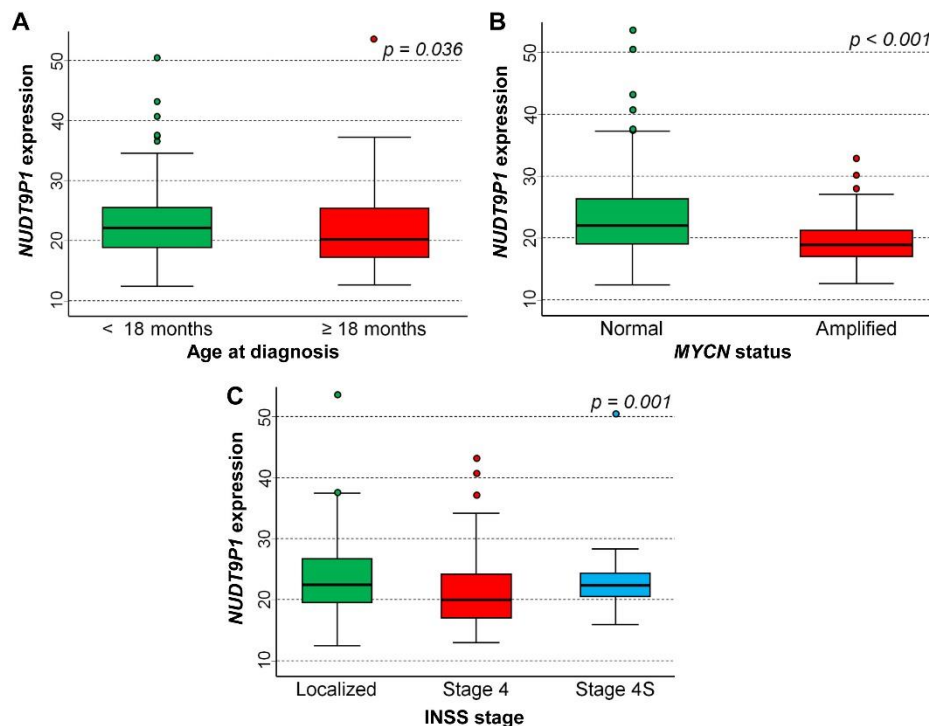
Association between *NUDT9P1* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 498 neuroblastoma patients in the SEQC-498 data set. (A) Age; (B) *MYCN* status; (C) INSS stage.

Supplementary Figure S19



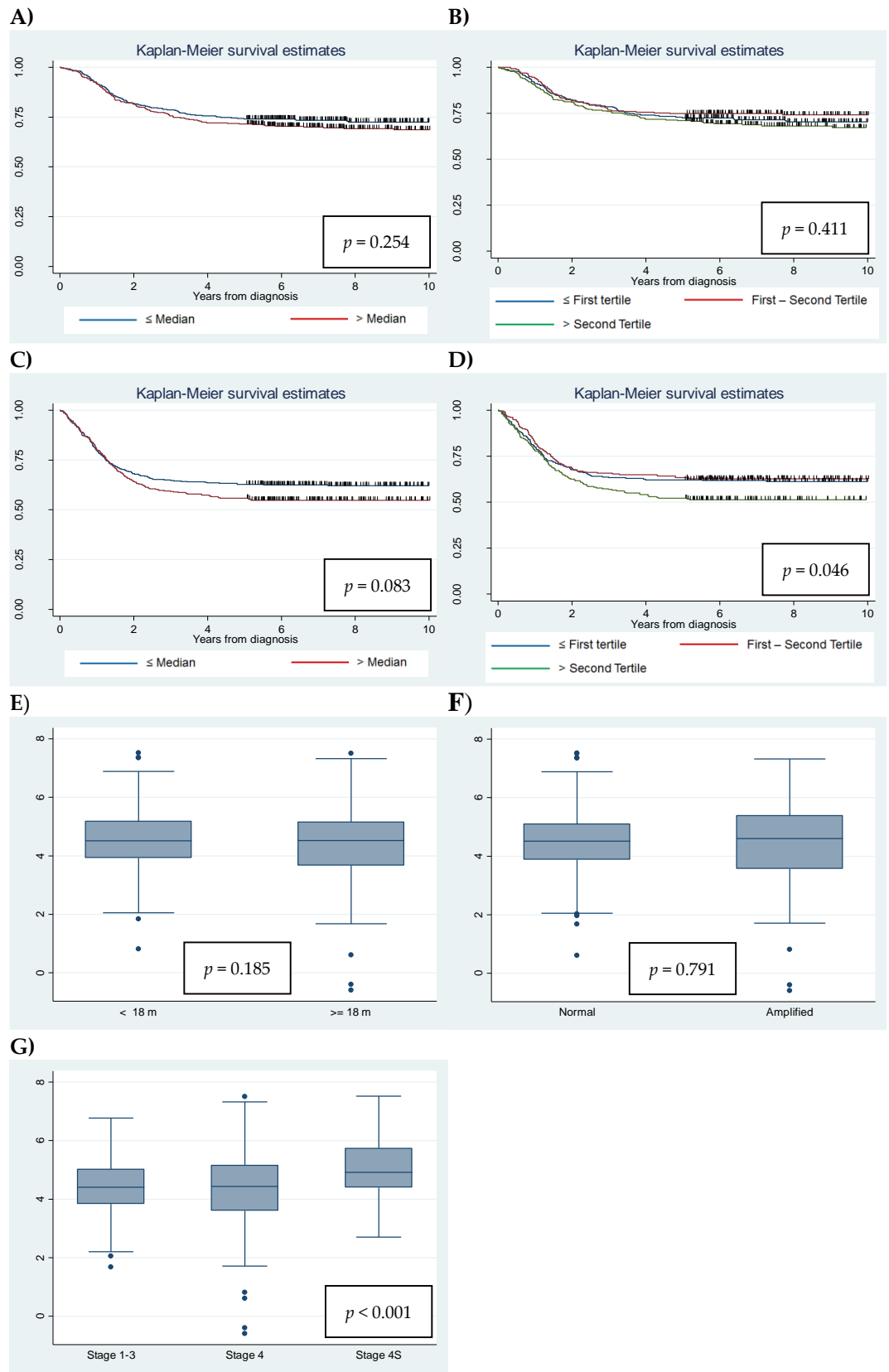
Survival analyses of 283 NB patients using the NRC-283 dataset for *NUDT9P1* gene expression. Overall survival, cut-off on the median(A) or tertile (B) expression value; Progression free survival, cut-off on the median (C) or tertile (D) expression value. Five-year survival estimates and their related 95% CI are shown.

Supplementary Figure S20



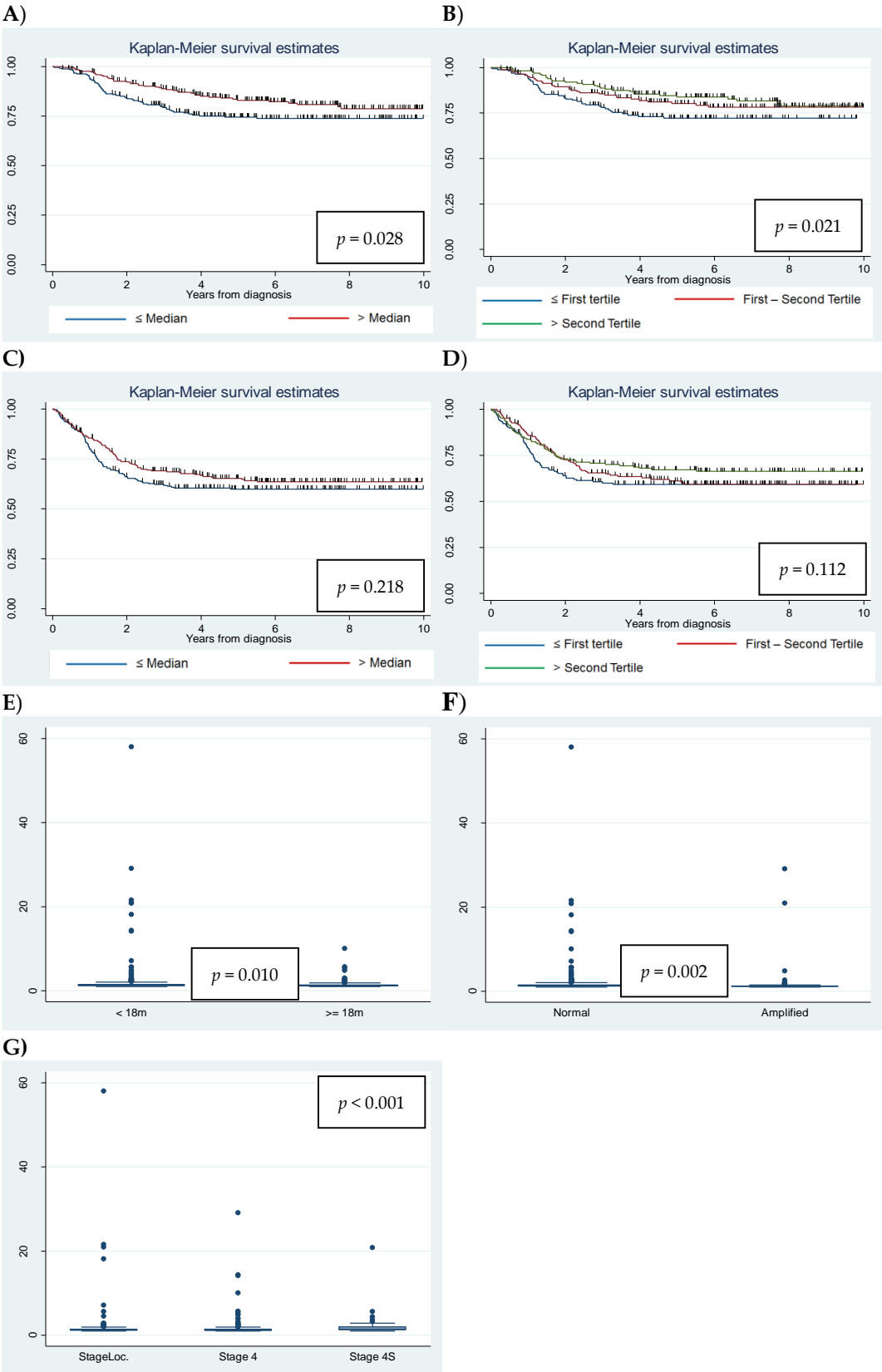
Association between *NUDT9P1* gene expression and the main patient characteristics at diagnosis evaluated on the cohort of 283 neuroblastoma patients in the NRC-283 data set. (A) Age; (B) *MYCN* status; (C) INSS stage.

Supplementary Figure S21



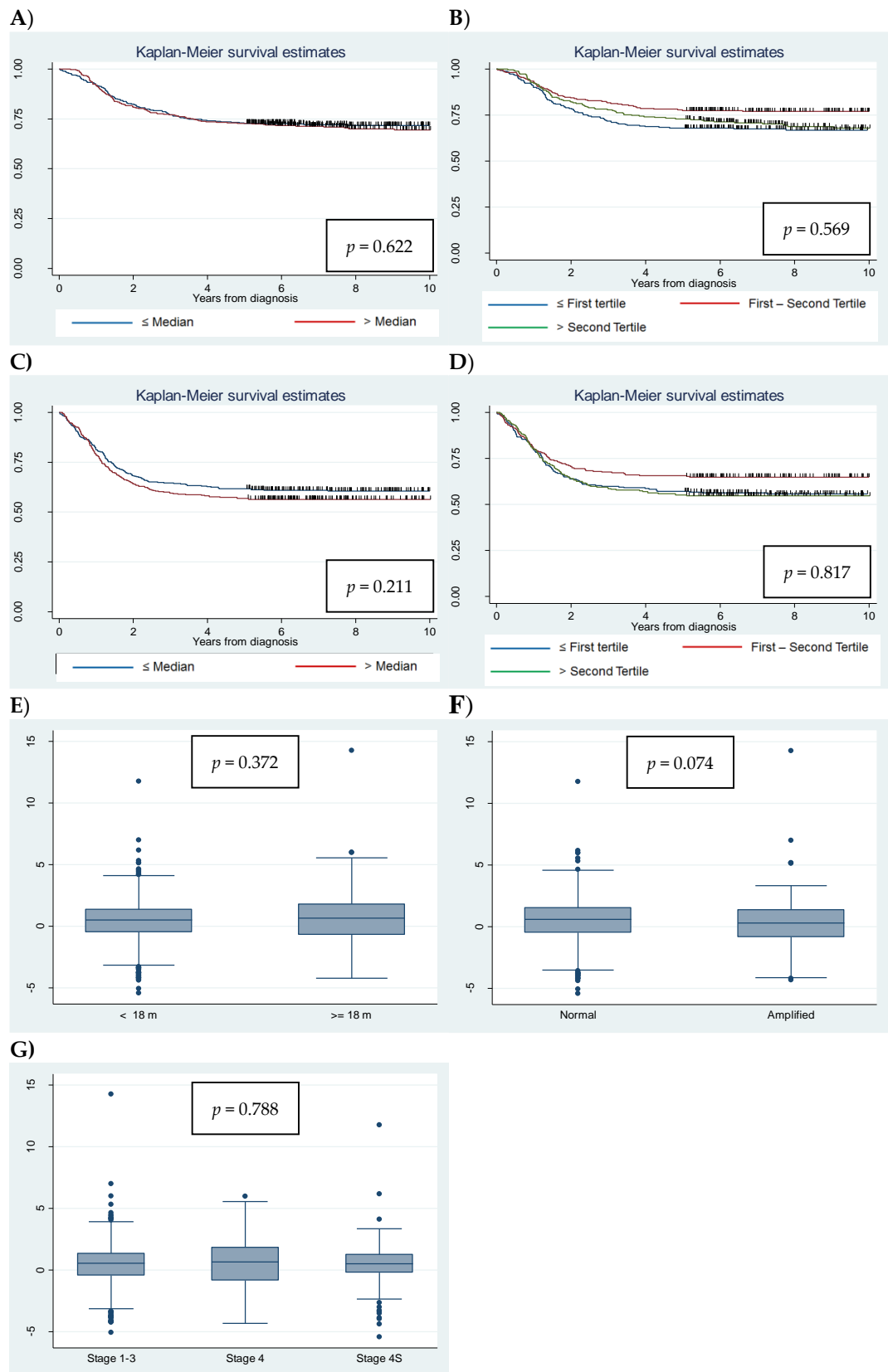
ACTA2 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S22



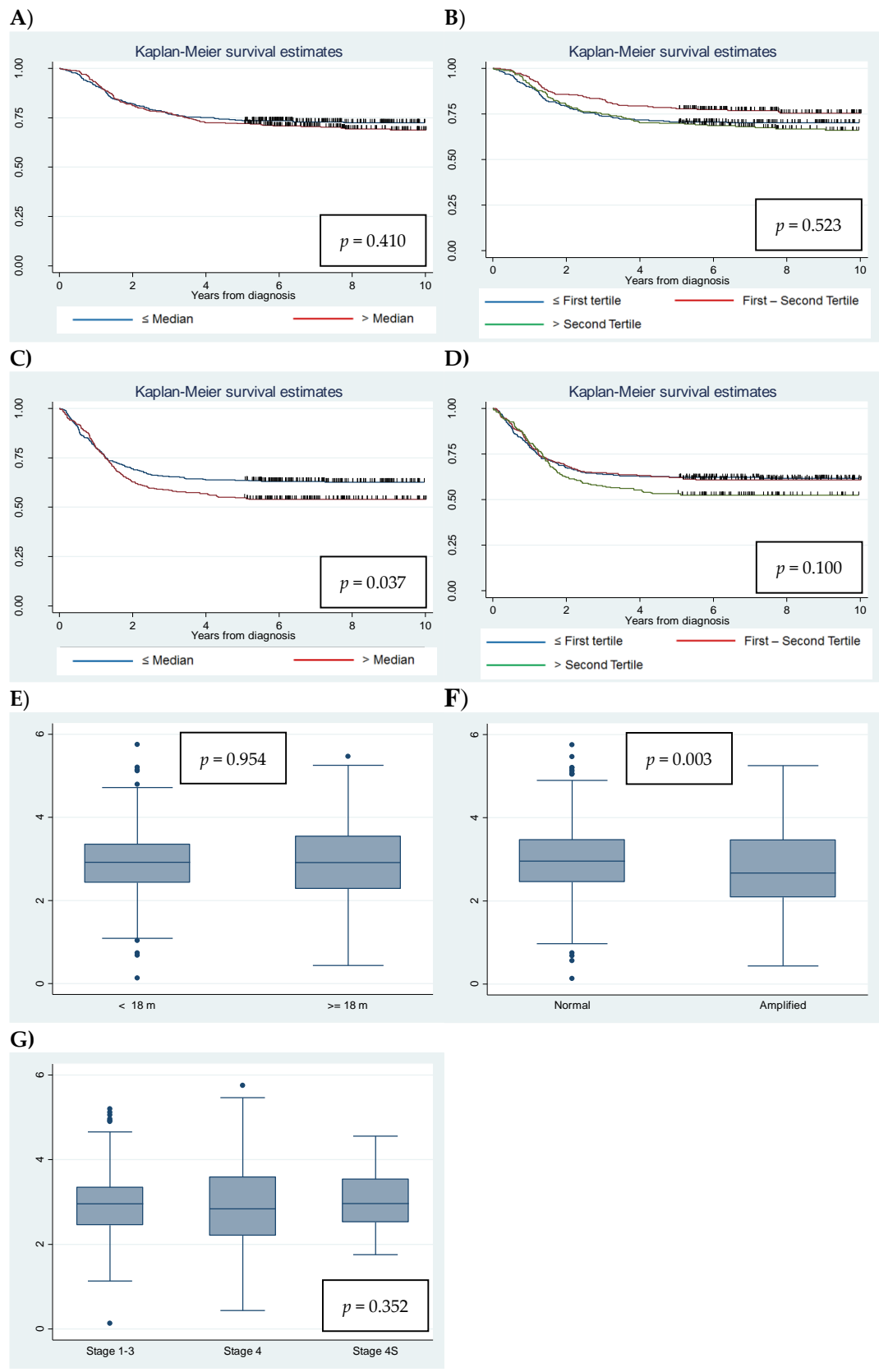
ANKRD1 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S23



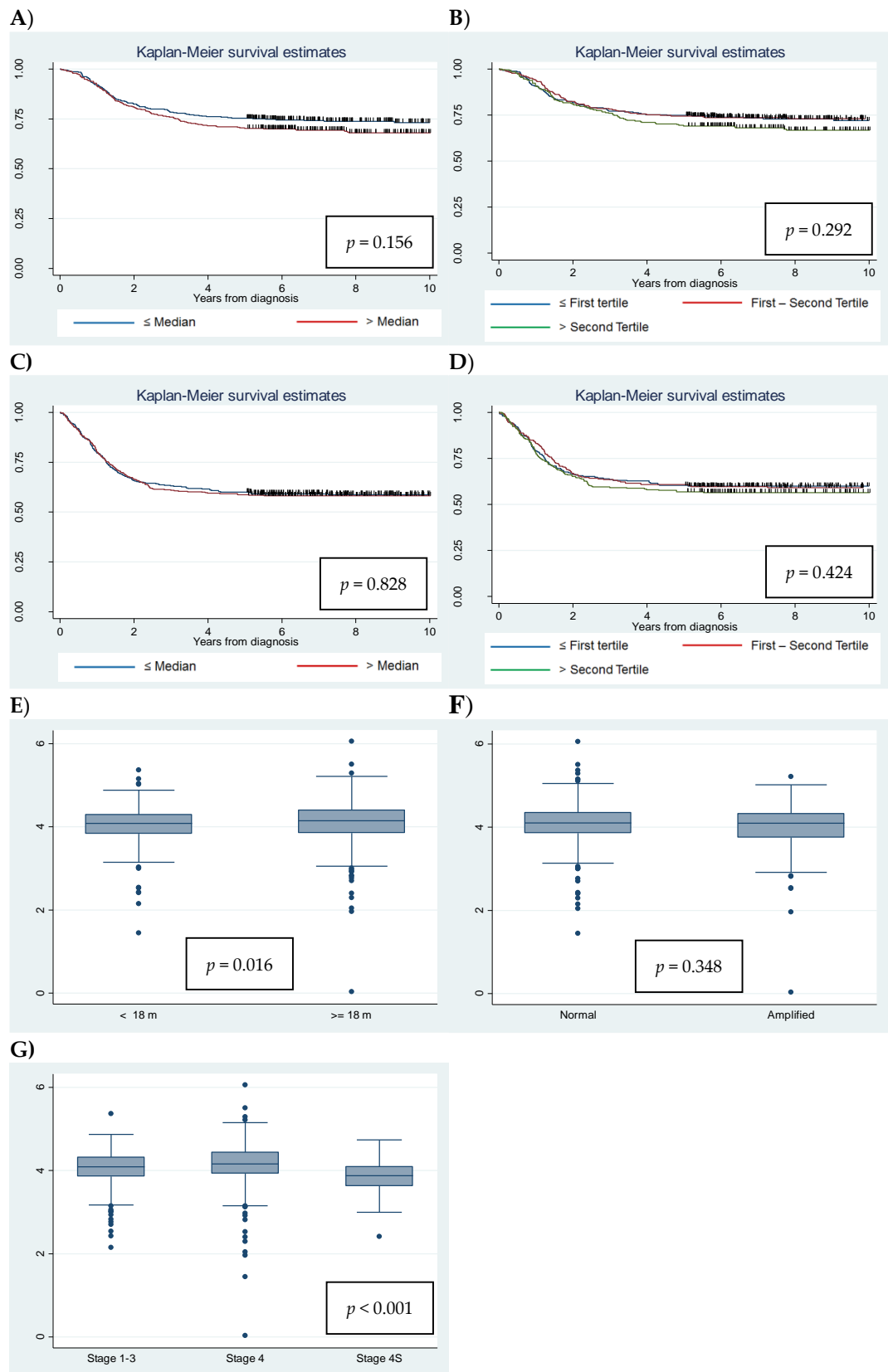
ANKRD22 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S24



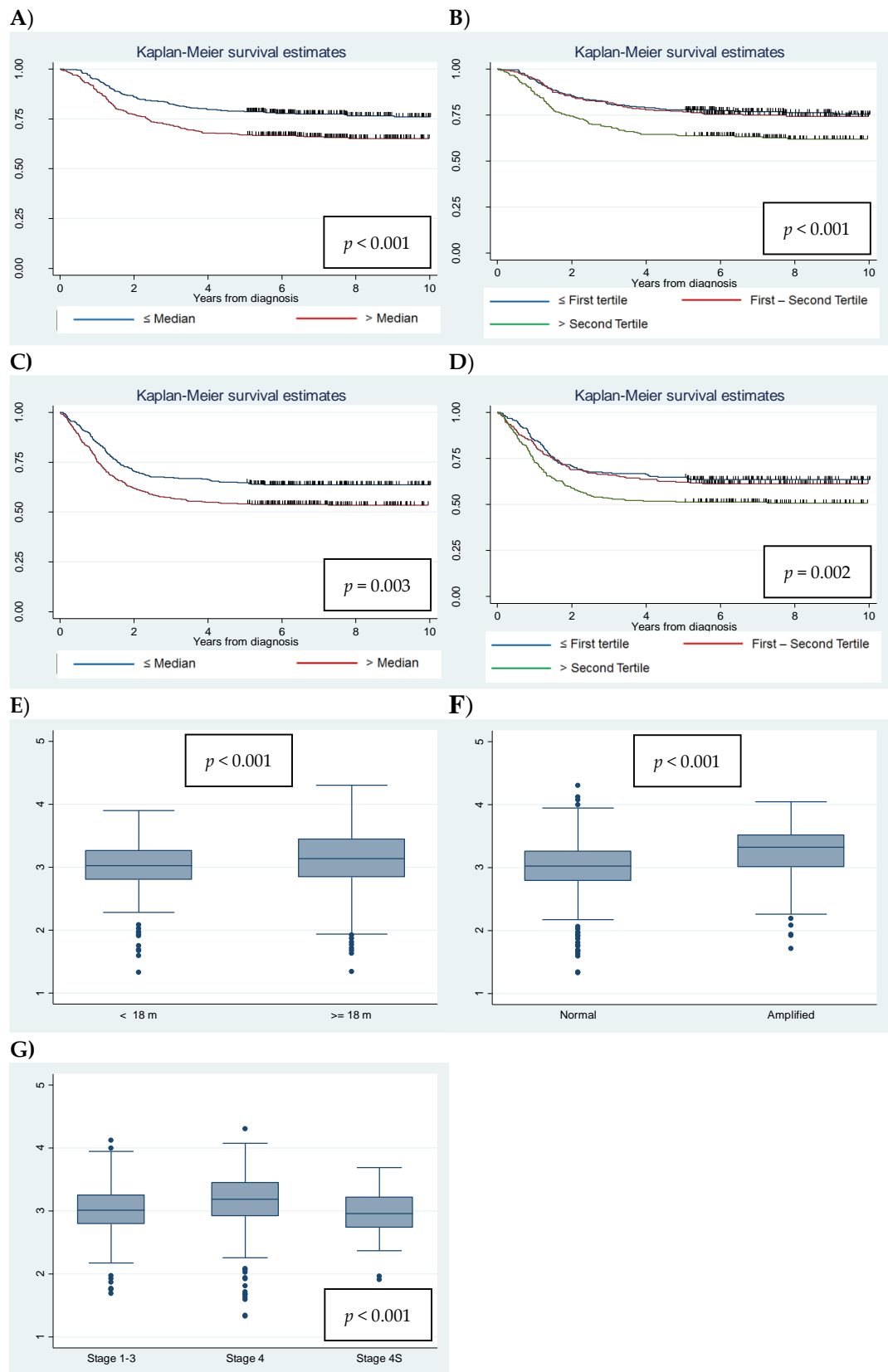
ANXA11 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S25



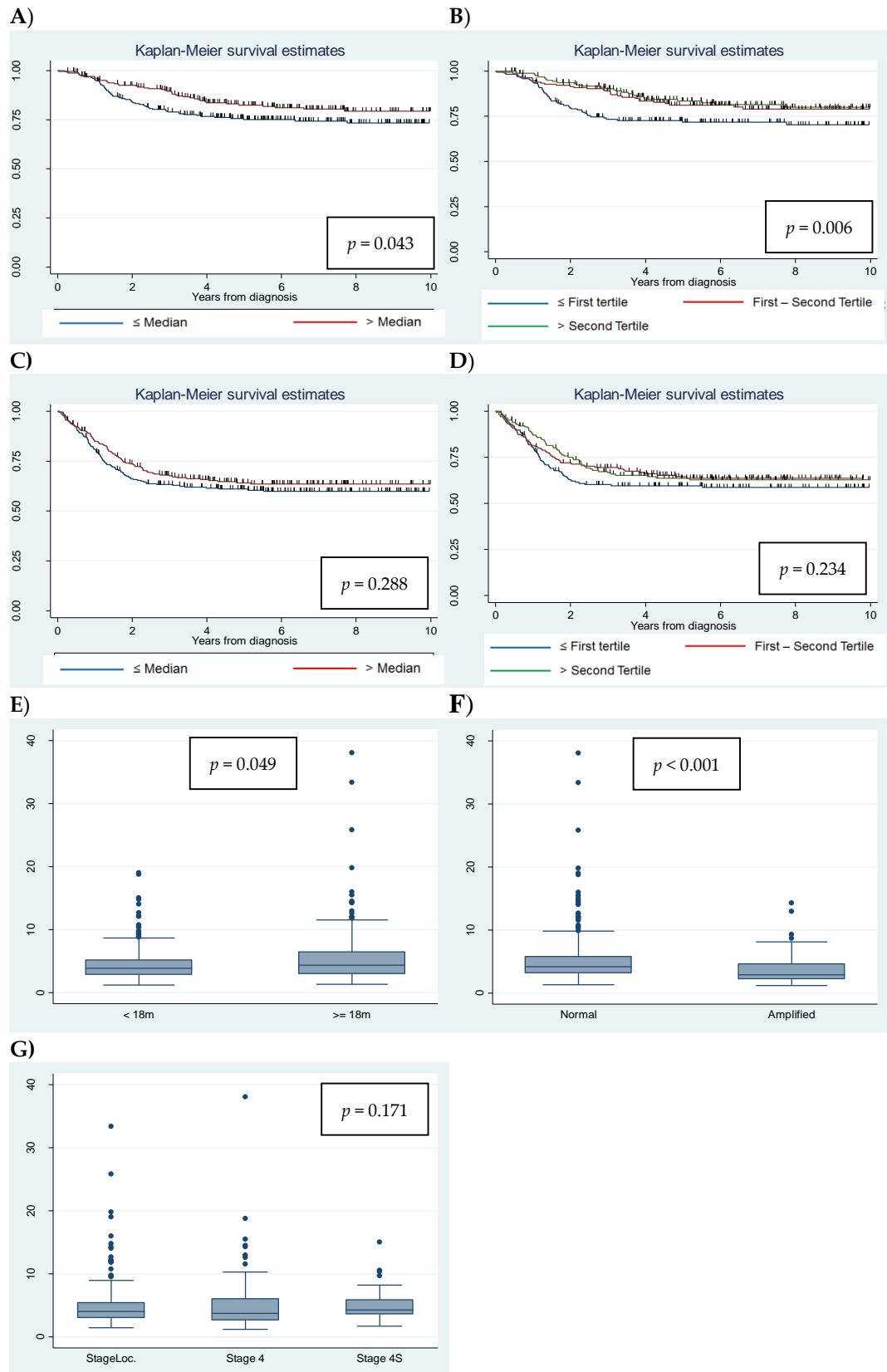
ATAD1 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S26



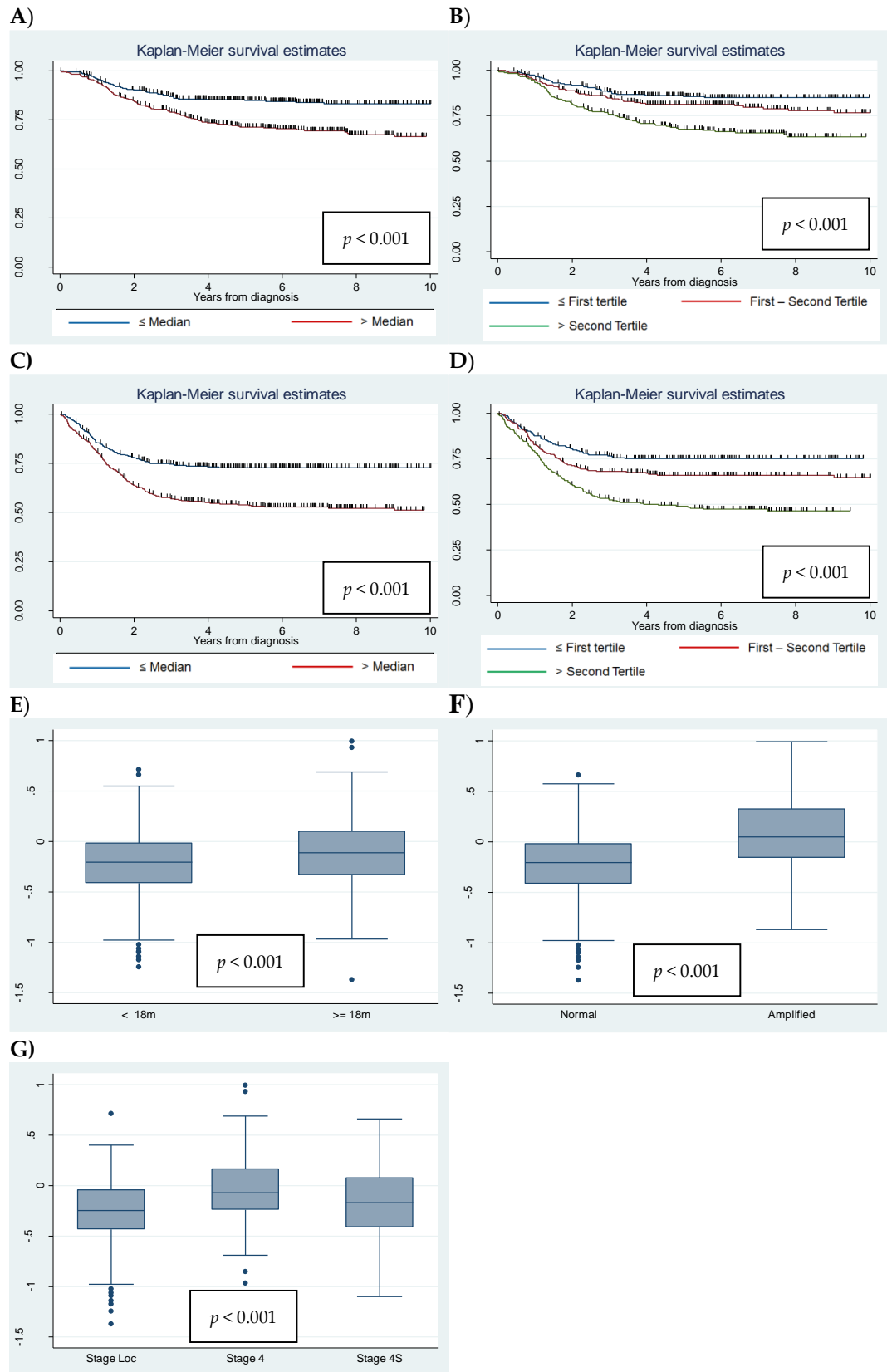
BMPR1A gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S27



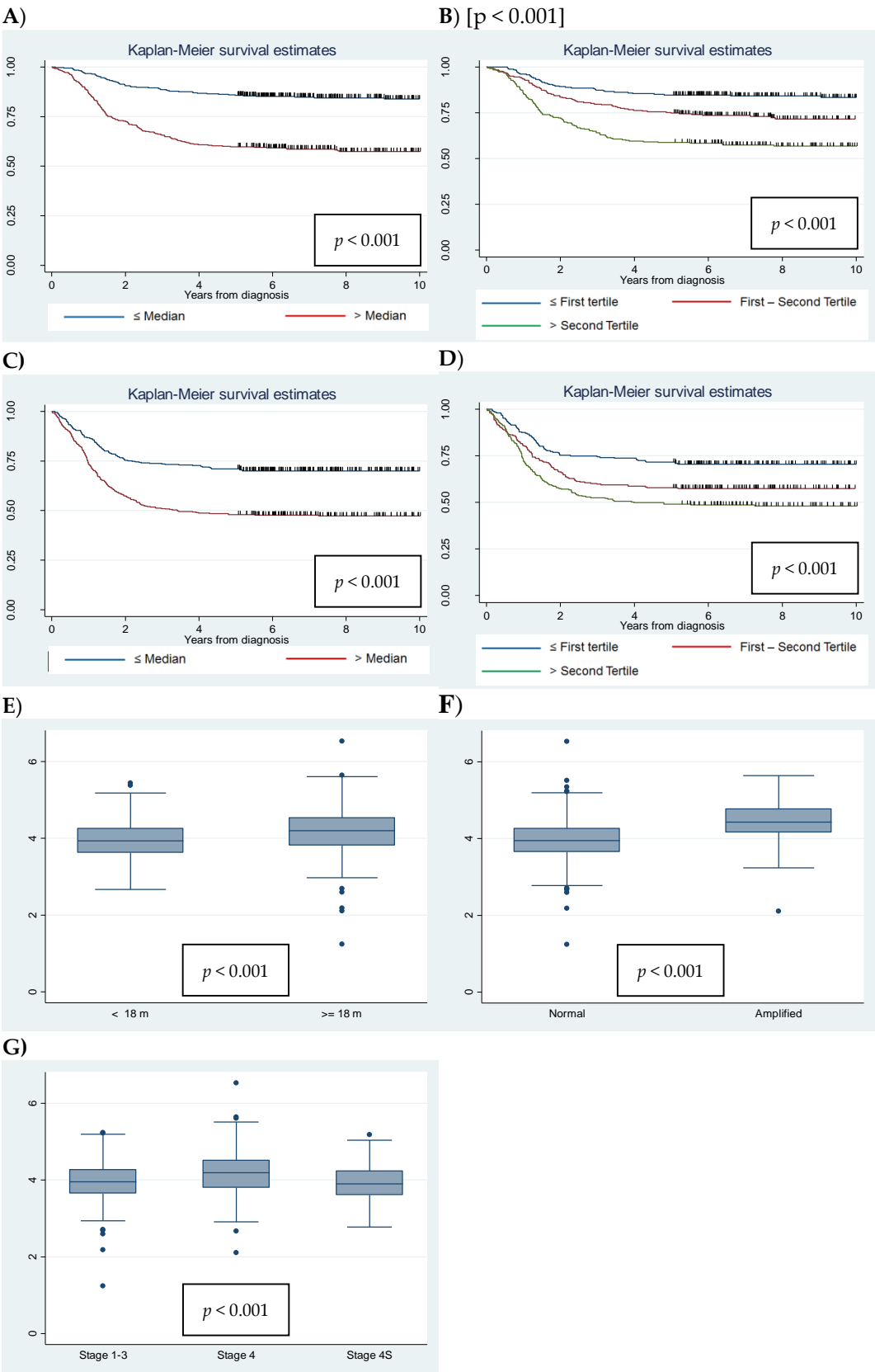
C10orf116 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S28



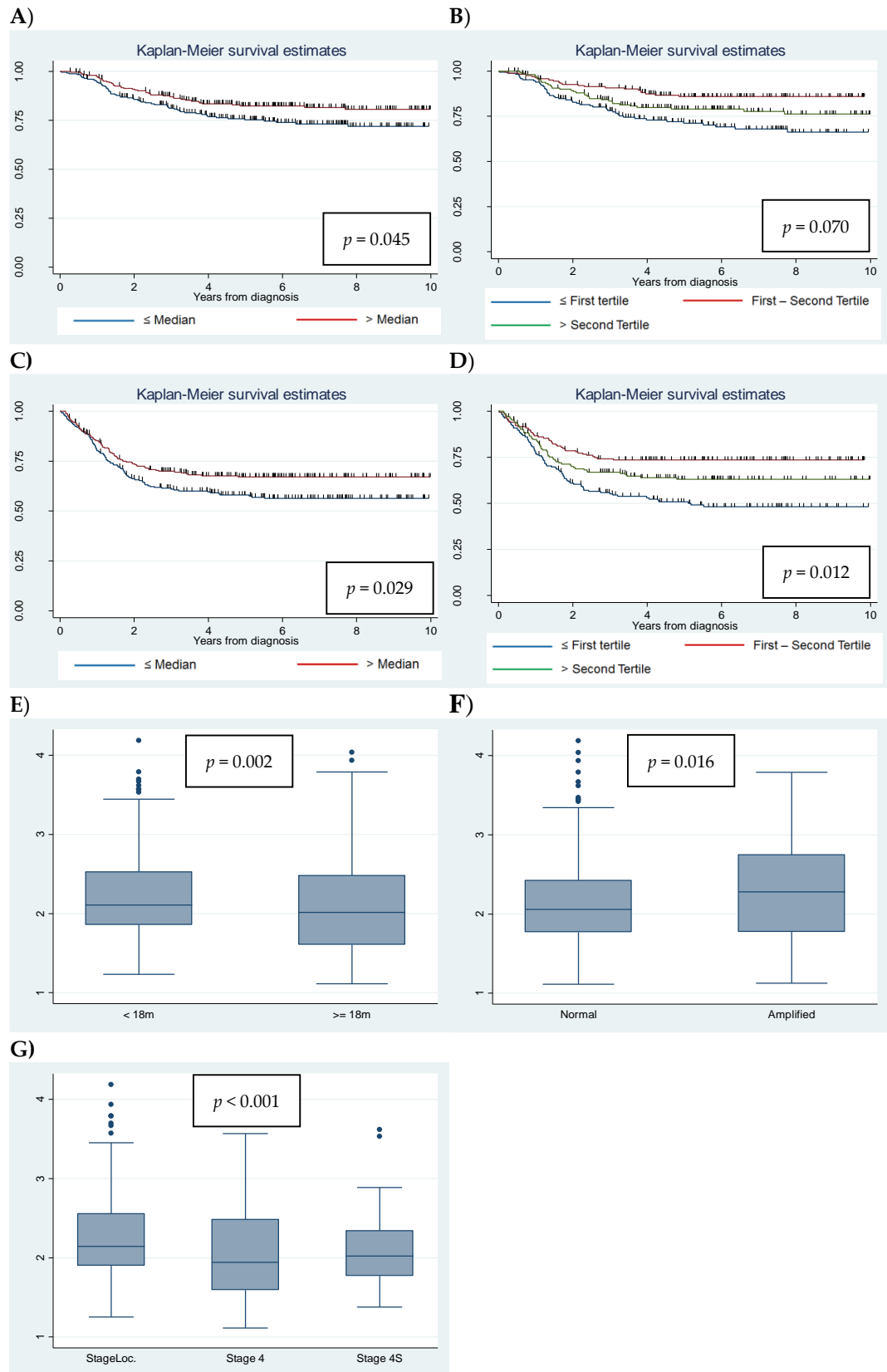
C10orf57 (alias *FLJ3263*, Agilent probe: A_23_P97853) gene expression and its association with survival and clinical characteristics in a cohort of 709 NB patients in the E-MTAB-1781 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S29



