

# Building Complex Graphics from Simple Plot Types

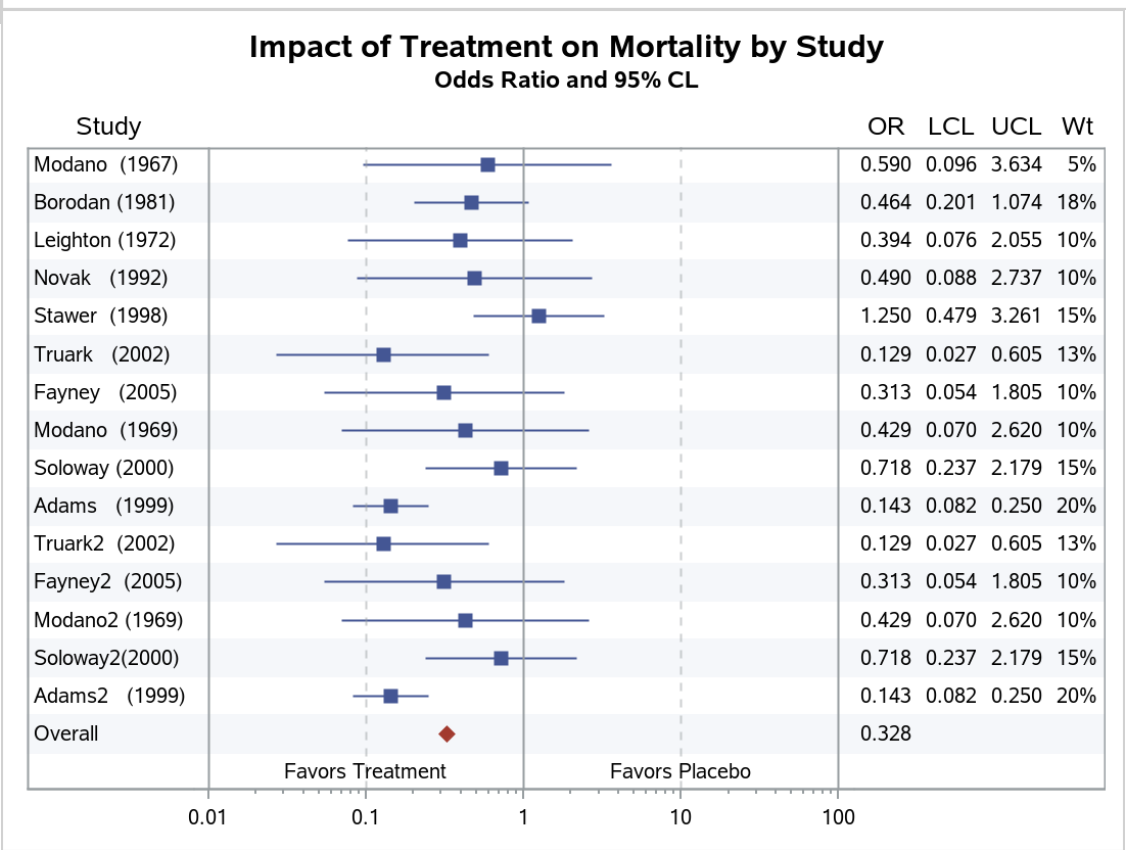
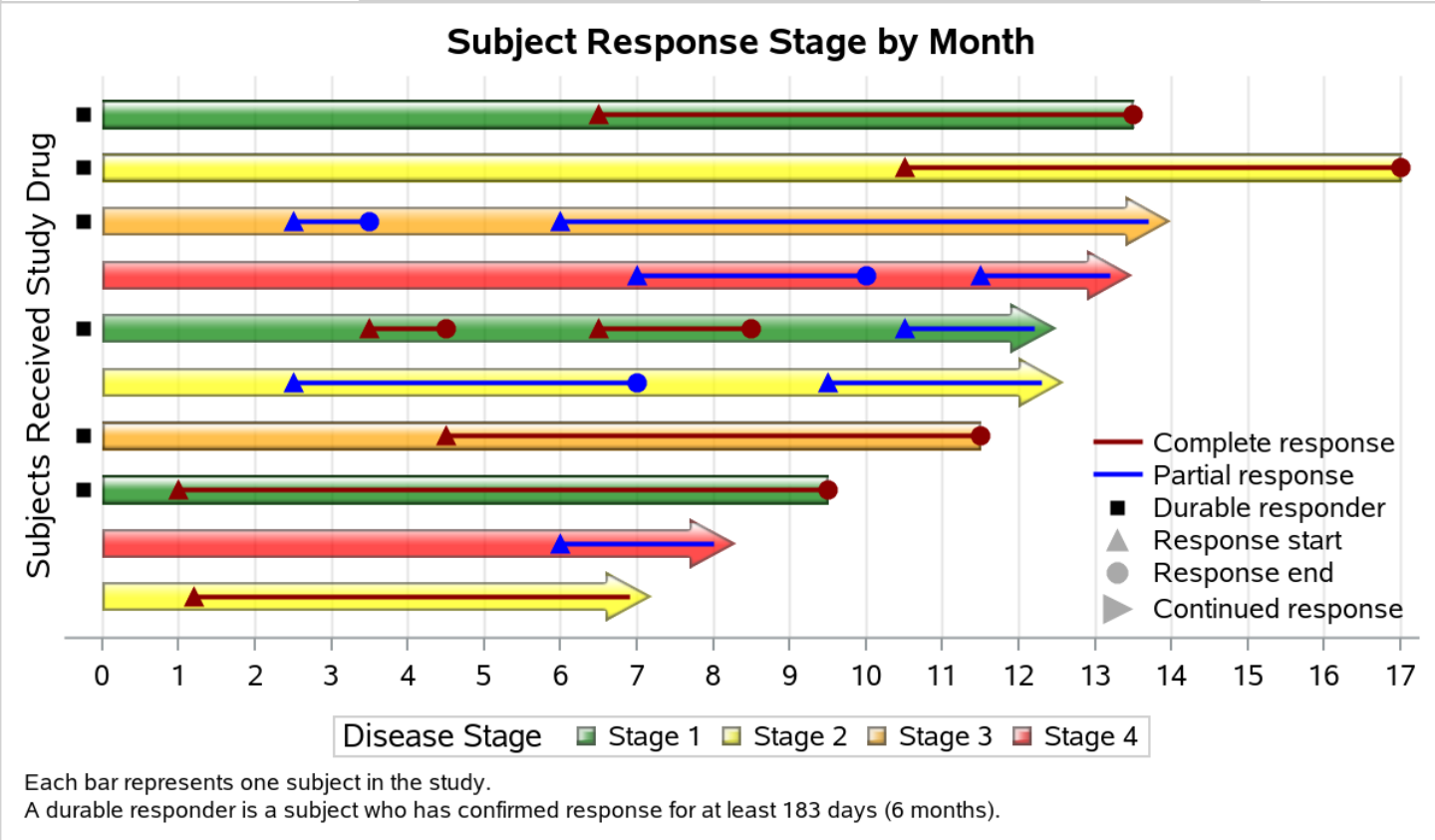
