Figure 1- Molecular Determinants of Response to Neoadjuvant Therapy in Triple-Negative Breast Cancer

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```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----------------------- tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.2     v tibble    3.3.0
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.1.0
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```r
library(readxl)
library(DiagrammeR)
library(ggpubr)
library(ggsurvfit)
```

#Figure 1A - Consort Diagram

```r
g <- grViz("
  digraph consort_diagram {
    graph [compound=true, rankdir=TB, splines=line]
    node [shape=box, style=filled, fillcolor=lightgrey, fontname=helvetica, fontsize=16,      width=6]

    // Enrollment
    enrolled [label='Assessed for eligibility and signed informed consent (n=695)', fillcolor=lightblue]
    excluded [label='Did not meet inclusion criteria (n=45)', fillcolor=lightcoral]

    // Procedure
    protocol  [label='Initiated protocol procedures (n=650)', fillcolor=lightblue]
    deviation [label='Deviated significantly from protocol (n=4)', fillcolor = lightcoral]
    withdraw [label='Withdrew consent prior to surgery (n=97)', fillcolor = lightcoral]
    no_us [label='Did not undergo ultrasound after completion of AC (n=16)', fillcolor=lightcoral]
    us [label='Underwent ultrasound after completion of AC (n=533)', fillcolor=lightblue]
    unmeasure [label='Breast tumor ill-defined and unmeasurable (n=1)', fillcolor=lightcoral]

    // Analysis
    analysis [label='Included in clinical analysis (n=549)', fillcolor=lightblue]
    vol_analysis [label='Included in Volumetric Analysis (n=532)', fillcolor = lightblue]
```

```
    // Blank_connection_nodes

  blank1[label = '', width = 0.01, height = 0.01]
  blank2[label = '', width = 0.01, height = 0.01]
  blank3[label = '', width = 0.01, height = 0.01]
  blank4[label = '', width = 0.01, height = 0.01]
  blank5[label = '', width = 0.01, height = 0.01]


    // Connections
    enrolled -> blank1[dir=none]
    blank1 ->protocol
    blank1 -> excluded
    protocol -> blank2[dir=none]
    blank2 -> blank3[dir=none]
    blank2 -> deviation
    blank3 -> withdraw
    blank3 ->analysis
    analysis -> blank4[dir=none]
    blank4 -> no_us
    blank4 -> us
    us -> blank5[dir=none]
    blank5 -> unmeasure
    blank5 -> vol_analysis



  {rank=same;blank1;excluded;};
  {rank=same;blank2;deviation;};
  {rank=same;blank3;withdraw;};
  {rank=same;blank4; no_us;};
  {rank=same;blank5; unmeasure;}

  }
")

g
```
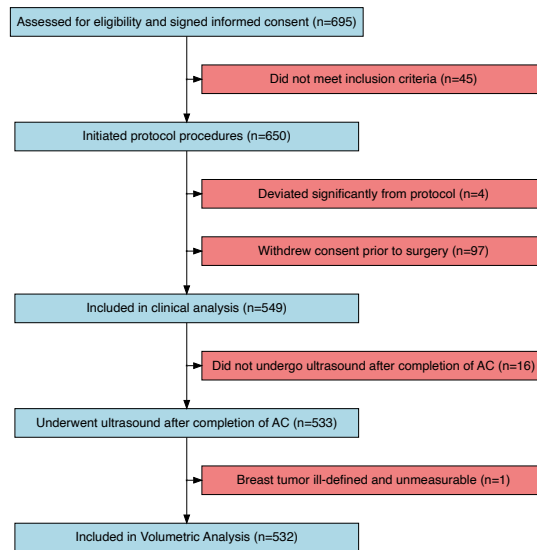
file:////private/var/folders/cc/drkqs5pn4bv6q3ldzfl2gzh80000gn/T/RtmpwLyPqY/file58332e460469/widget5&

Assessed for eligibility and signed informed consent (n=695)

Did not meet inclusion criteria (n=45)

Initiated protocol procedures (n=650)

Deviated significantly from protocol (n=4)

Withdrew consent prior to surgery (n=97)

Included in clinical analysis (n=549)

Did not undergo ultrasound after completion of AC (n=16)

Underwent ultrasound after completion of AC (n=533)

Breast tumor ill-defined and unmeasurable (n=1)

Included in Volumetric Analysis (n=532)

#Figure 1B - Waterfall Plot - showing tumor percent volumne change from baseline

```r
#Import data
W <-read_excel("/Users/hahill/Desktop/Figure_1_code_ARTEMIS/waterfall_plot.xlsx")