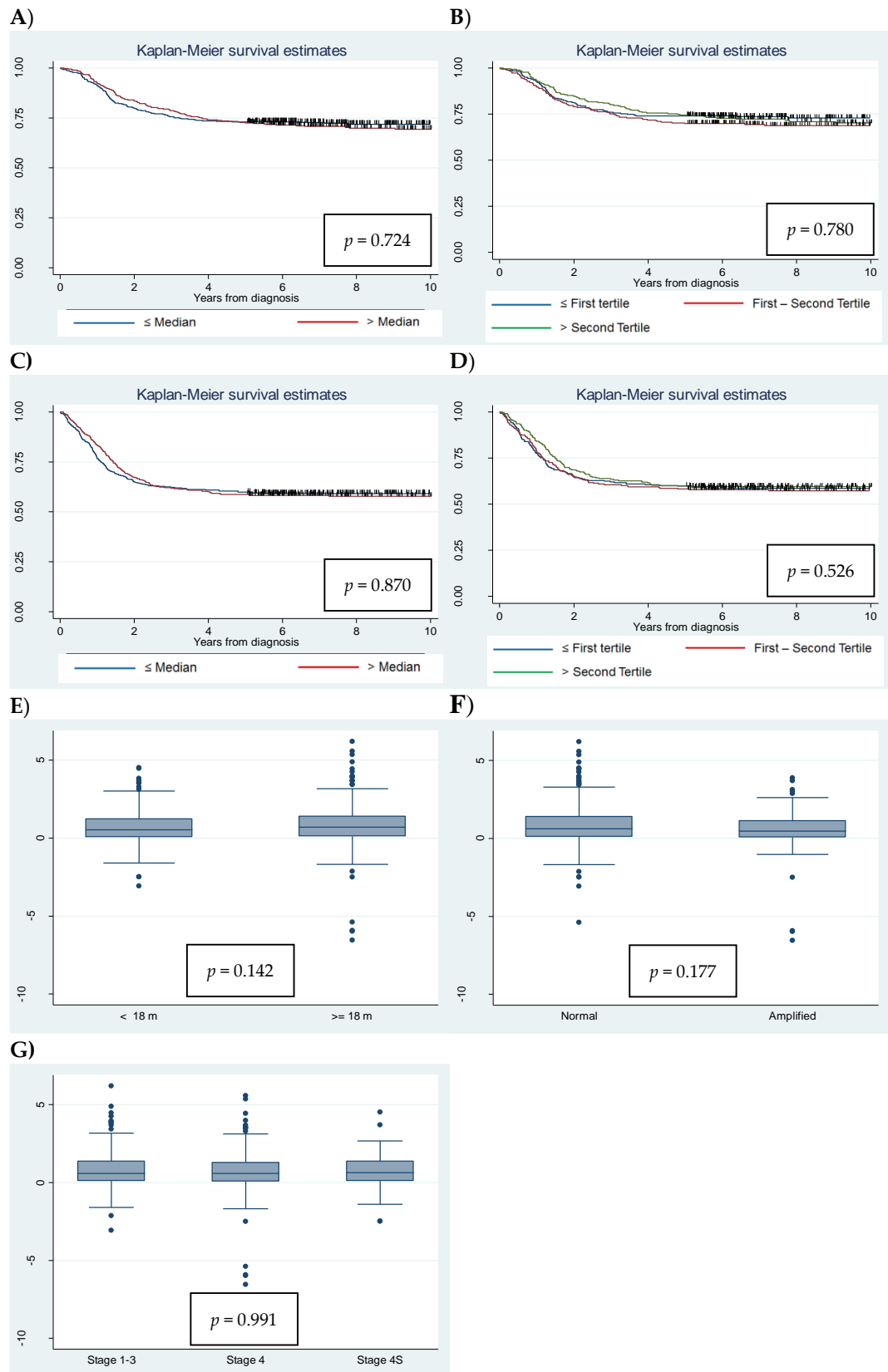
C10orf58 (alias *FAM213A*) gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S30



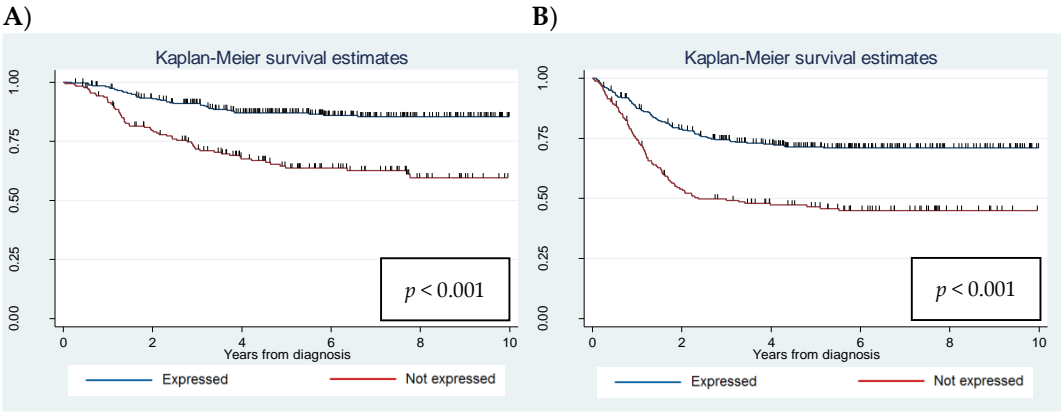
CFL1P1 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S31



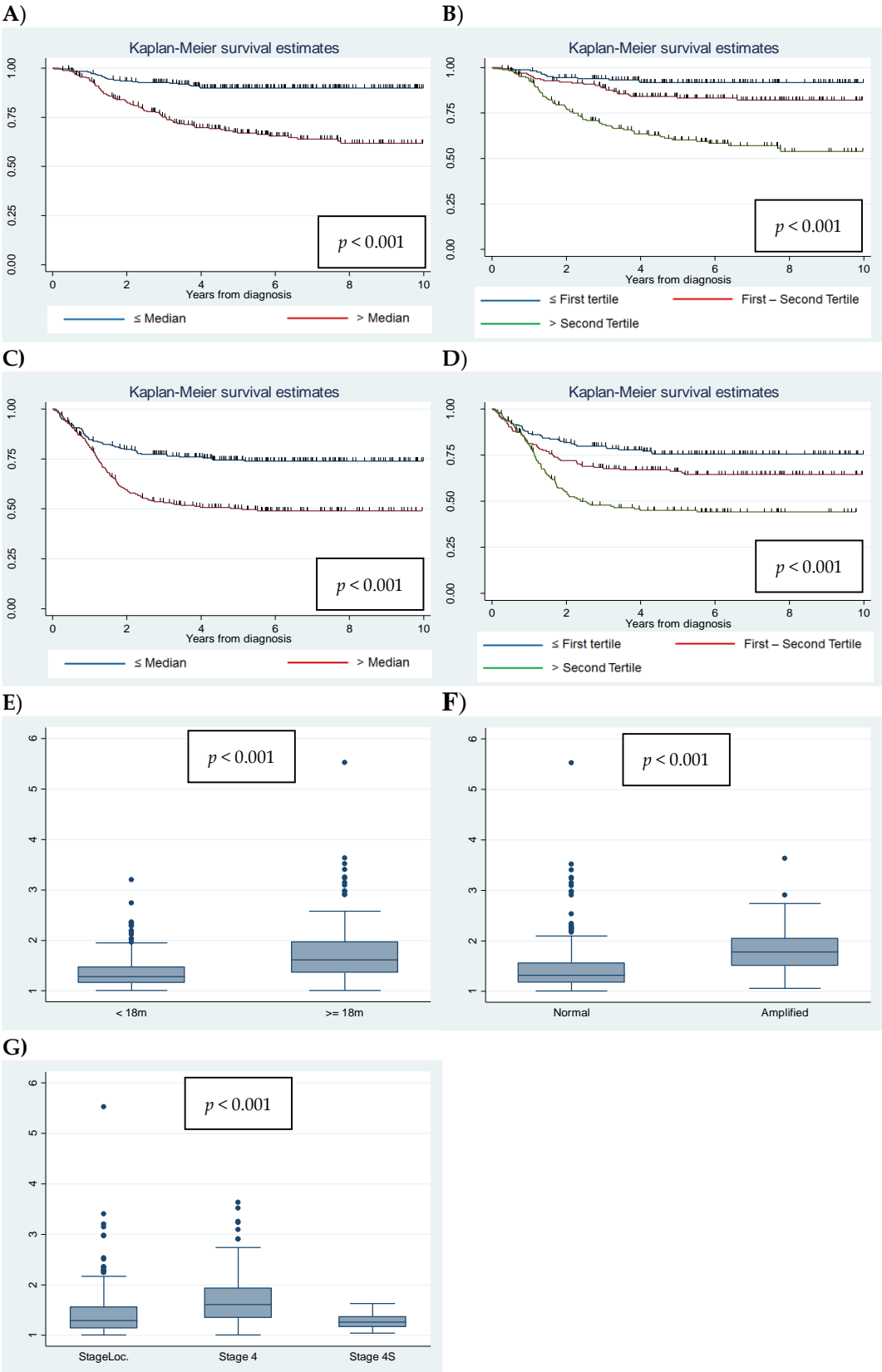
CH25H gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S32



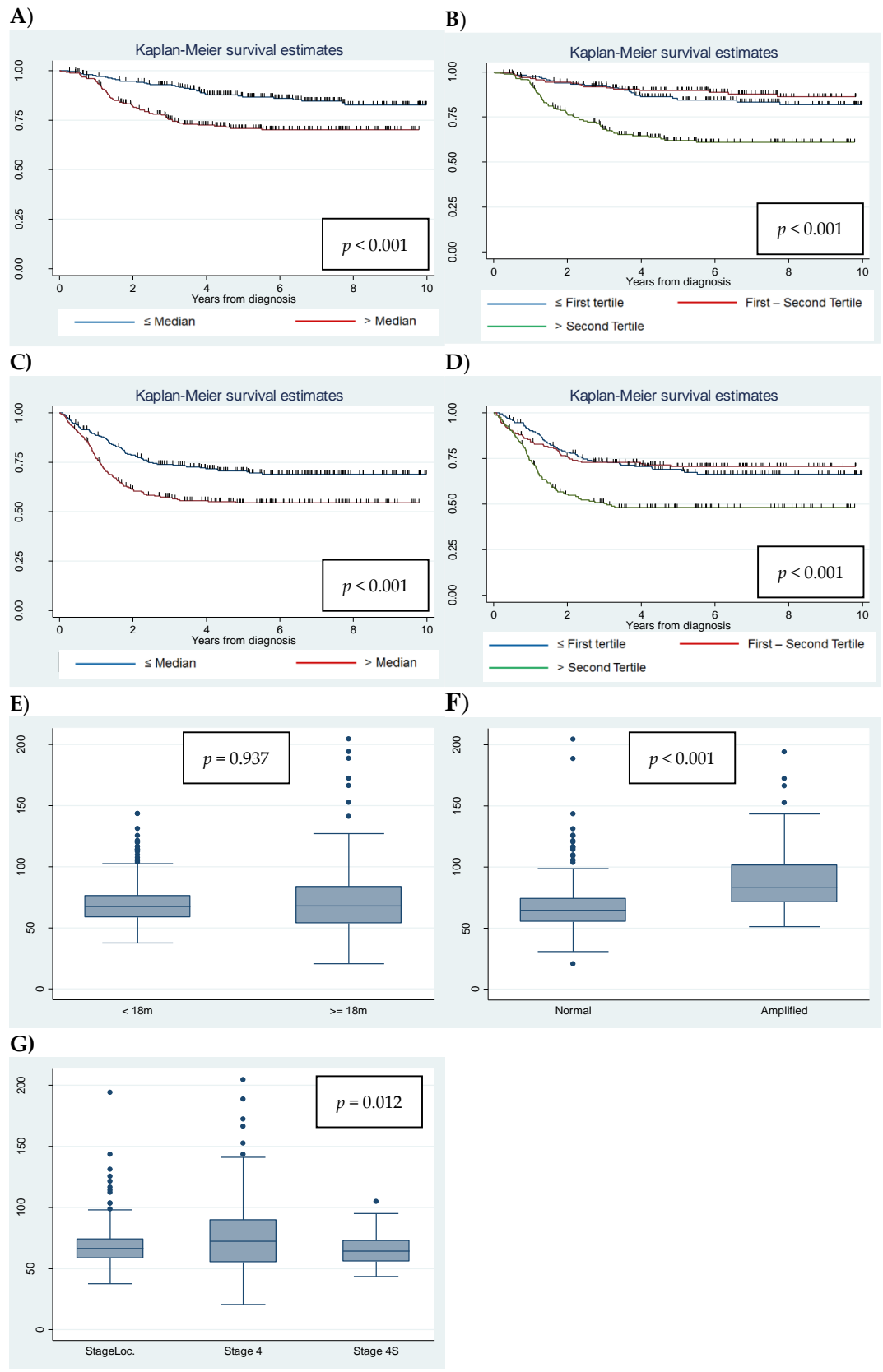
DYDC1 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, gene expression yes/not; (B) Event Free Survival, gene expression yes/not.

Supplementary Figure S33



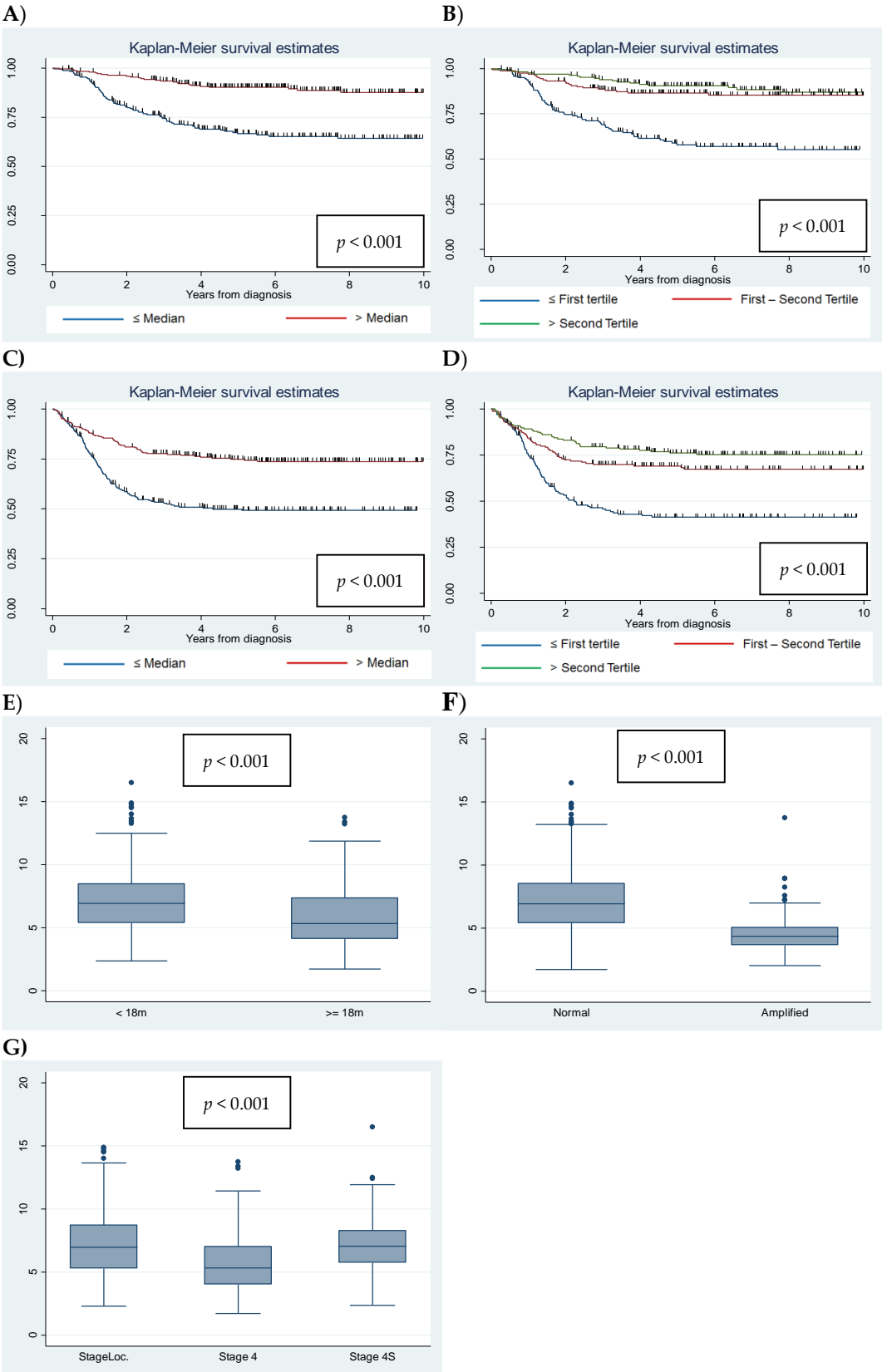
DYDC2 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S34



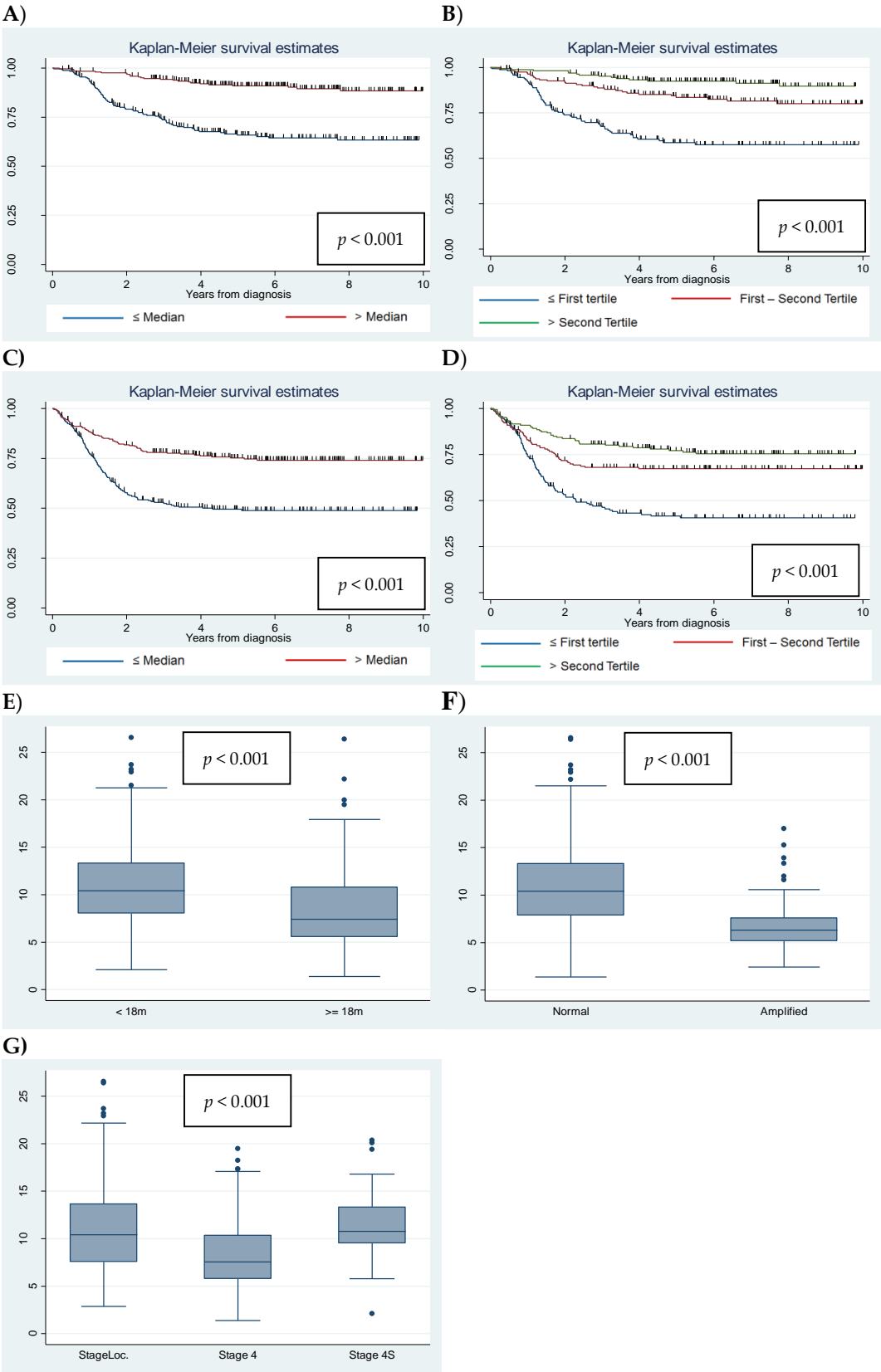
EIF5AL1 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S35



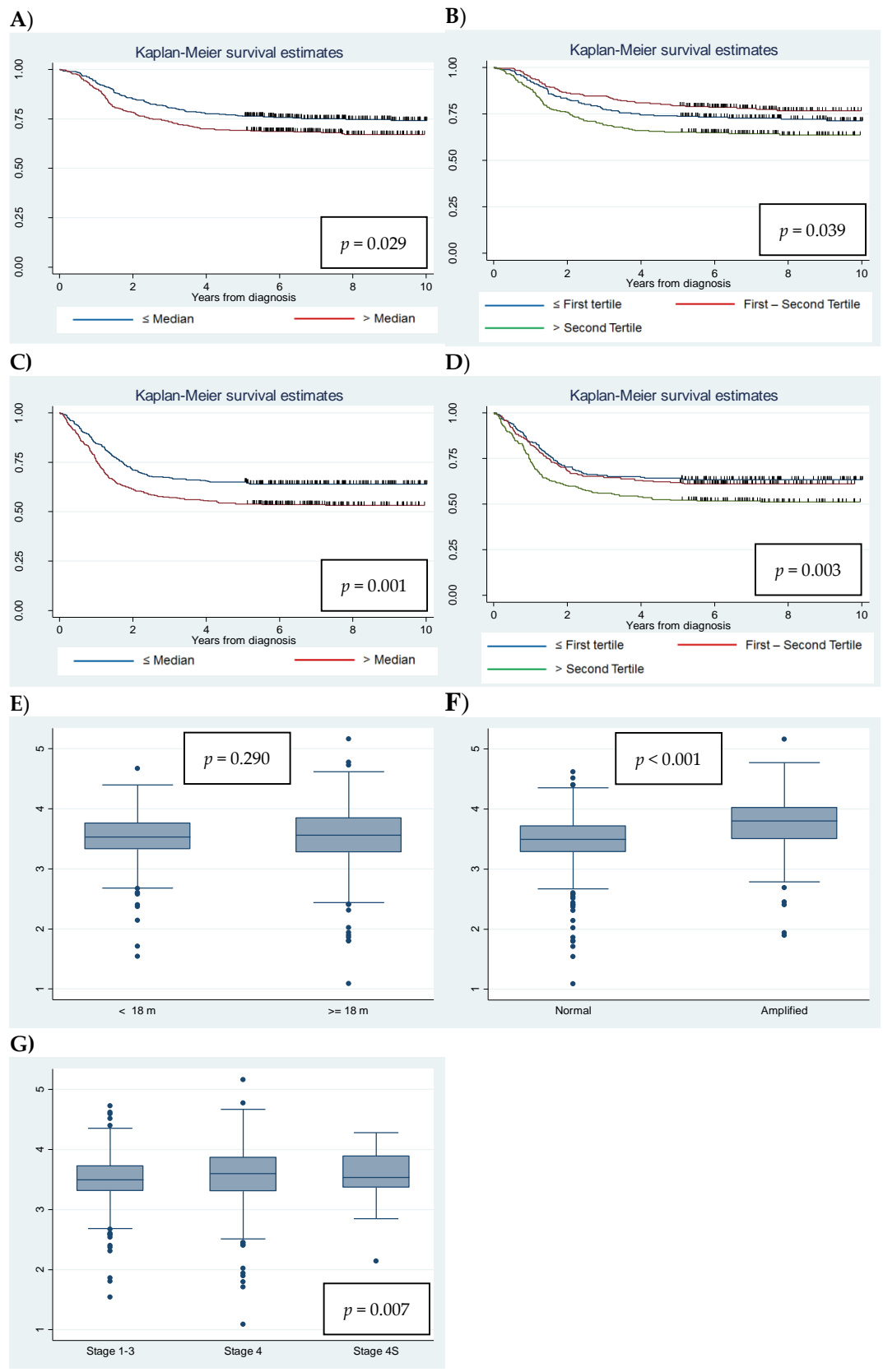
FAM22A gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S36



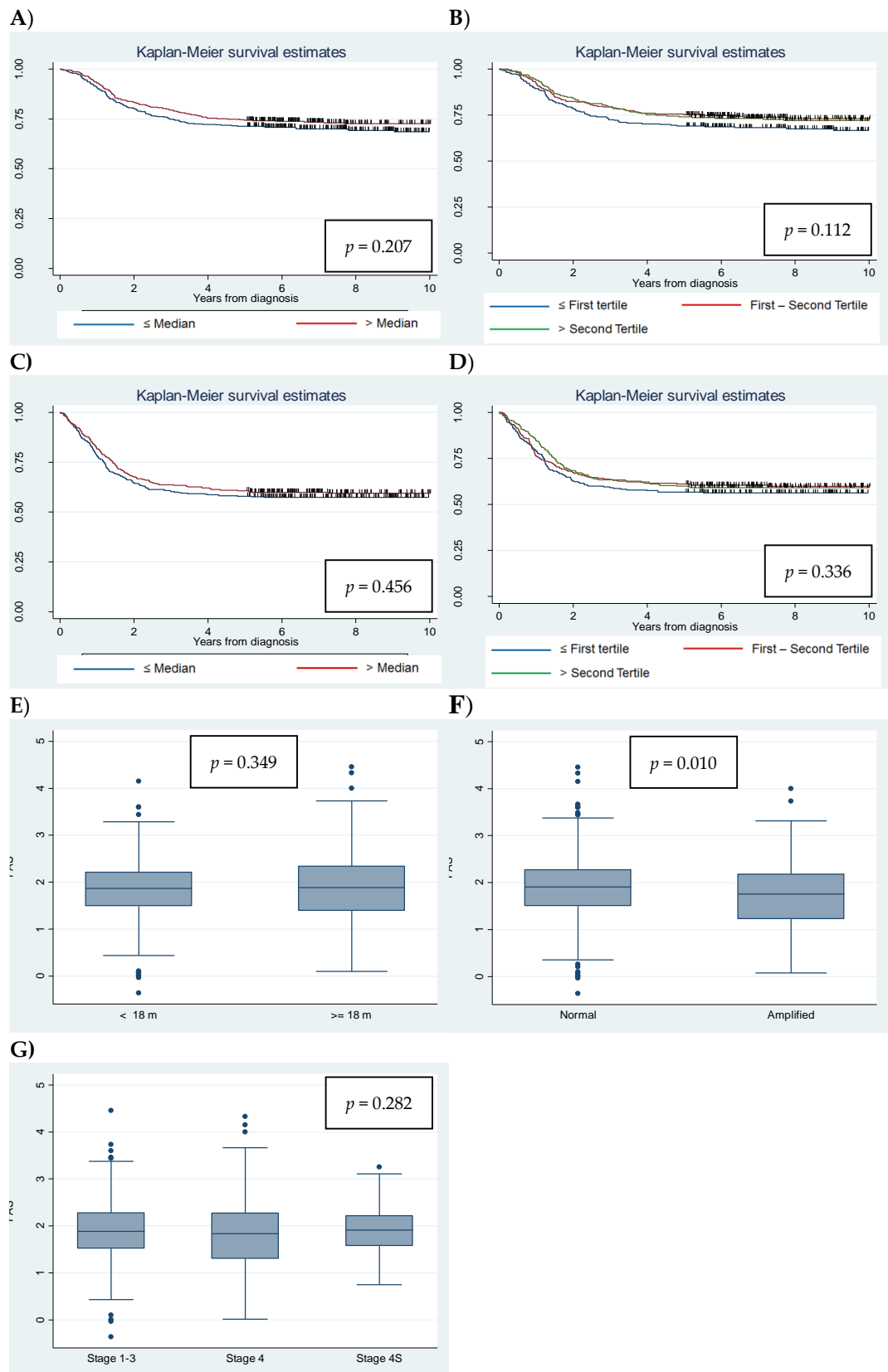
FAM22D gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S37



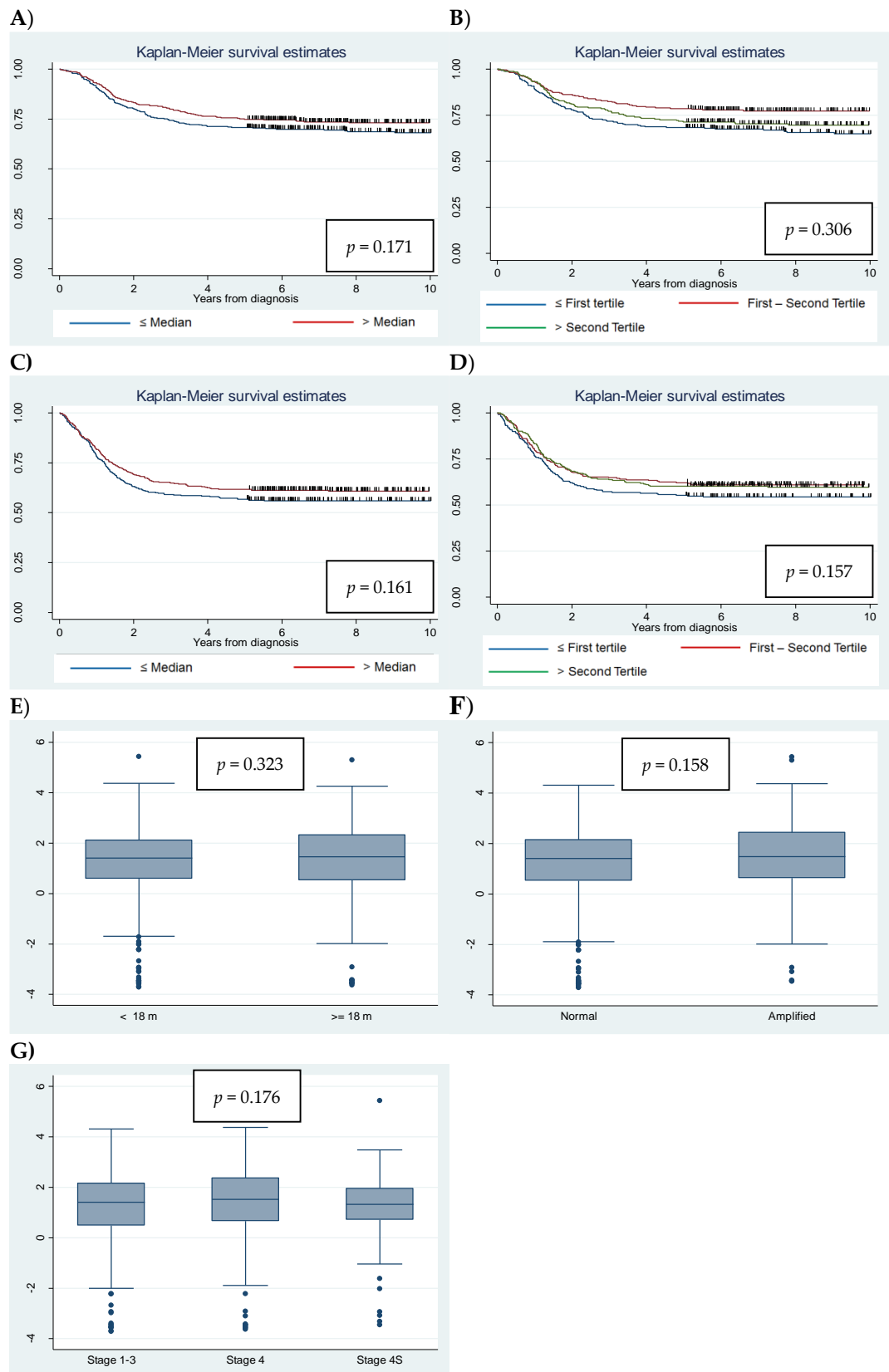
FAM35A gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S38



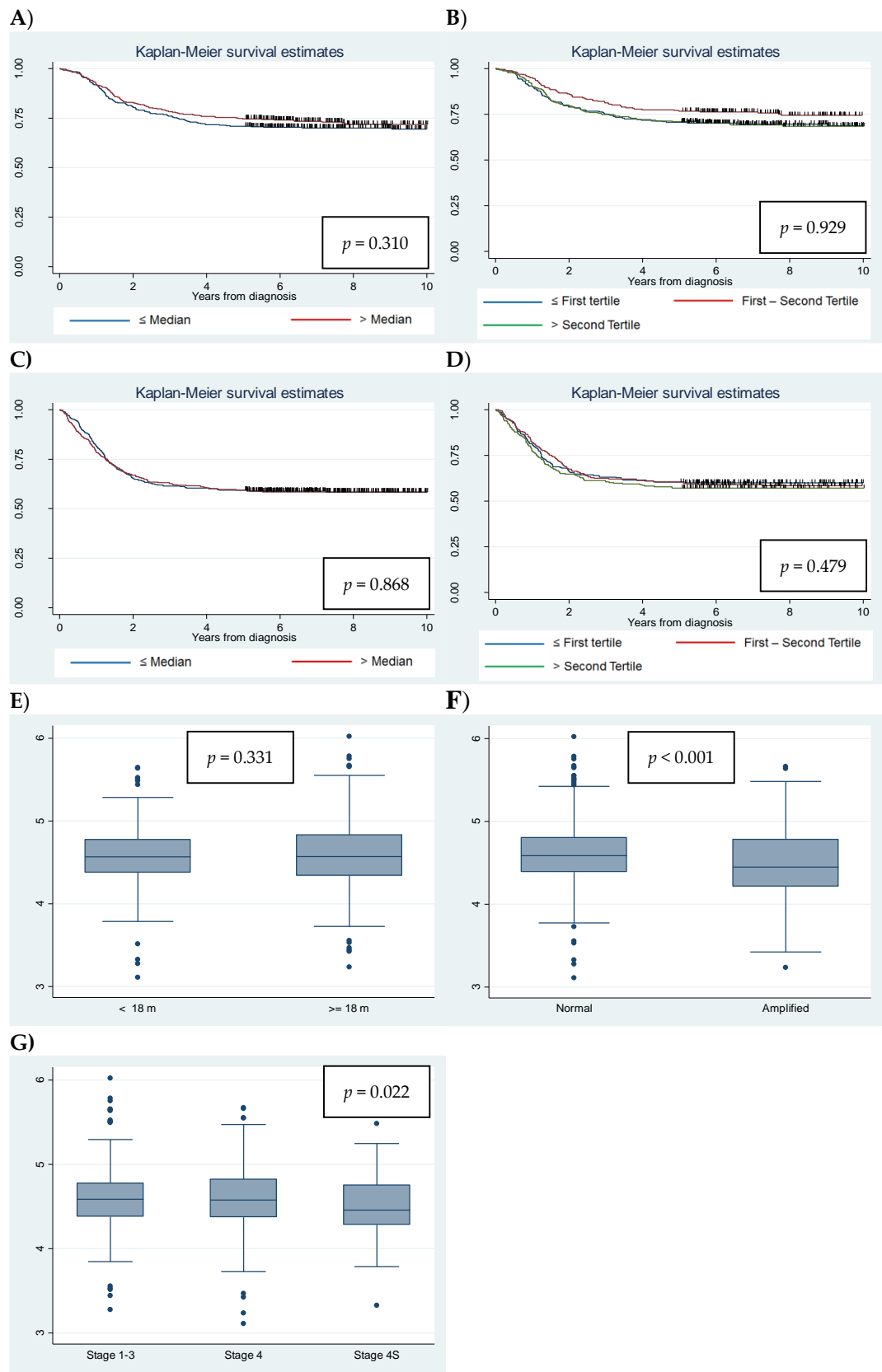
FAS gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S39



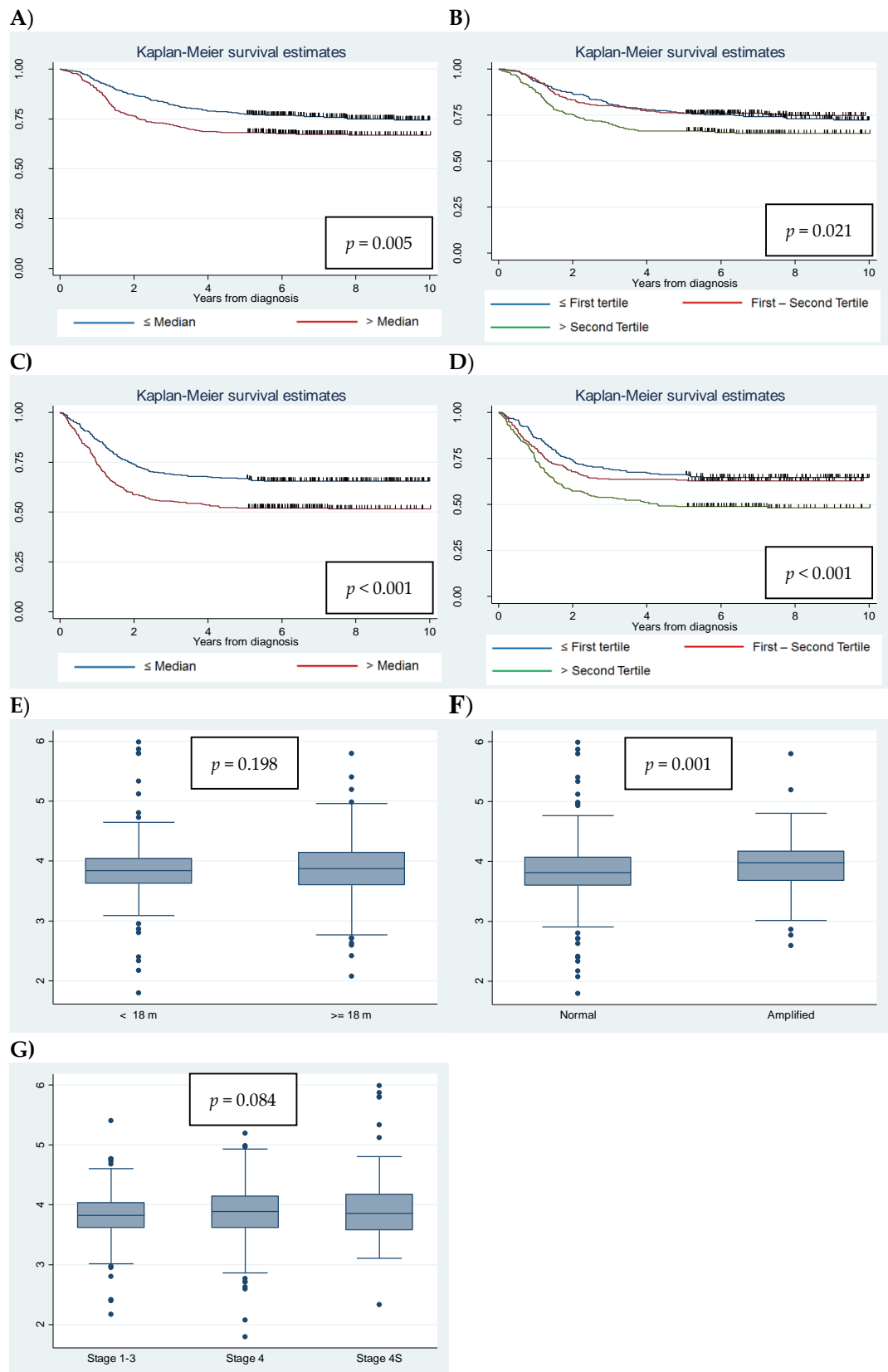
FLJ37201 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S40



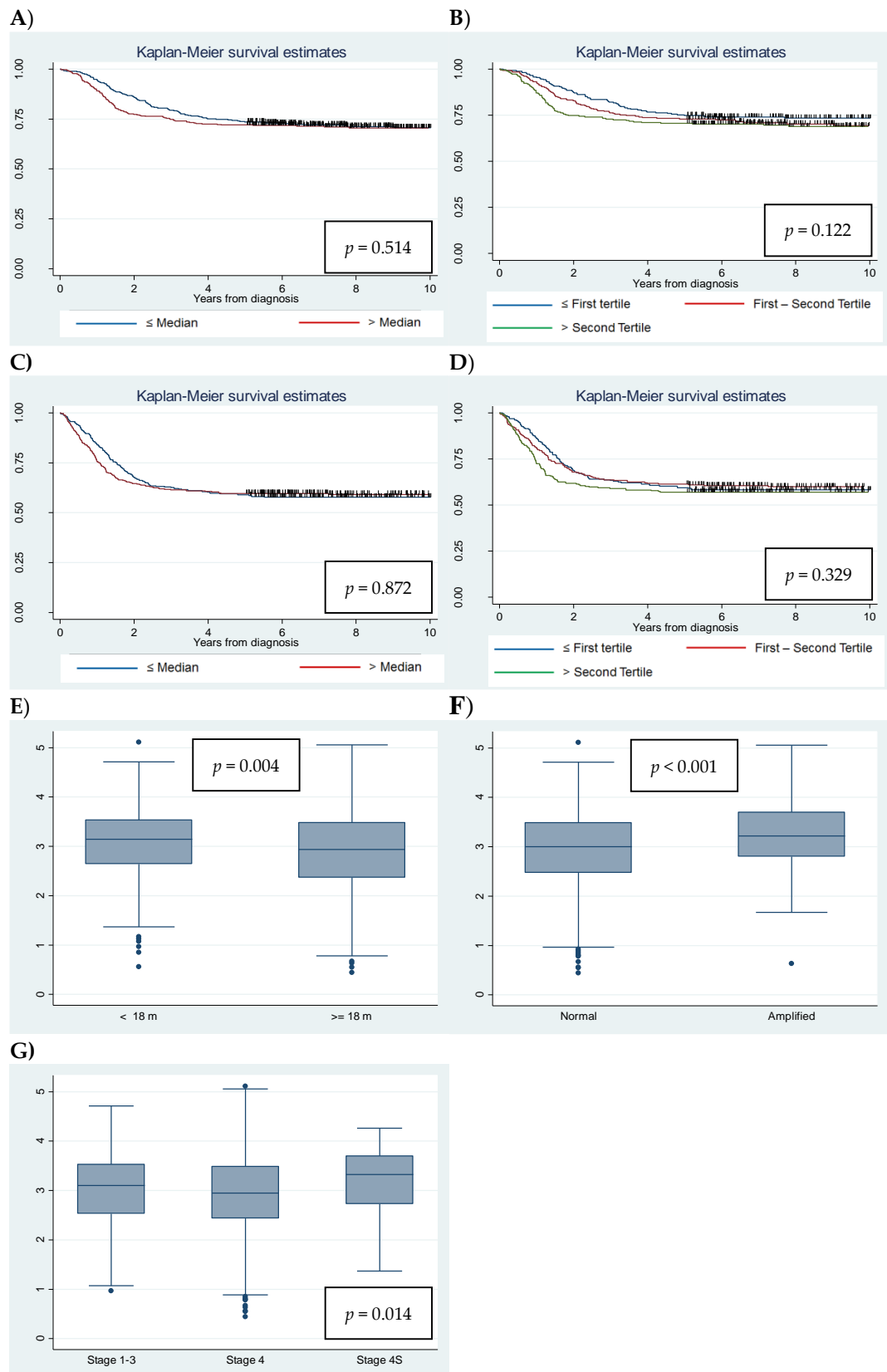
GHITM gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S41