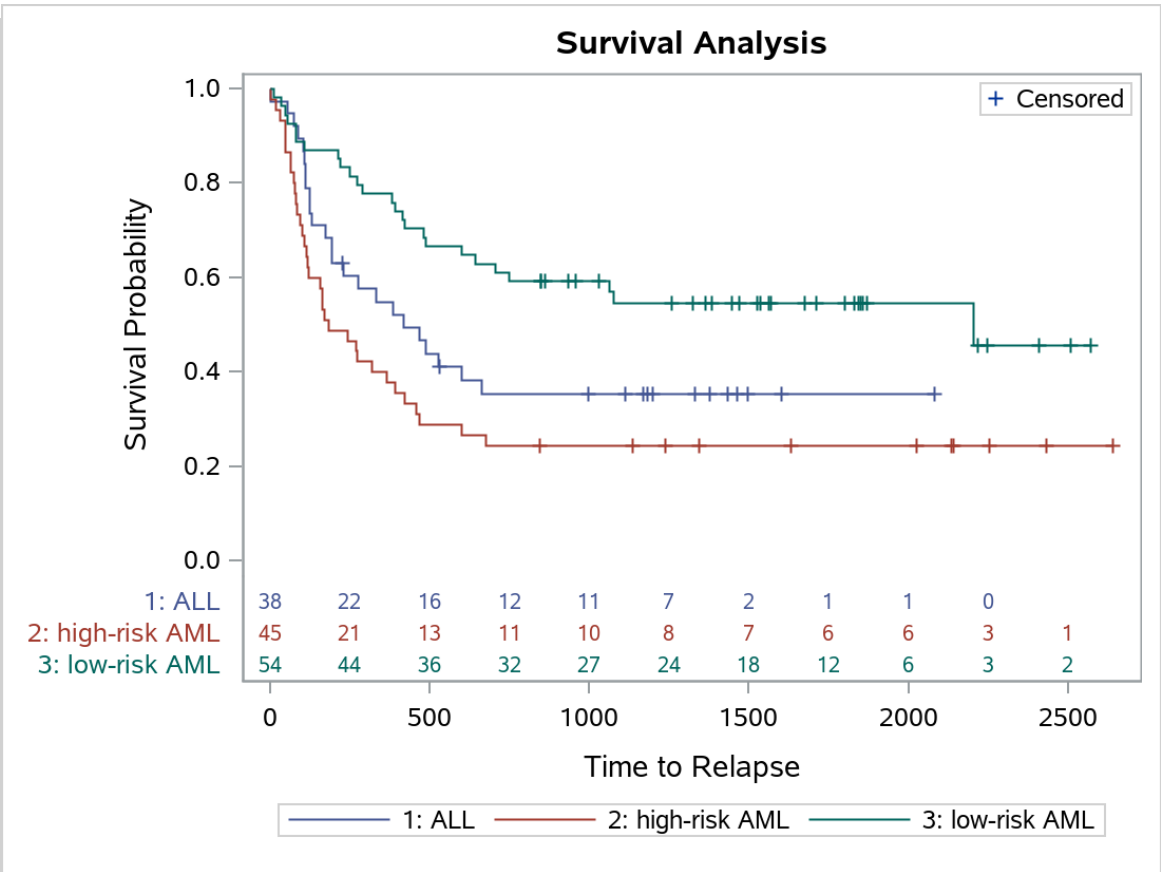
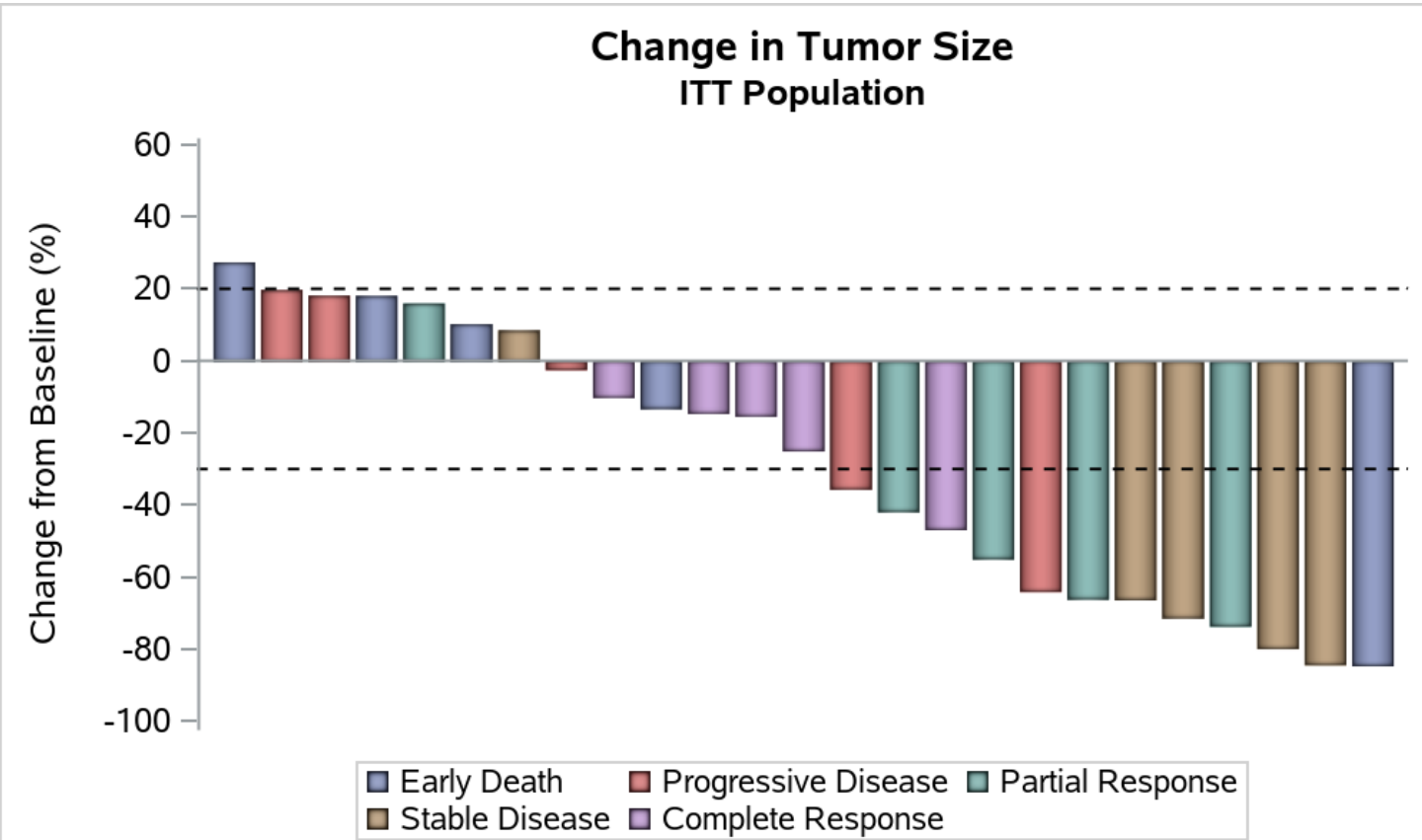
Dan Heath, SAS Data Visualization R&D