#Plot data

W <- W %>% arrange(desc(change))

col <- (ifelse(W$`number AC`==1,
               "#00A087",
        ifelse(W$`number AC` == 2,
               "#CF3759",
        ifelse(W$`number AC` == 3,
               "#FFD700","#A5D5D8"))))

wf<- barplot(W$change,
             col=col,
             border=col,
             space=0.5,
             ylim=c(-100,500),
             main = "Change in Tumor Volume (%) from Baseline",
             cex.axis=1.5,
             legend.text= c( "1","2","3","4"),
             args.legend=list(title="Cycles of AC", fill=c("#00A087","#CF3759","#FFD700","#A5D5D8"), b
```
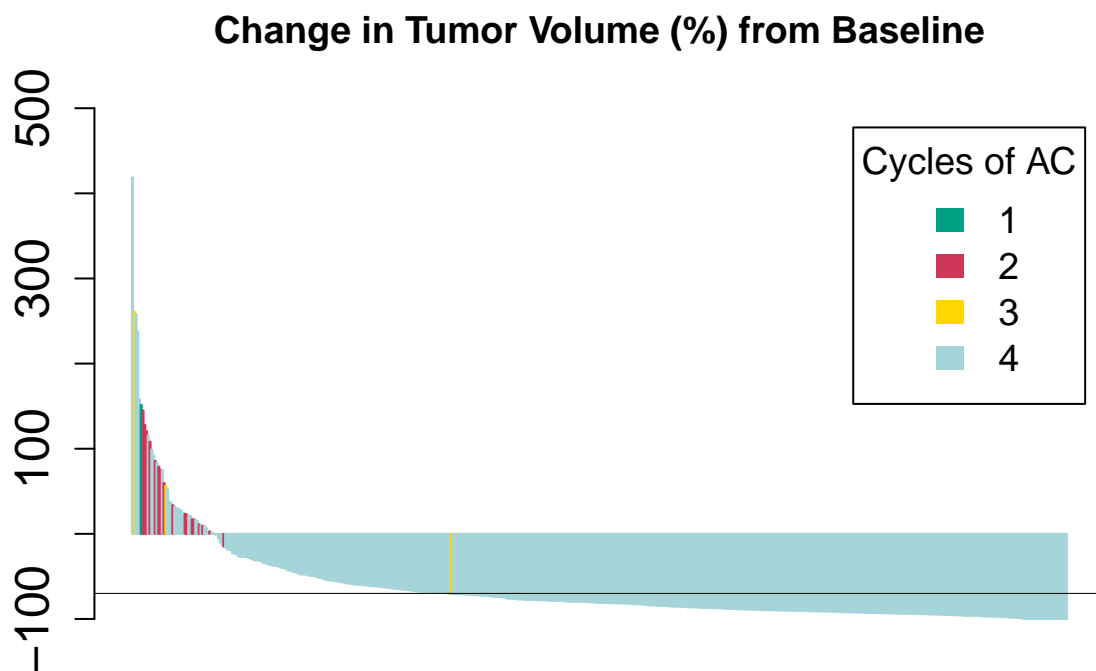

#Figure 1C - Event-free Survuval by Response to AC - please see analysis code for more information

```
#Import survival data
survival_art <-read_excel("/Users/hahill/Desktop/Figure_1_code_ARTEMIS/ARTEMIS_survival.xlsx")


p <- survfit2(Surv(time_efs, event_efs) ~ sensitive_cat, data = survival_art) |>
  ggsurvfit(linewidth = 1) +
  add_confidence_interval() +
  add_quantile(y_value = 0, color = "gray50", linewidth = 0.75)


q <- p + coord_cartesian(ylim = c(0, 1.00)) +
  labs(x= "Time (Weeks)", title = "Event-free Suvival (EFS) by Response to AC") +
  scale_color_manual(values = c('#efac71','#4682B4')) +
  scale_fill_manual(values = c('#efac71','#4682B4')) +
  scale_x_continuous(limits = c(0,90), expand=(c(0,0)))+
  scale_y_continuous(limits = c(0,1), expand=(c(0,0)))+
  add_pvalue(location  = "annotation", x = 80, y = 0.5)