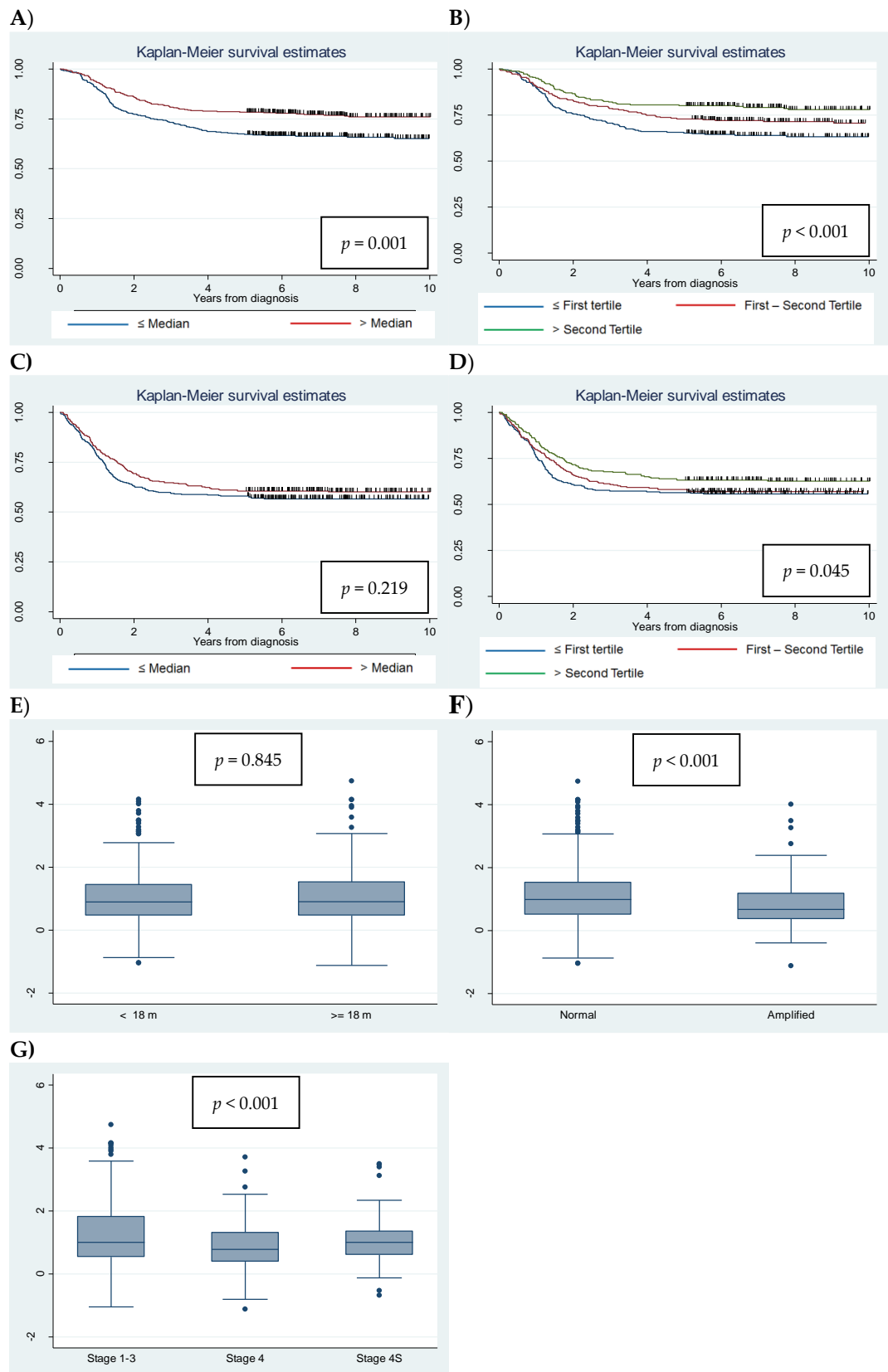
GLUD1 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S42



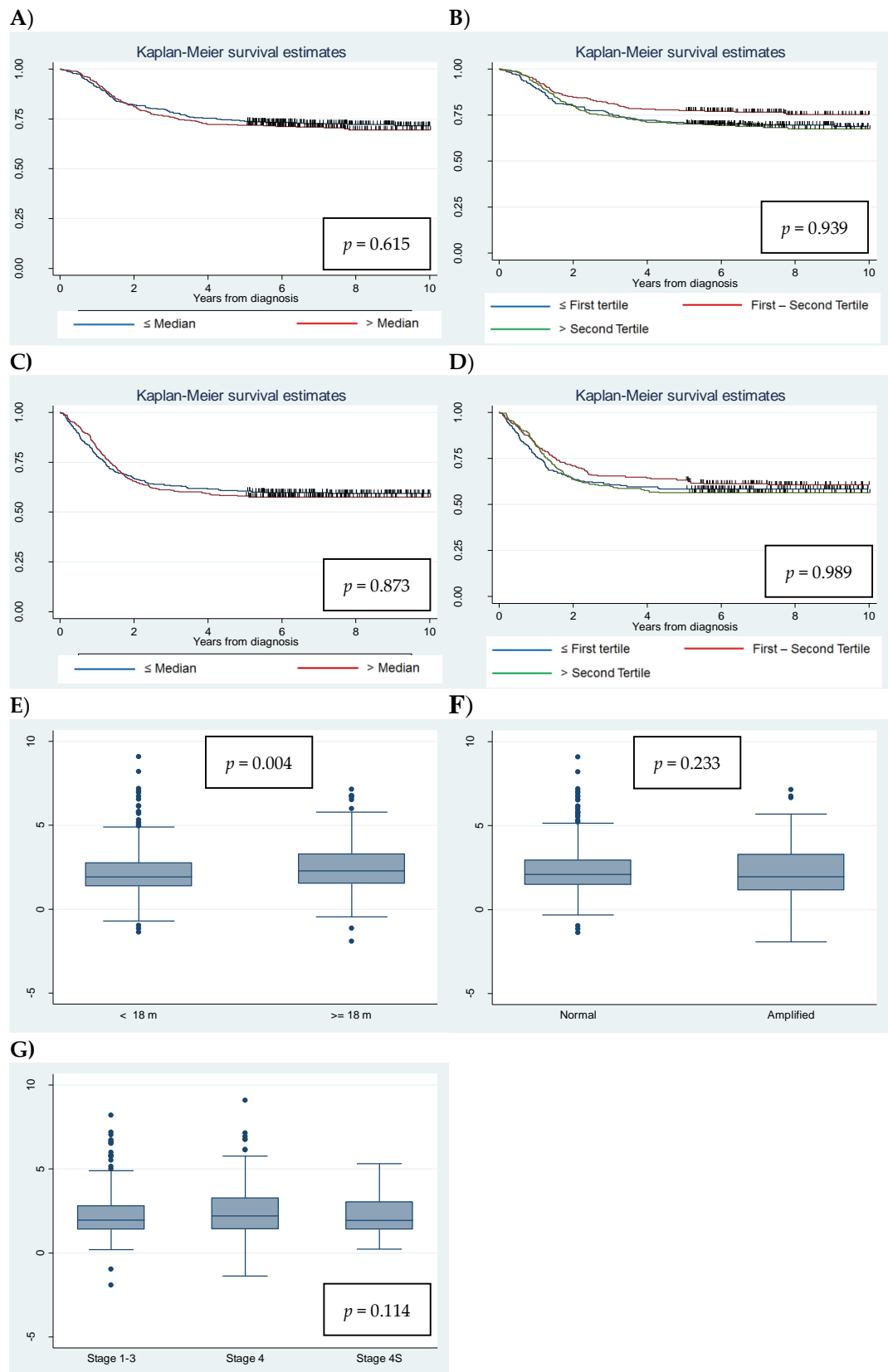
GRID1 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S43



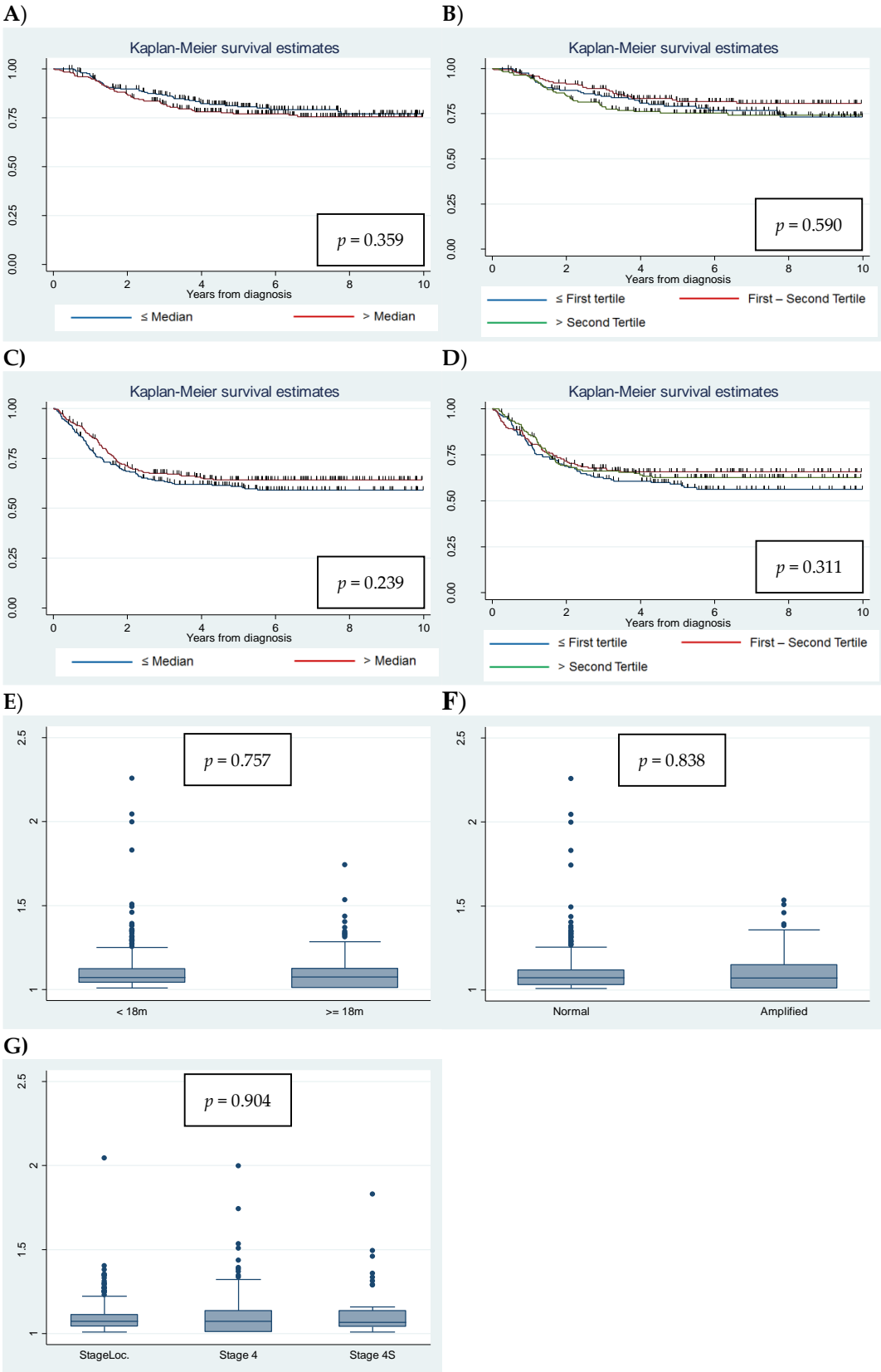
HTR7 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S44



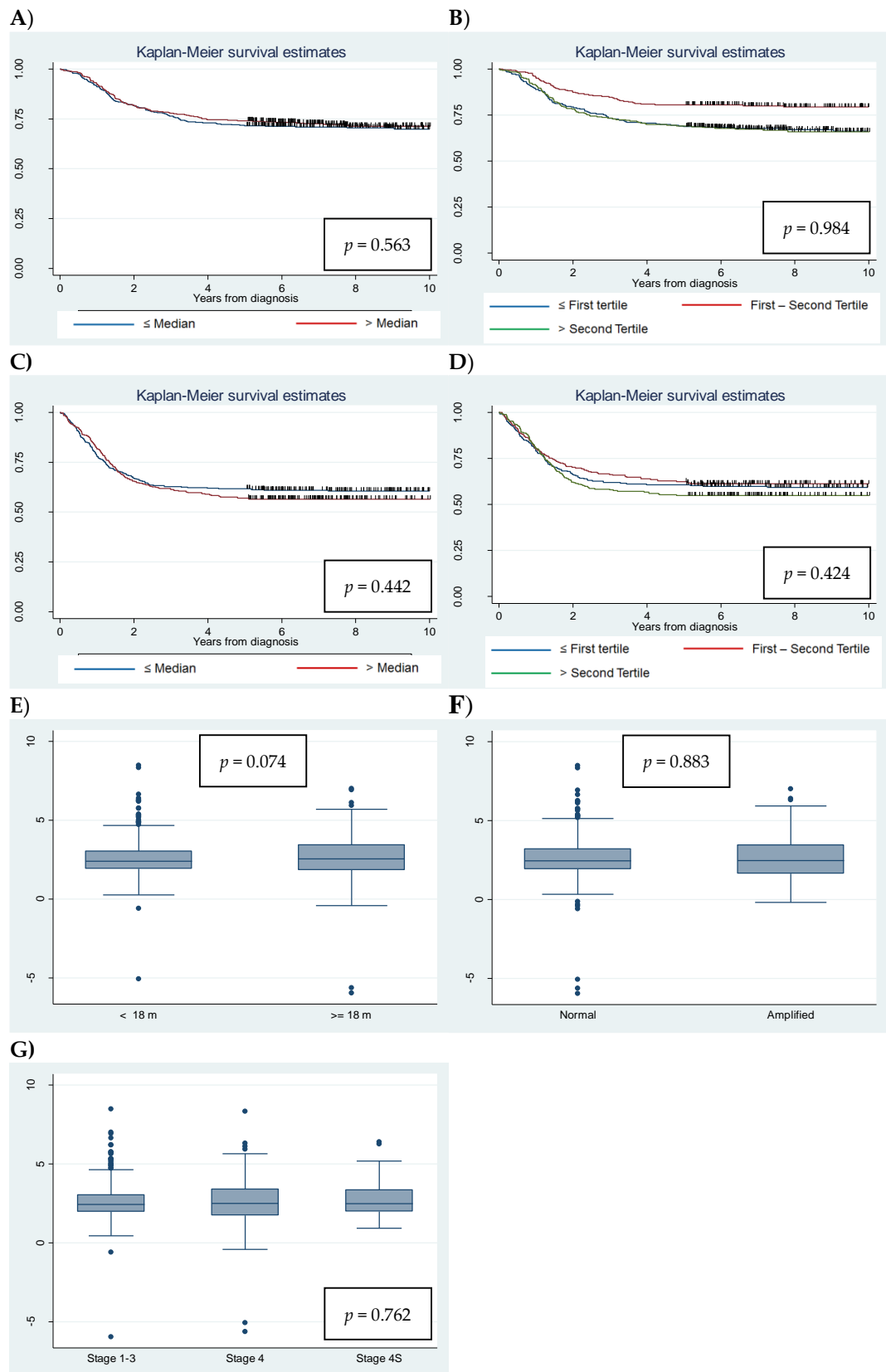
IFIT1 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S45



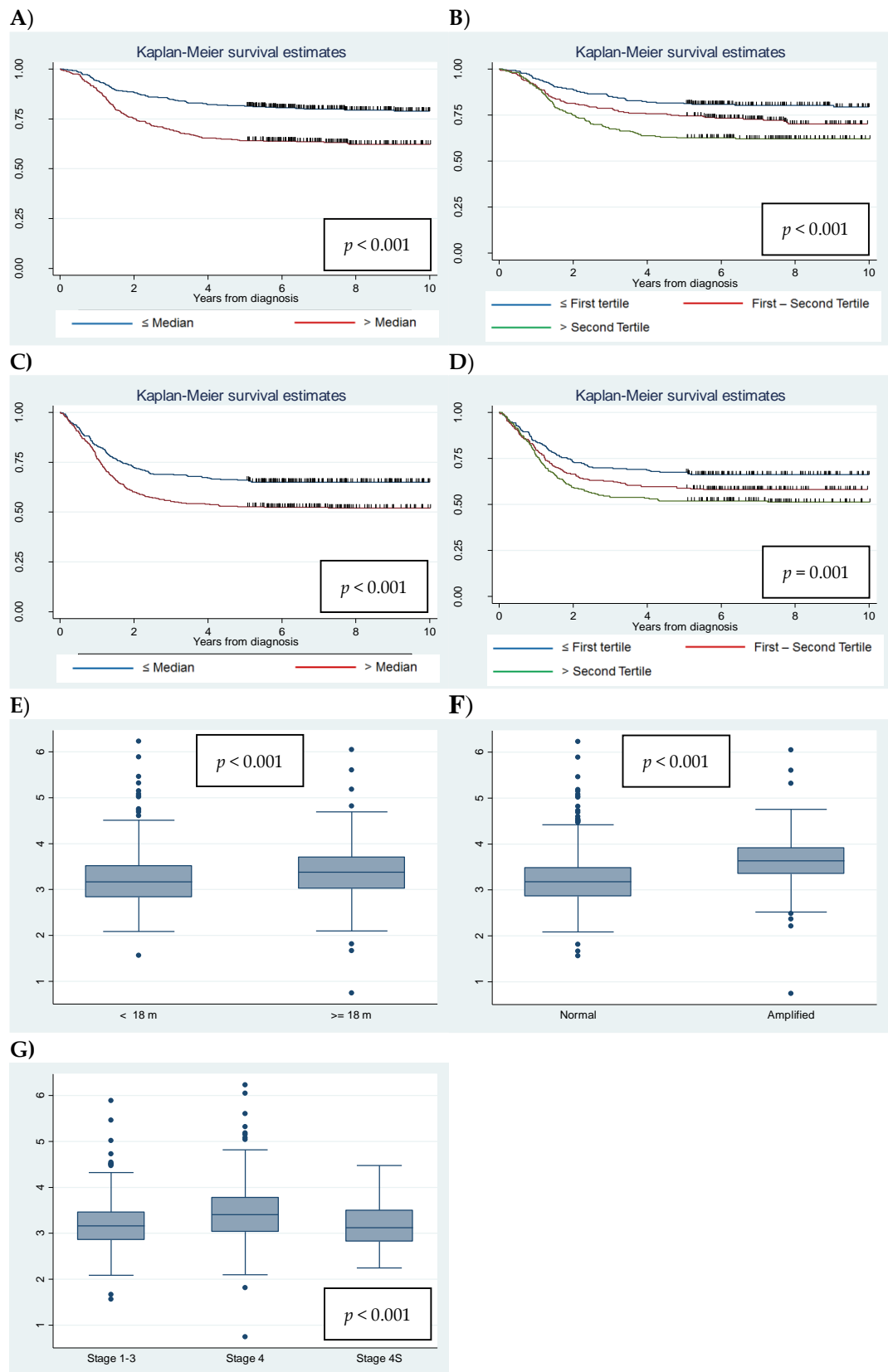
IFIT1L (alias *IFIT1B*) gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S46



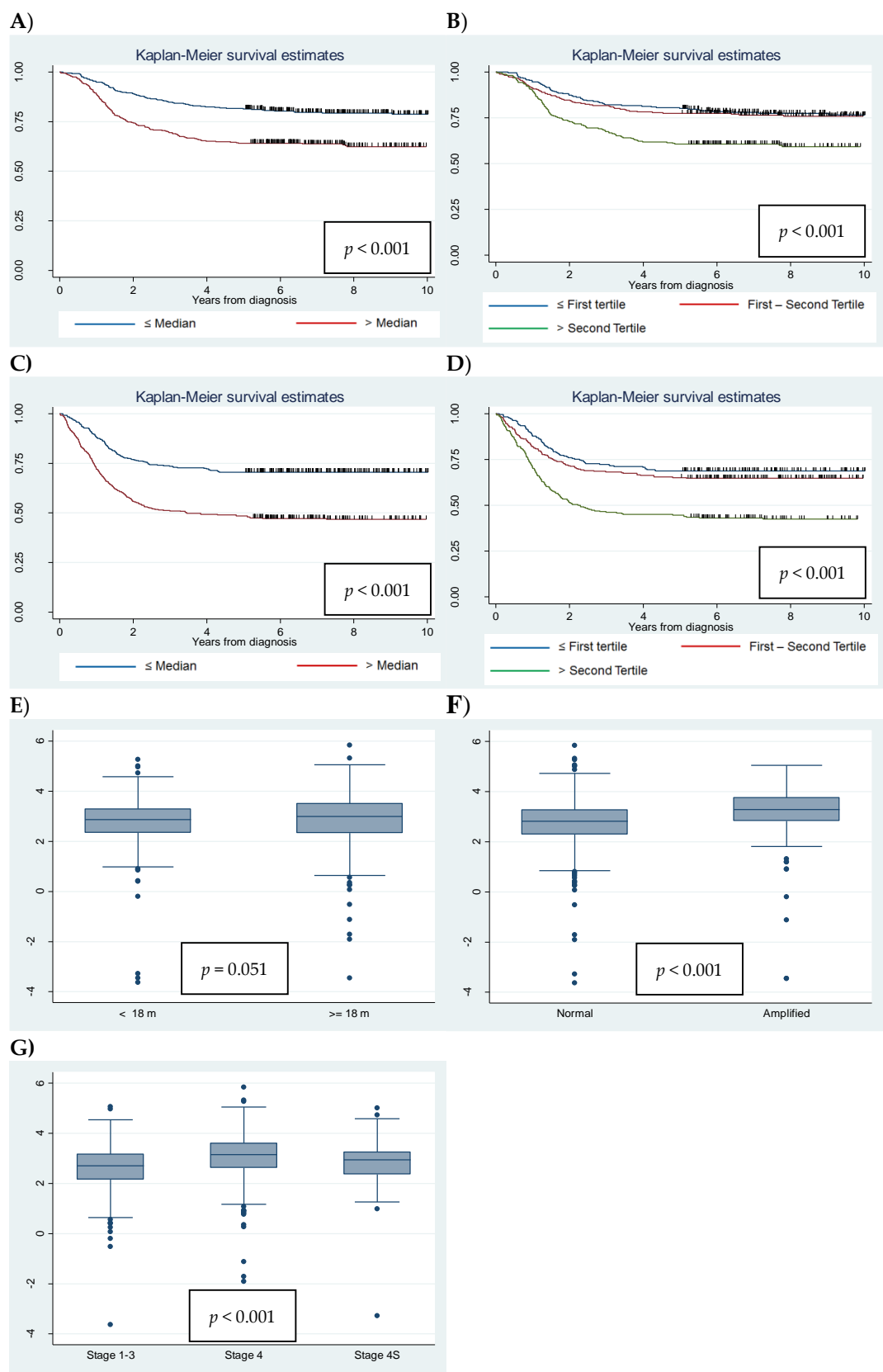
IFIT3 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S47



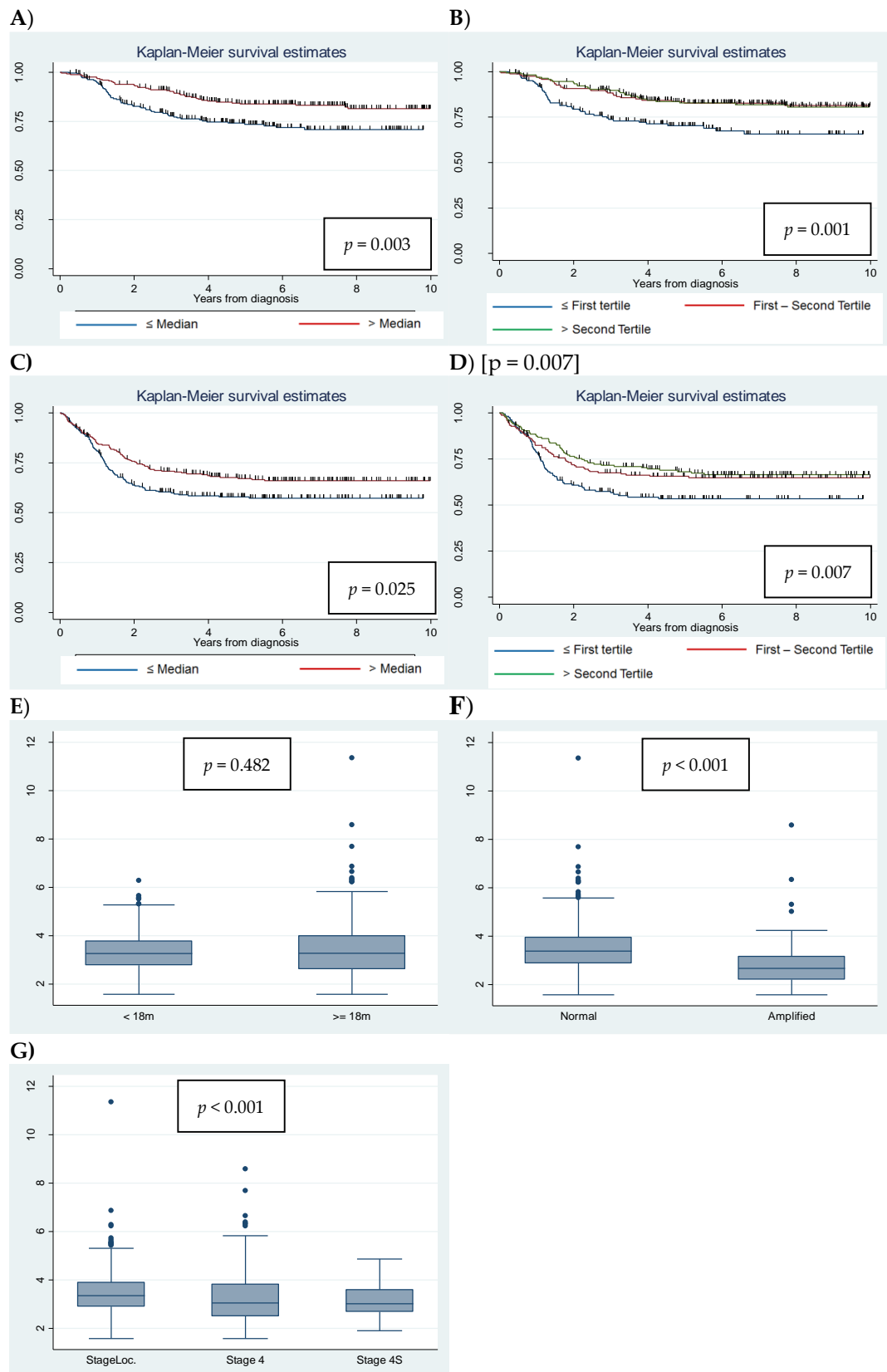
IFIT5 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S48



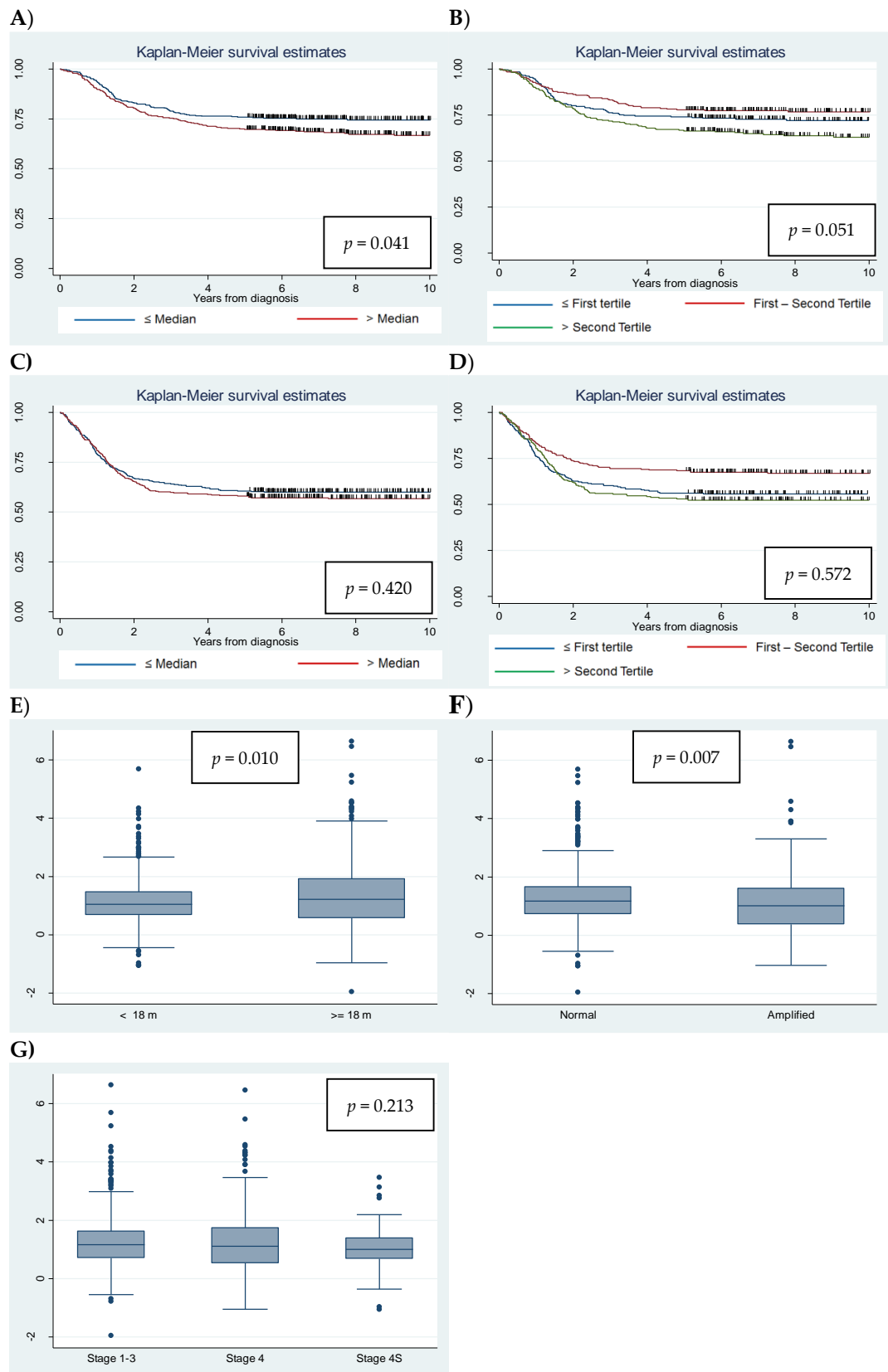
KIF20B gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S49



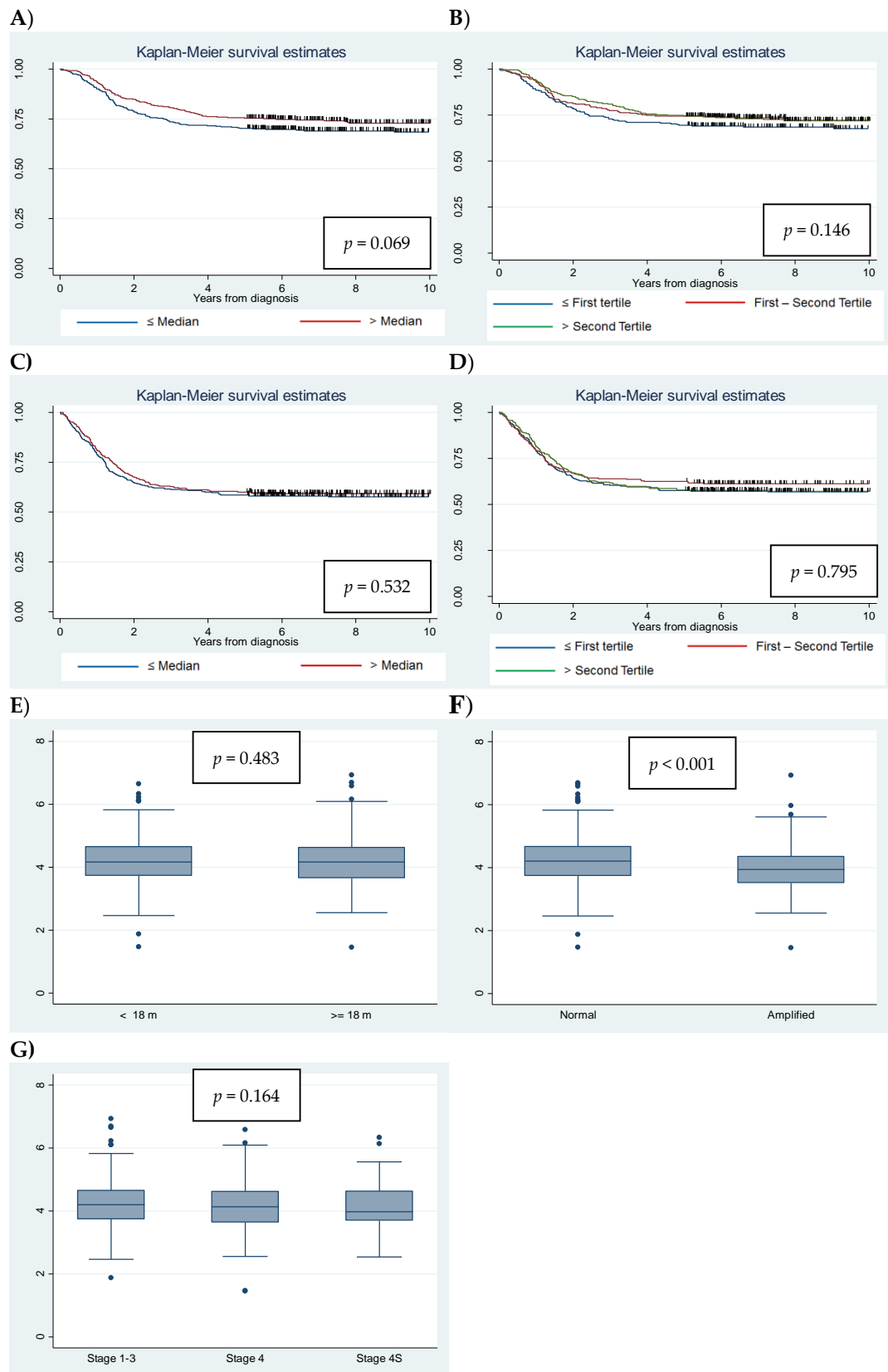
KILLIN (alia *KLLN*) gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S50



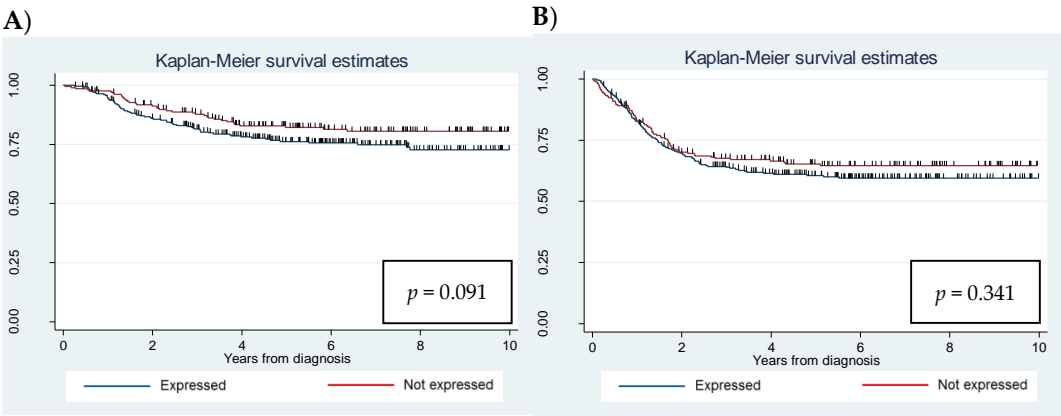
LDB3 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S51



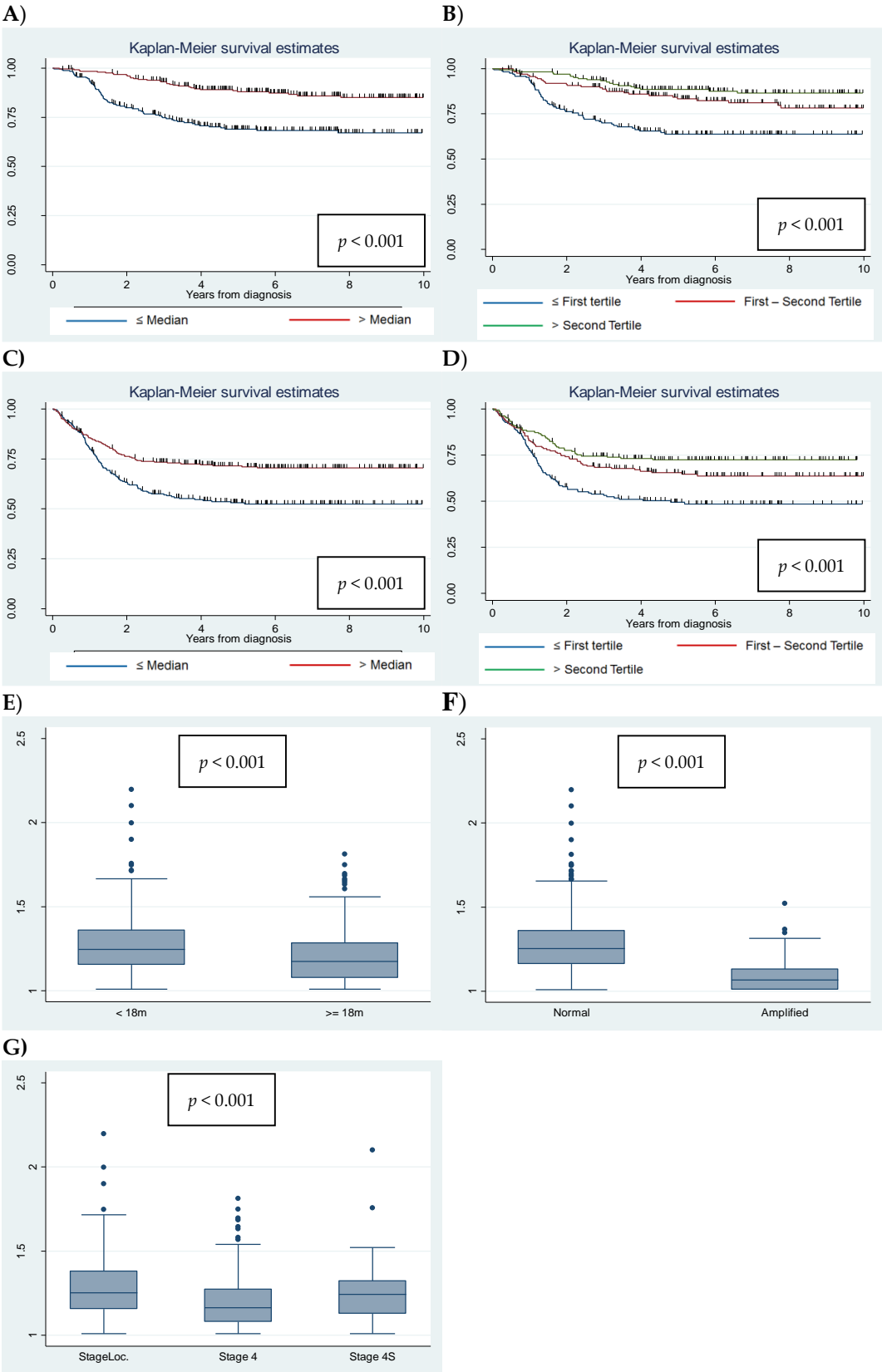
LIPA gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S52



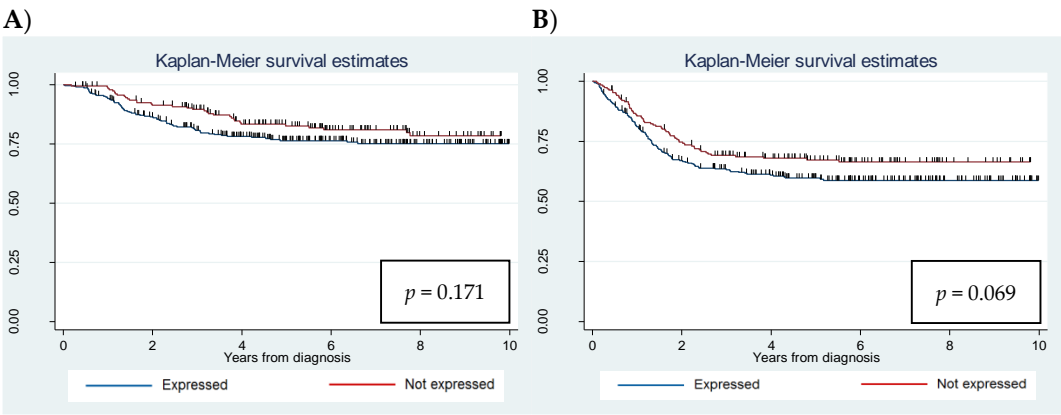
LIPF gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, gene expression yes/not; (B) Event Free Survival, gene expression yes/not.