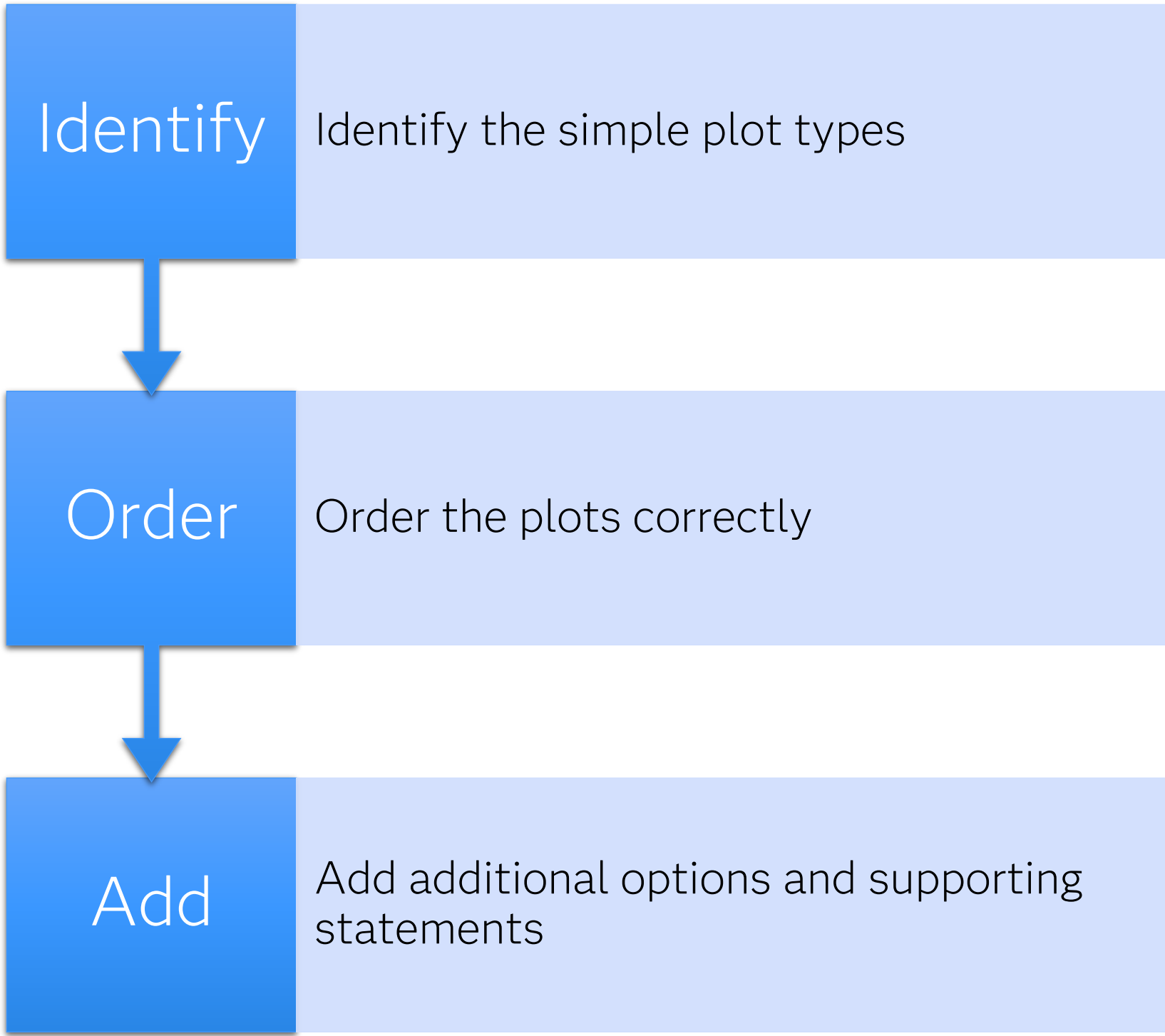
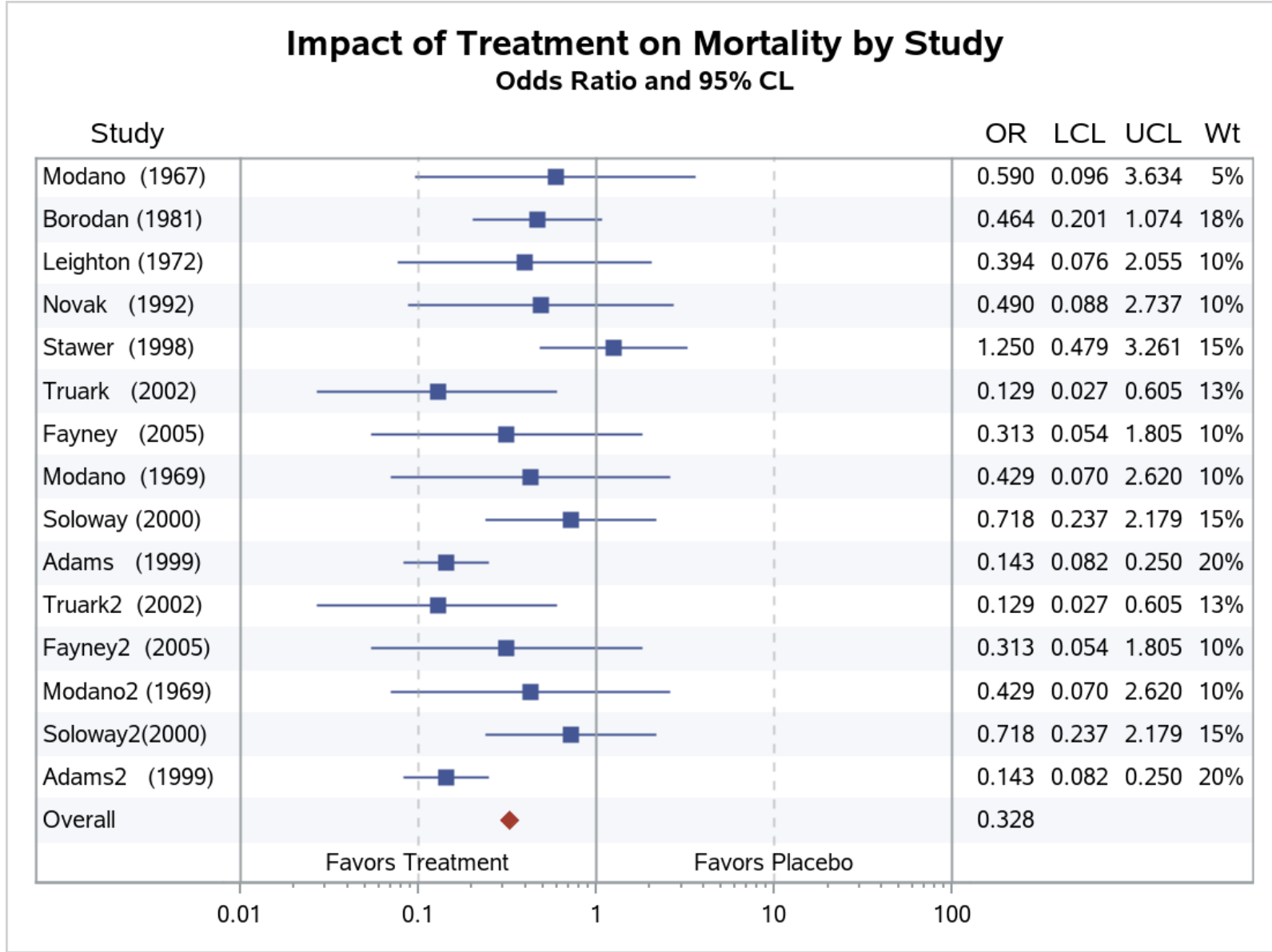
# Proverb