q
```
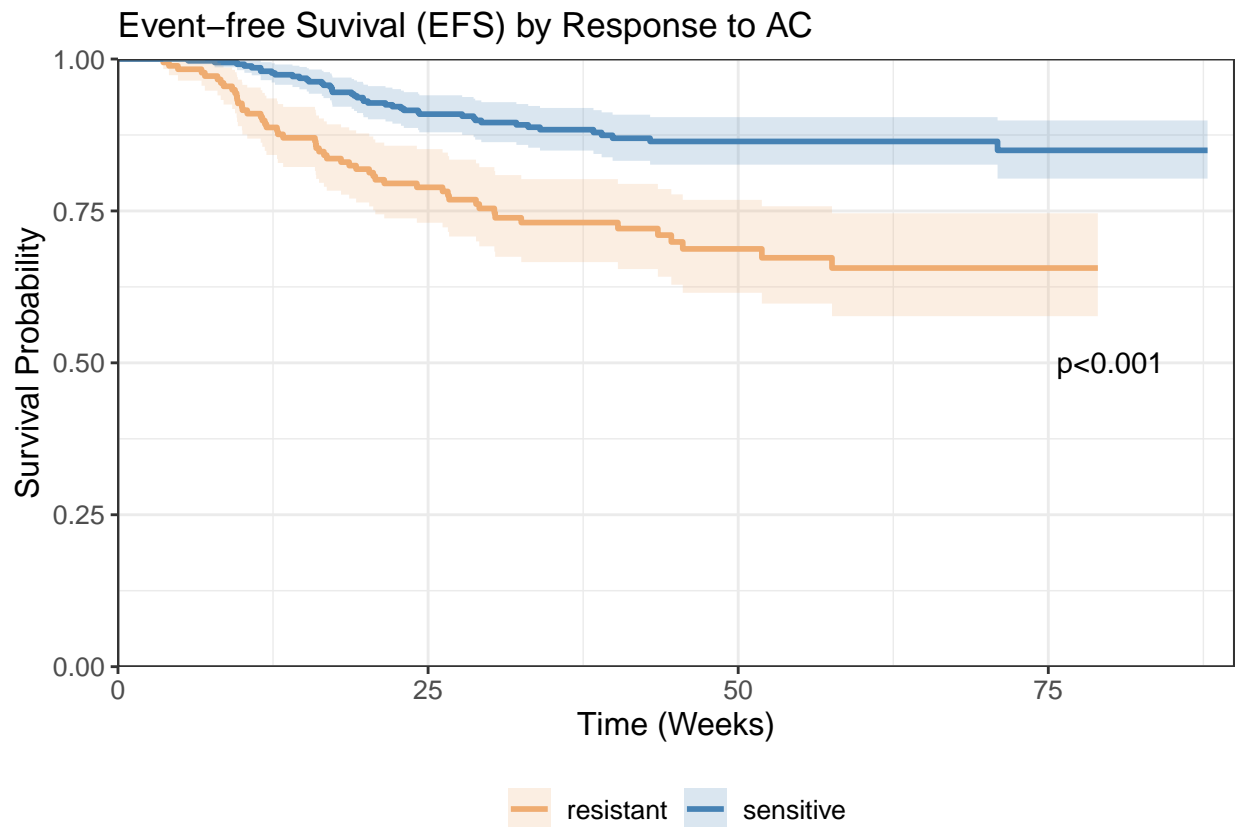

#Figure 2D - Flowchart of Patients and clinical outcomes

```
g = grViz("
    digraph G{
    compound = true
    rankdir = LR
    node [fontname='helvetica', shape=box, width = 4, style = filled,  color=lightgrey]
```

```
edge [arrowhead = none]

tab1 [label='@@1']
tab2 [label='@@2']

subgraph cluster_one {

node[shape=box, style = filled, fillcolor = lightsteelblue];
edge[arrowhead=none];
style = dashed;
fontname = 'helvetica-bold';
rank = LR;

node[shape = box, style = filled, color = black];
tab3 [label='@@3']
tab7 [label='@@7']
tab8 [label='@@8']
tab9 [label='@@9']
tab10 [label='@@10']
tab11 [label='@@11']
tab12 [label='@@12']

tab3-> tab7
tab3-> tab8
tab7 -> tab12
tab7 -> tab11
tab8 -> tab10
tab8 -> tab9

}

subgraph cluster_two {

node[shape=box, style = filled, fillcolor = peachpuff];
edge[arrowhead=none];
style = dashed;
fontname = 'helvetica-bold';
rank = LR;

node[shape = box, style = filled, color = black];

tab4 [label='@@4']
tab5 [label='@@5']
tab6 [label='@@6']
tab13[label='@@13']
tab14[label='@@14']
tab15[label='@@15']
tab16[label='@@16']

tab4 -> tab5
tab4 -> tab6
tab5 -> tab13
tab5 -> tab14
```

```
    tab6 -> tab15
    tab6 -> tab16

    }

    {rank=min tab1->tab2}
    tab1 -> tab3
    tab1 -> tab4
    }

    [1]:'All Patients (n=549)'
    [2]:'No Sensitivity Data (n=17)'
    [3]:'Sensitive to AC (n=352)'
    [4]:'Resistant to AC (n=180)'
    [5]:'Standard of Care (n=76)'
    [6]:'Experiemental Treatment (n=103)'
    [7]:'Standard of Care (n=338)'
    [8]:'Experimental Treatment (n=8)'
    [9]:'pCR (n=4)'
    [10]:'Residual Disease (n=4)'
    [11]:'pCR (n=187)'
    [12]:'Residual Disease (n=151)'
    [13]:'pCR (n=12)'
    [14]:'Residual Disease (n=64)'
    [15]:'pCR (n=14)'
    [16]:'Residual Disease (n=89)'
")

g
```

file:////private/var/folders/cc/drkqs5pn4bv6q3ldzfl2gzh80000gn/T/RtmpwLyPqY/file5833639133e9/widget58