Supplementary Figure S53



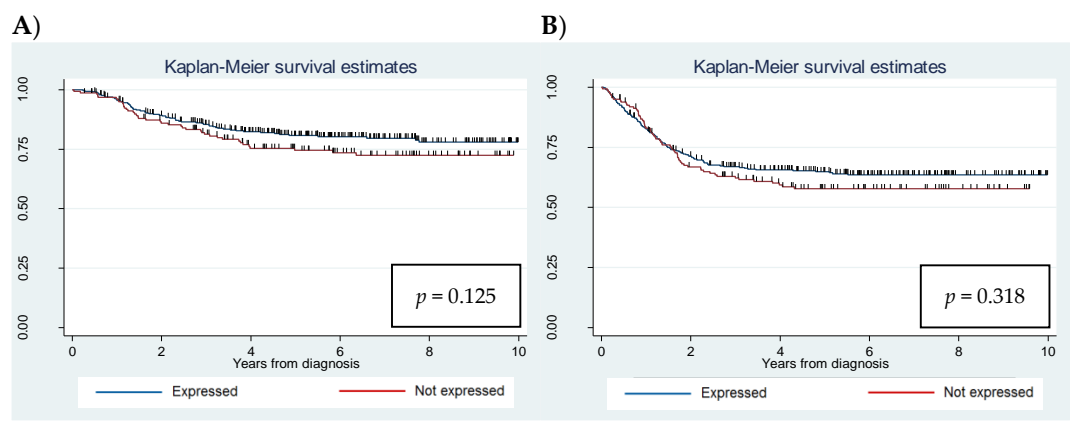
LIPJ gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S54



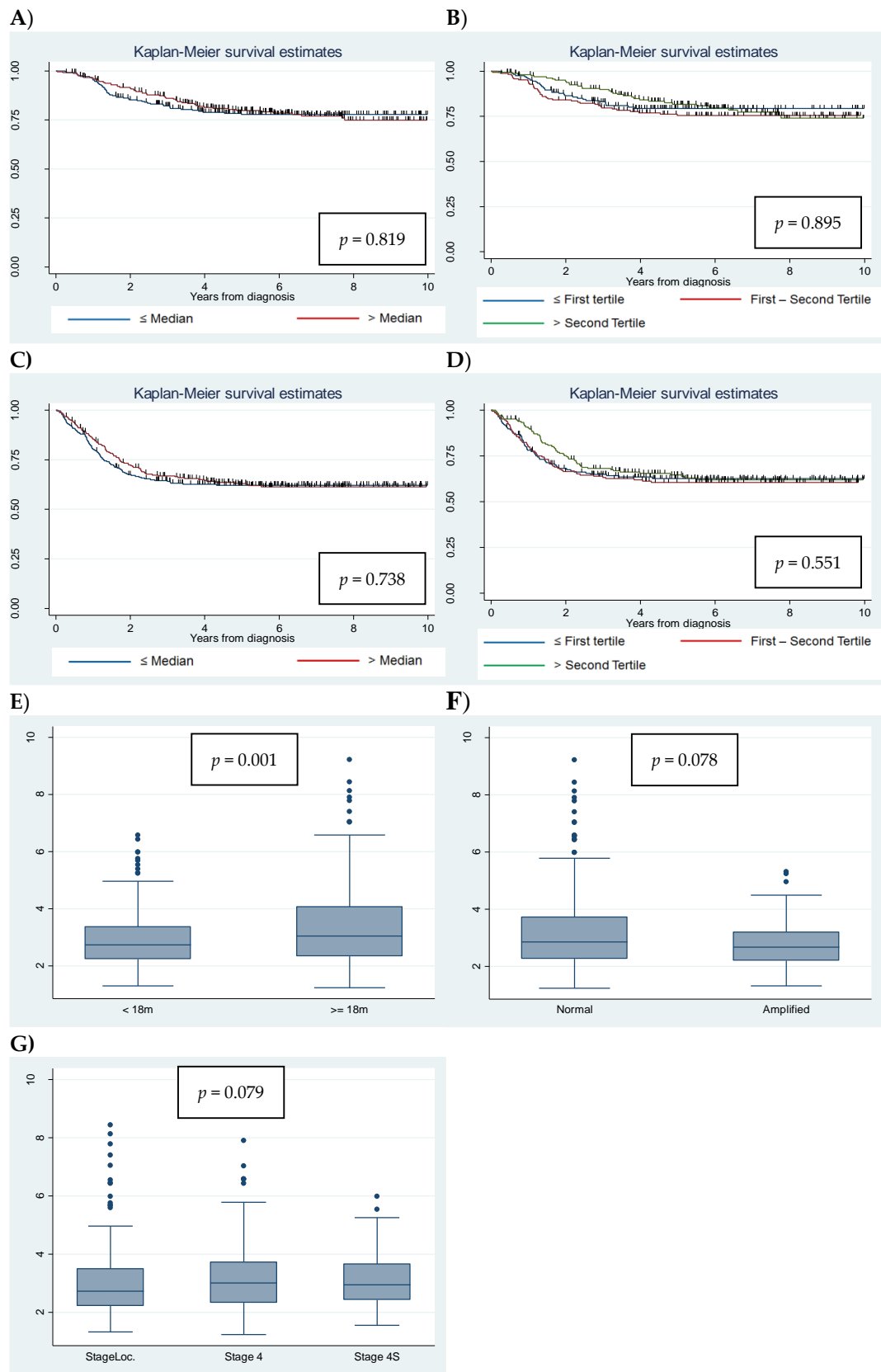
LIPM gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, gene expression yes/not; (B) Event Free Survival, gene expression yes/not.

Supplementary Figure S55



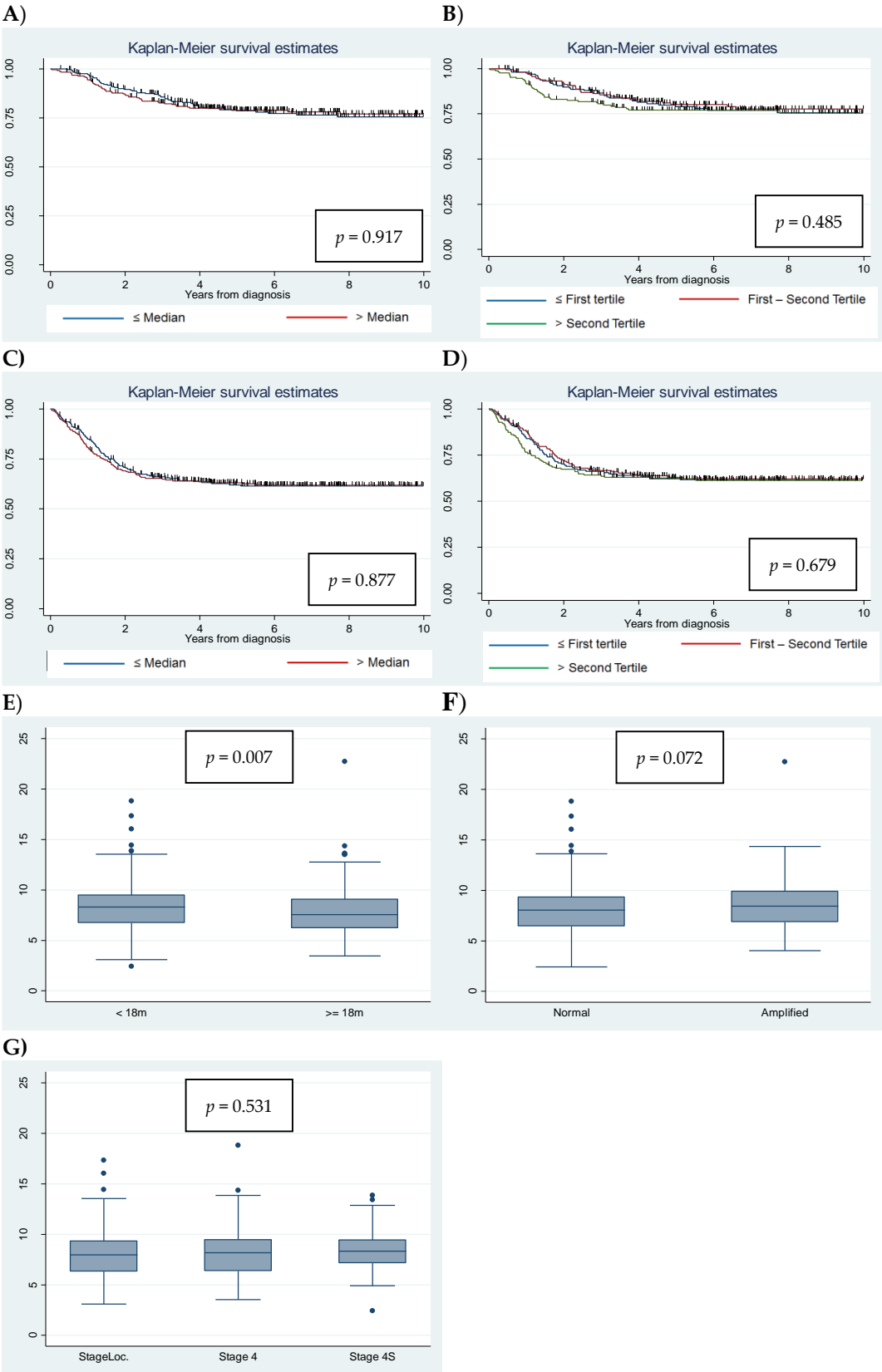
LIPN gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, gene expression yes/not; (B) Event Free Survival, gene expression yes/not.

Supplementary Figure S56



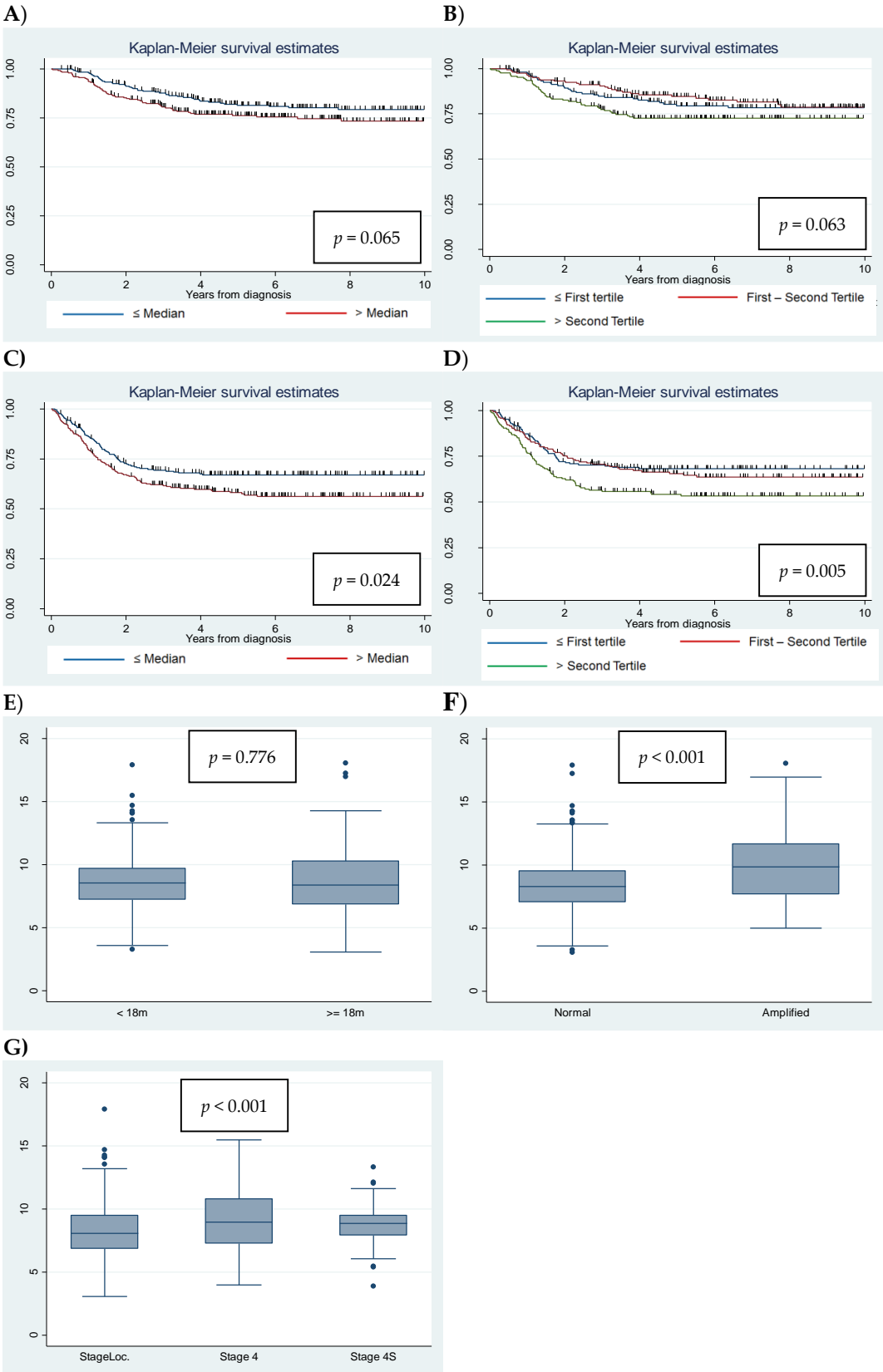
LOC219347(alias: TMEM254A1) gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S57



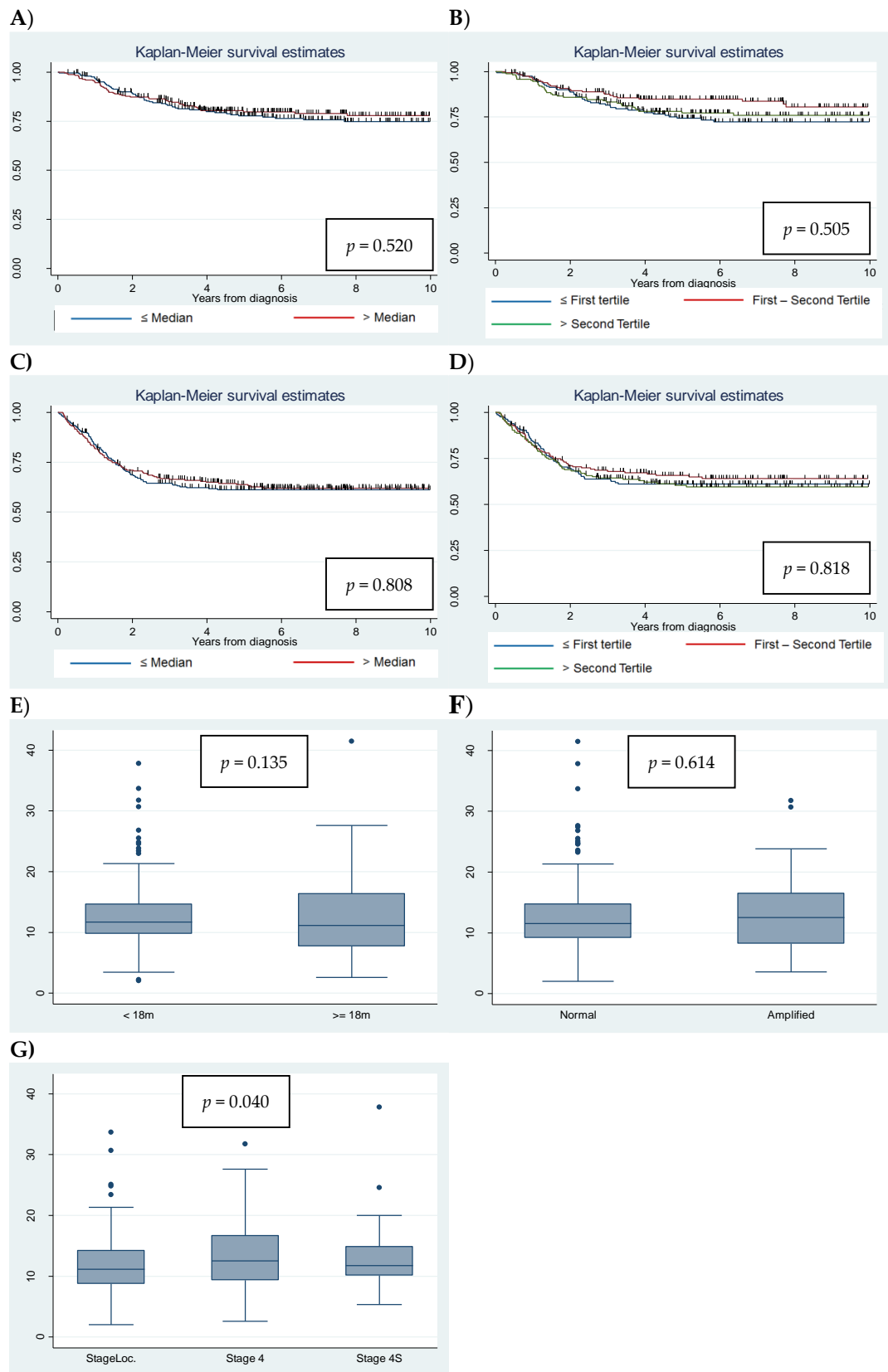
LOC439994 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S58



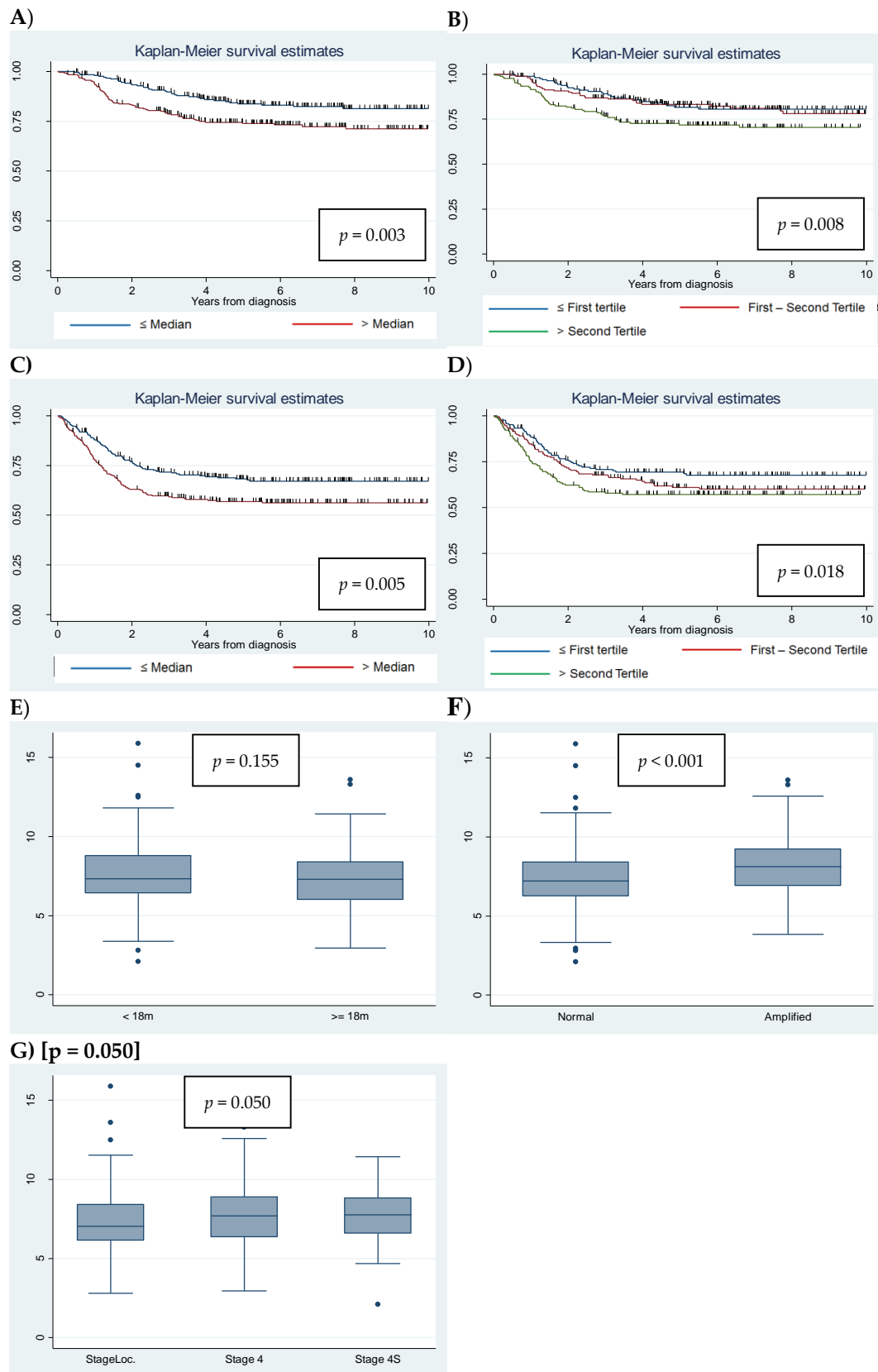
LOC642361 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S59



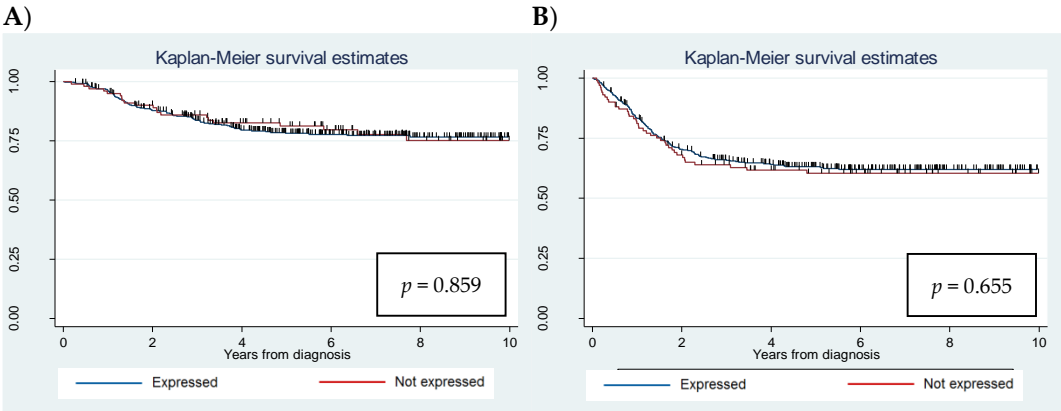
LOC650623 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S60



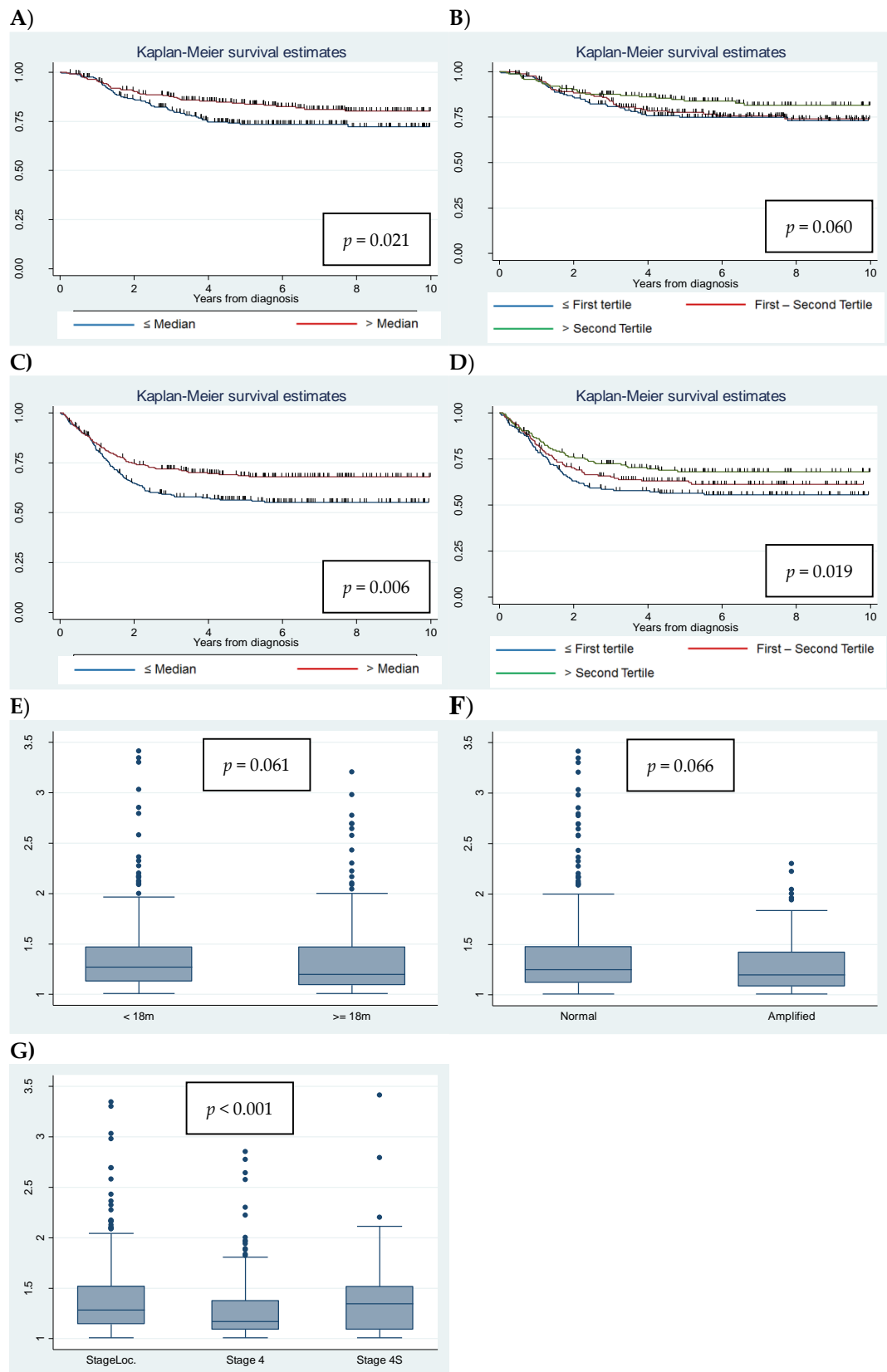
LOC728190 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S61



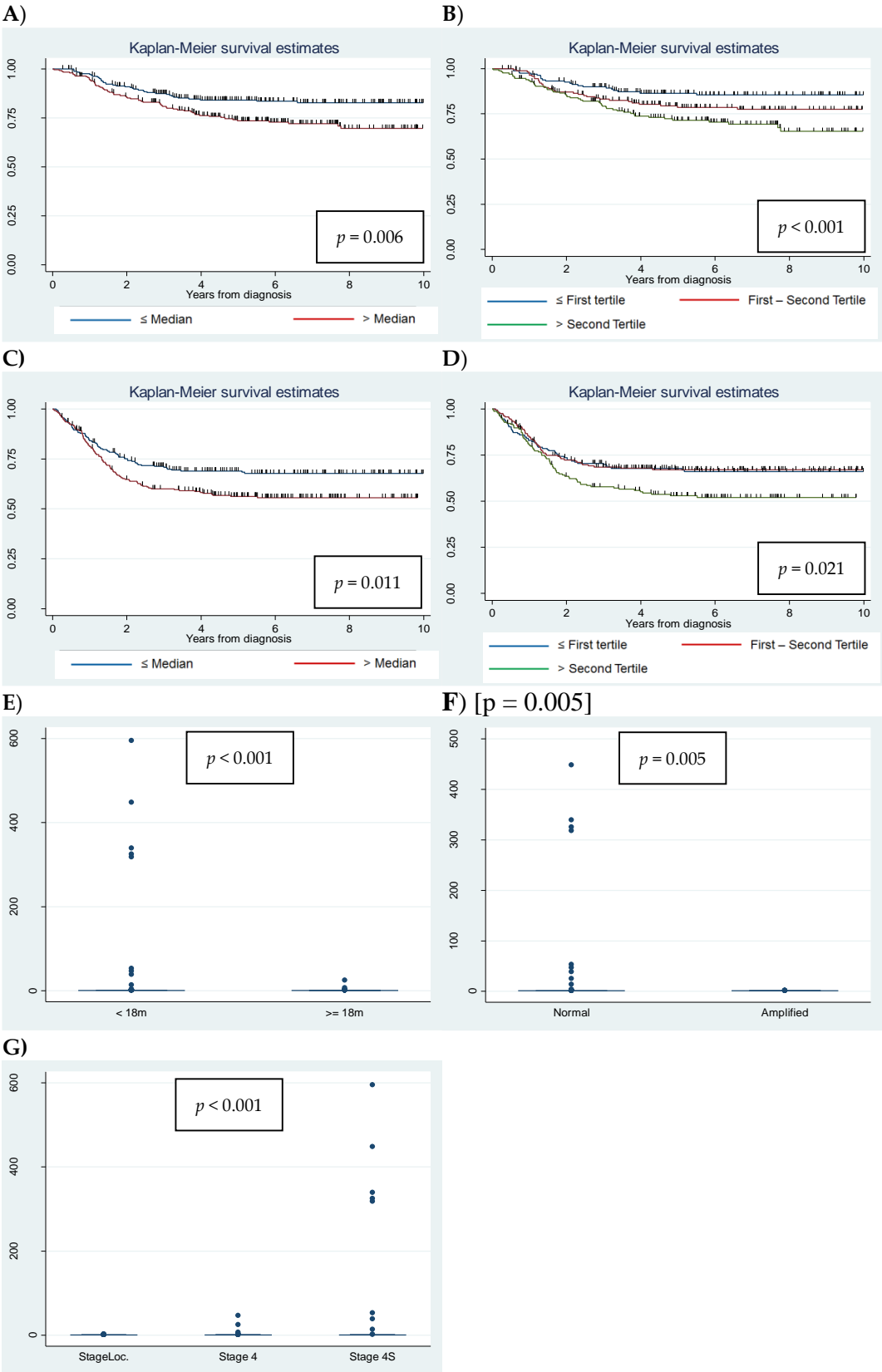
LRIT1 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, gene expression yes/not; (B) Event Free Survival, gene expression yes/not.

Supplementary Figure S62



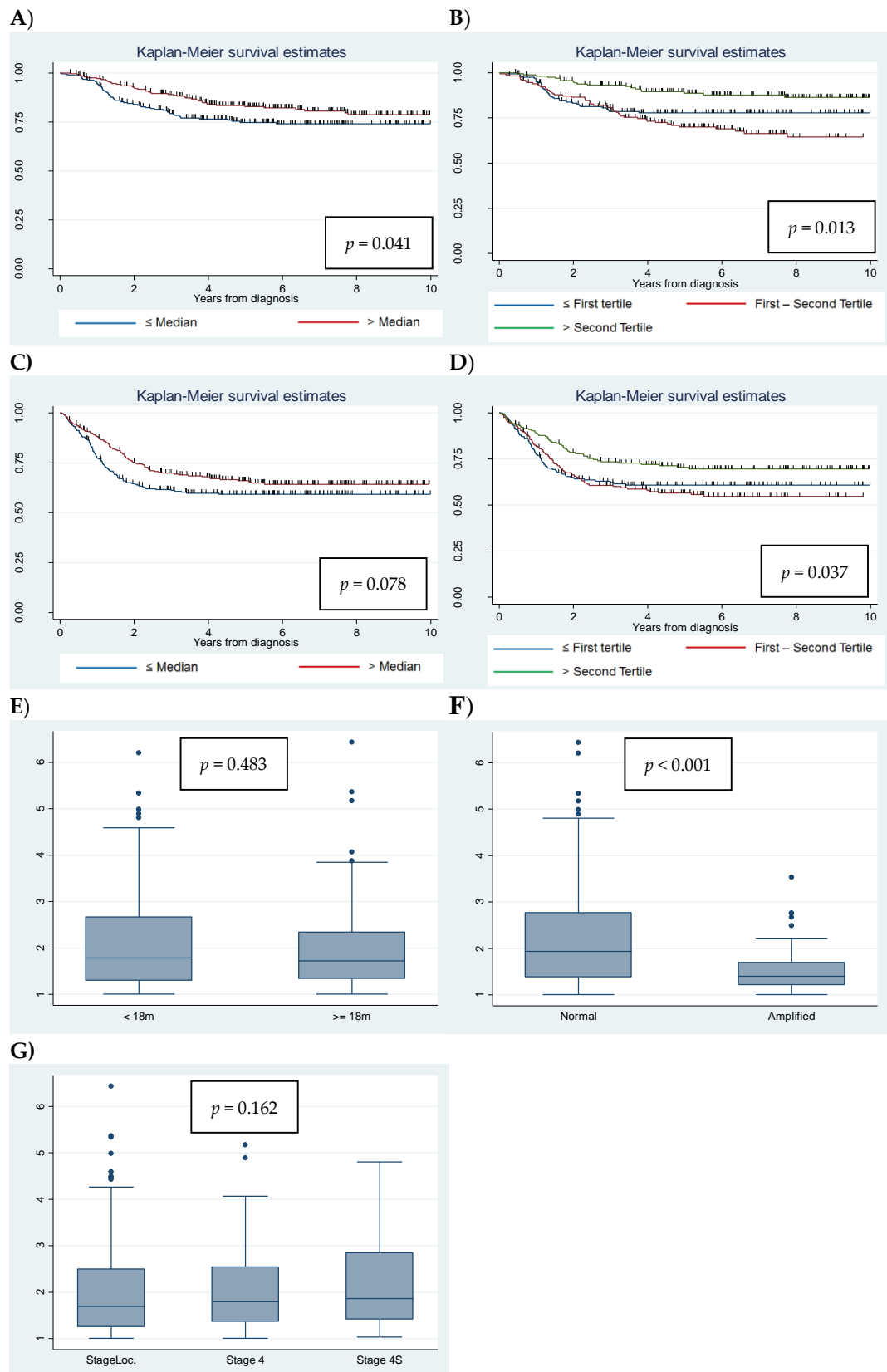
LRIT2 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S63



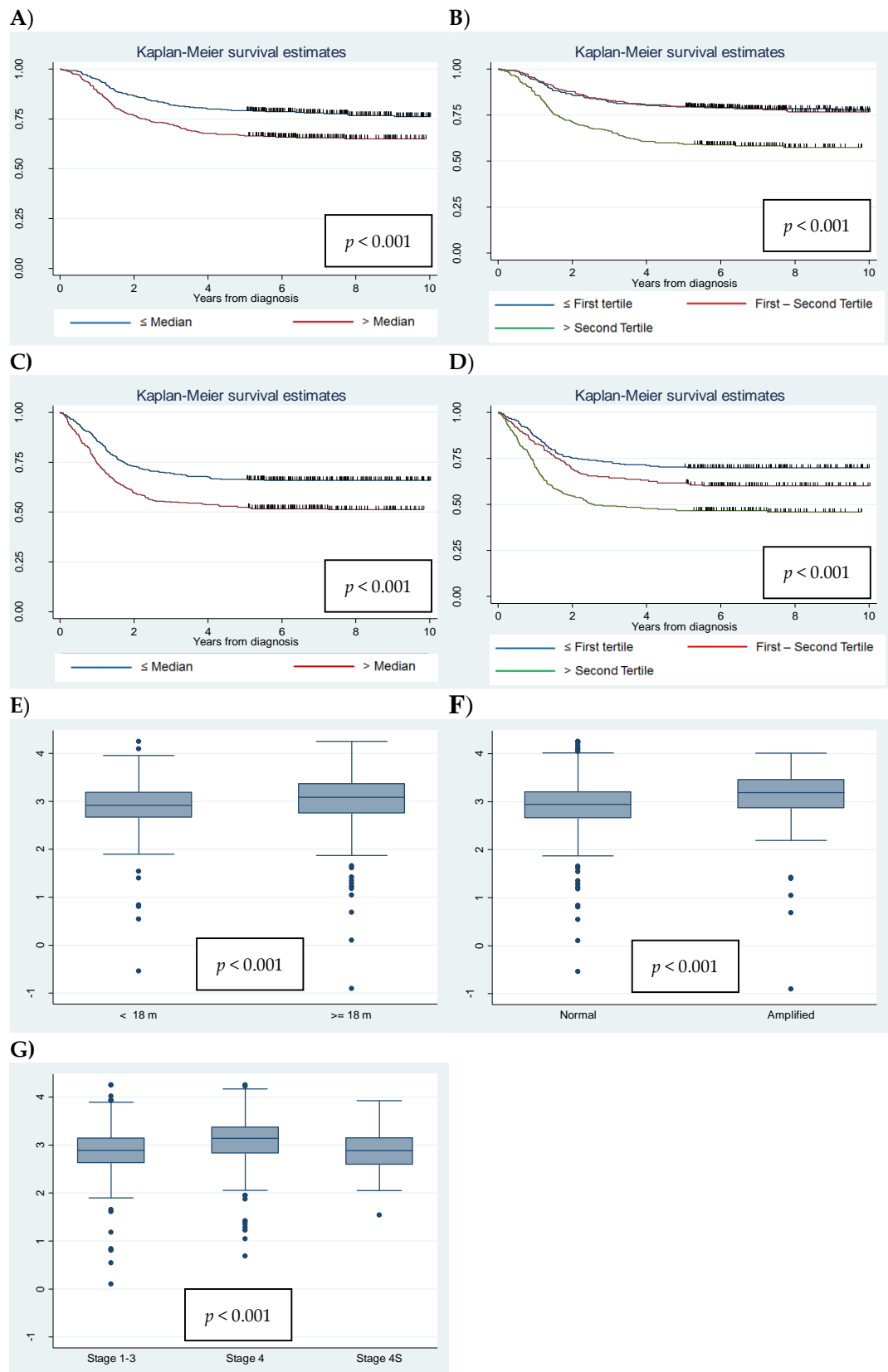
MAT1A gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S64



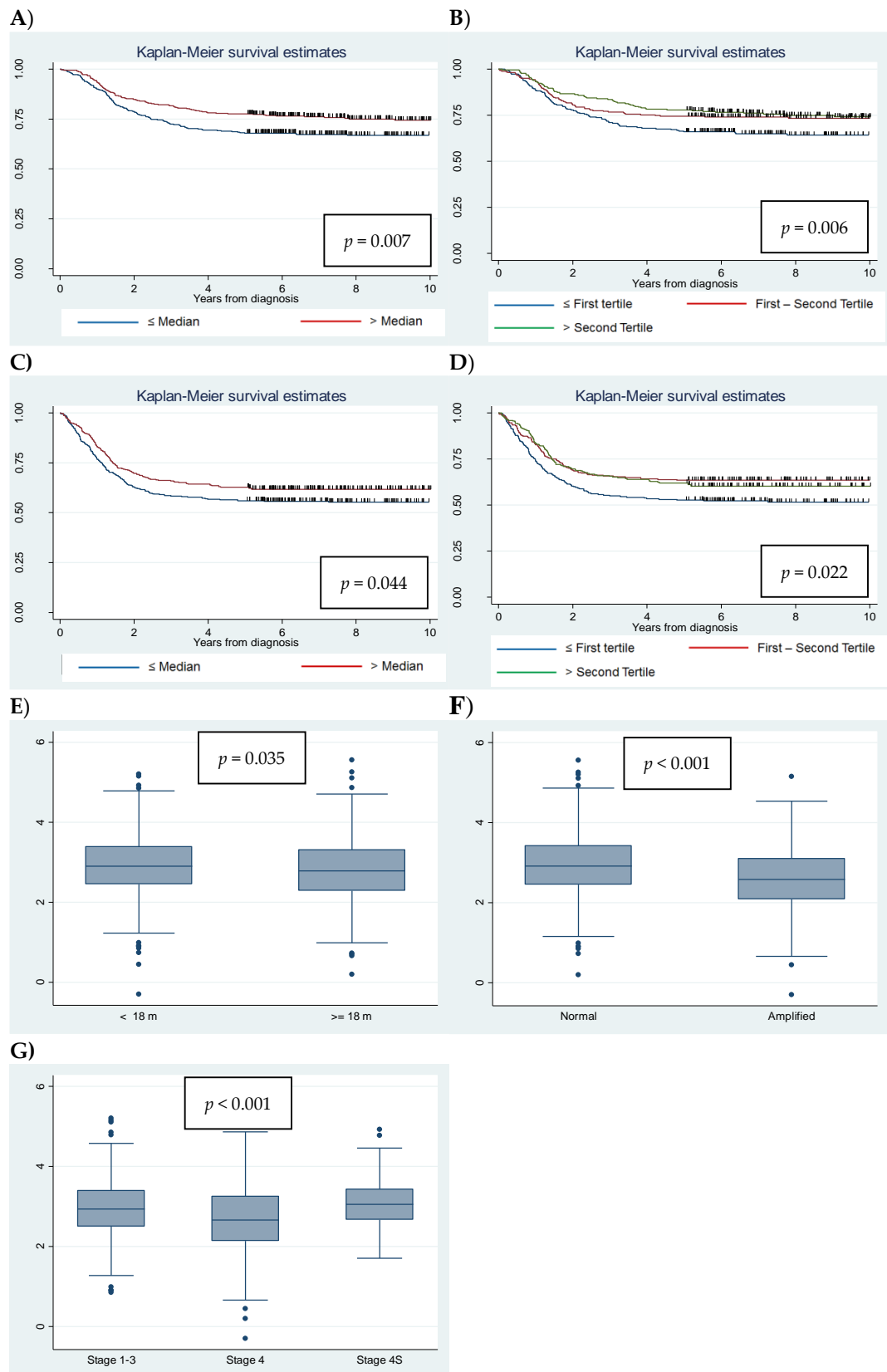
MBL1P gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S65



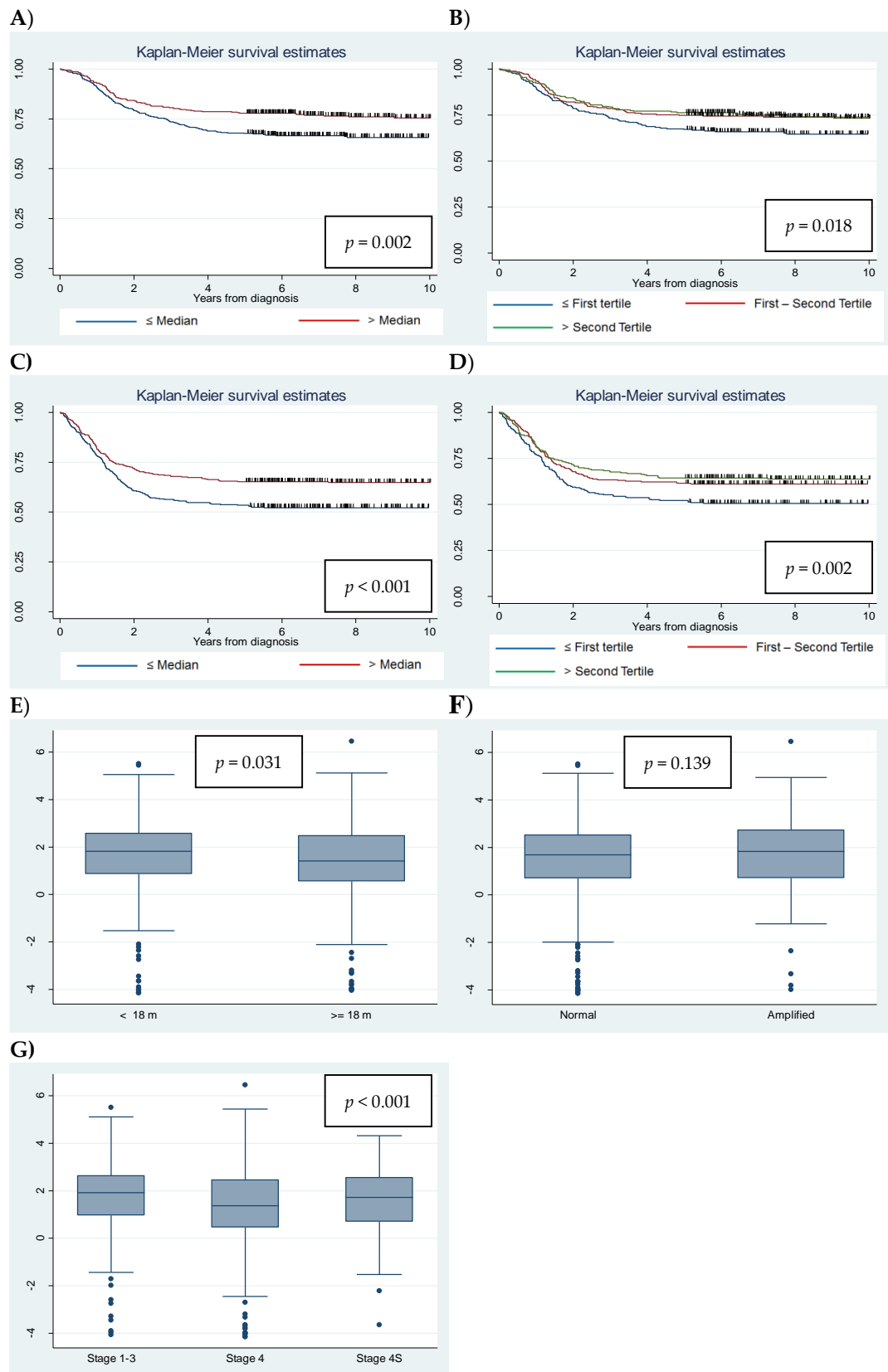
MINPP1 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S66