“If you give a man a fish, you feed him for a day. If you teach a man to fish, you feed him for a lifetime.”

# Clinical Graphics



# Steps to Create a Complex Plot

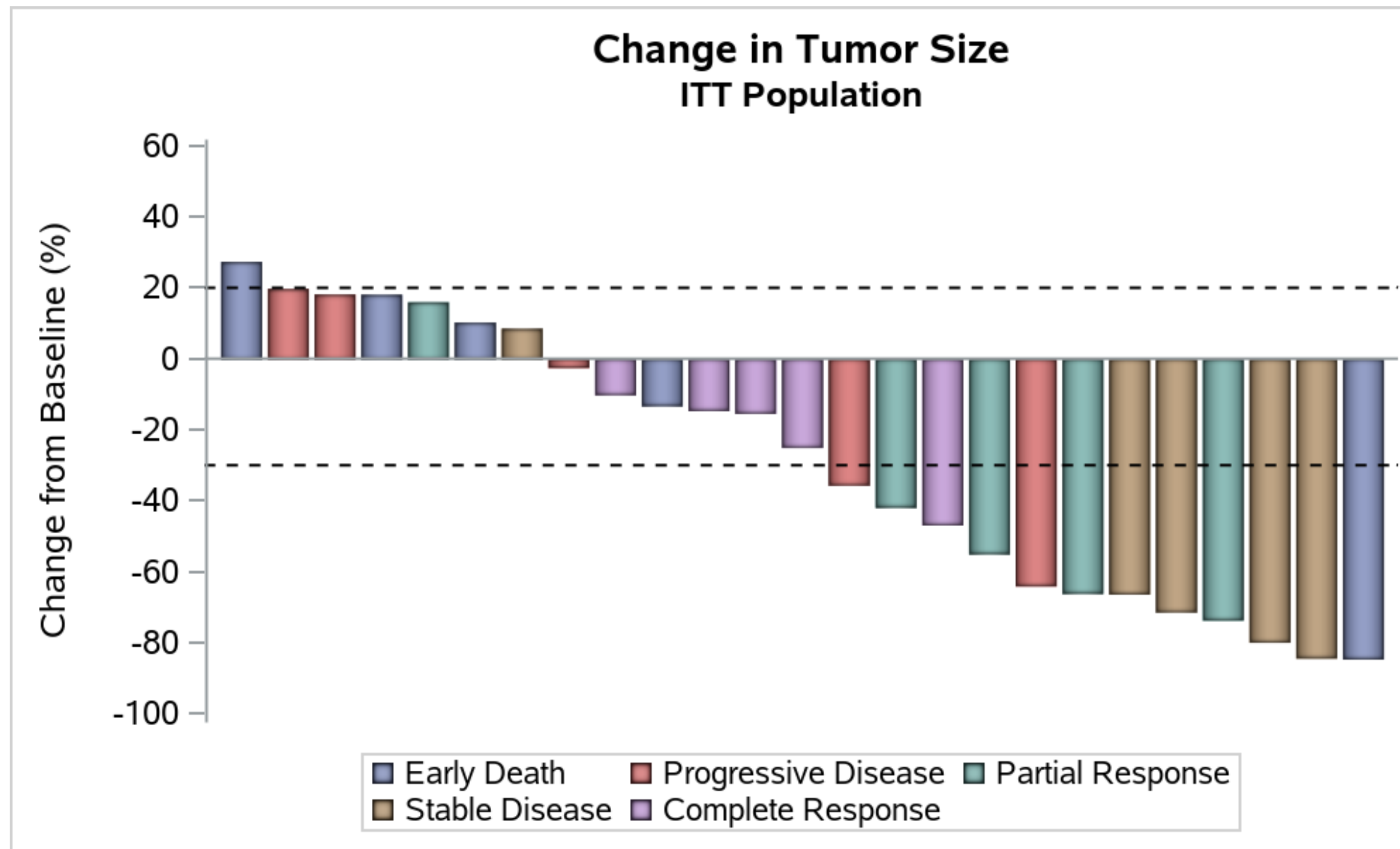


# Creative Use of Plot Types

- Band
- HighLow
- Text
- Scatter
- RefLine



# Waterfall Plot



# Waterfall Plot

## Code

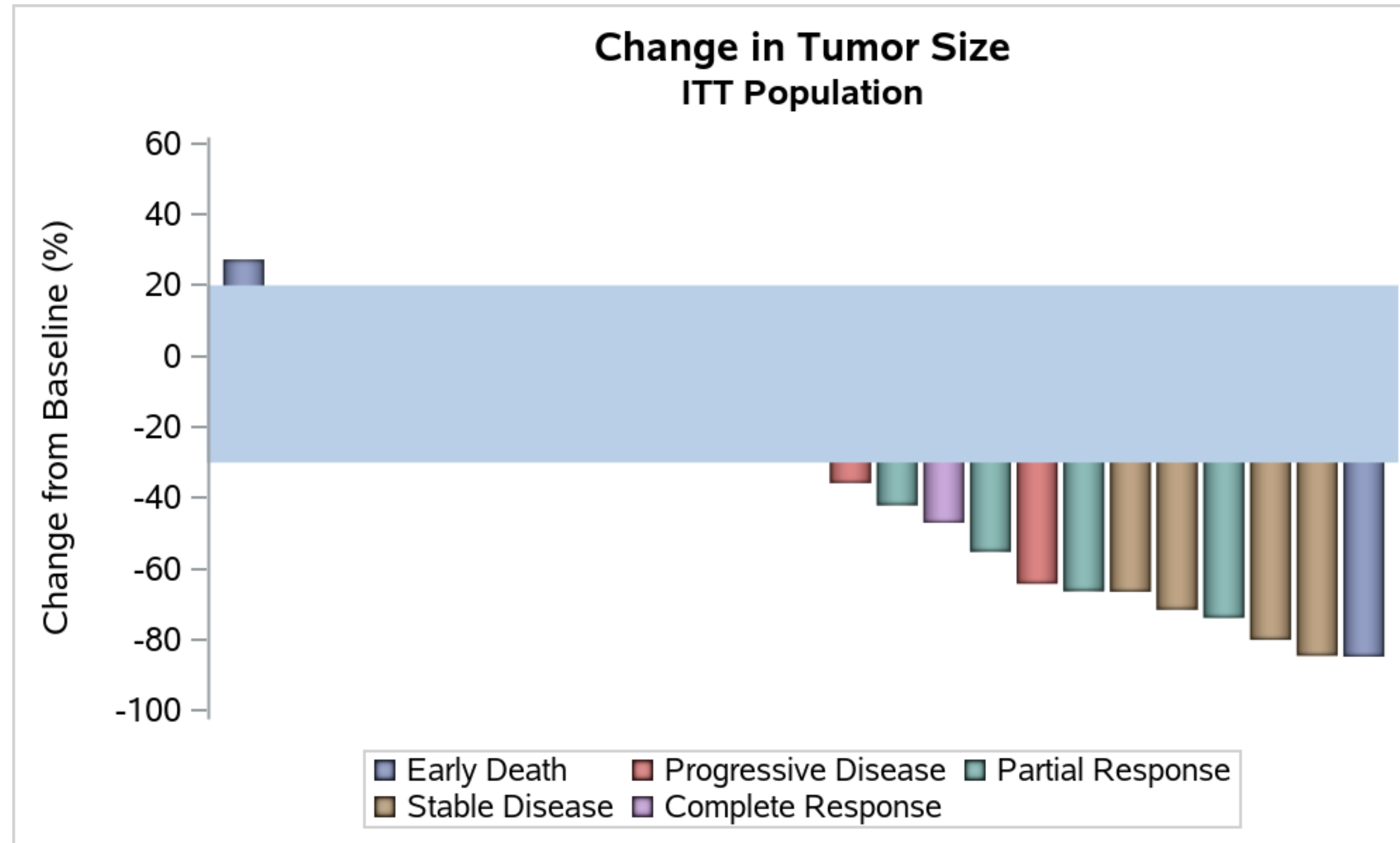
```
proc sort data=TumorSize out=TumorSizeDesc;  
  by descending change;  
run;  
  
title 'Change in Tumor Size';  
title2 'ITT Population';  
proc sgplot data=TumorSizeDesc nowall noborder;  
  format label $resp.;  
  vbarparm category=cid response=change / group=label dataskin=pressed;  
  refline 20 -30 / lineattrs=(color=black pattern=shortdash);  
  xaxis display=none;  
  yaxis values=(60 to -100 by -20);  
  keylegend / title='';  
run;
```

# Replace a REFLINE with a BAND

```
title 'Change in Tumor Size';
title2 'ITT Population';
proc sgplot data=TumorSizeDesc nowall noborder;
  format label $resp.;
  vbarparm category=cid response=change / group=label dataskin=pressed;
  band x=cid upper=20 lower=-30;
  xaxis display=none;
  yaxis values=(60 to -100 by -20);
  keylegend / title='';
run;
```



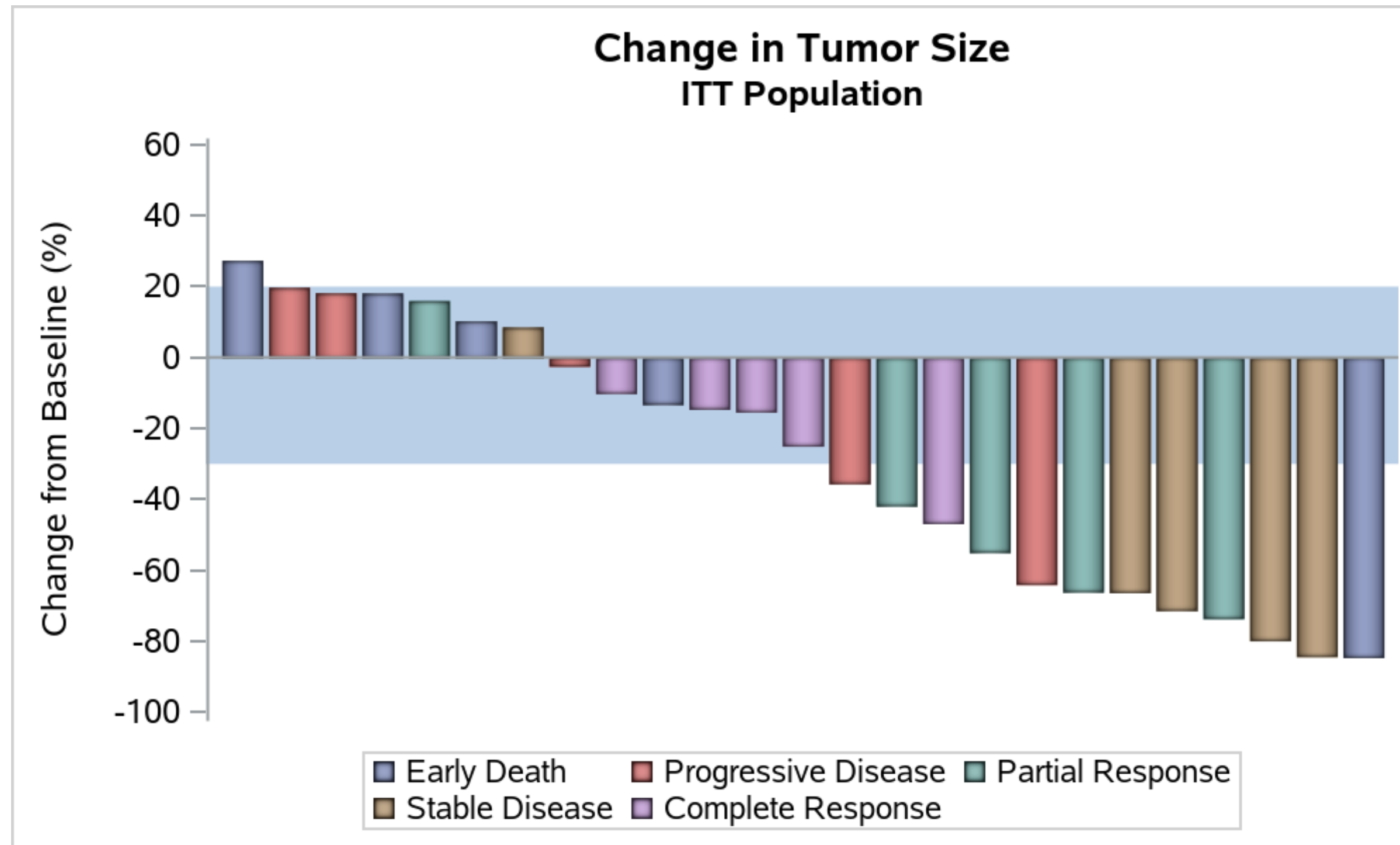
# Replace a REFLINE with a BAND



# Replace a REFLINE with a BAND

```
title 'Change in Tumor Size';  
title2 'ITT Population';  
proc sgplot data=TumorSizeDesc nowall noborder;  
    format label $resp.;  
    band x=cid upper=20 lower=-30;  
    vbarparm category=cid response=change / group=label dataskin=pressed;  
    xaxis display=none;  
    yaxis values=(60 to -100 by -20);  
    keylegend / title='';  
run;
```