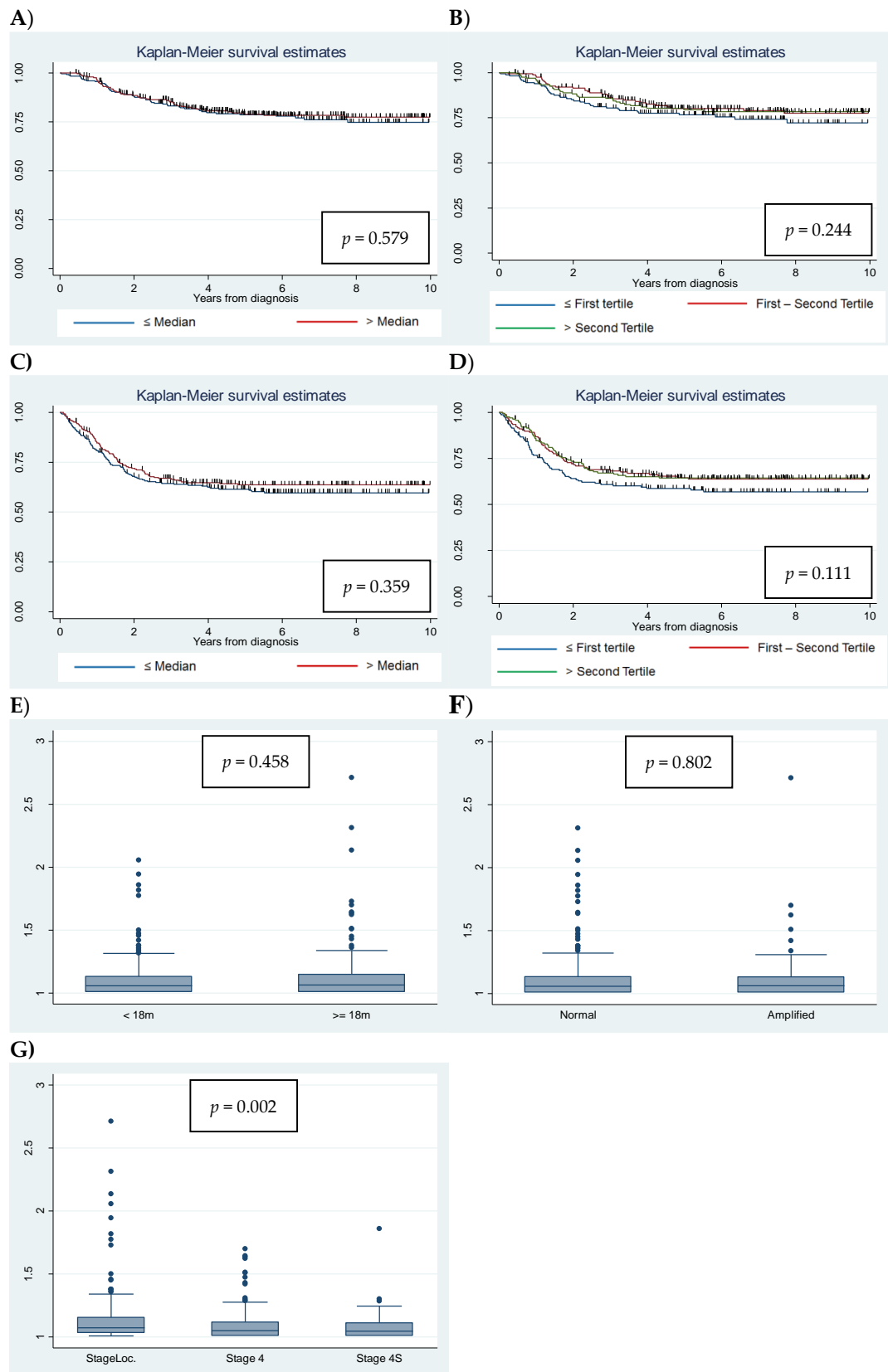
MMRN2 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S67



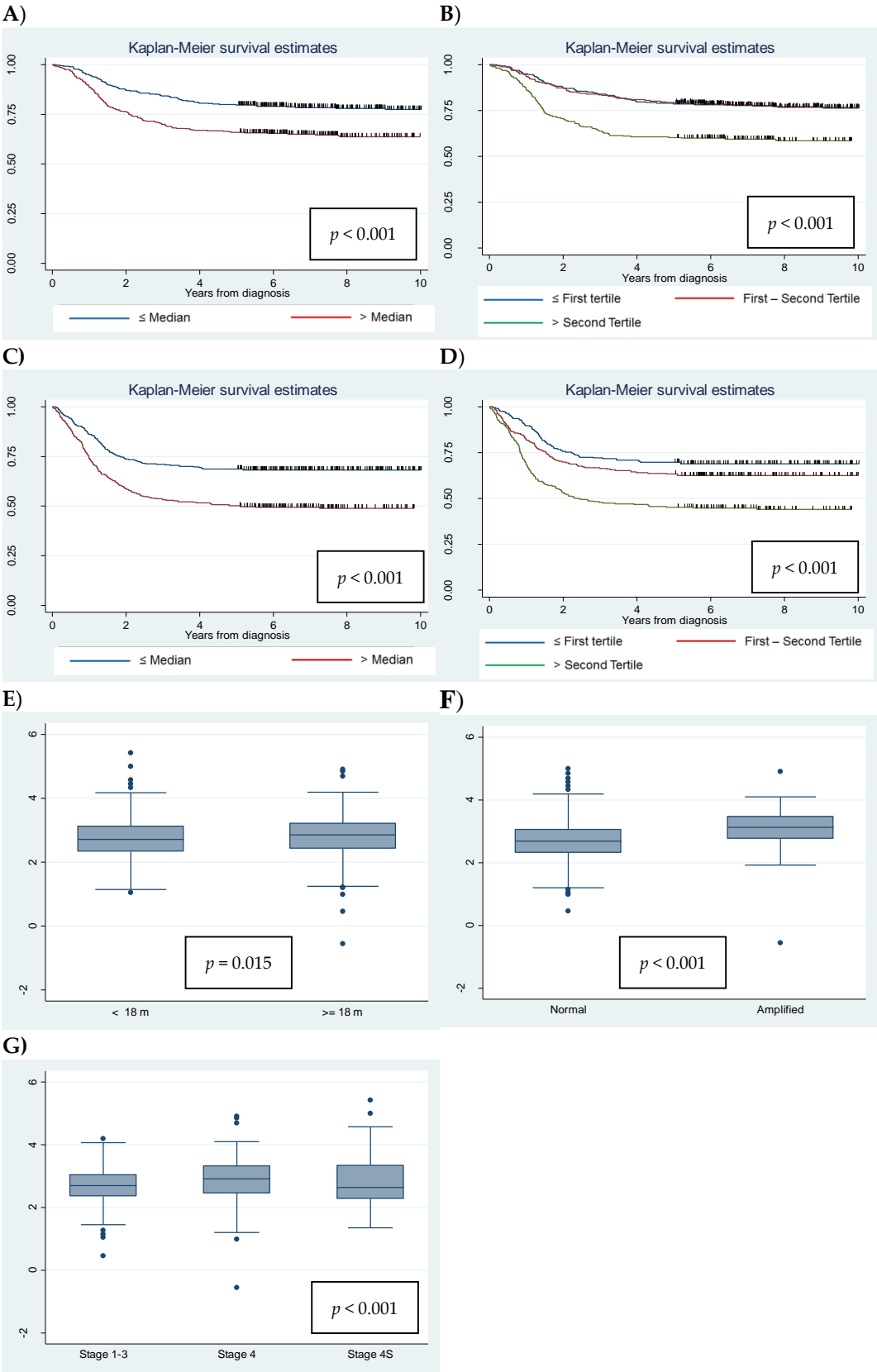
NRG3 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S68



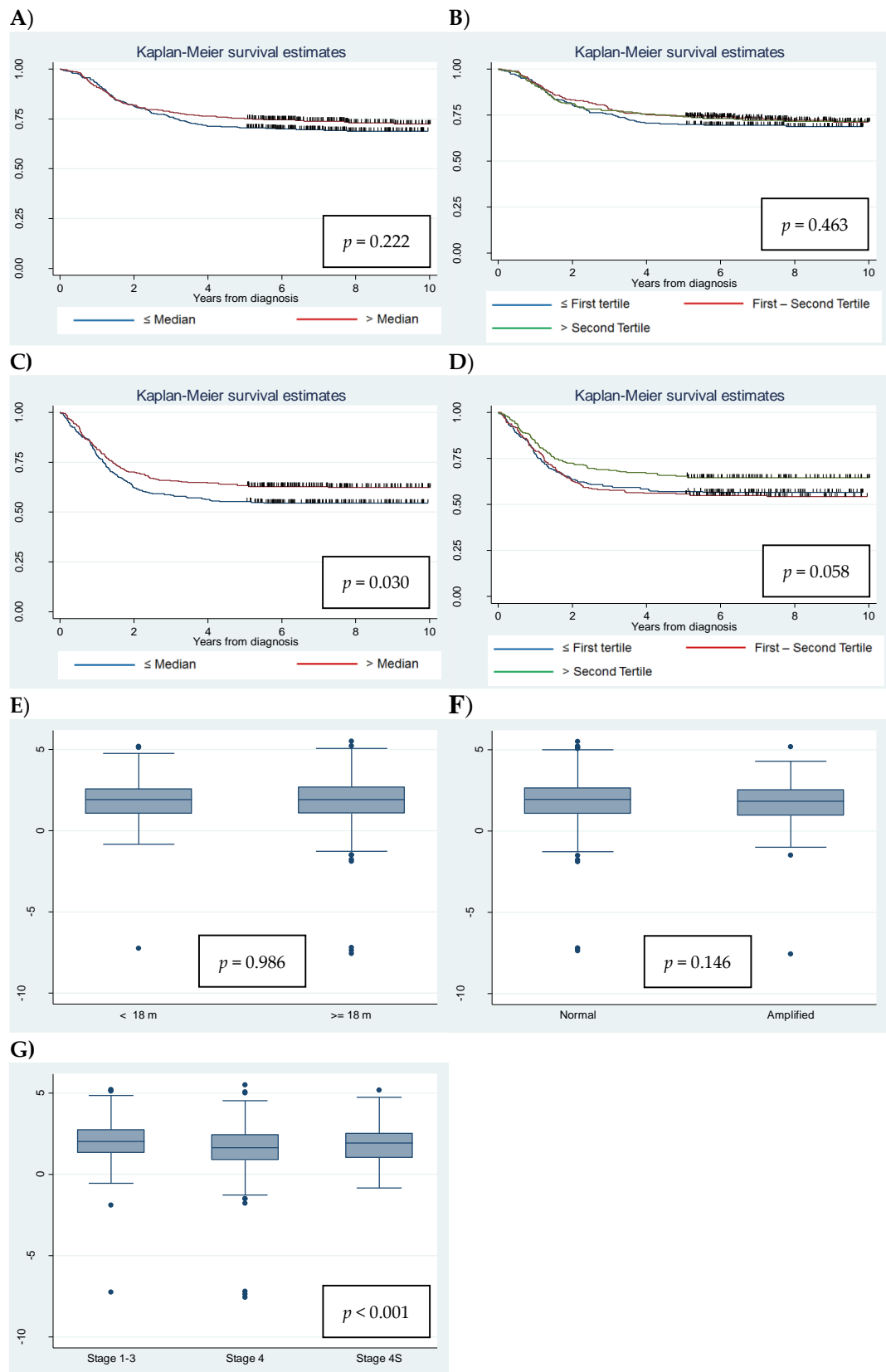
OPN4 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S69



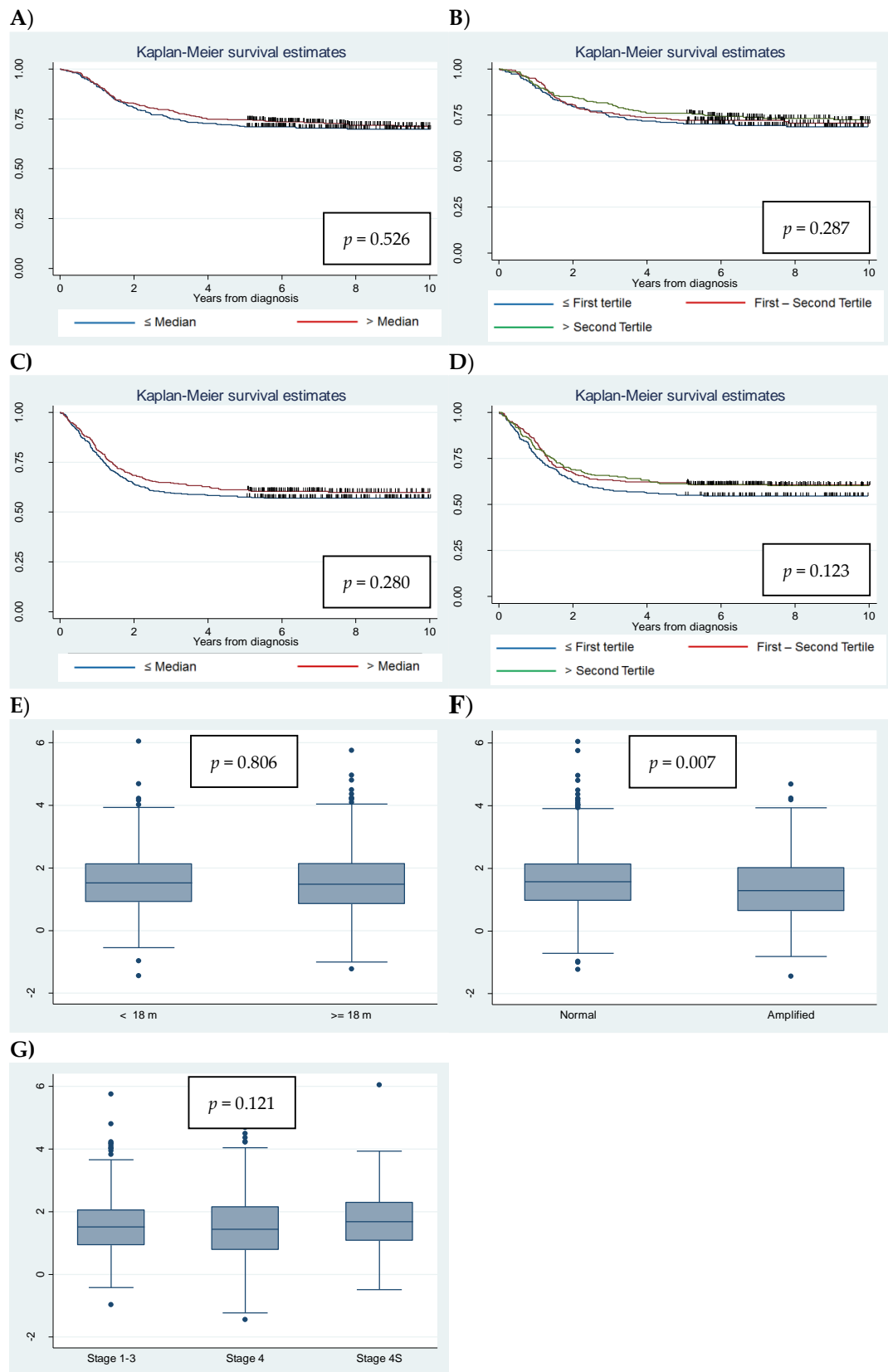
PANK1 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S70



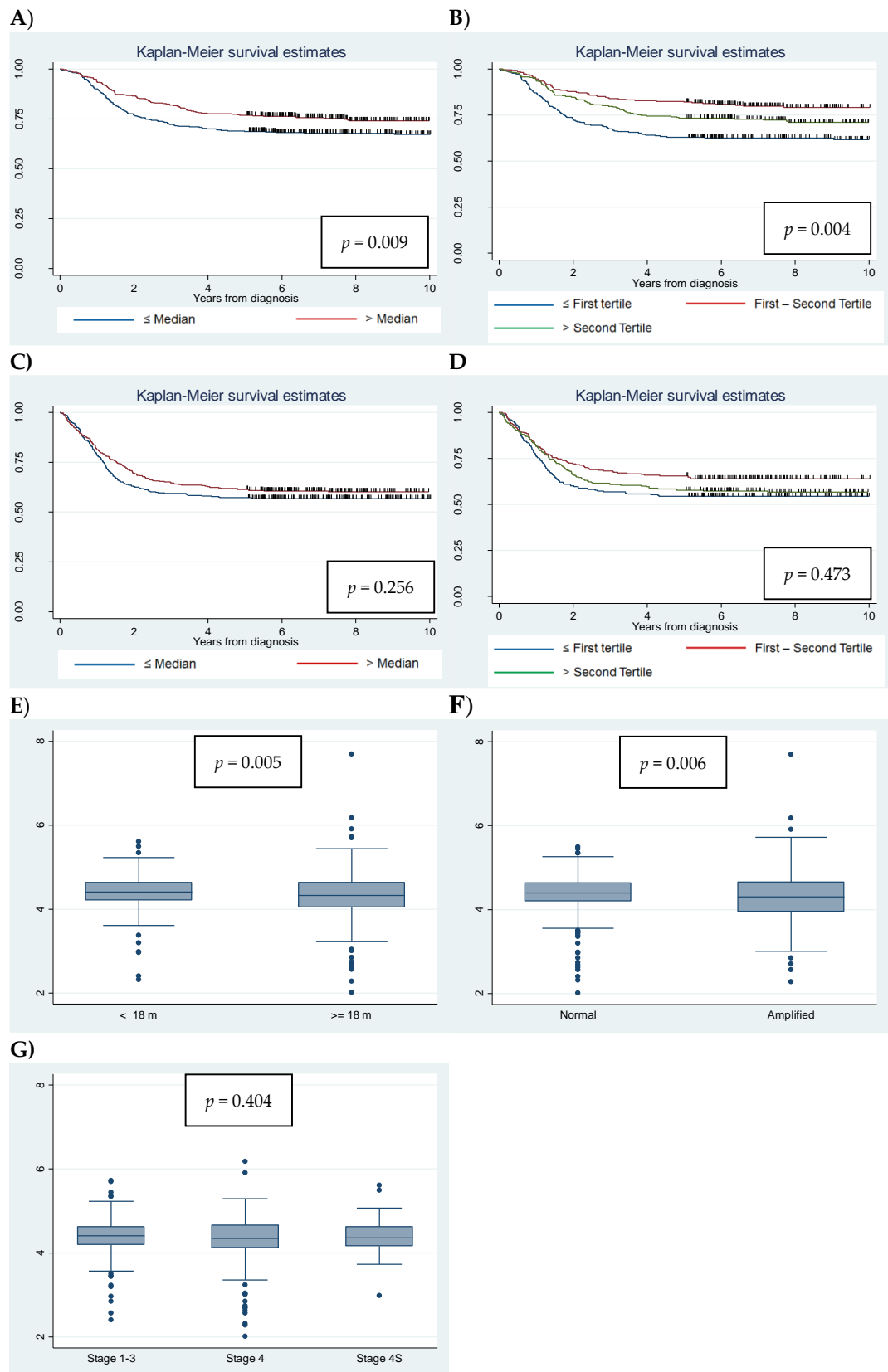
PCDH21 (alias *CDHR1*) gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S71



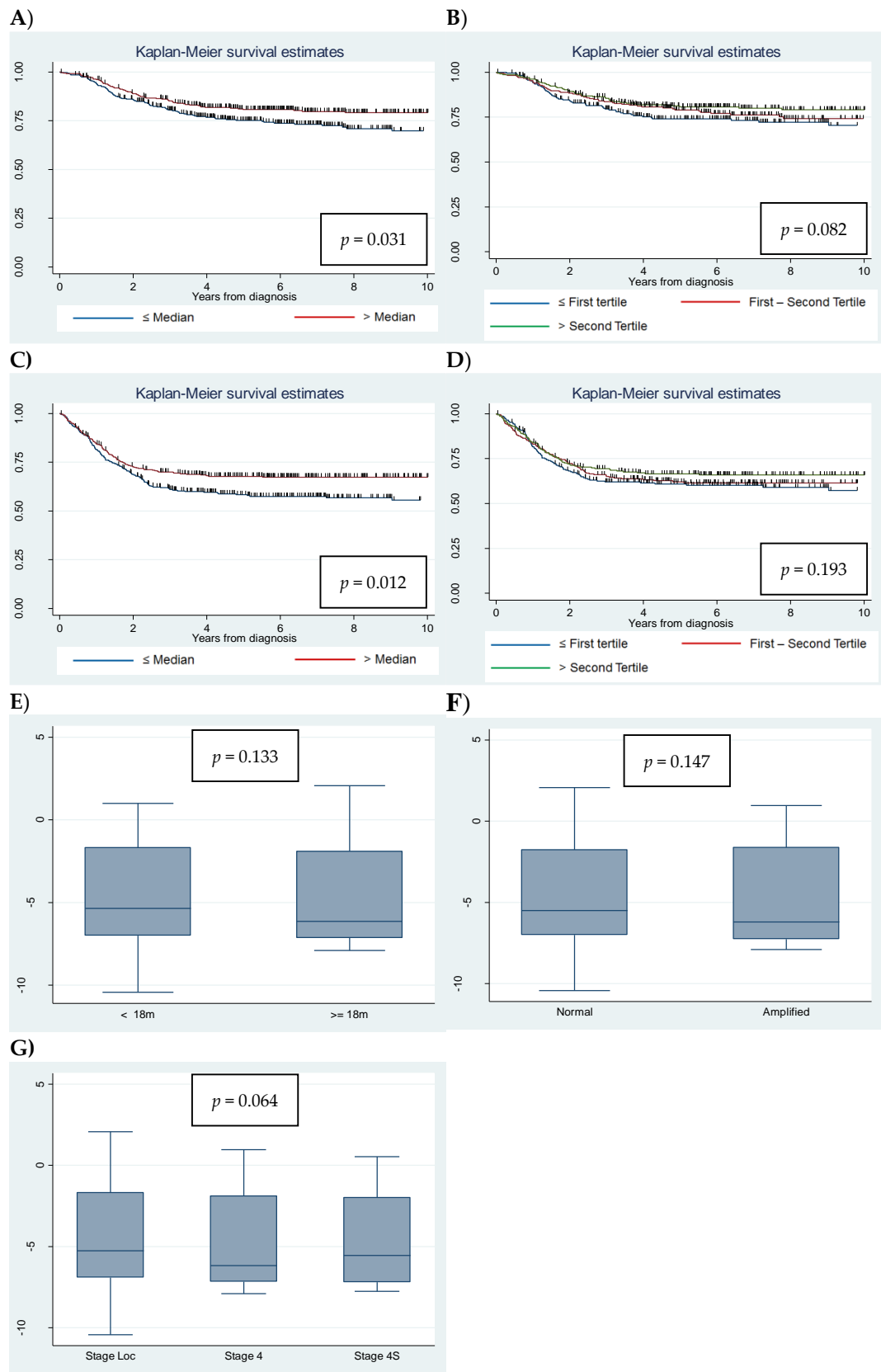
PLAC9 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S72



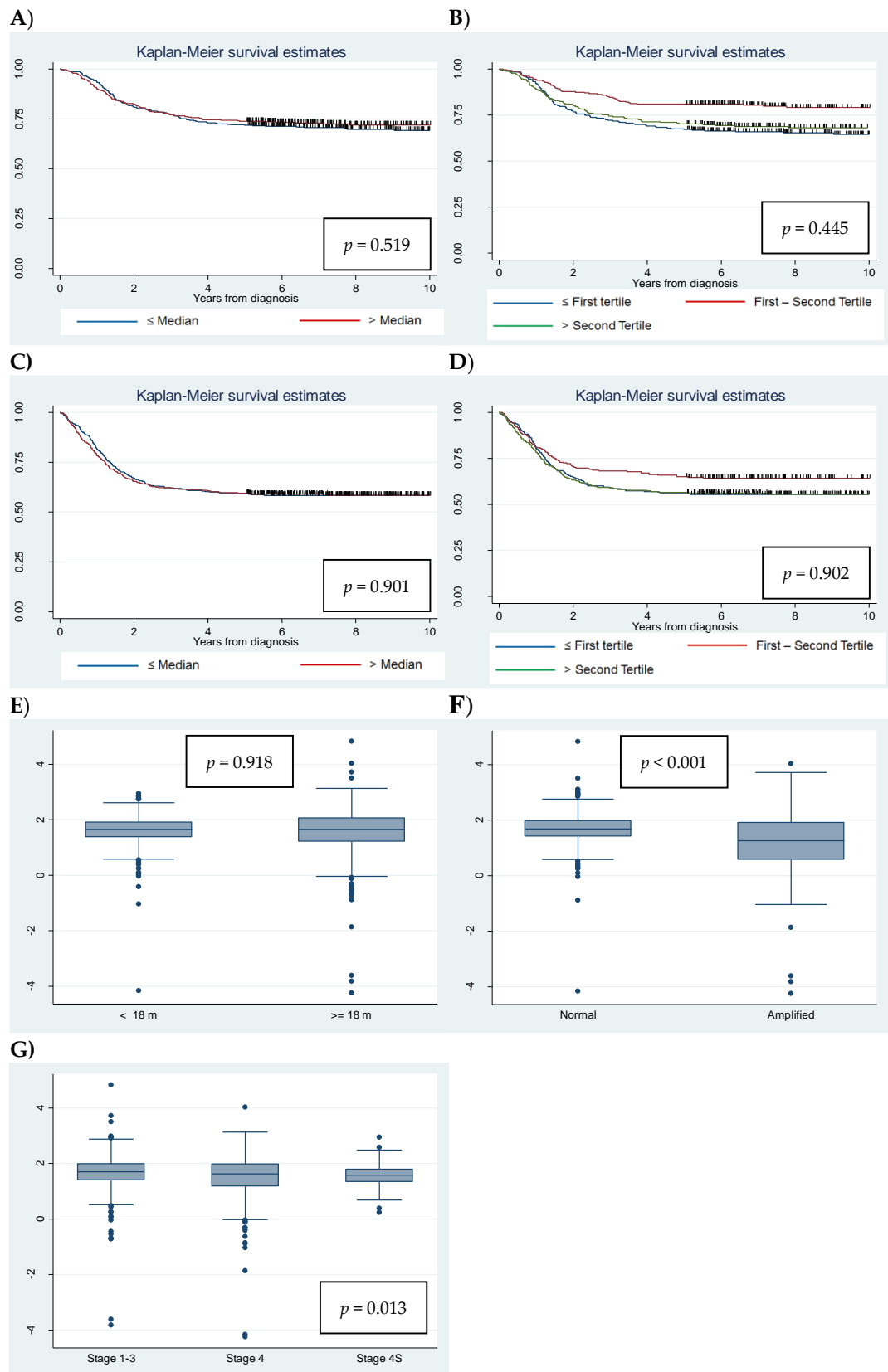
PTEN gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S73



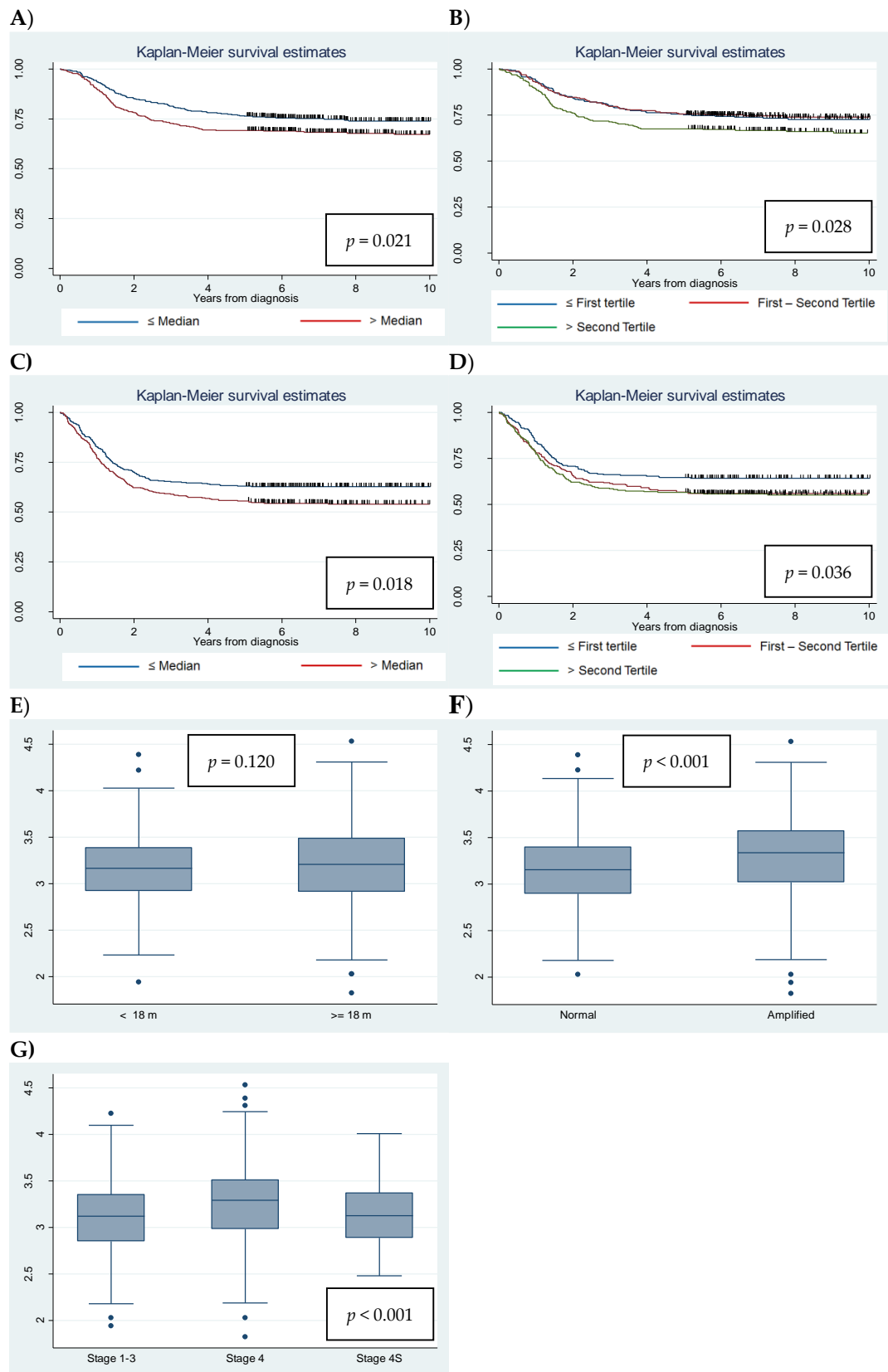
RGR gene expression and its association with survival and clinical characteristics in a cohort of 709 NB patients in the E-MTAB-1781 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S74



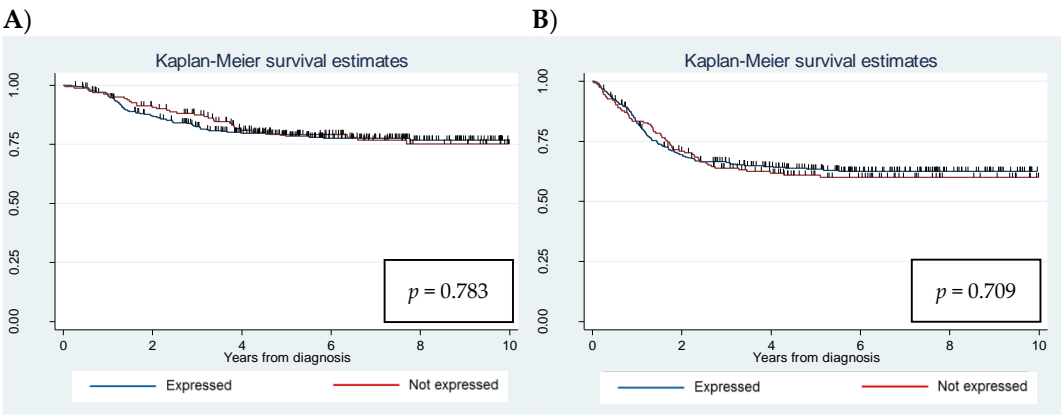
RNLS gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S75



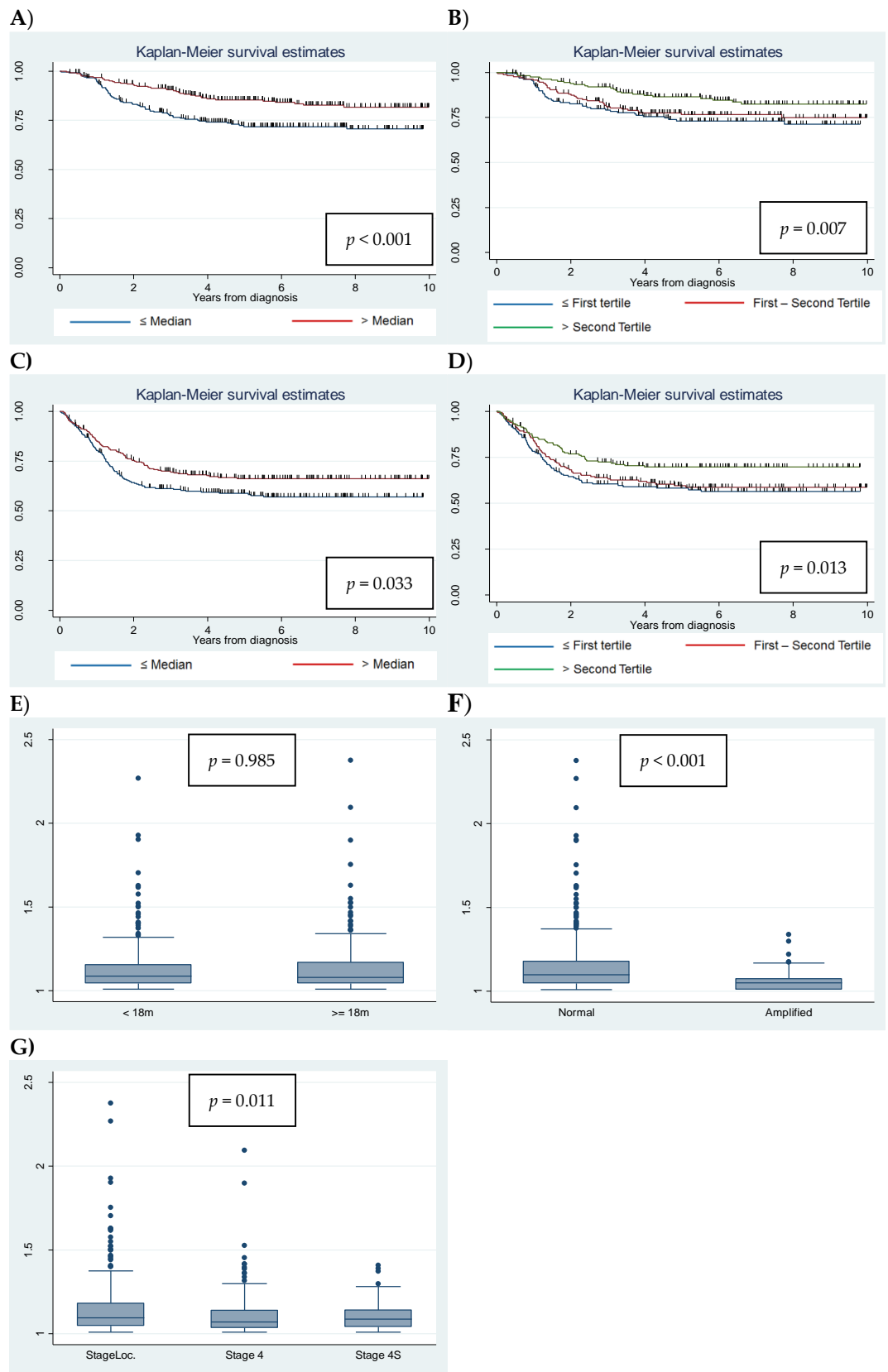
RPP30 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S76



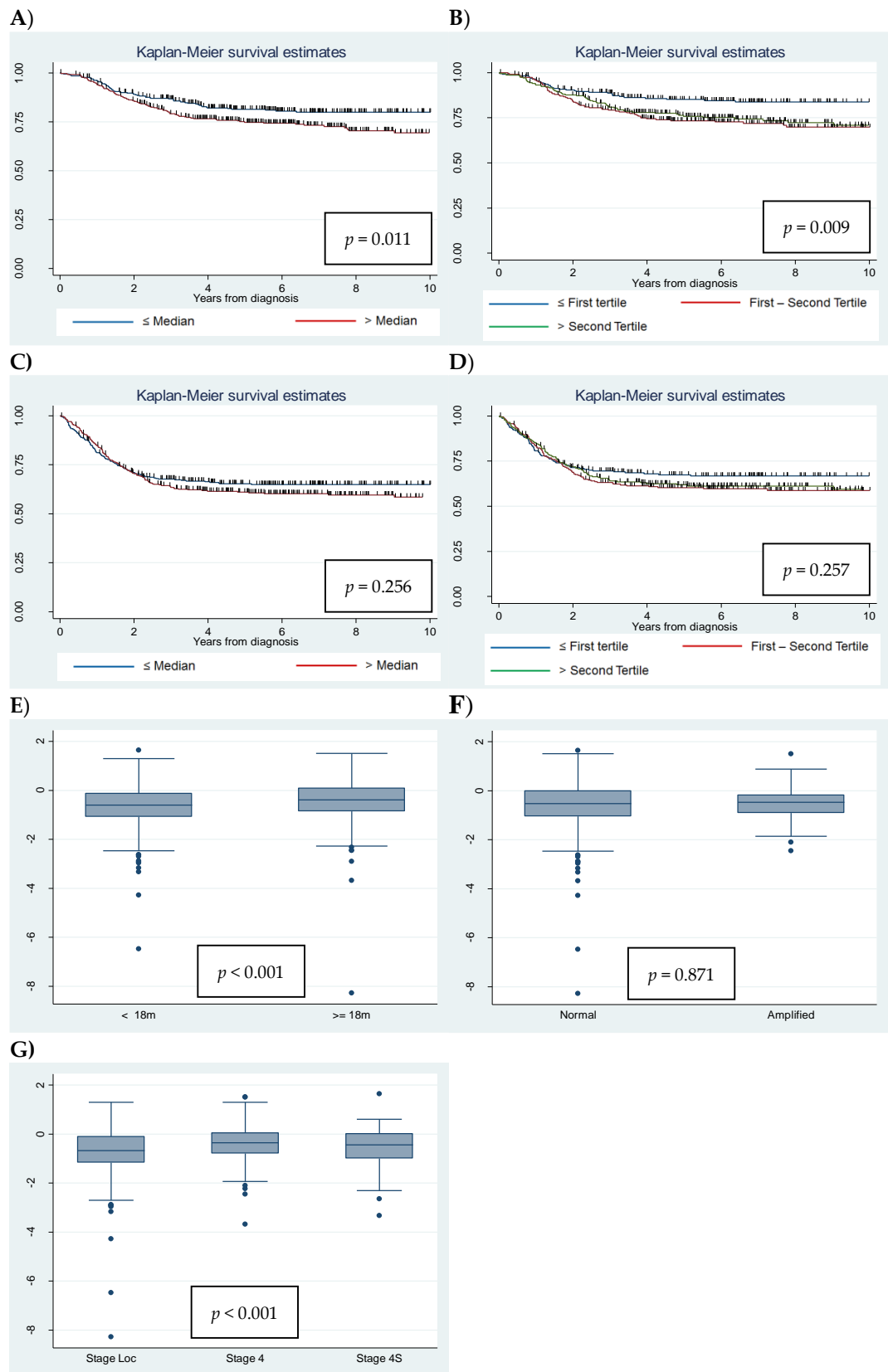
SFTP1 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, gene expression yes/not; (B) Event Free Survival, gene expression yes/not.

Supplementary Figure S77



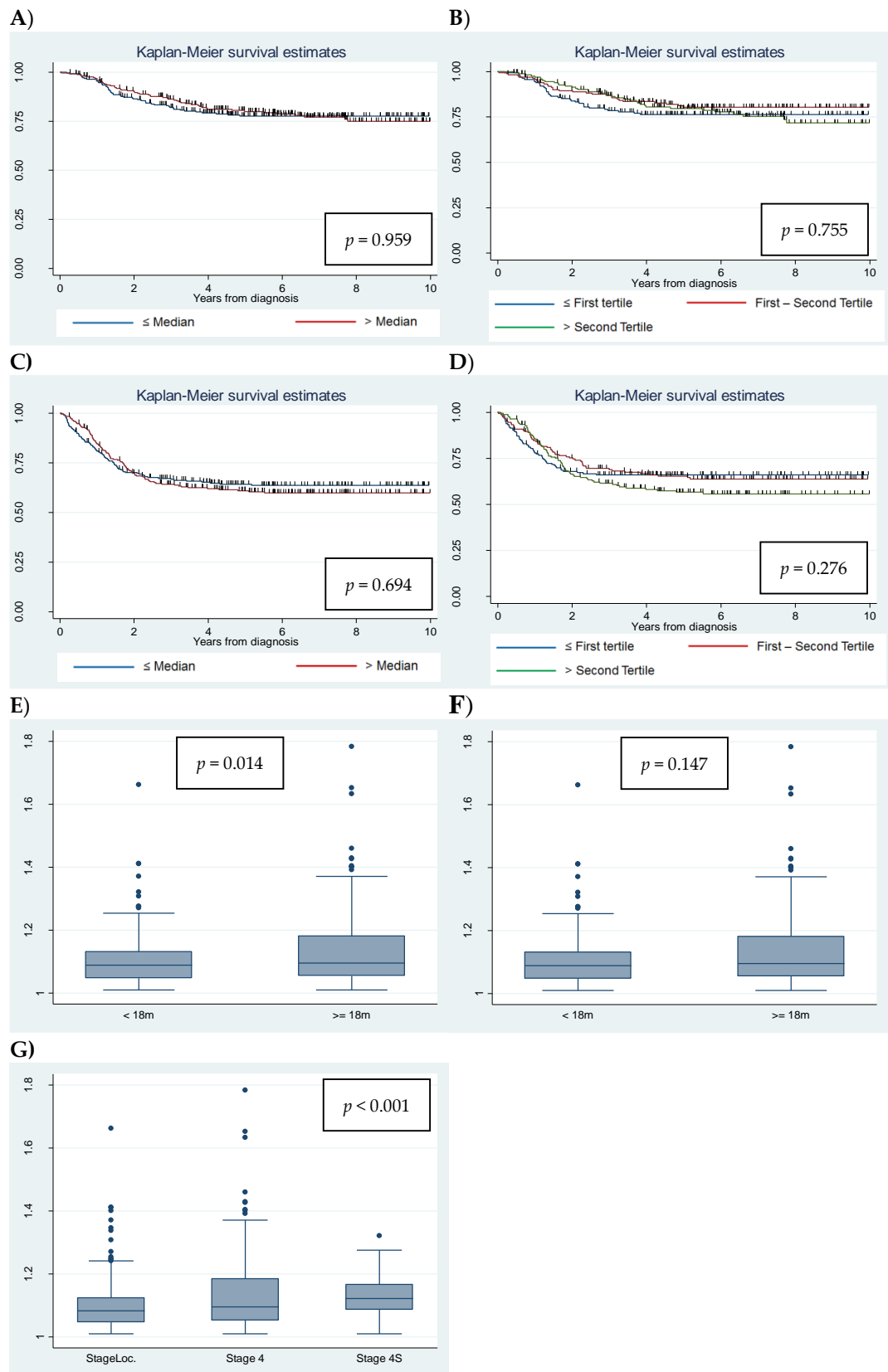
SFTPA2 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S78



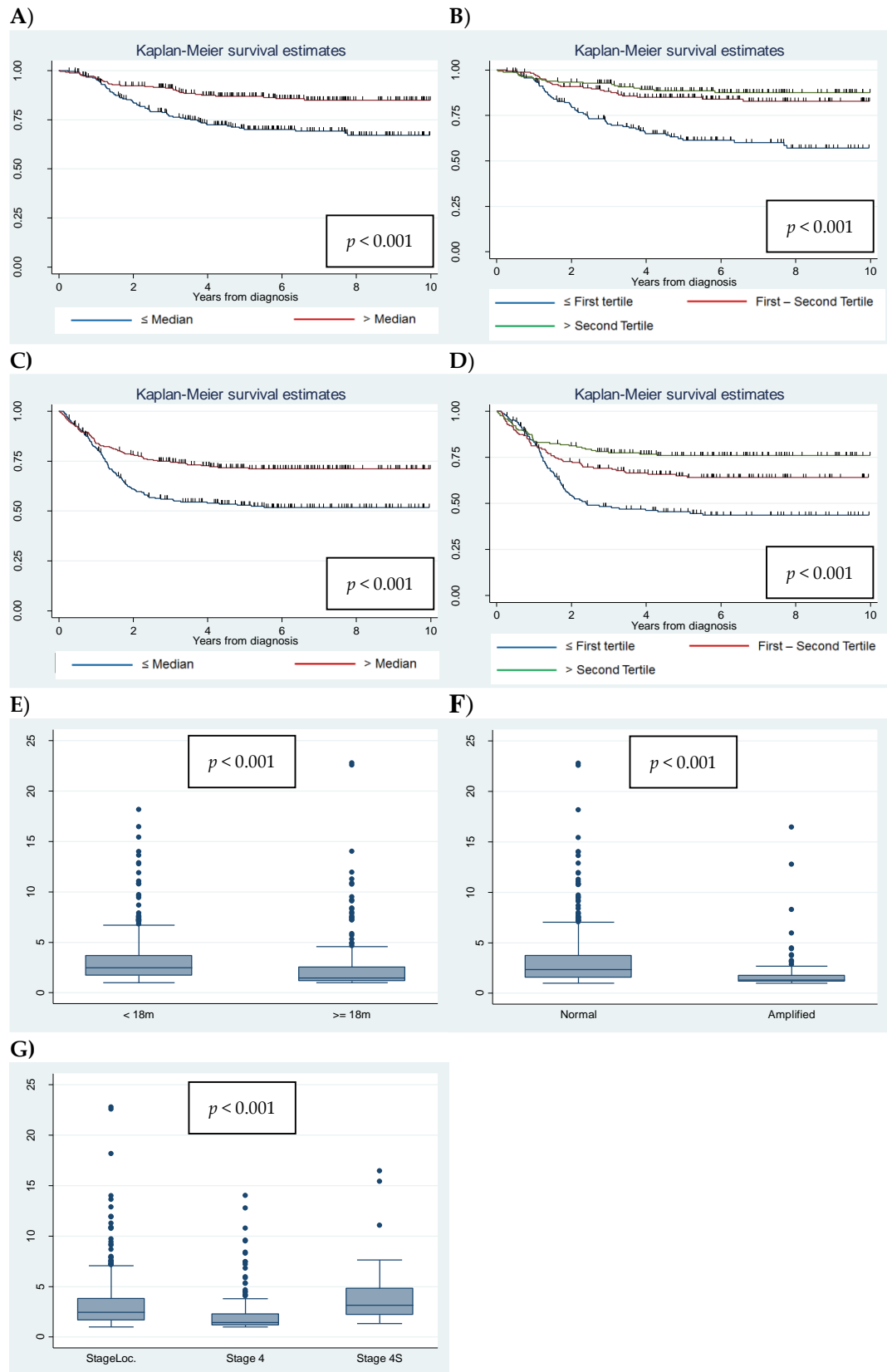
SFTPD gene expression and its association with survival and clinical characteristics in a cohort of 709 NB patients in the E-MTAB-1781 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S79



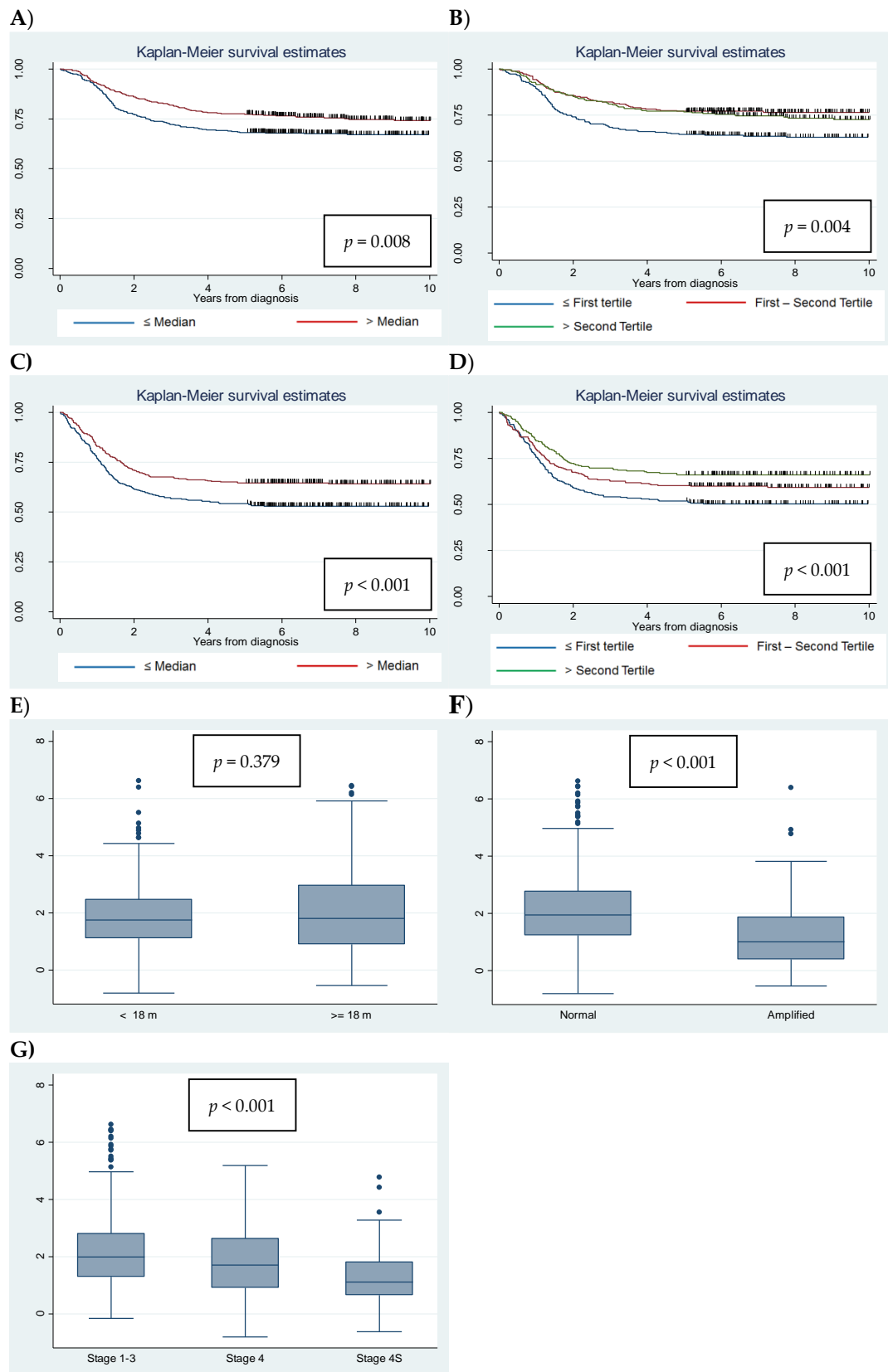
SH2D4B gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S80



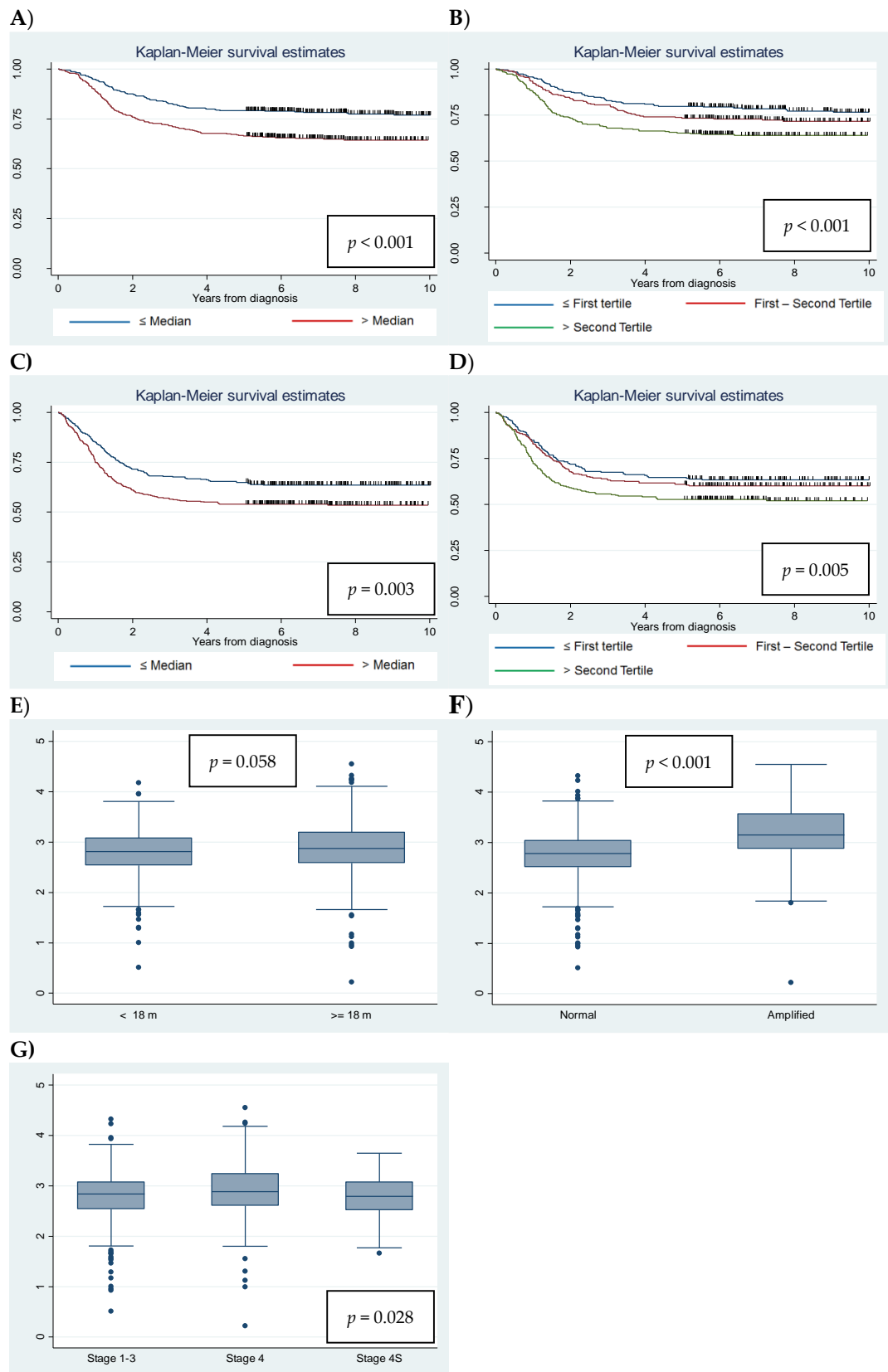
SLC16A12 gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S81



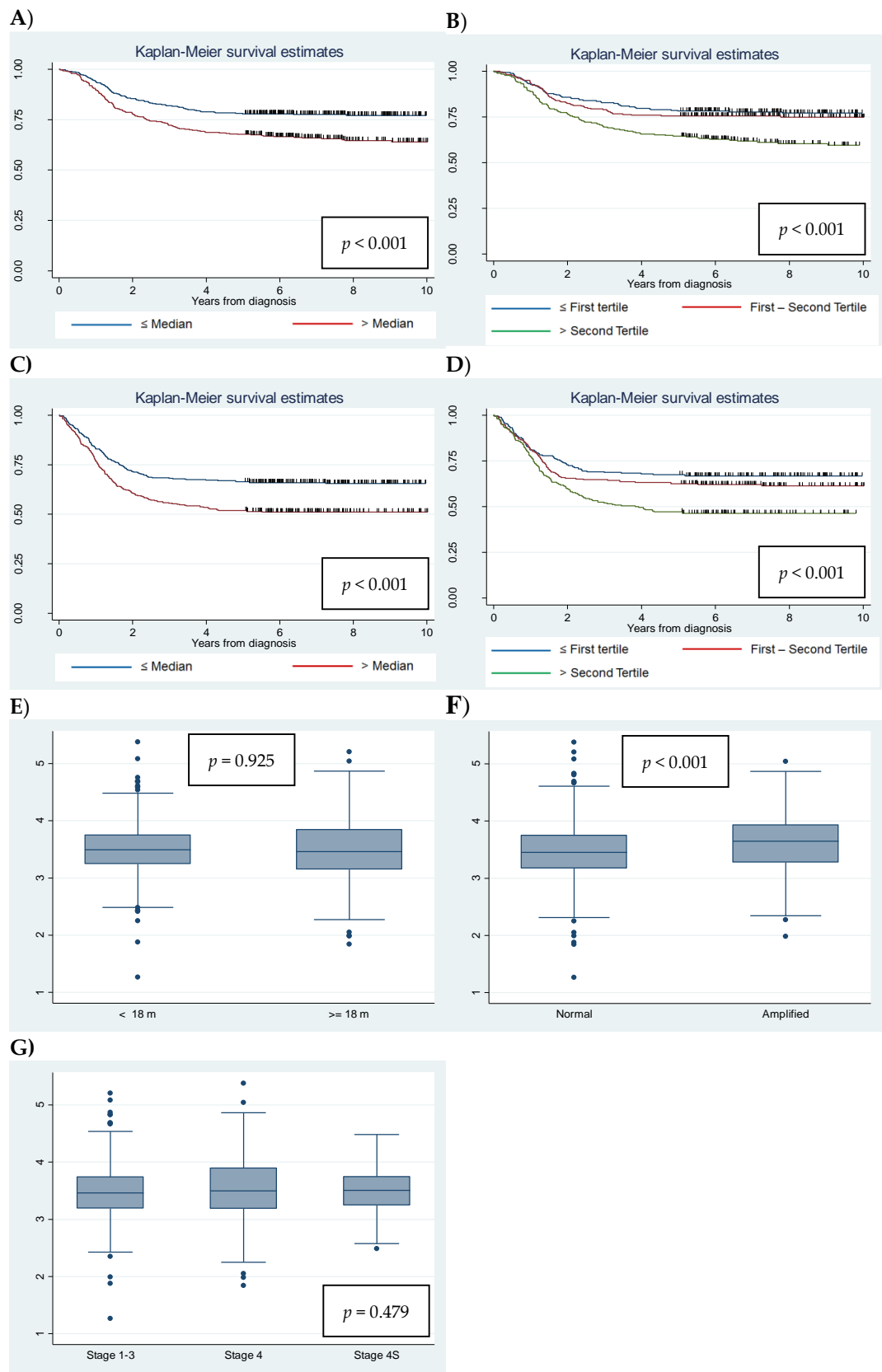
SNCG gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Figure S82



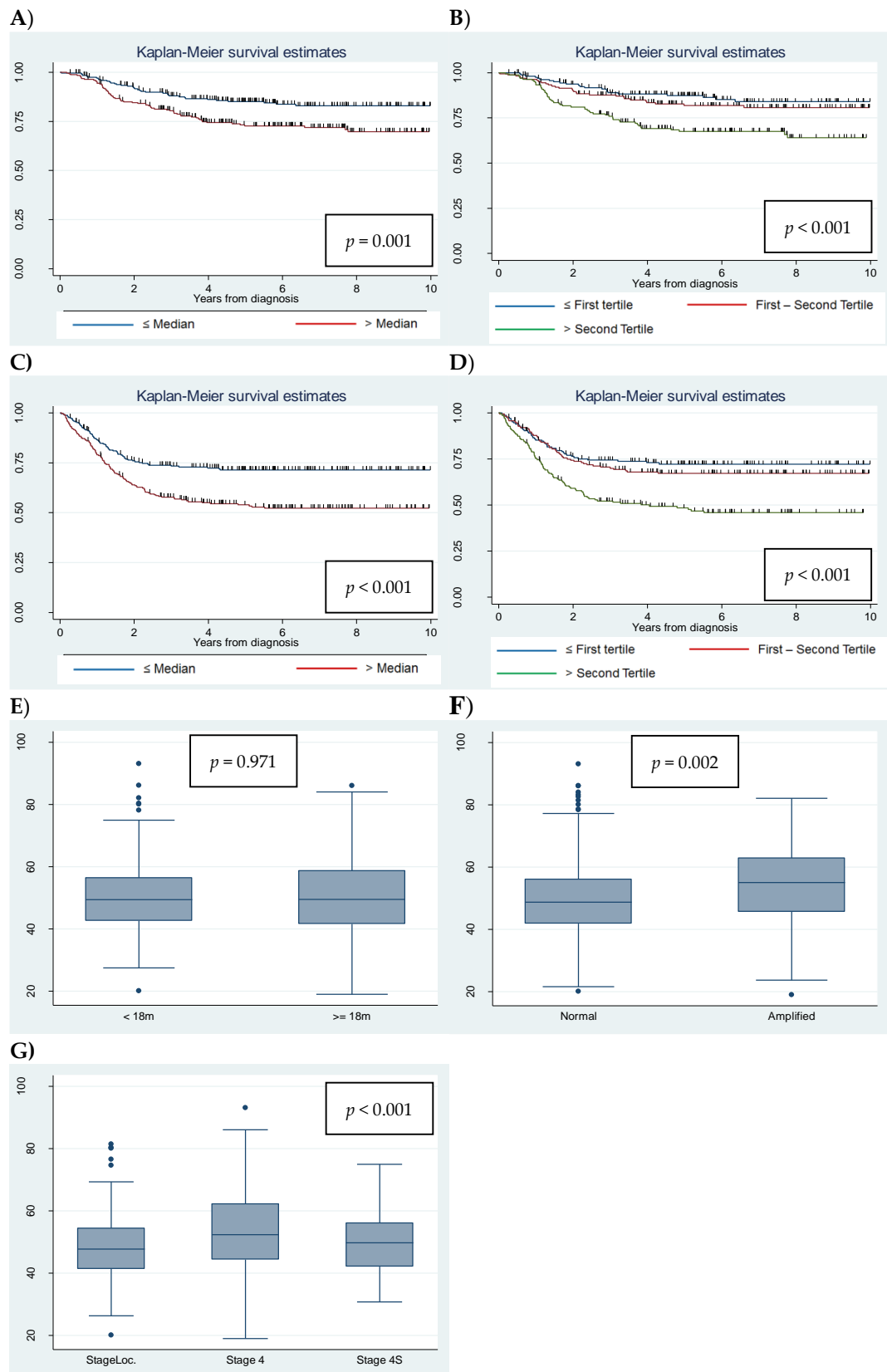
STAMBPL1 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S83



TSPAN14 gene expression and its association with survival and clinical characteristics in a cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) *MYCN* status; (G) INSS stage.

Supplementary Figure S84



WAPAL gene expression and its association with survival and clinical characteristics in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset. (A) Overall survival, cut-off based on the median expression value; (B) Overall survival, cut-off based on tertile expression values; (C) Event free survival, cut-off based on the median expression value; (D) Event free survival, cut-off based on tertile expression values; (E) Age at diagnosis; (F) MYCN status; (G) INSS stage.

Supplementary Tables

Supplementary Table S1. Demographic and clinical characteristics at diagnosis of the cohort of 260 neuroblastoma patients included in the analysis.

Patient characteristics	N	%
Age (months)		
0-17	98	37.7
18-59	124	47.7
≥ 60	38	14.6
Gender		
Male	138	53.1
Female	122	46.9
INSS Stage*		
Stage 1-2	61	23.6
Stage 3	47	18.2
Stage 4	132	51.2
Stage 4S	18	7.0
MYCN status		
Non-amplified	181	69.6
Amplified	79	30.4
Chromosome 10q loss		
No	234	90.0
Yes	26	10.0

* Two missing values

Supplementary Table S2. Association between chromosome 10q loss and other chromosome losses in a cohort of 260 neuroblastoma patients with segmental chromosome alterations at diagnosis.

Chromosome aberration	10q loss				<i>p</i>
	No (n = 234)		Yes (n = 26)		
	N	%	N	%	
1p loss	103	44.0	12	46.2	0.838
1q loss	9	3.9	1	3.9	0.999
2p loss	7	3.0	0	0.0	0.999
2q loss	10	4.3	1	3.9	0.999
3p loss	45	19.2	7	26.9	0.436
3q loss	2	0.9	1	3.9	0.272
4p loss	34	14.5	6	23.1	0.255
4q loss	6	2.6	3	11.5	0.050
5p loss	13	5.6	2	7.7	0.652
5q loss	9	3.9	1	3.9	0.999
6p loss	3	1.3	1	3.9	0.346
6q loss	21	9.0	3	11.5	0.718
7p loss	1	0.4	0	0.0	0.999
7q loss	2	0.9	1	3.9	0.272
8p loss	5	2.1	4	15.4	0.007
8q loss	7	3.0	1	3.9	0.575
9p loss	16	6.8	3	11.5	0.417
9q loss	13	5.6	3	11.5	0.206
10p loss	6	2.6	2	7.7	0.185
10q loss	-	-	-	-	-
11p loss	6	2.6	0	0.0	0.999
11q loss	86	36.8	11	42.3	0.670
12p loss	1	0.43	0	0.0	0.999
12q loss	3	1.3	0	0.0	0.999
13p loss	0	0.0	0	0.0	-
13q loss	2	0.9	1	3.9	0.272
14p loss	0	0.0	0	0.0	-
14q loss	21	9.0	4	15.4	0.292
15p loss	0	0.0	0	0.0	-
15q loss	14	6.0	1	3.9	0.999
16p loss	8	3.4	0	0.0	0.999
16q loss	10	4.3	2	7.7	0.342
17p loss	19	8.1	1	3.9	0.703
17q loss	4	1.7	0	0.0	0.999
18p loss	2	0.9	0	0.0	0.999
18q loss	2	0.9	0	0.0	0.999
19p loss	36	15.4	4	15.4	0.999
19q loss	10	4.3	5	19.2	0.010
20p loss	3	1.3	1	3.9	0.346
20q loss	0	0.0	0	0.0	-
21p loss	0	0.0	0	0.0	-
21q loss	5	2.1	3	11.5	0.036
22p loss	0	0.0	0	0.0	-
22q loss	13	5.6	2	7.7	0.652
Yp loss	9	3.9	1	3.9	0.999
Yq loss	7	3.0	1	3.9	0.575
Xp loss	2	0.9	0	0.0	0.999
Xq loss	1	0.43	0	0.0	0.999

Supplementary Table S3. Association between chromosome 10q loss and chromosomes gains in a cohort of 260 neuroblastoma patients with segmental chromosome alterations at diagnosis.

Chromosome aberration	10q loss				<i>p</i>
	No (n=234)		Yes (n=26)		
	N	%	N	%	
1p gain	12	5.1	2	7.7	0.638
1q gain	41	17.5	9	34.6	0.036
2p gain	108	46.2	12	46.2	0.999
2q gain	10	4.3	3	11.5	0.129
3p gain	3	1.3	1	3.9	0.346
3q gain	7	3.0	6	23.1	0.001
4p gain	2	0.9	1	3.9	0.272
4q gain	12	5.1	3	11.5	0.179
5p gain	4	1.7	3	11.5	0.024
5q gain	7	3.0	1	3.9	0.575
6p gain	13	5.6	6	23.1	0.006
6q gain	11	4.7	1	3.9	0.999
7p gain	6	2.6	1	3.9	0.526
7q gain	21	9.0	6	23.1	0.038
8p gain	2	0.9	0	0.0	0.999
8q gain	6	2.6	5	19.2	0.002
9p gain	5	2.1	1	3.9	0.472
9q gain	11	4.7	2	7.7	0.626
10p gain	2	0.9	0	0.0	0.999
10q gain	1	0.4	1	3.9	0.190
11p gain	29	12.4	5	19.2	0.355
11q gain	42	18.0	5	19.2	0.793
12p gain	4	1.7	1	3.9	0.412
12q gain	25	10.7	5	19.2	0.198
13p gain	0	0.0	0	0.0	-
13q gain	5	2.1	1	3.9	0.472
14p gain	0	0.0	0	0.0	-
14q gain	6	2.6	2	7.7	0.185
15p gain	0	0.0	0	0.0	-
15q gain	5	2.1	1	3.9	0.472
16p gain	0	0.0	0	0.0	-
16q gain	8	3.4	0	0.0	0.999
17p gain	2	0.9	2	7.7	0.051
17q gain	181	77.4	23	88.5	0.312
18p gain	3	1.3	1	3.9	0.346
18q gain	11	4.7	2	7.7	0.626
19p gain	5	2.1	0	0.0	0.999
19q gain	7	3.0	0	0.0	0.999
20p gain	3	1.3	0	0.0	0.999
20q gain	2	0.9	1	3.9	0.272
21p gain	0	0.0	0	0.0	-
21q gain	2	0.9	1	3.9	0.272
22p gain	0	0.0	0	0.0	-
22q gain	12	5.1	2	7.7	0.638
Yp gain	2	0.9	0	0.0	0.999
Yq gain	2	0.9	1	3.9	0.272
Xp gain	2	0.9	0	0.0	0.999
Xq gain	0	0.0	0	0.0	-

Supplementary Table S4 Survival of the cohort of 498 NB patients from the SEQC-498 data set, in relation to *AGAP11* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.025
≤ 4.664 (<i>reference</i>)	249/71	1	-		1	-	
> 4.664	249/34	0.43	0.28 – 0.64		0.62	0.41 – 0.95	
Tertiles				< 0.001			0.003
≤ 3.970 (<i>reference</i>)	166/58	1	-		1	-	
3.970 – 5.656	166/25	0.35	0.22 – 0.56		0.64	0.39 – 1.0	
> 5.656	166/22	0.31	0.19 – 0.51		0.49	0.30 – 0.82	
Continuous variable	498/105	0.79	0.71 – 0.89	< 0.001	0.92	0.83 – 1.01	0.072
Event Free Survival							
Median				0.002			0.146
≤ 4.664 (<i>reference</i>)	249/58	1	-		1	-	
> 4.664	249/75	0.63	0.47 – 0.84		0.80	0.59 – 1.1	
Tertiles				< 0.001			0.052
≤ 3.970 (<i>reference</i>)	166/79	1	-		1	-	
3.970 – 5.656	166/57	0.63	0.45 – 0.89		0.92	0.64 – 1.3	
> 5.656	166/47	0.50	0.35 – 0.72		0.69	0.47 – 1.0	
Continuous variable	498/183	0.87	0.80 – 0.94	0.001	0.93	0.87 – 1.0	0.064

N/O, Number of patients/Outcome (deaths for the overall and events for the event free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by MYCN status, age, and stage at diagnosis.

Supplementary Table S5. Survival of the cohort of 283 NB patients from the NRC-283 data set, in relation to *AGAP11* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.067			0.145
≤ 8.10 (reference)	137/44	1	-		1	-	
> 8.1	139/31	0.65	0.41 – 1.0		0.70	0.43 – 1.1	
Tertiles				0.029			0.199
≤ 6.8 (reference)	88/30	1	-		1	-	
6.8 – 9.8	94/27	0.84	0.50 – 1.4		0.88	0.52 – 1.5	
> 9.8	94/18	0.52	0.29 – 0.94		0.66	0.36 – 1.2	
Continuous variable	276/75	0.97	0.90 – 1.03	0.264	0.98	0.91 – 1.04	0.451
Progression Free Survival							
Median				0.520			0.949
≤ 8.1 (reference)	136/51	1	-		1	-	
> 8.1	139/46	0.88	0.59 – 1.3		0.99	0.65 – 1.5	
Tertiles				0.176			0.764
≤ 6.8 (reference)	87/35	1	-		1	-	
6.8 – 9.8	94/34	0.89	0.56 – 1.4		0.96	0.59 – 1.6	
> 9.8	94/28	0.71	0.43 – 1.2		0.92	0.54 – 1.6	
Continuous variable	275/973	0.98	0.93 – 1.04	0.504	0.99	0.94 – 1.05	0.875

N/O, Number of patients/Outcome (deaths for the overall and events for the progression free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by MYCN status, age, and stage at diagnosis.

Supplementary Table S6. Survival of the cohort of 786 NB patients from the Cangelosi *et al.* data set, in relation to *IFIT2* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>							
Median				<i>< 0.001</i>			<i>0.010</i>
≤ 2.391 (<i>reference</i>)	392/138	1	-		1	-	
> 2.391	394/91	0.59	0.45 – 0.77		0.70	0.54 – 0.92	
Tertiles				<i>< 0.001</i>			<i>0.080</i>
≤ 2.044 (<i>reference</i>)	262/105	1	-		1	-	
2.044 – 2.732	262/50	0.51	0.37 – 0.70		0.69	0.50 – 0.96	
> 2.732	262/64	0.53	0.39 – 0.72		0.77	0.56 – 1.1	
Continuous variable	786/229	0.65	0.56 – 0.76	<i>< 0.001</i>	0.87	0.75 – 0.99	<i>0.041</i>
<i>Event Free Survival</i>							
Median				<i>0.010</i>			<i>0.062</i>
≤ 2.391 (<i>reference</i>)	378/173	1	-		1	-	
> 2.391	391/147	0.75	0.60 – 0.93		0.81	0.65 – 1.0	
Tertiles				<i>0.002</i>			<i>0.129</i>
≤ 2.044 (<i>reference</i>)	250/125	1	-		1	-	
2.044 – 2.732	259/97	0.66	0.51 – 0.86		0.79	0.61 – 1.0	
> 2.732	260/98	0.65	0.50 – 0.85		0.81	0.62 – 1.1	
Continuous variable	769/320	0.76	0.67 – 0.87	<i>< 0.001</i>	0.89	0.78 – 1.0	<i>0.048</i>

N/O, Number of patients/Outcome (deaths for the overall and events for the event free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by *MYCN* status, age, and stage at diagnosis.

Supplementary Table S7. Survival of the cohort of 283 NB patients from the NRC-283 data set, in relation to *IFIT2* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>							
Median				0.040			0.938
≤ 34.9 (<i>reference</i>)	139/46	1	-		1	-	
> 34.9	137/29	0.61	0.39 – 0.98		0.98	0.60 – 1.6	
Tertiles				0.009			0.644
≤ 28.6 (<i>reference</i>)	92/36	1	-		1	-	
28.6 – 43.7	92/18	0.37	0.21 – 0.65		0.50	0.28 – 0.90	
> 43.7	92/21	0.51	0.30 – 0.88		0.99	0.54 – 1.8	
Continuous variable	176/75	0.997	0.989 – 1.01	0.464	1.00	0.995 – 1.01	0.663
<i>Progression Free Survival</i>							
Median				0.161			0.947
≤ 34.9 (<i>reference</i>)	138/55	1	-		1	-	
> 34.9	137/42	0.75	0.50 – 1.1		1.0	0.67 – 1.5	
Tertiles				0.020			0.634
≤ 28.6 (<i>reference</i>)	91/44	1	-		1	-	
28.6 – 43.7	92/23	0.39	0.23 – 0.64		0.52	0.31 – 0.88	
> 43.7	92/30	0.60	0.37 – 0.95		0.94	0.57 – 1.6	
Continuous variable	275/970	1.00	0.99 – 1.01	0.947	1.00	0.997–1.008	0.415

N/O, Number of patients/Outcome (deaths for the overall and events for the progression free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by *MYCN* status, age, and stage at diagnosis.

Supplementary Table S8. Survival of the cohort of 786 NB patients from the Cangelosi *et al.* data set, in relation to PAPSS2 gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>							
Median				<i>< 0.001</i>			<i>0.177</i>
≤ 2.852 (<i>reference</i>)	393/148	1	-		1	-	
> 2.852	393/81	0.49	0.37 – 0.64		0.83	0.63 – 1.1	
Tertiles				<i>< 0.001</i>			<i>0.015</i>
≤ 2.468 (<i>reference</i>)	262/119	1	-		1	-	
2.468 – 3.198	262/60	0.44	0.32 – 0.60		0.79	0.58 – 1.1	
> 3.198	262/50	0.36	0.26 – 0.49		0.67	0.48 – 0.94	
Continuous variable	786/229	0.57	0.49 – 0.66	<i>< 0.001</i>	0.86	0.74 – 0.99	<i>0.029</i>
<i>Event Free Survival</i>							
Median				<i>0.003</i>			<i>0.985</i>
≤ 2.852 (<i>reference</i>)	381/179	1	-		1	-	
> 2.852	388/141	0.72	0.57 – 0.89		1.0	0.79 – 1.3	
Tertiles				<i><0.001</i>			<i>0.708</i>
≤ 2.468 (<i>reference</i>)	251/129	1	-		1	-	
2.468 – 3.198	259/99	0.67	0.52 – 0.87		0.97	0.74 – 1.3	
> 3.198	259/92	0.62	0.48 – 0.81		0.95	0.72 – 1.3	
Continuous variable	769/320	0.74	0.65 – 0.84	<i>< 0.001</i>	0.94	0.83 – 1.1	<i>0.345</i>

N/O, Number of patients/Outcome (deaths for the overall and events for the event free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by MYCN status, age, and stage at diagnosis.

Supplementary Table S9. Survival of the cohort of 283 NB patients from the NRC-283 data set, in relation to PAPSS2 gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>							
Median				0.025			0.821
≤ 77.1 (<i>reference</i>)	137/46	1	-		1	-	
> 77.1	139/29	0.59	0.37 – 0.94		0.95	0.58 – 1.5	
Tertiles				0.013			0.713
≤ 63.8 (<i>reference</i>)	90/34	1	-		1	-	
63.8 – 103.3	94/23	0.63	0.37 – 1.1		0.90	0.52 – 1.5	
> 103.3	92/18	0.50	0.28 – 0.89		0.90	0.49 – 1.7	
Continuous variable	276/75	0.997	0.993–1.00	0.075	1.00	0.997–1.003	0.981
<i>Progression Free Survival</i>							
Median				0.009			0.373
≤ 77.1 (<i>reference</i>)	136/59	1	-		1	-	
> 77.1	139/38	0.59	0.39 – 0.88		0.83	0.54 – 1.3	
Tertiles				0.015			0.635
≤ 63.8 (<i>reference</i>)	89/42	1	-		1	-	
63.8 – 103.3	94/30	0.65	0.41 – 1.04		0.92	0.57 – 1.5	
> 103.3	92/25	0.55	0.34 – 0.91		0.88	0.52 – 1.5	
Continuous variable	275/97	0.997	0.994–1.00	0.063	1.000	0.997–1.003	0.771

N/O, Number of patients/Outcome (deaths for the overall and events for the progression free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by MYCN status, age, and stage at diagnosis.

Supplementary Table S10. Survival of the cohort of 786 NB patients from the Cangelosi *et al.* data set, in relation to *PCGF5* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>							
Median				< 0.001			< 0.001
≤ 3.008 (<i>reference</i>)	393/161	1	-		1	-	
> 3.008	393/61	0.34	0.26 – 0.46		0.56	0.42 – 0.76	
Tertiles				< 0.001			< 0.001
≤ 2.719 (<i>reference</i>)	262/126	1	-		1	-	
2.719 – 3.218	262/62	0.41	0.30 – 0.56		0.71	0.52 – 0.97	
> 3.218	262/41	0.25	0.17 – 0.35		0.48	0.33 – 0.69	
Continuous variable	786/229	0.52	0.45 – 0.60	< 0.001	0.79	0.66 – 0.93	0.006
<i>Event Free Survival</i>							
Median				< 0.001			< 0.001
≤ 3.008 (<i>reference</i>)	379/198	1	-		1	-	
> 3.008	390/122	0.49	0.39 – 0.62		0.67	0.53 – 0.85	
Tertiles				< 0.001			0.006
≤ 2.719 (<i>reference</i>)	249/141	1	-		1	-	
2.719 – 3.218	259/98	0.57	0.44 – 0.74		0.82	0.63 – 1.1	
> 3.218	261/81	0.43	0.33 – 0.57		0.67	0.50 – 0.89	
Continuous variable	769/320	0.60	0.52 – 0.70	< 0.001	0.85	0.72 – 1.0	0.047

N/O, Number of patients/Outcome (deaths for the overall and events for the event free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by *MYCN* status, age, and stage at diagnosis.

Supplementary Table S11. Survival of the cohort of 283 NB patients from the NRC-283 data set, in relation to *PCGF5* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>							
Median				<i>< 0.001</i>			<i>0.239</i>
≤ 73.8 (<i>reference</i>)	138/49	1	-		1	-	
> 73.8	138/26	0.45	<i>0.28 – 0.73</i>		0.74	<i>0.44 – 1.2</i>	
Tertiles				<i>< 0.001</i>			<i>0.151</i>
≤ 64.7 (<i>reference</i>)	92/41	1	-		1	-	
64.7 – 85.6	91/15	0.29	<i>0.16 – 0.52</i>		0.55	<i>0.30 – 1.0</i>	
> 85.6	93/19	0.36	<i>0.21 – 0.62</i>		0.67	<i>0.37 – 1.2</i>	
Continuous variable	276/75	0.984	<i>0.976–0.993</i>	<i>< 0.001</i>	0.997	<i>0.989–1.004</i>	<i>0.388</i>
<i>Progression Free Survival</i>							
Median				<i>0.048</i>			<i>0.979</i>
≤ 73.8 (<i>reference</i>)	137/55	1	-		1	-	
> 73.8	138/42	0.67	<i>0.45 – 1.0</i>		1.0	<i>0.65 – 1.5</i>	
Tertiles				<i>0.006</i>			<i>0.703</i>
≤ 64.7 (<i>reference</i>)	91/45	1	-		1	-	
64.7 – 85.6	91/22	0.38	<i>0.23 – 0.64</i>		0.68	<i>0.39 – 1.2</i>	
> 85.6	93/30	0.53	<i>0.34 – 0.85</i>		0.90	<i>0.54 – 1.5</i>	
Continuous variable	275/97	0.992	<i>0.986–0.999</i>	<i>0.015</i>	1.0	<i>0.994–1.006</i>	<i>0.919</i>

N/O, Number of patients/Outcome (deaths for the overall and events for the progression free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by *MYCN* status, age, and stage at diagnosis.

Supplementary Table S12. Survival of the cohort of 498 NB patients from the SEQC-498 data set, in relation to *NUDT9P1* gene expression values, evaluated by the Cox model.

Gene expression	Univariable analysis				Multivariable analysis		
	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>							
Median				< 0.001			< 0.001
≤ 1.330 (<i>reference</i>)	249/80	1	-		1	-	
> 1.330	249/25	0.25	0.16 – 0.39		0.36	0.23 – 0.58	
Tertiles				< 0.001			< 0.001
≤ 1.237 (<i>reference</i>)	166/67	1	-		1	-	
1.237 – 1.412	162/25	0.28	0.17 – 0.44		0.56	0.34 – 0.92	
> 1.412	170/13	0.13	0.07 – 0.24		0.24	0.13 – 0.44	
Continuous variable	498/105	0.01	0.003 – 0.04	< 0.001	0.06	0.02 – 0.20	< 0.001
<i>Event Free Survival</i>							
Median				< 0.001			< 0.001
≤ 1.330 (<i>reference</i>)	249/198	1	-		1	-	
> 1.330	249/63	0.43	0.32 – 0.59		0.52	0.38 – 0.72	
Tertiles				< 0.001			< 0.001
≤ 1.237 (<i>reference</i>)	166/90	1	-		1	-	
1.237 – 1.412	162/55	0.48	0.35 – 0.68		0.71	0.49 – 1.0	
> 1.412	170/38	0.30	0.21 – 0.44		0.41	0.28 – 0.62	
Continuous variable	498/183	0.08	0.03 – 0.19	< 0.001	0.19	0.08 – 0.43	< 0.001

N/O, Number of patients/Outcome (deaths for the overall and events for the event free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by MYCN status, age, and stage at diagnosis.