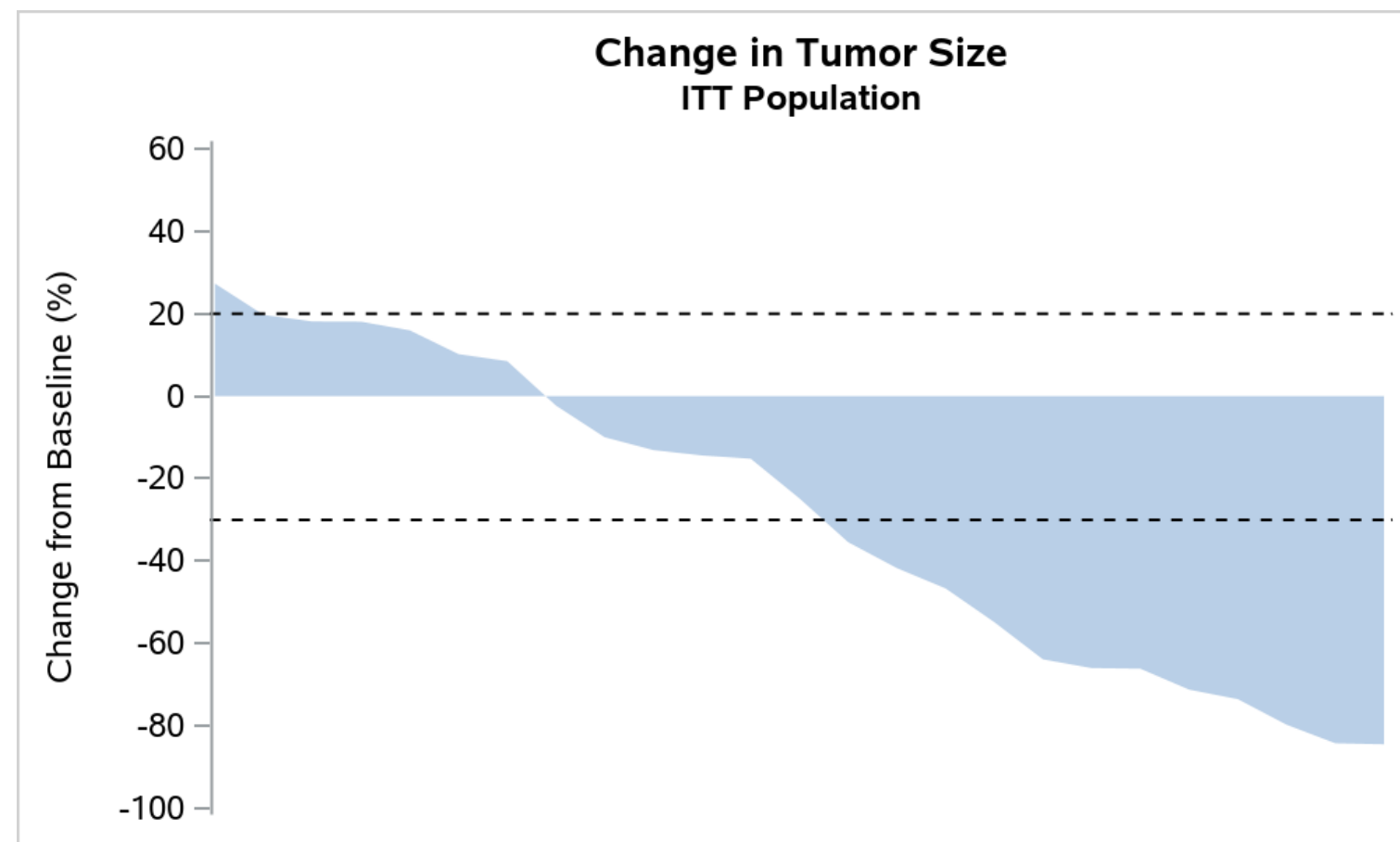
# Replace a REFLINE with a BAND



# Replace a REFLINE with a BAND

```
proc sgplot data=TumorSizeDesc nowall noborder;  
  format label $resp.;  
  vbarparm category=cid response=change / group=label dataskin=pressed  
    name="waterfall";  
  band x=cid upper=20 lower=-30 / lineattrs=(color=black pattern=shortdash)  
    nofill outline;  
  . . .  
run;
```

# Area Plot

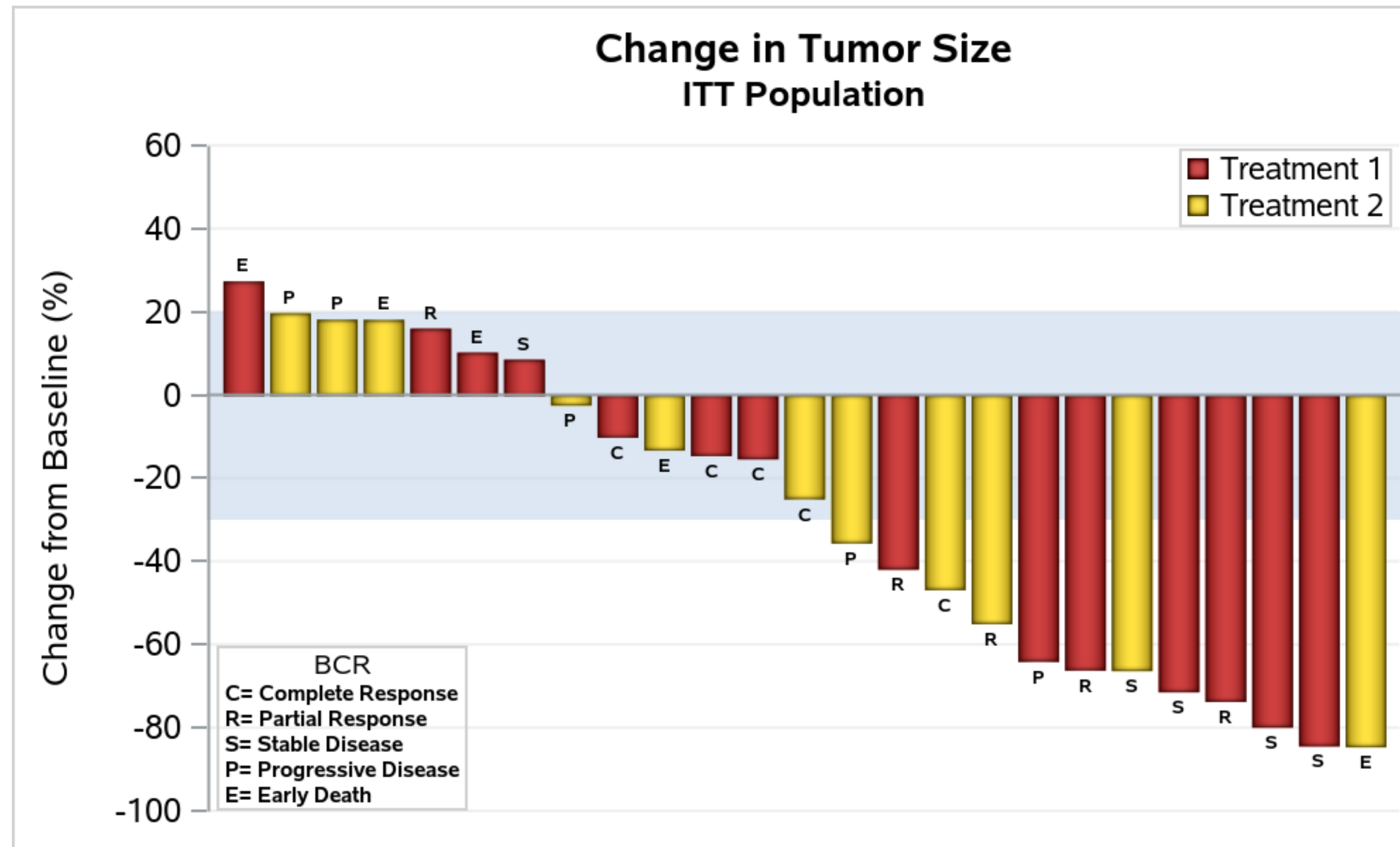


```
title 'Change in Tumor Size';
title2 'ITT Population';
proc sgplot data=TumorSizeDesc nowall
            noborder noautolegend;
    band x=cid upper=change lower=0 ;
    refline 20 -30 / lineattrs=(color=black
                                pattern=shortdash) ;
    xaxis display=none;
    yaxis values=(60 to -100 by -20) ;
run;
```



# Advanced Waterfall Plot

Two levels of classification



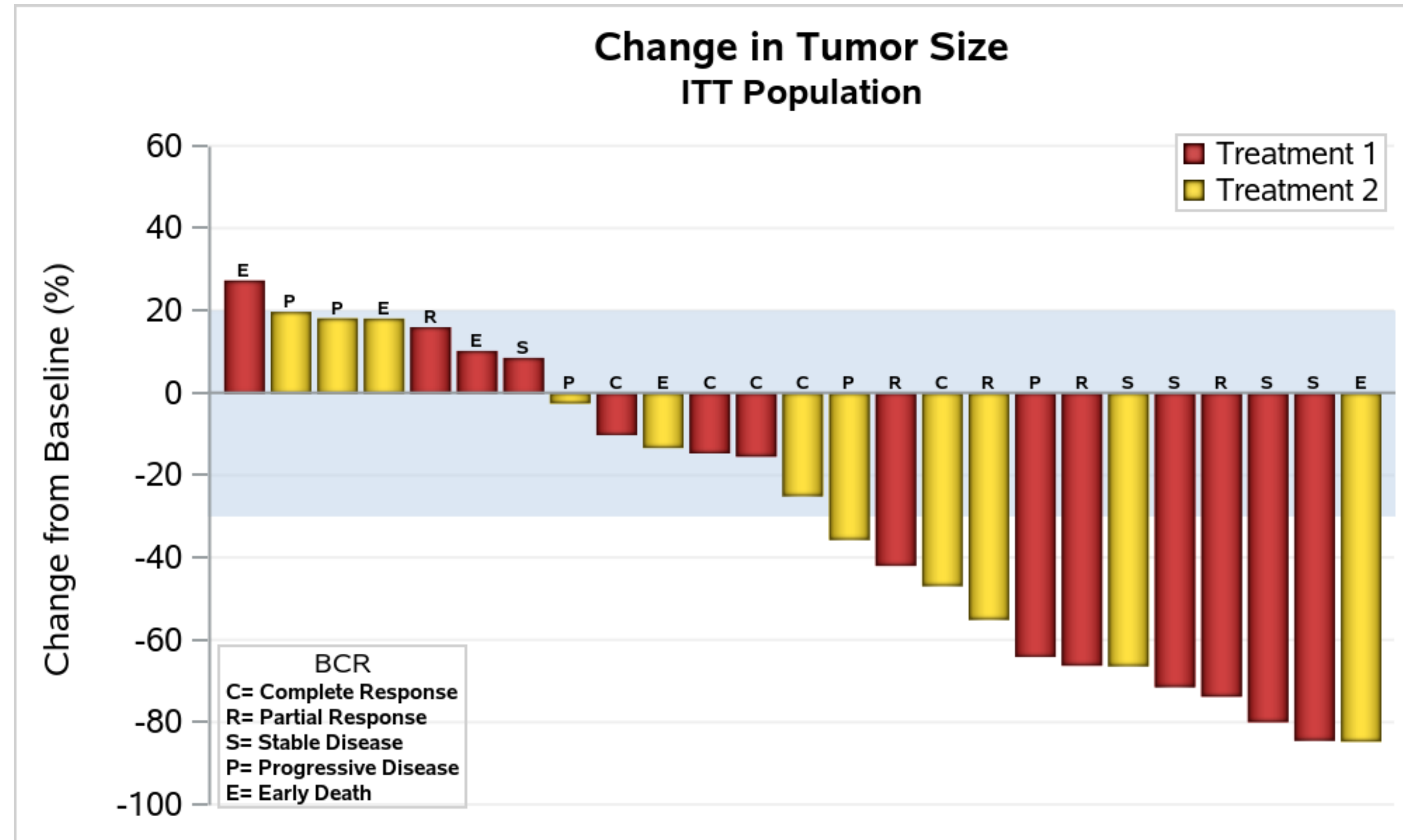
# Advanced Waterfall Plot

## Code

```
title 'Change in Tumor Size';
title2 'ITT Population';
proc sgplot data=TumorSizeDesc nowall noborder;
  styleattrs datacolors=(cxbf0000 gold) datacontrastcolors=(black) axisextent=data;
  band x=cid upper=20 lower=-30 / transparency=0.5;
  vbarparm category=cid response=change / group=group datalabel=label
          datalabelattrs=(size=5 weight=bold) groupdisplay=cluster name="waterfall"
          dataskin=preserved;
  xaxis display=none;
  yaxis values=(60 to -100 by -20) grid gridattrs=(color=cxf0f0f0);
  inset "C= Complete Response" "R= Partial Response" "S= Stable Disease"
        "P= Progressive Disease" "E= Early Death" / title='BCR'
        position=bottomleft border textattrs=(size=6 weight=bold) titleattrs=(size=7);
  keylegend "waterfall" / title='' location=inside position=topright across=1 border
opaque;
run;
```

# Advanced Waterfall Plot

Custom labeling





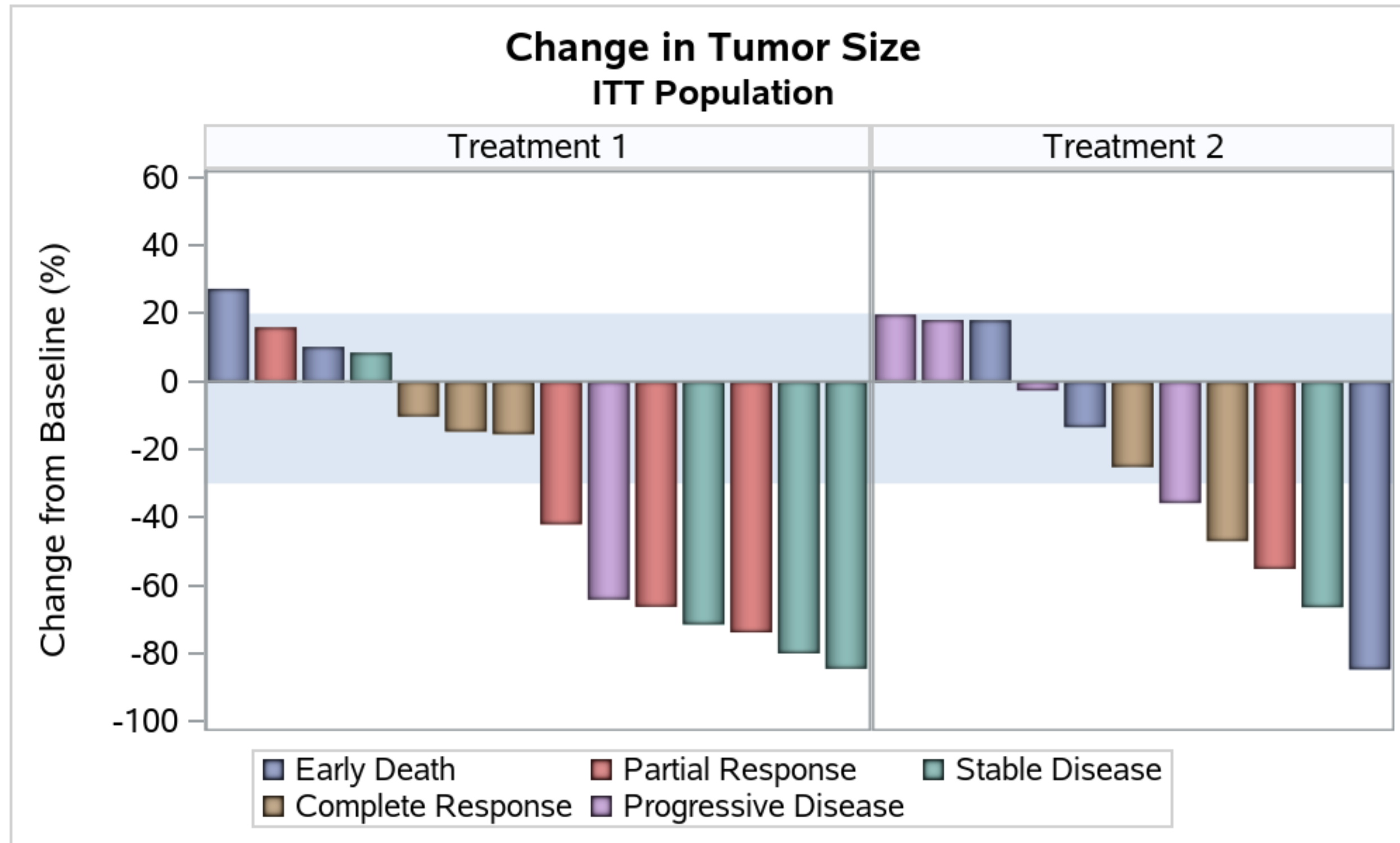
# Advanced Waterfall Plot

## Custom labeling code

```
data custom_label;  
set TumorSizeDesc;  
xlabel = cid;  
ylabel = ifn(change < 0, 0, change);  
run;  
  
proc sgplot data=custom_label nowall noborder;  
  styleattrs datacolors=(cxbf0000 gold) datacontrastcolors=(black)  
    axisextent=data;  
  band x=cid upper=20 lower=-30 / transparency=0.5;  
  vbarparm category=cid response=change / group=group groupdisplay=cluster  
    name="waterfall" dataskin=pressed;  
  text x=xlabel y=ylabel text=label / textattrs=(size=5 weight=bold)  
    position=top;  
  . . .  
run;
```