Supplementary Table S13. Survival of the cohort of 283 NB patients from the NRC-283 data set, in relation to *NUDT9P1* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>							
Median				< 0.001			0.444
≤ 21 (<i>reference</i>)	138/50	1	-		1	-	
> 21	138/25	0.40	0.25 – 0.65		0.82	0.48 – 1.42	
Tertiles				< 0.001			0.413
≤ 19.5 (<i>reference</i>)	91/39	1	-		1	-	
19.5 – 23.9	92/18	0.37	0.21 – 0.65		0.66	0.37 – 1.2	
> 23.9	93/18	0.35	0.20 – 0.61		0.83	0.45 – 1.5	
Continuous variable	276/75	0.91	0.87–0.96	< 0.001	0.97	0.93 – 1.02	0.237
<i>Progression Free Survival</i>							
Median				< 0.001			0.225
≤ 21.0 (<i>reference</i>)	137/62	1	-		1	-	
> 21.0	138/35	0.46	0.30 – 0.70		0.76	0.49 – 1.2	
Tertiles				< 0.001			0.175
≤ 19.5 (<i>reference</i>)	90/46	1	-		1	-	
19.5 – 23.9	92/28	0.49	0.31 – 0.79		0.79	0.49 – 1.3	
> 23.9	93/23	0.38	0.23 – 0.62		0.70	0.41 – 1.2	
Continuous variable	275/97	0.93	0.89 – 0.97	< 0.001	0.97	0.93 – 1.01	0.104

N/O, Number of patients/Outcome (deaths for the overall and events for the progression free survival); HR, Hazard Ratio. Multivariable analysis: HRs are adjusted by MYCN status, age, and stage at diagnosis.

Supplementary Table S14. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *ACTA2* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.254			0.585
≤ 4.518 (<i>reference</i>)	393/107	1	-		1	-	
> 4.518	393/122	1.2	0.90 – 1.5		1.1	0.83 – 1.4	
Tertiles				0.230			0.957
≤ 4.065 (<i>reference</i>)	262/77	1	-		1	-	
4.065 – 4.954	262/67	0.86	0.62 – 1.2		0.95	0.69 – 1.3	
> 4.954	262/85	1.1	0.83 – 1.5		0.99	0.73 – 1.4	
Continuous variable	786/229	0.97	0.86 – 1.1	0.664	0.99	0.89 – 1.1	0.914
Event Free Survival							
Median				0.083			0.251
≤ 4.518 (<i>reference</i>)	389/148	1	-		1	-	
> 4.518	380/172	1.2	0.97 – 1.5		1.1	0.91 – 1.4	
Tertiles				0.046			0.186
≤ 4.065 (<i>reference</i>)	259/101	1	-		1	-	
4.065 – 4.954	257/96	0.93	0.70 – 1.2		1.00	0.75 – 1.3	
> 4.954	253/123	1.3	1.0 – 1.7		1.2	0.91 – 1.6	
Continuous variable	769/320	1.08	0.97 – 1.2	0.150	1.07	0.97 – 1.17	0.199

N/O = Number of patients/Outcome (deaths for the overall and events for the event free survival). HR: Hazard Ratio. Multivariable analysis: HRs are adjusted by *MYCN* status, age, and stage at diagnosis.

Supplementary Table S15. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *ANKRD1* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.028			0.227
≤ 1.236 (reference)	249/61	1	-		1	-	
> 1.236	249/44	0.65	0.44 – 0.96		0.78	0.53 – 1.2	
Tertiles				0.021			0.326
≤ 1.155 (reference)	166/44	1	-		1	-	
1.155 – 1.399	166/32	0.69	0.44 – 1.1		0.67	0.43 – 1.1	
> 1.399	166/29	0.58	0.36 – 0.93		0.82	0.51 – 1.3	
Continuous variable	498/105	1.00	0.94 – 1.06	0.915	1.04	0.98 – 1.1	0.318
Event Free Survival							
Median				0.218			0.549
≤ 1.236 (reference)	249/96	1	-		1	-	
> 1.236	249/87	0.83	0.62 – 1.1		0.91	0.68 – 1.2	
Tertiles				0.113			0.421
≤ 1.155 (reference)	166/66	1	-		1	-	
1.155 – 1.399	166/63	0.88	0.63 – 1.2		0.89	0.63 – 1.3	
> 1.399	166/54	0.75	0.52 – 1.1		0.86	0.59 – 1.3	
Continuous variable	498/183	1.05	1.02 – 1.09	0.014	1.07	1.03 – 1.11	0.002

Supplementary Table S16. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *ANRKD22* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.623			0.177
≤ 0.562 (reference)	393/111	1	-		1	-	
> 0.562	393/118	1.1	0.82 – 1.4		1.2	0.92 – 1.6	
Tertiles				0.569			0.679
≤ -0.202 (reference)	262/86	1	-		1	-	
-0.202 – 1.171	262/61	0.66	0.48 – 0.92		1.1	0.78 – 1.5	
> 1.171	262/82	0.92	0.68 – 1.2		1.1	0.78 – 1.4	
Continuous variable	786/229	1.02	0.95 – 1.09	0.602	1.06	0.99 – 1.1	0.098
Event Free Survival							
Median							
≤ 0.562 (reference)				0.211			0.197
> 0.562	384/151	1	-		1	-	
Tertiles	385/169	1.2	0.92 – 1.4		1.2	0.93 – 1.4	
≤ -0.202 (reference)				0.817			0.654
-0.202 – 1.171	254/112	1	-		1	-	
> 1.171	259/91	0.76	0.58 – 1.0		1.0	0.75 – 1.3	
Median	256/117	1.0	0.79 – 1.3		1.1	0.82 – 1.4	
Continuous variable	769/320	1.03	0.97 – 1.09	0.385	1.04	0.98 – 1.09	0.217

Supplementary Table S17. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *ANXA11* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.410			0.028
≤ 2.922 (reference)	393/108	1	-		1	-	
> 2.922	393/121	1.1	0.86 – 1.4		1.3	1.0 – 1.7	
Tertiles				0.523			0.157
≤ 2.578 (reference)	262/79	1	-		1	-	
2.578 – 3.253	262/62	0.74	0.53 – 1.0		1.1	0.81 – 1.6	
> 3.253	262/88	1.1	0.81 – 1.5		1.2	0.92 – 1.7	
Continuous variable	786/229	1.04	0.89 – 1.21	0.652	1.13	0.98 – 1.3	0.097
Event Free Survival							
Median				0.037			0.004
≤ 2.922 (reference)	393/147	1	-		1	-	
> 2.922	376/173	1.3	1.0 – 1.6		1.4	1.1 – 1.7	
Tertiles				0.100			0.038
≤ 2.578 (reference)	262/101	1	-		1	-	
2.578 – 3.253	261/102	1.0	0.76 – 1.3		1.3	1.0 – 1.8	
> 3.253	246/117	1.2	0.96– 1.6		1.3	1.0 – 1.7	
Continuous variable	769/320	1.11	0.97 – 1.28	0.120	1.16	1.02 – 1.32	0.023

Supplementary Table S18. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *ATAD1* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.156			0.389
≤ 4.096 (<i>reference</i>)	393/105	1	-		1	-	
> 4.096	393/124	1.2	0.93 – 1.6		1.1	0.86 – 1.5	
Tertiles				0.292			0.811
≤ 3.935 (<i>reference</i>)	262/73	1	-		1	-	
3.935 – 4.259	262/71	0.95	0.69 – 1.3		0.97	0.70 – 1.4	
> 4.259	262/85	1.2	0.86 – 1.6		1.0	0.75 – 1.4	
Continuous variable	786/229	1.01	0.76 – 1.34	0.947	0.98	0.76 – 1.26	0.868
Event Free Survival							
Median				0.828			0.753
≤ 4.096 (<i>reference</i>)	377/155	1	-		1	-	
> 4.096	392/165	1.0	0.82 – 1.3		0.96	0.77 – 1.2	
Tertiles				0.424			0.937
≤ 3.935 (<i>reference</i>)	247/99	1	-		1	-	
3.935 – 4.259	260/106	1.0	0.76 – 1.3		0.99	0.75 – 1.3	
> 4.259	262/115	1.1	0.85 – 1.5		1.0	0.76 – 1.3	
Continuous variable	769/320	1.03	0.80 – 1.34	0.808	0.99	0.78 – 1.27	0.955

Supplementary Table S19. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *BMPR1A* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.764
≤ 3.070 (reference)	393/93	1	-		1	-	
> 3.070	393/136	1.6	1.2 – 2.1		0.96	0.73 – 1.3	
Tertiles				< 0.001			0.601
≤ 2.924 (reference)	262/63	1	-		1	-	
2.924 – 3.249	262/68	1.1	0.77 – 1.5		1.1	0.79 – 1.6	
> 3.249	262/98	1.8	1.3 – 2.4		0.93	0.67– 1.3	
Continuous variable	786/229	1.92	1.4 – 2.7	< 0.001	0.94	0.70 – 1.2	0.654
Event Free Survival							
Median				0.003			0.937
≤ 3.070 (reference)	377/138	1	-		1	-	
> 3.070	392/182	1.4	1.1 – 1.8		0.99	0.79 – 1.2	
Tertiles				0.002			0.907
≤ 2.924 (reference)	247/91	1	-		1	-	
2.924 – 3.249	261/101	1.1	0.82 – 1.4		1.1	0.81 – 1.4	
> 3.249	261/128	1.5	1.2 – 2.0		0.99	0.74 – 1.3	
Continuous variable	764/320	1.63	1.22– 2.17	0.001	0.99	0.75 – 1.29	0.919

Supplementary Table S20. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *C10orf116* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.043			0.386
≤ 3.999 (<i>reference</i>)	249/62	1	-		1	-	
> 3.999	249/43	0.67	0.45 – 0.99		0.84	0.56 – 1.3	
Tertiles				0.006			0.031
≤ 3.293 (<i>reference</i>)	166/47	1	-		1	-	
3.293 – 4.982	166/31	0.59	0.38 – 0.93		0.81	0.51 – 1.3	
> 4.982	166/27	0.53	0.33 – 0.85		0.58	0.36 – 0.96	
Continuous variable	498/105	0.97	0.90 – 1.03	0.272	0.98	0.92 – 1.03	0.441
Event Free Survival							
Median				0.288			0.970
≤ 3.999 (<i>reference</i>)	249/97	1	-		1	-	
> 3.999	249/86	0.85	0.64 – 1.1		0.99	0.73 – 1.3	
Tertiles				0.234			0.511
≤ 3.293 (<i>reference</i>)	166/67	1	-		1	-	
3.293 – 4.982	166/58	0.82	0.58 – 1.2		1.0	0.71 – 1.5	
> 4.982	166/58	0.81	0.57 – 1.1		0.88	0.61 – 1.3	
Continuous variable	498/183	0.98	0.94 – 1.03	0.474	0.99	0.95 – 1.03	0.636

Supplementary Table S21. Survival of the cohort of 709 NB patients in the E-MTAB-1781 *in silico* dataset, in relation to *C10orf57* (alias *FLJ3263*, Agilent probe: A_23_P97853) gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.993
≤ -0.170 (<i>reference</i>)	354/55	1	-		1	-	
> -0.170	355/106	2.0	1.5 – 2.8		1.00	0.71 – 1.4	
Tertiles				< 0.001			0.920
≤ -0.301 (<i>reference</i>)	236/33	1	-		1	-	
-0.301 – -0.041	236/48	1.5	0.96 – 2.3		0.99	0.63 – 1.6	
> -0.041	237/80	2.7	1.8 – 4.0		0.98	0.64 – 1.5	
Continuous variable	709/161	3.56	2.21 – 5.74	< 0.001	0.72	0.44 – 1.2	0.178
Event Free Survival							
Median				< 0.001			0.084
≤ -0.170 (<i>reference</i>)	343/92	1	-		1	-	
> -0.170	352/164	1.9	1.5 – 2.5		1.3	0.97 – 1.7	
Tertiles				< 0.001			0.046
≤ -0.301 (<i>reference</i>)	227/55	1	-		1	-	
-0.301 – -0.041	232/80	1.5	1.1 – 2.1		1.3	0.89 – 1.8	
> -0.041	236/121	2.5	1.8 – 3.5		1.4	1.0 – 2.0	
Continuous variable	695/256	2.73	1.87 – 3.98	< 0.001	1.07	0.72 – 1.59	0.742

Supplementary Table S22. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *C10orf58* (alias *FAM213A*) gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.003
≤ 4.032 (<i>reference</i>)	393/62	1	-		1	-	
> 4.032	393/167	3.2	2.4 – 4.4		1.6	1.2 – 2.2	
Tertiles				< 0.001			0.082
≤ 3.804 (<i>reference</i>)	262/43	1	-		1	-	
3.804 – 4.260	262/74	1.8	1.3 – 2.7		1.3	0.86 – 1.9	
> 4.260	262/112	3.1	2.2 – 4.5		1.4	0.96 – 2.0	
Continuous variable	786/229	2.57	2.04 – 3.25	< 0.001	1.21	0.94 – 1.57	0.137
Event Free Survival							
Median				< 0.001			0.016
≤ 4.032 (<i>reference</i>)	377/113	1	-		1	-	
> 4.032	392/207	2.1	1.7 – 2.6		1.4	1.1 – 1.7	
Tertiles				< 0.001			0.168
≤ 3.804 (<i>reference</i>)	247/73	1	-		1	-	
3.804 – 4.260	261/112	1.6	1.2 – 2.2		1.3	0.95 – 1.7	
> 4.260	261/135	2.1	1.6 – 2.8		1.3	0.93 – 1.7	
Continuous variable	769/320	1.86	1.5 – 2.3	< 0.001	1.15	0.92 – 1.4	0.224

Supplementary Table S23. Survival of the cohort of 498 NB patients in the SEQC-498. *in silico* dataset, in relation to *CFL1P1* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.045			0.035
≤ 2.078 (<i>reference</i>)	249/61	1	-		1	-	
> 2.078	249/44	0.67	0.46 – 0.99		0.65	0.44 – 0.97	
Tertiles				0.070			0.286
≤ 1.882 (<i>reference</i>)	166/48	1	-		1	-	
1.882 – 2.342	166/22	0.40	0.24 – 0.66		0.57	0.34 – 0.96	
> 2.342	166/35	0.69	0.45 – 1.1		0.79	0.51 – 1.2	
Continuous variable	498/105	0.71	0.48 – 1.04	0.075	0.82	0.57 – 1.2	0.262
Event Free Survival							
Median				0.029			0.043
≤ 2.078 (<i>reference</i>)	249/104	1	-		1	-	
> 2.078	249/79	0.72	0.54 – 0.97		0.73	0.54 – 0.99	
Tertiles				0.012			0.084
≤ 1.882 (<i>reference</i>)	166/82	1	-		1	-	
1.882 – 2.342	166/43	0.46	0.32 – 0.67		0.60	0.41 – 0.88	
> 2.342	166/58	0.67	0.48 – 0.94		0.75	0.52 – 1.1	
Continuous variable	498/183	0.74	0.55 – 1.00	0.043	0.82	0.62 – 1.1	0.156

Supplementary Table S24. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *CH25H* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.724			0.559
≤ 0.587 (reference)	393/110	1	-		1	-	
> 0.587	393/119	1.0	0.81 – 1.4		1.1	0.83 – 1.4	
Tertiles				0.780			0.568
≤ 0.264 (reference)	262/71	1	-		1	-	
0.264 – 1.058	262/81	1.2	0.84 – 1.6		1.2	0.90 – 1.7	
> 1.058	262/77	1.0	0.76 – 1.4		1.1	0.80 – 1.5	
Continuous variable	486/229	0.97	0.86 – 1.1	0.564	1.01	0.91 – 1.13	0.789
Event Free Survival							
Median				0.870			0.793
≤ 0.587 (reference)	389/160	1	-		1	-	
> 0.587	380/160	0.98	0.79 – 1.2		0.97	0.78 – 1.2	
Tertiles				0.527			0.648
≤ 0.264 (reference)	261/109	1	-		1	-	
0.264 – 1.058	256/109	1.0	0.78 – 1.3		0.99	0.76 – 1.3	
> 1.058	252/102	0.92	0.70 – 1.2		0.94	0.72 – 1.2	
Continuous variable	769/320	0.95	0.86 – 1.04	0.306	0.98	0.89 – 1.07	0.665

Supplementary Table S25. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *DYDC1* gene expression, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival				< 0.001			0.023
≤ 1.01* (reference)	321/43	1	-		1	-	
≤ 1.01*	177/62	3.1	2.1 – 4.5		1.6	1.1 – 2.4	
Event Free Survival				< 0.001			0.007
≤ 1.01* (reference)	321/89	1	-		1	-	
> 1.01	177/94	2.3	1.8 – 3.1		1.5	1.1 – 2.1	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S26. Association between *DYDC1* gene expression and main patients characteristics at diagnosis in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset.

Patients characteristics	Gene expression ≤ 1.01*		Gene expression > 1.01		<i>p</i>
	N	%	N	%	
MYCN status					< 0.001
Not amplified	283	70.6	118	29.4	
Amplified	36	39.1	56	60.9	
Age					< 0.001
≤ 18 months	224	73.4	81	26.6	
> 18 months	97	50.3	96	49.7	
Stage					< 0.001
Localized	191	72.9	71	27.1	
Stage 4	90	49.2	93	50.8	
Stage 4S	40	75.5	13	24.5	
Total	321	64.5	177	35.5	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S27. Survival of the cohort of 498 NB patients in the SEQC-498. *in silico* dataset, in relation to *DYDC2* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.290
≤ 1.373 (<i>reference</i>)	249/24	1	-		1	-	
> 1.373	249/81	4.1	2.6 – 6.4		1.3	0.79 – 2.2	
Tertiles				< 0.001			0.105
≤ 1.255 (<i>reference</i>)	166/13	1	-		1	-	
1.255 – 1.563	166/27	2.2	1.1 – 4.2		1.0	0.52 – 2.0	
> 1.563	166/65	6.4	3.5 – 11.6		1.5	0.77 – 2.9	
Continuous variable	498/105	2.14	1.75 – 2.60	< 0.001	1.53	1.10 – 2.12	0.021
Event Free Survival							
Median				< 0.001			0.551
≤ 1.373 (<i>reference</i>)	249/63	1	-		1	-	
> 1.373	249/120	2.2	1.6 – 3.0		1.1	0.78 – 1.6	
Tertiles				< 0.001			0.635
≤ 1.255 (<i>reference</i>)	166/39	1	-		1	-	
1.255 – 1.563	166/57	1.6	1.0 – 2.4		1.0	0.66 – 1.6	
> 1.563	166/87	2.8	1.9 – 4.0		1.1	0.71 – 1.7	
Continuous variable	498/183	1.9	1.6 – 2.3	< 0.001	1.35	1.01 – 1.80	0.055

Supplementary Table S28. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *EIF5AL1* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.157
≤ 67.788 (reference)	249/35	1	-		1	-	
> 67.788	249/70	2.3	1.5 – 3.4		1.4	0.88 – 2.2	
Tertiles				< 0.001			0.012
≤ 60.288 (reference)	166/25	1	-		1	-	
60.288 – 74.043	166/19	0.76	0.42 – 1.4		1.1	0.59 – 2.0	
> 74.043	166/61	3.0	1.9 – 4.7		1.9	1.1 – 3.1	
Continuous variable	498/105	1.02	1.01 – 1.03	< 0.001	1.01	1.00 – 1.01	0.163
Event Free Survival							
Median				< 0.001			0.036
≤ 67.788 (reference)	249/73	1	-		1	-	
> 67.788	249/110	1.7	1.3 – 2.3		1.4	1.0 – 2.0	
Tertiles				< 0.001			0.011
≤ 60.288 (reference)	166/52	1	-		1	-	
60.288 – 74.043	166/47	0.94	0.64 – 1.4		1.2	0.81 – 1.8	
> 74.043	166/84	2.0	1.4 – 2.8		1.6	1.1 – 2.4	
Continuous variable	498/183	1.01	1.00 – 1.02	< 0.001	1.01	1.00 – 1.01	0.019

Supplementary Table S29. Survival of the cohort of 498 NB patients in the SEQC-498. *in silico* dataset, in relation to *FAM22A* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.069
≤ 6.476 (reference)	249/78	1	-		1	-	
> 6.476	249/27	0.28	0.18 – 0.44		0.65	0.40 – 1.0	
Tertiles				< 0.001			0.056
≤ 5.292 (reference)	166/64	1	-		1	-	
5.292 – 7.470	166/22	0.28	0.17 – 0.46		0.68	0.40 – 1.2	
> 7.470	166/19	0.22	0.13 – 0.37		0.60	0.34 – 1.1	
Continuous variable	498/105	0.76	0.69 – 0.83	< 0.001	0.95	0.87 – 1.04	0.258
Event Free Survival							
Median				< 0.001			0.027
≤ 6.476 (reference)	249/120	1	-		1	-	
> 6.476	249/63	0.43	0.31 – 0.58		0.68	0.49 – 0.96	
Tertiles				< 0.001			0.016
≤ 5.292 (reference)	166/91	1	-		1	-	
5.292 – 7.470	166/52	0.47	0.33 – 0.66		0.78	0.53 – 1.1	
> 7.470	166/40	0.33	0.23 – 0.48		0.60	0.40 – 0.92	
Continuous variable	498/183	0.82	0.77 – 0.88	< 0.001	0.93	0.87 – 1.0	0.044

Supplementary Table S30. Survival of the cohort of 498 NB patients in the SEQC-498. *in silico* dataset, in relation to *FAM22D* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.022
≤ 9.545 (reference)	249/80	1	-		1	-	
> 9.545	249/25	0.25	0.16 – 0.39		0.57	0.35 – 0.93	
Tertiles				< 0.001			0.029
≤ 7.601 (reference)	166/62	1	-		1	-	
7.601 – 11.590	166/28	0.35	0.22 – 0.55		0.93	0.56 – 1.5	
> 11.590	166/15	0.17	0.10 – 0.30		0.50	0.27 – 0.93	
Continuous variable	498/105	0.82	0.78 – 0.87	< 0.001	0.94	0.88 – 0.99	0.023
Event Free Survival							
Median				< 0.001			0.017
≤ 9.545 (reference)	249/121	1	-		1	-	
> 9.545	249/62	0.42	0.31 – 0.57		0.66	0.47 – 0.93	
Tertiles				< 0.001			0.012
≤ 7.601 (reference)	166/91	1	-		1	-	
7.601 – 11.590	166/53	0.48	0.34 – 0.67		0.80	0.54 – 1.2	
> 11.590	166/39	0.31	0.22 – 0.46		0.59	0.39 – 0.89	
Continuous variable	498/183	0.88	0.84 – 0.91	< 0.001	0.94	0.90 – 0.98	0.002

Supplementary Table S31. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *FAM35A* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.029			0.037
≤ 3.536 (reference)	393/102	1	-		1	-	
> 3.536	393/127	1.3	1.0 – 1.7		0.74	0.55 – 0.98	
Tertiles				0.039			0.077
≤ 3.396 (reference)	262/75	1	-		1	-	
3.396 – 3.697	262/60	0.77	0.55 – 1.1		0.86	0.61 – 1.2	
> 3.697	262/94	1.4	1.0 – 1.8		0.74	0.53 – 1.0	
Continuous variable	786/229	1.26	0.91 – 1.7	0.161	0.82	0.64 – 1.1	0.124
Event Free Survival							
Median				0.001			0.746
≤ 3.536 (reference)	377/137	1	-		1	-	
> 3.536	392/183	1.4	1.1 – 1.8		1.0	0.82 – 1.3	
Tertiles				0.003			0.714
≤ 3.396 (reference)	246/91	1	-		1	-	
3.396 – 3.697	262/102	1.1	0.81 – 1.4		1.1	0.84 – 1.5	
> 3.697	261/127	1.5	1.1 – 1.9		1.1	0.79 – 1.4	
Continuous variable	769/320	1.55	1.15 – 2.09	0.004	1.05	0.80 – 1.37	0.740

Supplementary Table S32. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *FAS* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.207			0.906
≤ 1.871 (reference)	393/122	1	-		1	-	
> 1.871	393/107	0.85	0.65 – 1.1		0.98	0.76 – 1.3	
Tertiles				0.112			0.324
≤ 1.626 (reference)	262/87	1	-		1	-	
1.626 – 2.143	262/70	0.77	0.56 – 1.1		0.89	0.65 – 1.2	
> 2.143	262/72	0.78	0.57 – 1.1		0.85	0.62 – 1.2	
Continuous variable	786/229	0.85	0.70 – 1.04	0.118	0.96	0.80 – 1.15	0.644
Event Free Survival							
Median				0.456			0.958
≤ 1.871 (reference)	378/161	1	-		1	-	
> 1.871	391/159	0.92	0.74 – 1.1		1.00	0.81 – 1.3	
Tertiles				0.337			0.600
≤ 1.626 (reference)	247/108	1	-		1	-	
1.626 – 2.143	260/105	0.90	0.69 – 1.2		0.98	0.75 – 1.3	
> 2.143	262/107	0.88	0.67 – 1.1		0.93	0.71 – 1.2	
Continuous variable	769/320	0.97	0.82 – 1.15	0.732	1.03	0.88 – 1.22	0.679

Supplementary Table S33. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *FLJ37201* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.171			0.019
≤ 1.418 (reference)	393/123	1	-		1	-	
> 1.418	393/106	0.83	0.64 – 1.1		0.73	0.56 – 0.95	
Tertiles				0.306			0.063
≤ 0.887 (reference)	262/90	1	-		1	-	
0.887 – 1.956	262/59	0.61	0.44 – 0.85		0.69	0.50 – 0.97	
> 1.956	262/80	0.86	0.64 – 1.2		0.75	0.55 – 1.0	
Continuous variable	786/229	0.98	0.89 – 1.06	0.580	0.93	0.86 – 1.01	0.107
Event Free Survival							
Median				0.161			0.024
≤ 1.418 (reference)	377/166	1	-		1	-	
> 1.418	392/154	0.85	0.69 – 1.1		0.77	0.62 – 0.97	
Tertiles				0.157			0.030
≤ 0.887 (reference)	248/113	1	-		1	-	
0.887 – 1.956	259/102	0.82	0.63 – 1.1		0.85	0.65 – 1.1	
> 1.956	262/105	0.82	0.63 – 1.1		0.74	0.57 – 0.97	
Continuous variable	769/320	0.98	0.90 – 1.06	0.601	0.94	0.87 – 1.01	0.125

Supplementary Table S34. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *GHITM* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.310			0.270
≤ 4.571 (reference)	392/120	1	-		1	-	
> 4.571	394/109	0.87	0.67 – 1.1		1.2	0.89 – 1.5	
Tertiles				0.929			0.165
≤ 4.435 (reference)	262/81	1	-		1	-	
4.435 – 4.726	262/67	0.78	0.56 – 1.1		1.1	0.79 – 1.6	
> 4.726	262/81	0.99	0.72 – 1.3		1.3	0.91 – 1.7	
Continuous variable	786/229	0.79	0.55 – 1.13	0.191	1.03	0.73 – 1.5	0.859
Event Free Survival							
Median				0.868			0.232
≤ 4.571 (reference)	376/156	1	-		1	-	
> 4.571	393/164	1.0	0.82 – 1.3		1.1	0.92 – 1.4	
Tertiles				0.479			0.214
≤ 4.435 (reference)	247/99	1	-		1	-	
4.435 – 4.726	261/109	1.0	0.78 – 1.3		1.2	0.92 – 1.6	
> 4.726	261/112	1.1	0.84 – 1.4		1.2	0.91 – 1.6	
Continuous variable	769/320	0.92	0.67 – 1.3	0.579	1.04	0.76 – 1.4	0.812

Supplementary Table S35. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *GLUD1* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.005			0.221
≤ 3.848 (<i>reference</i>)	393/99	1	-		1	-	
> 3.848	393/130	1.4	1.1 – 1.9		1.2	0.90 – 1.5	
Tertiles				0.021			0.693
≤ 3.689 (<i>reference</i>)	262/72	1	-		1	-	
3.689 – 4.006	262/65	0.92	0.66 – 1.3		0.97	0.69 – 1.4	
> 4.006	262/92	1.4	1.0 – 1.9		1.1	0.78 – 1.4	
Continuous variable	786/229	1.32	0.99 – 1.8	0.064	1.10	0.81 – 1.5	0.530
Event Free Survival							
Median				< 0.001			0.004
≤ 3.848 (<i>reference</i>)	377/131	1	-		1	-	
> 3.848	392/189	1.60	1.3 – 2.0		1.4	1.1 – 1.7	
Tertiles				< 0.001			0.022
≤ 3.689 (<i>reference</i>)	246/88	1	-		1	-	
3.689 – 4.006	261/97	1.1	0.83 – 1.5		1.1	0.82 – 1.5	
> 4.006	262/135	1.7	1.3 – 2.2		1.4	1.0 – 1.8	
Continuous variable	769/320	1.7	1.3 – 2.2	< 0.001	1.5	1.2 – 2.0	0.002

Supplementary Table S36. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *GRID1* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.514			0.501
≤ 3.059 (<i>reference</i>)	393/113	1	-		1	-	
> 3.059	393/116	1.1	0.84 – 1.4		1.1	0.84 – 1.4	
Tertiles				0.122			0.111
≤ 2.712 (<i>reference</i>)	262/70	1	-		1	-	
2.712 – 3.388	262/78	1.2	0.85 – 1.6		1.1	0.80 – 1.6	
> 3.388	262/81	1.3	0.93 – 1.8		1.3	0.94 – 1.8	
Continuous variable	786/229	1.15	0.96 – 1.38	0.125	1.18	0.99 – 1.41	0.059
Event Free Survival							
Median				0.873			0.993
≤ 3.059 (<i>reference</i>)	388/165	1	-		1	-	
> 3.059	381/155	1.0	0.82 – 1.3		1.0	0.80 – 1.3	
Tertiles				0.329			0.458
≤ 2.712 (<i>reference</i>)	259/109	1	-		1	-	
2.712 – 3.388	259/103	0.98	0.75 – 1.3		0.95	0.72 – 1.3	
> 3.388	251/108	1.1	0.88 – 1.5		1.1	0.84 – 1.5	
Continuous variable	769/320	1.03	0.89 – 1.2	0.699	1.04	0.90 – 1.2	0.597

Supplementary Table S37. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *HTR7* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.001			0.282
≤ 0.906 (<i>reference</i>)	393/134	1	-		1	-	
> 0.906	393/95	0.65	0.50 – 0.85		0.86	0.66 – 1.1	
Tertiles				< 0.001			0.160
≤ 0.604 (<i>reference</i>)	262/95	1	-		1	-	
0.604 – 1.294	262/77	0.76	0.56 – 1.0		0.86	0.63 – 1.2	
> 1.294	262/57	0.53	0.38 – 0.74		0.79	0.57 – 1.1	
Continuous variable	786/229	0.71	0.61 – 0.85	< 0.001	0.88	0.73 – 1.1	0.186
Event Free Survival							
Median				0.219			0.853
≤ 0.906 (<i>reference</i>)	381/165	1	-		1	-	
> 0.906	388/155	0.87	0.70 – 1.1		1.0	0.82 – 1.3	
Tertiles				0.045			0.783
≤ 0.604 (<i>reference</i>)	255/113	1	-		1	-	
0.604 – 1.294	253/110	0.93	0.72 – 1.2		1.0	0.79 – 1.3	
> 1.294	261/97	0.76	0.58 – 0.99		0.96	0.73 – 1.3	
Continuous variable	769/320	0.85	0.74 – 0.97	0.015	0.97	0.84 – 1.1	0.703

Supplementary Table S38. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *IFIT1* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.615			0.858
≤ 2.074 (<i>reference</i>)	393/111	1	-		1	-	
> 2.074	393/118	1.1	0.82 – 1.4		0.98	0.75 – 1.3	
Tertiles				0.939			0.733
≤ 1.638 (<i>reference</i>)	262/82	1	-		1	-	
1.638 – 2.675	262/63	0.72	0.52 – 1.0		0.84	0.60 – 1.2	
> 2.675	262/84	1.0	0.74 – 1.4		0.95	0.70 – 1.3	
Continuous variable	786/229	0.98	0.89 – 1.08	0.661	0.96	0.88 – 1.06	0.442
Event Free Survival							
Median				0.873			0.537
≤ 2.074 (<i>reference</i>)	380/155	1	-		1	-	
> 2.074	389/165	1.0	0.82 – 1.3		0.93	0.75 – 1.2	
Tertiles				0.989			0.487
≤ 1.638 (<i>reference</i>)	252/106	1	-		1	-	
1.638 – 2.675	258/101	0.87	0.66 – 1.1		0.94	0.71 – 1.2	
> 2.675	259/113	1.0	0.77 – 1.3		0.91	0.69 – 1.2	
Continuous variable	769/320	0.98	0.90 – 1.1	0.580	0.96	0.88 – 1.0	0.302

Supplementary Table S39. Survival of the cohort of 498 NB patients in the SEQC-498. *in silico* dataset, in relation to *IFIT1L* (alias *IFIT1B*) gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.359			0.127
≤ 1.074 (<i>reference</i>)	249/48	1	-		1	-	
> 1.074	249/57	1.2	0.81 – 1.8		1.4	0.92 – 2.0	
Tertiles				0.590			0.223
≤ 1.048 (<i>reference</i>)	163/35	1	-		1	-	
1.048 – 1.106	168/30	0.78	0.48 – 1.3		0.91	0.55 – 1.5	
> 1.106	167/40	1.1	0.71 – 1.8		1.3	0.84 – 2.1	
Continuous variable	498/105	3.29	1.05 – 10.3	0.069	7.79	2.29 – 26.5	0.005
Event Free Survival							
Median				0.239			0.333
≤ 1.074 (<i>reference</i>)	249/97	1	-		1	-	
> 1.074	249/86	0.84	0.63 – 1.1		0.86	0.64 – 1.2	
Tertiles				0.311			0.456
≤ 1.048 (<i>reference</i>)	163/67	1	-		1	-	
1.048 – 1.106	168/56	0.79	0.55 – 1.1		0.87	0.61 – 1.2	
> 1.106	167/60	0.84	0.59 – 1.2		0.88	0.62 – 1.2	
Continuous variable	498/183	0.89	0.27 – 2.90	0.848	0.97	0.29 – 3.3	0.956

Supplementary Table S40. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *IFIT3* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.563			0.177
≤ 2.459 (reference)	393/118	1	-		1	-	
> 2.459	393/111	0.93	0.71 – 1.2		0.84	0.64 – 1.1	
Tertiles				0.984			0.216
≤ 2.096 (reference)	262/87	1	-		1	-	
2.096 – 2.879	262/55	0.57	0.41 – 0.80		0.68	0.48 – 0.95	
> 2.879	262/87	1.0	0.74 – 1.3		0.82	0.61 – 1.1	
Continuous variable	786/229	0.93	0.84 – 1.03	0.160	0.93	0.84 – 1.02	0.131
Event Free Survival							
Median				0.442			0.840
≤ 2.459 (reference)	381/151	1	-		1	-	
> 2.459	388/169	1.1	0.88 – 1.4		0.98	0.78 – 1.2	
Tertiles				0.424			0.708
≤ 2.096 (reference)	252/103	1	-		1	-	
2.096 – 2.879	258/100	0.92	0.70 – 1.2		1.0	0.79 – 1.4	
> 2.879	259/117	1.1	0.85 – 1.4		0.95	0.72 – 1.2	
Continuous variable	769/320	0.96	0.88 – 1.1	0.416	0.95	0.87 – 1.0	0.290

Supplementary Table S41. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *IFIT5* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.480
≤ 3.253 (<i>reference</i>)	393/83	1	-		1	-	
> 3.253	393/146	2.0	1.5 – 2.6		1.1	0.83 – 1.5	
Tertiles				< 0.001			0.758
≤ 3.031 (<i>reference</i>)	261/54	1	-		1	-	
3.031 – 3.473	263/76	1.5	1.0 – 2.1		1.3	0.93 – 1.9	
> 3.473	262/99	2.1	1.5 – 2.9		0.99	0.70 – 1.4	
Continuous variable	786/229	1.47	1.21 – 1.79	< 0.001	0.92	0.74 – 1.1	0.479
Event Free Survival							
Median				< 0.001			0.988
≤ 3.253 (<i>reference</i>)	380/134	1	-		1	-	
> 3.253	389/186	1.5	1.2 – 1.9		1.0	0.79 – 1.3	
Tertiles				0.001			0.628
≤ 3.031 (<i>reference</i>)	249/85	1	-		1	-	
3.031 – 3.473	260/109	1.3	0.99 – 1.7		1.2	0.88 – 1.6	
> 3.473	260/126	1.6	1.2 – 2.1		0.94	0.70 – 1.3	
Continuous variable	769/320	1.26	1.06 – 1.51	0.010	0.91	0.75 – 1.1	0.314

Supplementary Table S42. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *KIF20B* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.213
≤ 2.923 (reference)	393/82	1	-		1	-	
> 2.923	393/147	2.1	1.6 – 2.7		1.2	0.90 – 1.6	
Tertiles				< 0.001			0.951
≤ 2.592 (reference)	262/60	1	-		1	-	
2.592 – 3.203	262/63	1.1	0.76 – 1.5		0.87	0.61 – 1.3	
> 3.203	262/106	2.0	1.5 – 2.8		0.97	0.69 – 1.4	
Continuous variable	786/229	1.39	1.19 – 1.63	< 0.001	1.05	0.92 – 1.1	0.412
Event Free Survival							
Median				< 0.001			< 0.001
≤ 2.923 (reference)	377/111	1	-		1	-	
> 2.923	392/209	2.2	1.8 – 2.8		1.6	1.2 – 2.0	
Tertiles				< 0.001			0.006
≤ 2.592 (reference)	246/77	1	-		1	-	
2.592 – 3.203	261/93	1.2	0.89 – 1.6		1.1	0.80 – 1.5	
> 3.203	262/150	2.3	1.8 – 3.1		1.5	1.1 – 2.0	
Continuous variable	769/320	1.60	1.39 – 1.8	< 0.001	1.29	1.12 – 1.48	< 0.001

Supplementary Table S43. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *KILLIN* (alias *KLLN*) gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.003			0.753
≤ 3.272 (reference)	249/63	1	-		1	-	
> 3.272	249/42	0.56	0.38 – 0.82		0.93	0.60 – 1.5	
Tertiles				0.001			0.989
≤ 2.915 (reference)	166/47	1	-		1	-	
2.915 – 3.618	166/29	0.48	0.30 – 0.77		1.02	0.61 – 1.72	
> 3.618	166/29	0.47	0.30 – 0.75		1.00	0.59 – 1.7	
Continuous variable	498/105	0.86	0.69 – 1.1	0.144	1.09	0.93 – 1.27	0.309
Event Free Survival							
Median				0.025			0.532
≤ 3.272 (reference)	249/101	1	-		1	-	
> 3.272	249/82	0.72	0.54 – 0.96		0.90	0.66 – 1.2	
Tertiles				0.007			0.402
≤ 2.915 (reference)	166/72	1	-		1	-	
2.915 – 3.618	166/57	0.69	0.49 – 0.98		0.94	0.64 – 1.4	
> 3.618	166/54	0.62	0.43 – 0.88		0.84	0.57 – 1.3	
Continuous variable	498/183	0.89	0.76 – 1.05	0.149	1.00	0.87 – 1.14	0.972

Supplementary Table S44. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *LDB3* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.041			0.002
≤ 1.127 (reference)	393/101	1	-		1	-	
> 1.127	393/128	1.3	1.0 – 1.7		1.5	1.2 – 2.0	
Tertiles				0.051			0.014
≤ 0.836 (reference)	262/74	1	-		1	-	
0.836 – 1.426	262/60	0.78	0.56 – 1.1		1.0	0.72 – 1.4	
> 1.426	262/95	1.3	0.98 – 1.8		1.5	1.1 – 2.0	
Continuous variable	786/229	1.15	1.01 – 1.30	0.035	1.11	0.99 – 1.23	0.080
Event Free Survival							
Median				0.420			0.086
≤ 1.127 (reference)	393/157	1	-		1	-	
> 1.127	376/163	1.1	0.88 – 1.4		1.2	0.97 – 1.5	
Tertiles				0.572			0.268
≤ 0.836 (reference)	262/116	1	-		1	-	
0.836 – 1.426	262/86	0.68	0.51 – 0.90		0.82	0.62 – 1.1	
> 1.426	245/118	1.1	0.84 – 1.4		1.2	0.90 – 1.5	
Continuous variable	769/320	1.10	0.98 – 1.23	0.106	1.08	0.97 – 1.19	0.168

Supplementary Table S45. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *LIPA* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.069			0.768
≤ 4.171 (<i>reference</i>)	393/125	1	-		1	-	
> 4.171	393/104	0.79	0.61 – 1.0		1.0	0.79 – 1.4	
Tertiles				0.146			0.655
≤ 3.838 (<i>reference</i>)	262/85	1	-		1	-	
3.838 – 4.479	262/72	0.81	0.59 – 1.1		0.88	0.64 – 1.2	
> 4.479	262/72	0.79	0.58 – 1.1		1.1	0.79 – 1.5	
Continuous variable	786/229	0.77	0.64 – 0.93	0.006	0.96	0.80 – 1.16	0.673
Event Free Survival							
Median				0.532			0.505
≤ 4.171 (<i>reference</i>)	377/160	1	-		1	-	
> 4.171	392/160	0.93	0.75 – 1.2		1.1	0.86 – 1.4	
Tertiles				0.795			0.353
≤ 3.838 (<i>reference</i>)	247/107	1	-		1	-	
3.838 – 4.479	261/101	0.88	0.67 – 1.2		0.93	0.70 – 1.2	
> 4.479	261/112	0.96	0.74 – 1.3		1.1	0.87 – 1.5	
Continuous variable	769/320	0.92	0.78 – 1.1	0.280	1.0	0.89 – 1.2	0.566

Supplementary Table S46. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *LIPF* gene expression, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival				0.089			0.750
≤ 1.01* (reference)	287/67	1	-		1	-	
≤ 1.01*	211/38	0.71	0.48 – 1.1		1.1	0.71 – 1.6	
Event Free Survival				0.339			0.864
≤ 1.01* (reference)	287/111	1	-		1	-	
> 1.01	211/72	0.87	0.64 – 1.2		1.0	0.75 – 1.4	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S47. Association between *LIPF* gene expression and main patients' characteristics at diagnosis in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset.

Patients characteristics	Gene expression ≤ 1.01*		Gene expression > 1.01		<i>p</i>
	N	%	N	%	
MYCN status					< 0.001
Not amplified	216	53.9	185	46.1	
Amplified	69	75.0	23	25.0	
Age					0.102
≤ 18 months	167	54.8	138	45.3	
> 18 months	120	62.2	73	37.8	
Stage					0.465
Localized	146	55.7	116	44.3	
Stage 4	112	61.2	71	38.8	
Stage 4S	29	54.7	24	45.3	
Total	287	57.6	177	35.5	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S48. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *LIPJ* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.947
≤ 1.219 (<i>reference</i>)	248/72	1	-		1	-	
> 1.219	250/33	0.36	0.24 – 0.55		0.98	0.58 – 1.7	
Tertiles				< 0.001			0.900
≤ 1.153 (<i>reference</i>)	166/55	1	-		1	-	
1.153 – 1.284	166/29	0.44	0.28 – 0.70		1.3	0.78 – 2.2	
> 1.284	166/21	0.30	0.18 – 0.49		1.0	0.53 – 1.9	
Continuous variable	498/105	0.02	0.01 – 0.09	< 0.001	0.72	0.16 – 3.22	0.660
Event Free Survival							
Median				< 0.001			0.811
≤ 1.219 (<i>reference</i>)	248/111	1	-		1	-	
> 1.219	250/72	0.56	0.42 – 0.76		0.96	0.67 – 1.4	
Tertiles				< 0.001			0.486
≤ 1.153 (<i>reference</i>)	166/81	1	-		1	-	
1.153 – 1.284	166/57	0.62	0.44 – 0.87		1.1	0.74 – 1.6	
> 1.284	166/45	0.46	0.32 – 0.66		0.86	0.55 – 1.3	
Continuous variable	498/183	0.11	0.04 – 0.30	< 0.001	0.60	0.21 – 1.74	0.342

Supplementary Table S49. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *LIPM* gene expression, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival				0.166			0.479
≤ 1.01* (reference)	309/70	1	-		1	-	
≤ 1.01*	189/35	0.75	0.50 – 1.1		1.2	0.75 – 1.9	
Event Free Survival				0.066			0.417
≤ 1.01* (reference)	309/122	1	-		1	-	
> 1.01	189/61	0.75	0.55 – 1.0		0.87	0.63 – 1.2	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S50. Association between *LIPM* gene expression and main patients characteristics at diagnosis in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset.

Patients characteristics	Gene expression ≤ 1.01*		Gene expression > 1.01		<i>p</i>
	N	%	N	%	
MYCN status					< 0.001
Not amplified	231	57.6	170	42.4	
Amplified	78	84.8	14	15.20	
Age					0.813
≤ 18 months	188	61.6	117	38.4	
> 18 months	121	62.7	72	37.3	
Stage					0.588
Localized	157	59.9	105	40.1	
Stage 4	118	64.5	65	35.5	
Stage 4S	34	64.2	19	35.8	
Total	309	62.1	189	37.1	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S51. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *LIPN* gene expression, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>				0.131			0.044
≤ 1.01* (<i>reference</i>)	336/64	1	-		1	-	
≤ 1.01*	162/41	1.4	0.91 – 2.0		1.5	1.0 – 2.3	
<i>Event Free Survival</i>				0.323			0.310
≤ 1.01* (<i>reference</i>)	336/118	1	-		1	-	
> 1.01	162/65	1.2	0.86 – 1.6		1.2	0.86 – 1.6	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S52. Association between *LIPN* gene expression and main patients characteristics at diagnosis in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset.

Patients characteristics	Gene expression ≤ 1.01*		Gene expression > 1.01		<i>p</i>
	N	%	N	%	
<i>MYCN</i> status					0.814
Not amplified	271	67.6	130	32.4	
Amplified	61	66.3	31	33.7	
Age					0.306
≤ 18 months	211	69.2	94	30.8	
> 18 months	125	64.8	68	35.2	
Stage					0.695
Localized	181	69.1	81	30.9	
Stage 4	121	66.1	62	33.9	
Stage 4S	34	64.2	19	35.8	
Total	336	67.5	162	32.5	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S53. Survival of the cohort of 498 NB patients in the SEQC-498. *in silico* dataset, in relation to *LOC219347*(*alias: TMEM254AS1*) gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.819			0.310
≤ 2.839 (<i>reference</i>)	249/53	1	-		1	-	
> 2.839	249/52	0.96	0.65 – 1.4		0.81	0.55 – 1.2	
Tertiles				0.895			0.199
≤ 2.416 (<i>reference</i>)	166/32	1	-		1	-	
2.416 – 3.297	166/40	1.2	0.76 – 1.9		0.98	0.61 – 1.6	
> 3.297	166/33	0.97	0.60 – 1.6		0.73	0.44 – 1.2	
Continuous variable	498/105	1.01	0.86 – 1.18	0.900	0.92	0.78 – 1.09	0.343
Event Free Survival							
Median				0.738			0.398
≤ 2.839 (<i>reference</i>)	249/92	1	-		1	-	
> 2.839	249/91	0.95	0.71 – 1.3		0.88	0.65 – 1.2	
Tertiles				0.551			0.136
≤ 2.416 (<i>reference</i>)	166/60	1	-		1	-	
2.416 – 3.297	166/64	1.0	0.73 – 1.5		0.98	0.69 – 1.4	
> 3.297	166/59	0.90	0.63 – 1.3		0.75	0.52 – 1.1	
Continuous variable	498/183	1.03	0.91 – 1.16	0.652	0.97	0.85 – 1.1	0.592

Supplementary Table S54. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *LOC439994* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.917			0.909
≤ 8.121 (<i>reference</i>)	249/52	1	-		1	-	
> 8.121	249/53	1.0	0.70 – 1.5		0.98	0.66 – 1.4	
Tertiles				0.485			0.348
≤ 7.086 (<i>reference</i>)	166/34	1	-		1	-	
7.086 – 8.948	166/32	0.93	0.57 – 1.5		0.96	0.59 – 1.6	
> 8.948	166/39	1.2	0.74 – 1.9		1.3	0.78 – 2.0	
Continuous variable	498/105	1.04	0.96 – 1.12	0.315	1.01	0.94 – 1.09	0.725
Event Free Survival							
Median				0.877			0.878
≤ 8.121 (<i>reference</i>)	249/91	1	-		1	-	
> 8.121	249/92	1.0	0.77 – 1.4		1.0	0.76 – 1.4	
Tertiles				0.679			0.457
≤ 7.086 (<i>reference</i>)	166/60	1	-		1	-	
7.086 – 8.948	166/60	0.97	0.68 – 1.4		1.0	0.70 – 1.4	
> 8.948	166/63	1.1	0.76 – 1.5		1.1	0.80 – 1.6	
Continuous variable	498/183	1.01	0.95 – 1.1	0.675	1.0	0.95 – 1.1	0.811

Supplementary Table S55. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *LOC642361* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.064			0.451
≤ 8.493 (<i>reference</i>)	249/45	1	-		1	-	
> 8.493	249/60	1.4	0.98 – 2.1		1.2	0.78 – 1.7	
Tertiles				0.063			0.860
≤ 7.584 (<i>reference</i>)	166/32	1	-		1	-	
7.584 – 9.351	165/28	0.87	0.52 – 1.4		0.92	0.55 – 1.5	
> 9.351	167/45	1.5	0.96 – 2.4		0.95	0.60 – 1.5	
Continuous variable	498/105	1.13	1.04 – 1.22	0.003	1.02	0.94 – 1.09	0.690
Event Free Survival							
Median				0.024			0.247
≤ 8.493 (<i>reference</i>)	249/79	1	-		1	-	
> 8.493	249/104	1.4	1.0 – 1.9		1.2	0.88 – 1.6	
Tertiles				0.005			0.385
≤ 7.584 (<i>reference</i>)	166/51	1	-		1	-	
7.584 – 9.351	165/56	1.1	0.76 – 1.6		1.1	0.75 – 1.6	
> 9.351	167/76	1.6	1.2 – 2.3		1.2	0.81 – 1.7	
Continuous variable	498/183	1.09	1.03 – 1.16	0.004	1.02	0.96 – 1.09	0.431

Supplementary Table S56. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *LOC650623* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.520			0.207
≤ 11.615 (reference)	249/56	1	-		1	-	
> 11.615	249/49	0.88	0.60 – 1.3		0.78	0.53 – 1.1	
Tertiles				< 0.001			0.347
≤ 10.052 (reference)	166/42	1	-		1	-	
10.052 – 13.799	165/27	0.62	0.38 – 1.0		0.83	0.51 – 1.4	
> 13.799	167/36	0.87	0.56 – 1.4		0.81	0.51 – 1.3	
Continuous variable	498/105	0.985	0.946 – 1.03	0.455	0.98	0.95 – 1.02	0.341
Event Free Survival							
Median				0.808			0.244
≤ 11.615 (reference)	249/93	1	-		1	-	
> 11.615	249/90	0.96	0.72 – 1.3		0.84	0.62 – 1.1	
Tertiles				0.818			0.698
≤ 10.052 (reference)	166/62	1	-		1	-	
10.052 – 13.799	165/57	0.90	0.63 – 1.3		1.0	0.70 – 1.5	
> 13.799	167/64	1.0	0.73 – 1.5		0.93	0.65 – 1.3	
Continuous variable	498/183	1.00	0.97 – 1.02	0.831	0.99	0.96 – 1.02	0.370

Supplementary Table S57. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *LOC728190* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.002			0.085
≤ 7.325 (<i>reference</i>)	248/39	1	-		1	-	
> 7.325	250/66	1.8	1.2 – 2.7		1.4	0.95 – 2.1	
Tertiles				0.008			0.124
≤ 6.601 (<i>reference</i>)	166/28	1	-		1	-	
6.601 – 8.152	166/30	1.1	0.66 – 1.8		1.1	0.64 – 1.8	
> 8.152	166/47	1.8	1.1 – 2.9		1.4	0.89 – 2.3	
Continuous variable	498/105	1.14	1.03 – 1.25	0.011	1.08	0.98 – 1.19	0.132
Event Free Survival							
Median				0.005			0.083
≤ 7.325 (<i>reference</i>)	248/77	1	-		1	-	
> 7.325	250/106	1.5	1.1 – 2.0		1.3	0.96 – 1.8	
Tertiles				0.018			0.098
≤ 6.601 (<i>reference</i>)	166/51	1	-		1	-	
6.601 – 8.152	166/62	1.3	0.88 – 1.8		1.2	0.84 – 1.8	
> 8.152	166/70	1.5	1.1 – 2.2		1.4	0.94 – 2.0	
Continuous variable	498/183	1.07	1.00 – 1.16	0.066	1.05	0.97 – 1.13	0.229

Supplementary Table S58. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *LRIT1* gene expression, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival				0.858			0.729
≤ 1.01* (reference)	397/84	1	-		1	-	
≤ 1.01*	101/21	0.96	0.59 – 1.5		1.1	0.67 – 1.8	
Event Free Survival				0.658			0.226
≤ 1.01* (reference)	397/144	1	-		1	-	
> 1.01	101/39	1.1	0.76 – 1.5		1.3	0.88 – 1.8	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S59. Association between *LRIT1* gene expression and main patients characteristics at diagnosis in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset.

Patients characteristics	Gene expression ≤ 1.01*		Gene expression > 1.01		<i>p</i>
	N	%	N	%	
MYCN status					0.180
Not amplified	315	78.6	86	21.5	
Amplified	78	84.8	14	15.2	
Age					0.624
≤ 18 months	241	79.0	64	21.0	
> 18 months	156	80.8	37	19.2	
Stage					0.260
Localized	206	78.6	56	21.4	
Stage 4	152	83.1	31	16.9	
Stage 4S	39	73.6	14	26.4	
Total	397	79.7	101	20.3	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S60. Survival of the cohort of 498 NB patients in the SEQC-498. *in silico* dataset, in relation to *LRIT2* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.021			0.915
≤ 1.236 (reference)	249/62	1	-		1	-	
> 1.236	249/43	0.63	0.43 – 0.94		1.0	0.69 – 1.5	
Tertiles				0.059			0.961
≤ 1.148 (reference)	165/40	1	-		1	-	
1.148 – 1.383	167/38	0.90	0.58 – 1.4		1.3	0.85 – 2.1	
> 1.383	166/27	0.62	0.38 – 1.0		0.98	0.60 – 1.6	
Continuous variable	498/105	0.46	0.24 – 0.88	0.009	0.67	0.38 – 1.2	0.141
Event Free Survival							
Median				0.006			0.416
≤ 1.236 (reference)	249/106	1	-		1	-	
> 1.236	249/77	0.67	0.50 – 0.89		0.88	0.65 – 1.2	
Tertiles				0.019			0.394
≤ 1.148 (reference)	165/70	1	-		1	-	
1.148 – 1.383	167/62	0.83	0.59 – 1.2		1.0	0.71 – 1.4	
> 1.383	166/51	0.65	0.45 – 0.93		0.85	0.59 – 1.2	
Continuous variable	498/183	0.59	0.38 – 0.93	0.014	0.74	0.49 – 1.12	0.147

Supplementary Table S61. Survival of the cohort of 498 NB patients in the SEQC-498. *in silico* dataset, in relation to *MAT1A* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.006			0.731
≤ 1.066 (reference)	249/40	1	-		1	-	
> 1.066	249/65	1.7	1.2 – 2.6		1.1	0.72 – 1.6	
Tertiles				< 0.001			0.516
≤ 1.040 (reference)	166/23	1	-		1	-	
1.040 – 1.104	166/34	1.5	0.90 – 2.6		1.2	0.68 – 2.0	
> 1.104	166/48	2.3	1.4 – 3.7		1.2	0.72 – 2.0	
Continuous variable	498/105	0.99	0.96 – 1.02	0.135	0.99	0.97 – 1.02	0.579
Event Free Survival							
Median				0.010			0.518
≤ 1.066 (reference)	249/77	1	-		1	-	
> 1.066	249/106	1.5	1.1 – 2.0		1.1	0.82 – 1.5	
Tertiles				0.021			0.796
≤ 1.040 (reference)	166/54	1	-		1	-	
1.040 – 1.104	166/53	0.97	0.66 – 1.4		0.81	0.55 – 1.2	
> 1.104	166/76	1.5	1.1 – 2.1		1.0	0.72 – 1.5	
Continuous variable	498/183	1.00	0.99 – 1.003	0.964	1.002	0.999 – 1.01	0.229

Supplementary Table S62. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *MBL1P* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.041			0.675
≤ 1.743 (<i>reference</i>)	249/61	1	-		1	-	
> 1.743	249/44	0.67	0.45 – 0.99		1.1	0.68 – 1.8	
Tertiles				0.013			0.968
≤ 1.414 (<i>reference</i>)	165/36	1	-		1	-	
1.414 – 2.233	167/50	1.4	0.90 – 2.1		1.6	1.0 – 2.5	
> 2.233	166/19	0.47	0.27 – 0.82		0.83	0.44 – 1.6	
Continuous variable	498/105	0.71	0.56 – 0.91	0.003	0.91	0.69 – 1.2	0.489
Event Free Survival							
Median				0.078			0.410
≤ 1.743 (<i>reference</i>)	249/99	1	-		1	-	
> 1.743	249/84	0.77	0.58 – 1.0		0.87	0.61 – 1.2	
Tertiles				0.037			0.307
≤ 1.414 (<i>reference</i>)	165/63	1	-		1	-	
1.414 – 2.233	167/72	1.1	0.78 – 1.5		1.1	0.76 – 1.5	
> 2.233	166/48	0.67	0.46 – 0.97		0.79	0.51 – 1.2	
Continuous variable	498/183	0.83	0.70 – 0.98	0.025	0.90	0.75 – 1.1	0.287

Supplementary Table S63. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *MINPP1* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.992
≤ 2.989 (reference)	393/91	1	-		1	-	
> 2.989	393/138	1.7	1.3 – 2.2		1.0	0.76 – 1.3	
Tertiles				< 0.001			0.297
≤ 2.813 (reference)	262/58	1	-		1	-	
2.813 – 3.169	262/61	1.0	0.72 – 1.5		0.76	0.53 – 1.1	
> 3.169	262/110	2.2	1.6 – 3.0		1.1	0.81 – 1.6	
Continuous variable	786/229	1.97	1.47 – 2.65	< 0.001	1.13	0.87 – 1.46	0.354
Event Free Survival							
Median				< 0.001			0.235
≤ 2.989 (reference)	376/128	1	-		1	-	
> 2.989	393/192	1.6	1.3 – 2.0		1.1	0.91 – 1.4	
Tertiles				< 0.001			0.015
≤ 2.813 (reference)	246/74	1	-		1	-	
2.813 – 3.169	261/105	1.4	1.0 – 1.9		1.1	0.84 – 1.5	
> 3.169	262/141	2.2	1.7 – 2.9		1.4	1.1 – 1.9	
Continuous variable	769/320	2.15	1.66 – 2.79	< 0.001	1.42	1.09 – 1.83	0.007

Supplementary Table S64. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *MMRN2* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.007			0.583
≤ 2.863 (<i>reference</i>)	393/131	1	-		1	-	
> 2.863	393/98	0.70	0.54 – 0.91		0.93	0.71 – 1.2	
Tertiles				0.006			0.269
≤ 2.525 (<i>reference</i>)	262/93	1	-		1	-	
2.525 – 3.187	262/70	0.71	0.52 – 0.97		1.0	0.74 – 1.4	
> 3.187	262/66	0.65	0.47 – 0.89		0.83	0.60 – 1.1	
Continuous variable	786/229	0.82	0.69 – 0.96	0.017	1.02	0.88 – 1.18	0.795
Event Free Survival							
Median				0.044			0.688
≤ 2.863 (<i>reference</i>)	393/176	1	-		1	-	
> 2.863	376/144	0.80	0.64 – 0.99		0.95	0.76 – 1.2	
Tertiles				0.022			0.351
≤ 2.525 (<i>reference</i>)	262/126	1	-		1	-	
2.525 – 3.187	260/96	0.70	0.53 – 0.91		0.89	0.68 – 1.2	
> 3.187	247/98	0.74	0.57 – 0.96		0.88	0.67 – 1.2	
Continuous variable	769/320	0.87	0.75 – 1.00	0.054	1.00	0.87 – 1.1	0.972

Supplementary Table S65. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *NRG3* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.002			0.026
≤ 1.714 (reference)	393/135	1	-		1	-	
> 1.714	393/94	0.66	0.51– 0.86		0.74	0.56 – 0.97	
Tertiles				0.018			0.126
≤ 1.097 (reference)	262/92	1	-		1	-	
1.097 – 2.249	262/70	0.73	0.53 – 0.99		0.83	0.61 – 1.1	
> 2.249	262/67	0.69	0.50 – 0.94		0.78	0.57 – 1.1	
Continuous variable	786/229	0.93	0.86 – 1.00	0.078	0.96	0.89 – 1.03	0.299
Event Free Survival							
Median				< 0.001			0.007
≤ 1.714 (reference)	389/187	1	-		1	-	
> 1.714	380/133	0.67	0.54 – 0.84		0.73	0.58 – 0.92	
Tertiles				0.002			0.017
≤ 1.097 (reference)	259/129	1	-		1	-	
1.097 – 2.249	257/100	0.72	0.56 – 0.94		0.78	0.60 – 1.0	
> 2.249	253/91	0.66	0.50 – 0.86		0.72	0.55 – 0.95	
Continuous variable	769/320	0.93	0.87 – 0.99	0.025	0.95	0.90 – 1.02	0.145

Supplementary Table S66. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *OPN4* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.578			0.764
≤ 1.062 (reference)	248/54	1	-		1	-	
> 1.062	250/51	0.90	0.61 – 1.3		0.94	0.64 – 1.4	
Tertiles				0.244			0.441
≤ 1.036 (reference)	165/40	1	-		1	-	
1.036 – 1.107	167/32	0.73	0.46 – 1.2		0.68	0.42 – 1.1	
> 1.107	166/33	0.76	0.48 – 1.2		0.84	0.52 – 1.3	
Continuous variable	498/105	1.45	0.54 – 3.94	0.483	1.52	0.54 – 4.26	0.450
Event Free Survival							
Median				0.360			0.586
≤ 1.062 (reference)	248/95	1	-		1	-	
> 1.062	250/88	0.87	0.65 – 1.2		0.92	0.68 – 1.2	
Tertiles				0.111			0.288
≤ 1.036 (reference)	165/68	1	-		1	-	
1.036 – 1.107	167/58	0.76	0.54 – 1.1		0.75	0.53 – 1.1	
> 1.107	166/57	0.75	0.53 – 1.1		0.83	0.58 – 1.2	
Continuous variable	498/183	1.13	0.49 – 2.59	0.782	1.21	0.52 – 2.83	0.671

Supplementary Table S67. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *PANK1* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.312
≤ 2.773 (reference)	393/88	1	-		1	-	
> 2.773	393/141	1.8	1.4 – 2.4		1.2	0.87 – 1.5	
Tertiles				< 0.001			0.096
≤ 2.516 (reference)	262/61	1	-		1	-	
2.516 – 3.026	262/60	0.99	0.69 – 1.4		0.88	0.61 – 1.3	
> 3.026	262/108	2.1	1.5 – 2.9		1.3	0.92 – 1.8	
Continuous variable	786/229	1.57	1.29 – 1.93	< 0.001	1.12	0.90 – 1.38	0.327
Event Free Survival							
Median				< 0.001			0.009
≤ 2.773 (reference)	380/122	1	-		1	-	
> 2.773	389/198	1.8	1.5 – 2.3		1.4	1.1 – 1.7	
Tertiles				< 0.001			< 0.001
≤ 2.516 (reference)	251/79	1	-		1	-	
2.516 – 3.026	259/97	1.3	0.95 – 1.7		1.2	0.86 – 1.6	
> 3.026	259/144	2.3	1.7 – 3.0		1.6	1.2 – 2.2	
Continuous variable	769/320	1.61	1.35 – 1.91	< 0.001	1.30	1.08 – 1.57	0.006

Supplementary Table S68. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *PCDH21* (alias *CDHR1*) gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.222			0.590
≤ 1.923 (<i>reference</i>)	393/123	1	-		1	-	
> 1.923	393/106	0.85	0.66 – 1.1		1.1	0.83 – 1.4	
Tertiles				0.463			0.211
≤ 1.376 (<i>reference</i>)	262/82	1	-		1	-	
1.376 – 2.383	262/73	0.87	0.64 – 1.2		1.1	0.77 – 1.5	
> 2.383	262/74	0.89	0.65 – 1.2		1.2	0.89 – 1.7	
Continuous variable	786/229	0.92	0.84 – 1.01	0.079	1.01	0.92 – 1.11	0.825
Event Free Survival							
Median				0.030			0.406
≤ 1.923 (<i>reference</i>)	387/176	1	-		1	-	
> 1.923	382/144	0.78	0.63 – 0.98		0.91	0.73 – 1.1	
Tertiles				0.058			0.775
≤ 1.376 (<i>reference</i>)	260/113	1	-		1	-	
1.376 – 2.383	255/116	1.0	0.81 – 1.4		1.2	0.91 – 1.5	
> 2.383	254/91	0.76	0.58 – 1.0		0.95	0.72 – 1.3	
Continuous variable	769/320	0.93	0.86 – 1.00	0.054	0.99	0.91 – 1.07	0.732

Supplementary Table S69. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *PLAC9* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.526			0.646
≤ 1.501 (<i>reference</i>)	393/118	1	-		1	-	
> 1.501	393/111	0.92	0.71 – 1.2		1.1	0.82 – 1.4	
Tertiles				0.288			0.646
≤ 1.118 (<i>reference</i>)	262/82	1	-		1	-	
1.118 – 1.897	262/75	0.90	0.66 – 1.2		0.97	0.71 – 1.3	
> 1.897	262/72	0.84	0.61 – 1.2		0.93	0.68 – 1.3	
Continuous variable	786/229	0.96	0.85 – 1.10	0.592	1.00	0.88 – 1.12	0.974
Event Free Survival							
Median				0.280			0.892
≤ 1.501 (<i>reference</i>)	393/170	1	-		1	-	
> 1.501	376/150	0.89	0.71 – 1.1		0.98	0.79 – 1.2	
Tertiles				0.123			0.358
≤ 1.118 (<i>reference</i>)	262/120	1	-		1	-	
1.118 – 1.897	262/103	0.81	0.62 – 1.1		0.90	0.69 – 1.2	
> 1.897	245/97	0.81	0.62 – 1.1		0.88	0.68 – 1.2	
Continuous variable	769/320	0.97	0.86 – 1.09	0.610	0.99	0.89 – 1.11	0.901

Supplementary Table S70. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *PTEN* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.009			0.190
≤ 4.383 (<i>reference</i>)	393/130	1	-		1	-	
> 4.383	393/99	0.71	0.54 – 0.92		0.84	0.64 – 1.1	
Tertiles				0.004			0.048
≤ 4.233 (<i>reference</i>)	262/101	1	-		1	-	
4.233 – 4.552	262/54	0.46	0.33 – 0.64		0.62	0.44 – 0.87	
> 4.552	262/74	0.65	0.48 – 0.88		0.75	0.55 – 1.0	
Continuous variable	786/229	0.66	0.51 – 0.85	0.003	0.86	0.70 – 1.06	0.164
Event Free Survival							
Median				0.257			0.702
≤ 4.383 (<i>reference</i>)	379/164	1	-		1	-	
> 4.383	390/156	0.88	0.71 – 1.1		0.96	0.77 – 1.2	
Tertiles				0.474			0.702
≤ 4.233 (<i>reference</i>)	248/113	1	-		1	-	
4.233 – 4.552	261/94	0.72	0.55 – 0.95		0.84	0.64 – 1.1	
> 4.552	260/113	0.91	0.70 – 1.2		0.95	0.73 – 1.2	
Continuous variable	769/320	0.87	0.68 – 1.12	0.293	0.98	0.80 – 1.2	0.832

Supplementary Table S71. Survival of the cohort of 709 NB patients in the E-MTAB-1781 *in silico* dataset, in relation to *RGR* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.031			0.554
≤ -5.690 (<i>reference</i>)	353/90	1	-		1	-	
> -5.690	356/71	0.71	0.52 – 0.97		0.91	0.66 – 1.2	
Tertiles				0.082			0.554
≤ -6.745 (<i>reference</i>)	236/59	1	-		1	-	
-6.745 – -2.613	236/54	0.84	0.58 – 1.2		1.0	0.69 – 1.5	
> -2.613	237/48	0.71	0.49 – 1.0		0.89	0.60 – 1.3	
Continuous variable	709/161	0.94	0.89 – 1.00	0.049	0.97	0.92 – 1.03	0.410
Event Free Survival							
Median				0.012			0.206
≤ -5.690 (<i>reference</i>)	349/144	1	-		1	-	
> -5.690	346/112	0.73	0.57 – 0.93		0.85	0.66 – 1.1	
Tertiles				0.193			0.503
≤ -6.745 (<i>reference</i>)	232/90	1	-		1	-	
-6.745 – -2.613	235/89	0.94	0.70 – 1.3		1.1	0.79 – 1.4	
> -2.613	228/77	0.82	0.60 – 1.1		0.90	0.66 – 1.2	
Continuous variable	695/256	0.95	0.91 – 1.0	0.051	0.97	0.93 – 1.0	0.201

Supplementary Table S72. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *RNLS* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.519			0.083
≤ 1.653 (<i>reference</i>)	393/120	1	-		1	-	
> 1.653	393/109	0.92	0.71 – 1.2		1.3	0.97 – 1.7	
Tertiles				0.445			0.065
≤ 1.428 (<i>reference</i>)	262/91	1	-		1	-	
1.428 – 1.843	262/56	0.56	0.40 – 0.79		1.0	0.70 – 1.4	
> 1.843	262/82	0.90	0.67 – 1.2		1.3	0.98 – 1.8	
Continuous variable	786/229	0.84	0.73 – 0.98	0.033	1.14	0.98 – 1.34	0.082
Event Free Survival							
Median				0.901			0.137
≤ 1.653 (<i>reference</i>)	382/160	1	-		1	-	
> 1.653	387/160	1.0	0.81 – 1.3		1.2	0.95 – 1.5	
Tertiles				0.902			0.094
≤ 1.428 (<i>reference</i>)	256/114	1	-		1	-	
1.428 – 1.843	255/92	0.78	0.59 – 1.0		1.1	0.82 – 1.5	
> 1.843	258/114	1.0	0.78 – 1.3		1.3	0.96 – 1.7	
Continuous variable	769/320	0.93	0.80 – 1.1	0.342	1.1	0.98 – 1.3	0.081

Supplementary Table S73. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *RPP30* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.021			0.782
≤ 3.175 (reference)	393/101	1	-		1	-	
> 3.175	393/128	1.4	1.0 – 1.8		0.96	0.74 – 1.3	
Tertiles				0.028			0.356
≤ 3.017 (reference)	262/70	1	-		1	-	
3.017 – 3.346	262/68	0.98	0.70 – 1.4		1.1	0.79 – 1.6	
> 3.346	262/91	1.4	1.0 – 1.9		0.87	0.63 – 1.2	
Continuous variable	786/229	1.48	1.07 – 2.05	0.019	0.87	0.65 – 1.15	0.327
Event Free Survival							
Median				0.018			0.854
≤ 3.175 (reference)	387/145	1	-		1	-	
> 3.175	382/175	1.3	1.0 – 1.6		1.0	0.81 – 1.3	
Tertiles				0.037			0.696
≤ 3.017 (reference)	257/93	1	-		1	-	
3.017 – 3.346	259/114	1.3	0.98 – 1.7		1.3	1.0 – 1.8	
> 3.346	253/113	1.3	1.0 – 1.8		0.95	0.72 – 1.3	
Continuous variable	769/320	1.41	1.07– 1.84	0.015	0.96	0.74 – 1.3	0.777

Supplementary Table S74. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *SFTPA1* gene expression, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
<i>Overall Survival</i>				0.782			0.890
≤ 1.01* (<i>reference</i>)	335/71	1	-		1	-	
≤ 1.01*	163/341	0.94	0.63 – 1.4		1.0	0.68 – 1.6	
<i>Event Free Survival</i>				0.710			0.417
≤ 1.01* (<i>reference</i>)	335/120	1	-		1	-	
> 1.01	163/63	1.1	0.78 – 1.4		1.1	0.83 – 1.6	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S75. Association between *SFTPA1* gene expression and main patients characteristics at diagnosis in a cohort of 498 NB patients in the SEQC-498 *in silico* dataset.

Patients characteristics	Gene expression ≤ 1.01*		Gene expression > 1.01		<i>p</i>
	N	%	N	%	
<i>MYCN</i> status					0.006
Not amplified	259	64.6	142	35.4	
Amplified	73	79.4	19	20.7	
Age					0.670
≤ 18 months	203	66.6	102	33.4	
> 18 months	132	68.4	61	31.6	
Stage					0.977
Localized	177	67.6	85	32.4	
Stage 4	123	67.2	60	32.8	
Stage 4S	35	66.0	18	34.0	
Total	335	67.3	163	32.73	

* Allegedly corresponding to the absence of gene expression.

Supplementary Table S76. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *SFTPA2* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.575
≤ 1.086 (reference)	248/66	1	-		1	-	
> 1.086	250/39	0.52	0.35 – 0.77		0.88	0.57 – 1.4	
Tertiles				0.007			0.318
≤ 1.053 (reference)	164/42	1	-		1	-	
1.053 – 1.122	168/38	0.82	0.53 – 1.3		0.90	0.57 – 1.4	
> 1.122	166/25	0.51	0.31 – 0.83		0.77	0.45 – 1.3	
Continuous variable	498/105	0.06	0.01 – 0.40	< 0.001	0.33	0.05 – 2.06	0.196
Event Free Survival							
Median				0.033			0.761
≤ 1.086 (reference)	248/101	1	-		1	-	
> 1.086	250/82	0.73	0.54 – 0.98		0.95	0.69 – 1.3	
Tertiles				0.013			0.119
≤ 1.053 (reference)	164/67	1	-		1	-	
1.053 – 1.122	168/67	0.90	0.64 – 1.3		0.91	0.64 – 1.3	
> 1.122	166/49	0.63	0.43 – 0.91		0.73	0.50 – 1.1	
Continuous variable	498/183	0.24	0.07 – 0.77	0.008	0.43	0.13 – 1.43	0.142

Supplementary Table S77. Survival of the cohort of 709 NB patients in the E-MTAB-1781 *in silico* dataset, in relation to *SFTPD* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.010			0.495
≤ -0.519 (<i>reference</i>)	354/66	1	-		1	-	
> -0.519	355/95	1.5	1.1 – 2.1		1.1	0.81 – 1.5	
Tertiles				0.009			0.369
≤ -0.854 (<i>reference</i>)	236/36	1	-		1	-	
-0.854 – -0.205	236/64	1.9	1.2 – 2.8		1.1	0.74 – 1.7	
> -0.205	237/61	1.8	1.2 – 2.7		1.2	0.79 – 1.9	
Continuous variable	709/161	1.36	1.11 – 1.66	0.002	1.19	0.95 – 1.5	0.119
Event Free Survival							
Median				0.256			0.475
≤ -0.519 (<i>reference</i>)	353/120	1	-		1	-	
> -0.519	342/136	1.2	0.90 – 1.5		0.91	0.71 – 1.2	
Tertiles				0.257			0.460
≤ -0.854 (<i>reference</i>)	235/75	1	-		1	-	
-0.854 – -0.205	235/93	1.2	0.91 – 1.7		0.91	0.66 – 1.2	
> -0.205	225/88	1.2	0.88 – 1.6		0.88	0.64 – 1.2	
Continuous variable	695/256	1.12	0.96 – 1.31	0.124	0.96	0.83 – 1.12	0.646

Supplementary Table S78. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *SH2D4B* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.959			0.667
≤ 1.091 (<i>reference</i>)	248/52	1	-		1	-	
> 1.091	250/53	0.99	0.68 – 1.5		0.92	0.62 – 1.4	
Tertiles				0.755			0.243
≤ 1.064 (<i>reference</i>)	165/37	1	-		1	-	
1.064 – 1.125	165/31	0.78	0.49 – 1.3		1.0	0.62 – 1.6	
> 1.125	168/37	0.93	0.59 – 1.5		0.76	0.48 – 1.2	
Continuous variable	498/105	2.03	0.36 – 11.60	0.440	0.56	0.09 – 3.40	0.519
Event Free Survival							
Median				0.694			0.780
≤ 1.091 (<i>reference</i>)	248/87	1	-		1	-	
> 1.091	250/96	1.1	0.79 – 1.4		0.96	0.71 – 1.3	
Tertiles				0.275			0.931
≤ 1.064 (<i>reference</i>)	165/55	1	-		1	-	
1.064 – 1.125	165/57	0.97	0.67 – 1.4		1.1	0.76 – 1.6	
> 1.125	168/71	1.2	0.85 – 1.7		0.99	0.69 – 1.4	
Continuous variable	498/183	3.50	1.04 – 11.8	0.057	1.02	0.28 – 3.81	0.972

Supplementary Table S79. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *SLC16A12* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.836
≤ 2.070 (reference)	249/71	1	-		1	-	
> 2.070	249/34	0.42	0.28 – 0.63		1.0	0.67 – 1.6	
Tertiles				< 0.001			0.861
≤ 1.559 (reference)	166/60	1	-		1	-	
1.559 – 2.847	166/26	0.36	0.22 – 0.56		0.96	0.60 – 1.5	
> 2.847	166/19	0.25	0.15 – 0.42		0.96	0.53 – 1.7	
Continuous variable	498/105	0.84	0.75 – 0.94	< 0.001	1.01	0.93 – 1.09	0.887
Event Free Survival							
Median				< 0.001			0.518
≤ 2.070 (reference)	249/113	1	-		1	-	
> 2.070	249/70	0.54	0.40 – 0.73		0.90	0.65 – 1.2	
Tertiles				< 0.001			0.418
≤ 1.559 (reference)	166/86	1	-		1	-	
1.559 – 2.847	166/58	0.59	0.42 – 0.82		1.1	0.79 – 1.6	
> 2.847	166/39	0.37	0.25 – 0.54		0.81	0.53 – 1.2	
Continuous variable	498/183	0.87	0.81 – 0.94	< 0.001	0.96	0.90 – 1.02	0.209

Supplementary Table S80. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *SNCG* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.008			0.868
≤ 1.774 (reference)	393/130	1	-		1	-	
> 1.774	393/99	0.70	0.54 – 0.92		1.0	0.77 – 1.4	
Tertiles				0.004			0.568
≤ 1.294 (reference)	262/98	1	-		1	-	
1.294 – 2.297	262/61	0.57	0.41 – 0.78		0.91	0.65 – 1.3	
> 2.297	262/70	0.65	0.48 – 0.88		1.1	0.80 – 1.6	
Continuous variable	786/229	0.82	0.73 – 0.92	< 0.001	1.0	0.89 – 1.1	0.972
Event Free Survival							
Median				< 0.001			0.182
≤ 1.774 (reference)	393/186	1	-		1	-	
> 1.774	376/134	0.69	0.55 – 0.86		0.85	0.67 – 1.1	
Tertiles				< 0.001			0.165
≤ 1.294 (reference)	262/131	1	-		1	-	
1.294 – 2.297	262/106	0.76	0.59 – 0.98		1.0	0.76 – 1.3	
> 2.297	245/83	0.60	0.45 – 0.78		0.80	0.59 – 1.1	
Continuous variable	769/320	0.79	0.72 – 0.88	< 0.001	0.89	0.80 – 0.98	0.022

Supplementary Table S81. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *STAMBPL1* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				<i>< 0.001</i>			<i>0.444</i>
≤ 2.844 (<i>reference</i>)	393/91	1	-		1	-	
> 2.844	393/138	1.7	1.3 – 2.2		1.1	0.84 – 1.5	
Tertiles				<i>< 0.001</i>			<i>0.690</i>
≤ 2.662 (<i>reference</i>)	262/61	1	-		1	-	
2.662 – 3.029	262/74	1.3	0.91 – 1.8		1.1	0.76 – 1.5	
> 3.029	262/94	1.8	1.3 – 2.5		1.1	0.75 – 1.5	
Continuous variable	786/229	1.91	1.46 – 2.50	<i>< 0.001</i>	1.1	0.87 – 1.4	<i>0.388</i>
Event Free Survival							
Median				<i>0.003</i>			<i>0.305</i>
≤ 2.844 (<i>reference</i>)	376/138	1	-		1	-	
> 2.844	393/182	1.4	1.1 – 1.8		1.1	0.89 – 1.4	
Tertiles				<i>0.005</i>			<i>0.495</i>
≤ 2.662 (<i>reference</i>)	246/91	1	-		1	-	
2.662 – 3.029	261/104	1.1	0.84 – 1.5		1.0	0.75 – 1.3	
> 3.029	262/125	1.5	1.1 – 1.9		1.1	0.82 – 1.5	
Continuous variable	769/320	1.61	1.28 – 2.03	<i>< 0.001</i>	1.19	0.94 – 1.49	<i>0.138</i>

Supplementary Table S82. Survival of the cohort of 786 NB patients in the Cangelosi et al. *in silico* dataset, in relation to *TSPAN14* gene expression values, evaluated by the Cox model.

Gene expression	N/O	Univariable analysis			Multivariable analysis		
		HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				< 0.001			0.003
≤ 3.486 (<i>reference</i>)	393/90	1	-		1	-	
> 3.486	393/139	1.7	1.3 – 2.2		1.5	1.1 – 2.0	
Tertiles				< 0.001			0.025
≤ 3.303 (<i>reference</i>)	262/60	1	-		1	-	
3.303 – 3.687	262/66	1.1	0.79 – 1.6		1.5	1.1 – 2.2	
> 3.687	262/103	1.9	1.4 – 2.6		1.5	1.1 – 2.0	
Continuous variable	786/229	1.59	1.24 – 2.04	< 0.001	1.2	0.98 – 1.6	0.069
Event Free Survival							
Median				< 0.001			0.002
≤ 3.486 (<i>reference</i>)	393/136	1	-		1	-	
> 3.486	376/184	1.6	1.3 – 2.0		1.4	1.1 – 1.8	
Tertiles				< 0.001			0.010
≤ 3.303 (<i>reference</i>)	262/88	1	-		1	-	
3.303 – 3.687	261/100	1.2	0.89 – 1.6		1.4	1.0 – 1.8	
> 3.687	246/132	1.8	1.4 – 2.3		1.4	1.1 – 1.9	
Continuous variable	769/320	1.67	1.33 – 2.09	< 0.001	1.38	1.11 – 1.71	0.004

Supplementary Table S83. Survival of the cohort of 498 NB patients in the SEQC-498 *in silico* dataset, in relation to *WAPAL* gene expression values, evaluated by the Cox model.

		Univariable analysis			Multivariable analysis		
Gene expression	N/O	HR	95%CI	<i>p</i>	HR	95%CI	<i>p</i>
Overall Survival							
Median				0.001			0.073
≤ 49.436 (<i>reference</i>)	249/37	1	-		1	-	
> 49.436	249/68	1.9	1.3 – 2.9		1.4	0.96 – 2.2	
Tertiles				< 0.001			0.027
≤ 44.612 (<i>reference</i>)	166/22	1	-		1	-	
44.612 – 54.125	166/29	1.3	0.75 – 2.3		1.4	0.79 – 2.4	
> 54.125	166/54	2.7	1.6 – 4.4		1.7	1.1 – 2.9	
Continuous variable	498/105	1.04	1.03 – 1.06	< 0.001	1.03	1.01 – 1.04	< 0.001
Event Free Survival							
Median				< 0.001			0.007
≤ 49.436 (<i>reference</i>)	249/68	1	-		1	-	
> 49.436	249/115	1.8	1.4 – 2.5		1.5	1.1 – 2.1	
Tertiles				< 0.001			0.008
≤ 44.612 (<i>reference</i>)	166/44	1	-		1	-	
44.612 – 54.125	166/53	1.2	0.79 – 1.8		1.1	0.76 – 1.7	
> 54.125	166/86	2.2	1.6 – 3.2		1.6	1.1 – 2.4	
Continuous variable	498/183	1.04	1.02 – 1.05	< 0.001	1.02	1.01 – 1.03	< 0.001