# Advanced Waterfall Plot

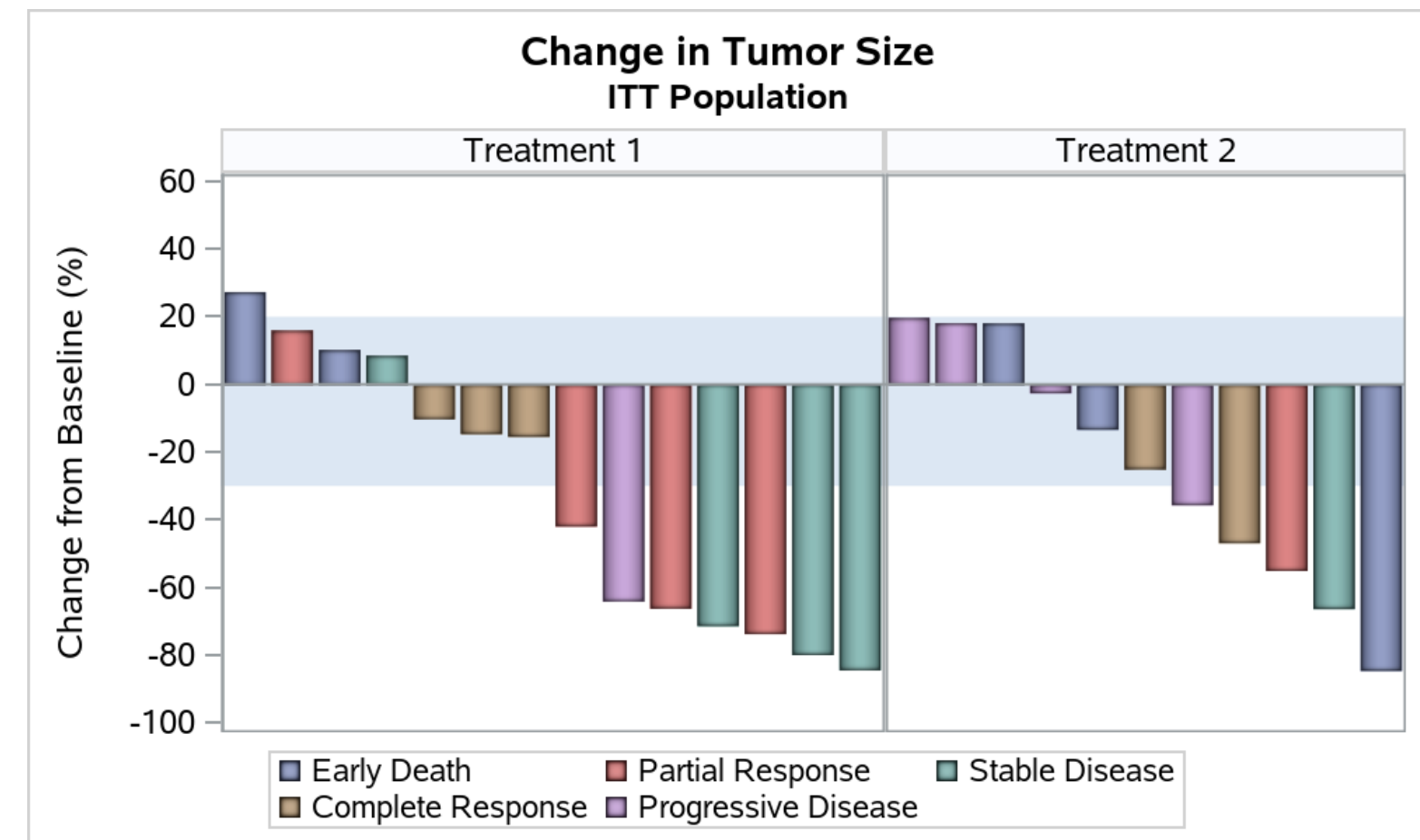
SGPANEL



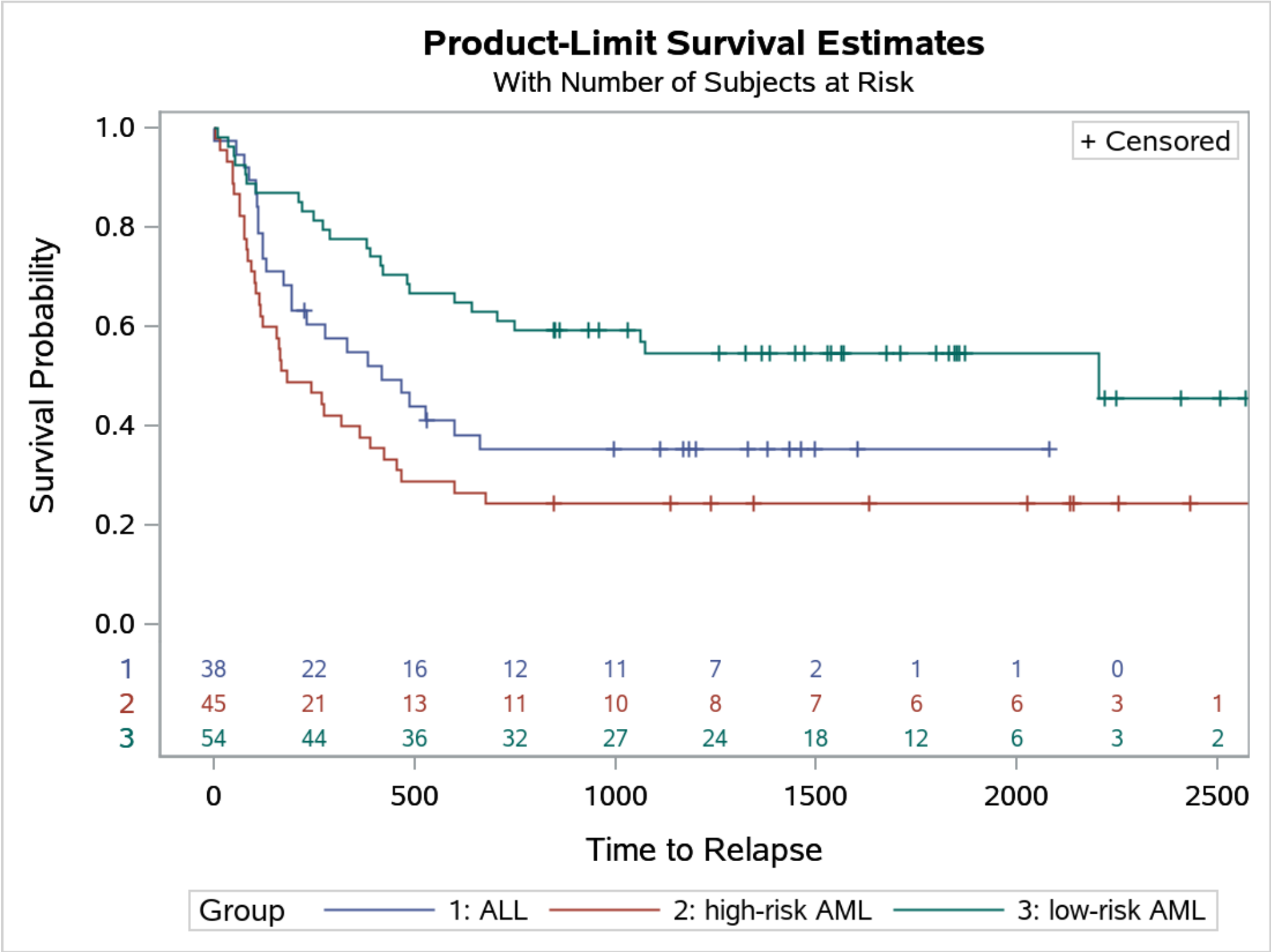
# Advanced Waterfall Plot

## SGPANEL

```
title 'Change in Tumor Size';
title2 'ITT Population';
proc sgpanel data=TumorSizeDesc;
  format label $resp.;
  panelby group / uniscale=row novarname proportional;
  band x=cid upper=20 lower=-30 / transparency=0.5;
  vbarparm category=cid response=change / group=label dataskin=preserved
        name="waterfall";
  colaxis display=none;
  rowaxis values=(60 to -100 by -20);
  keylegend "waterfall" / title='';
run;
```



# Survival Plot



# Survival Plot

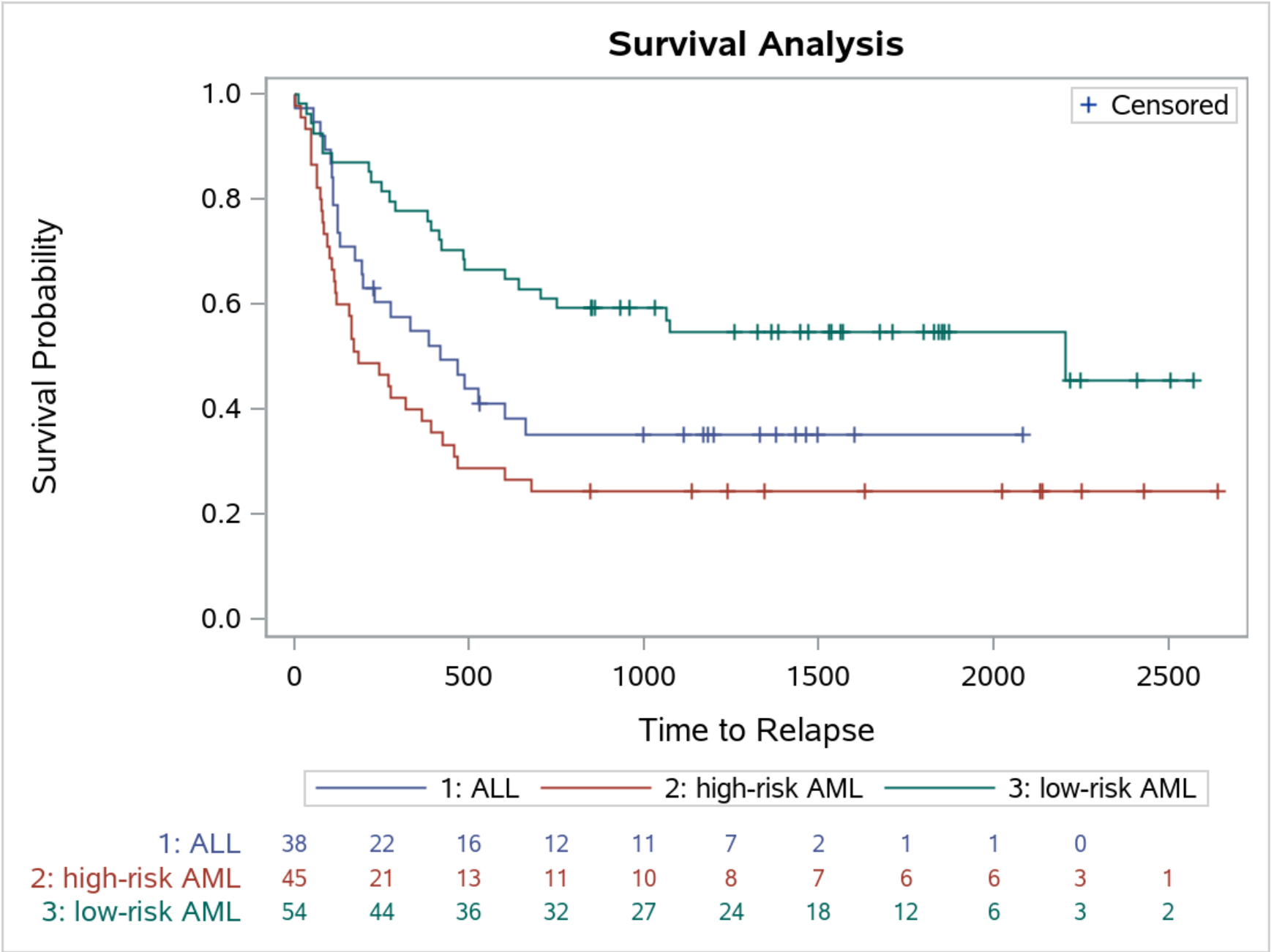
## Code

```
title "Survival Analysis";
proc sgplot data=OutSurvival;
    step x=time y=survival / group=stratum name='s';
    scatter x=time y=censored / group=stratum
            markerattrs=(symbol=plus);
    xaxistable atrisk / x=tatrisk class=stratum location=inside
            colorgroup=stratum;
    legenditem type=marker name='c' /
            markerattrs=GraphDataDefault(symbol=plus)
            label='Censored';
    yaxis min=0;
    keylegend 'c' / location=inside position=topright;
    keylegend 's' / outerpad=10;
run;
```



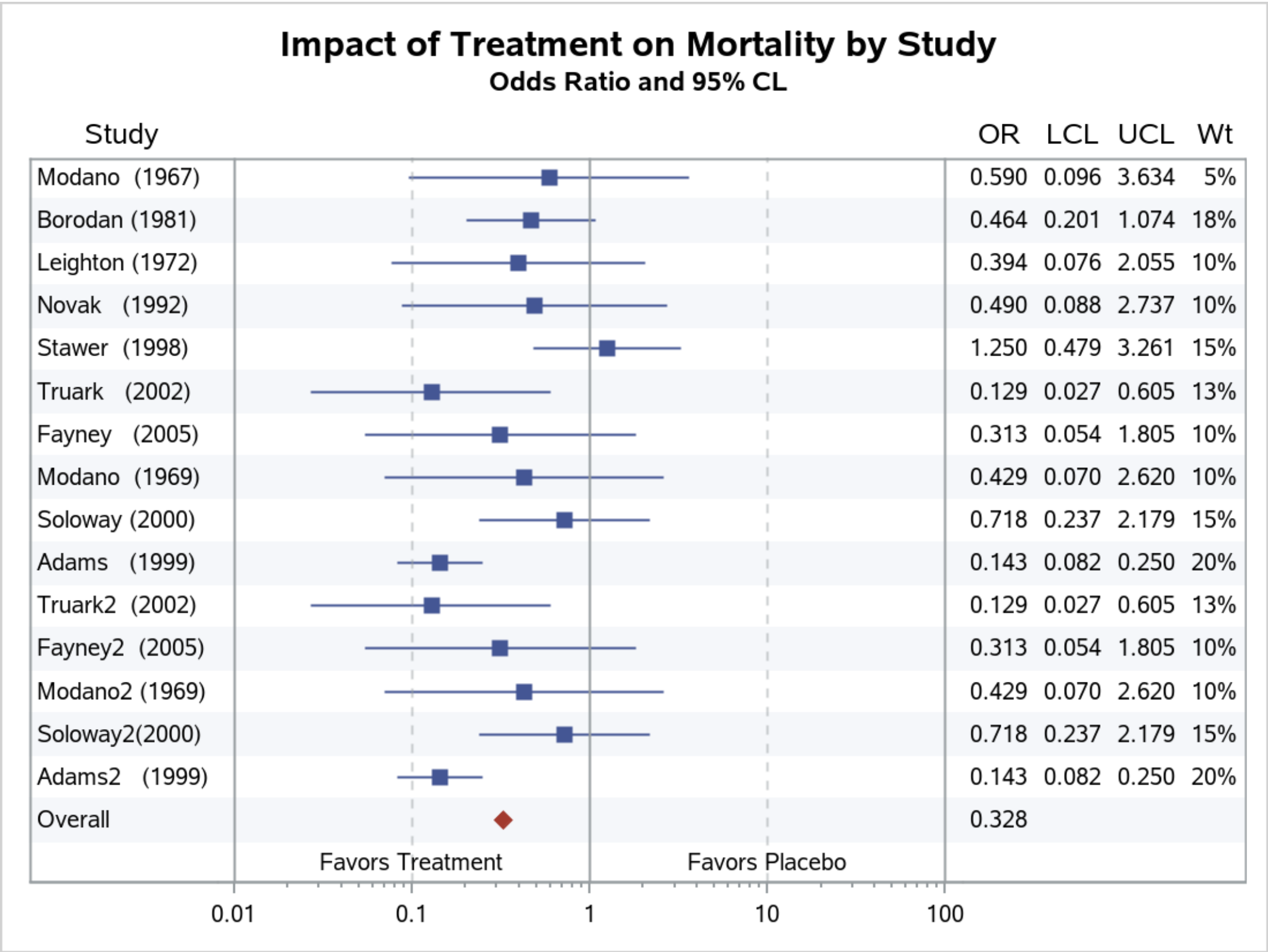
# Survival Plot

Outside axis table



xaxistable atrisk / x=tatrisk class=stratum location=outside colorgroup=stratum;

# Forest Plot



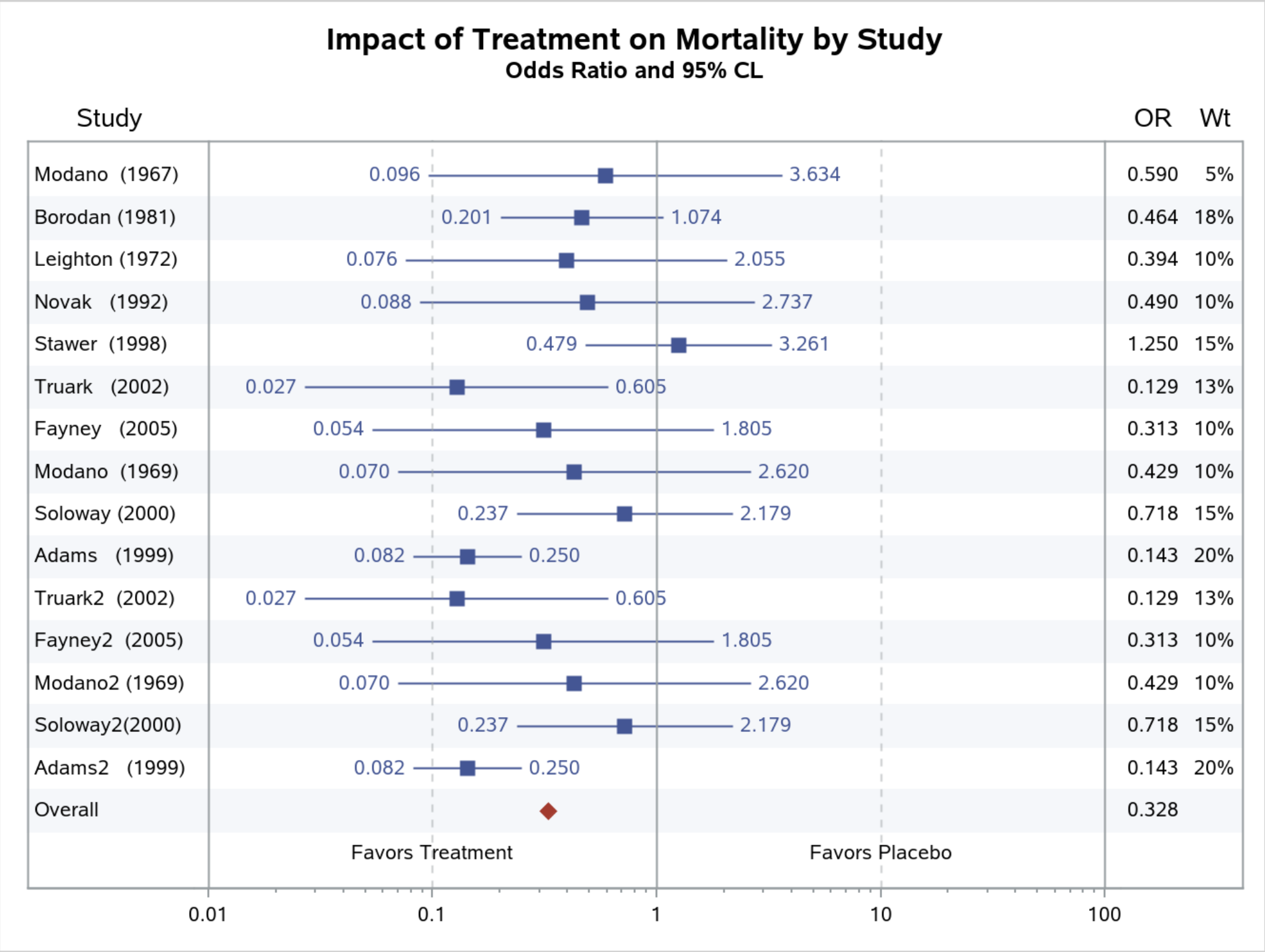
# Forest Plot

## Code

```
title "Impact of Treatment on Mortality by Study";
title2 h=8pt 'Odds Ratio and 95% CL';
ods graphics / attrpriority=none;
proc sgplot data=forest noautolegend nocycleattrs;
  styleattrs datasymbols=(squarefilled diamondfilled);
  scatter y=study x=or / xerrorupper=ucl xerrorlower=lcl group=grp noerrorcaps;
  refline 0.01 1 100 / axis=x noclip;
  refline 0.1 10 / axis=x lineattrs=(pattern=shortdash) transparency=0.5 noclip;
  text y=study x=xlbl text=lbl / position=center contributeoffsets=none;
  yaxistable study / y=study location=inside position=left;
  yaxistable or lcl ucl wt / y=study location=inside position=right nomissingchar;
  xaxis type=log max=100 minor display=(nolabel) valueattrs=(size=7);
  yaxis display=none fitpolicy=none reverse valueshalign=left colorbands=even
    valueattrs=(size=7) colorbandsattrs=Graphdatadefault(transparency=0.8);
run;
```



# Forest Plot with Labeled Limits

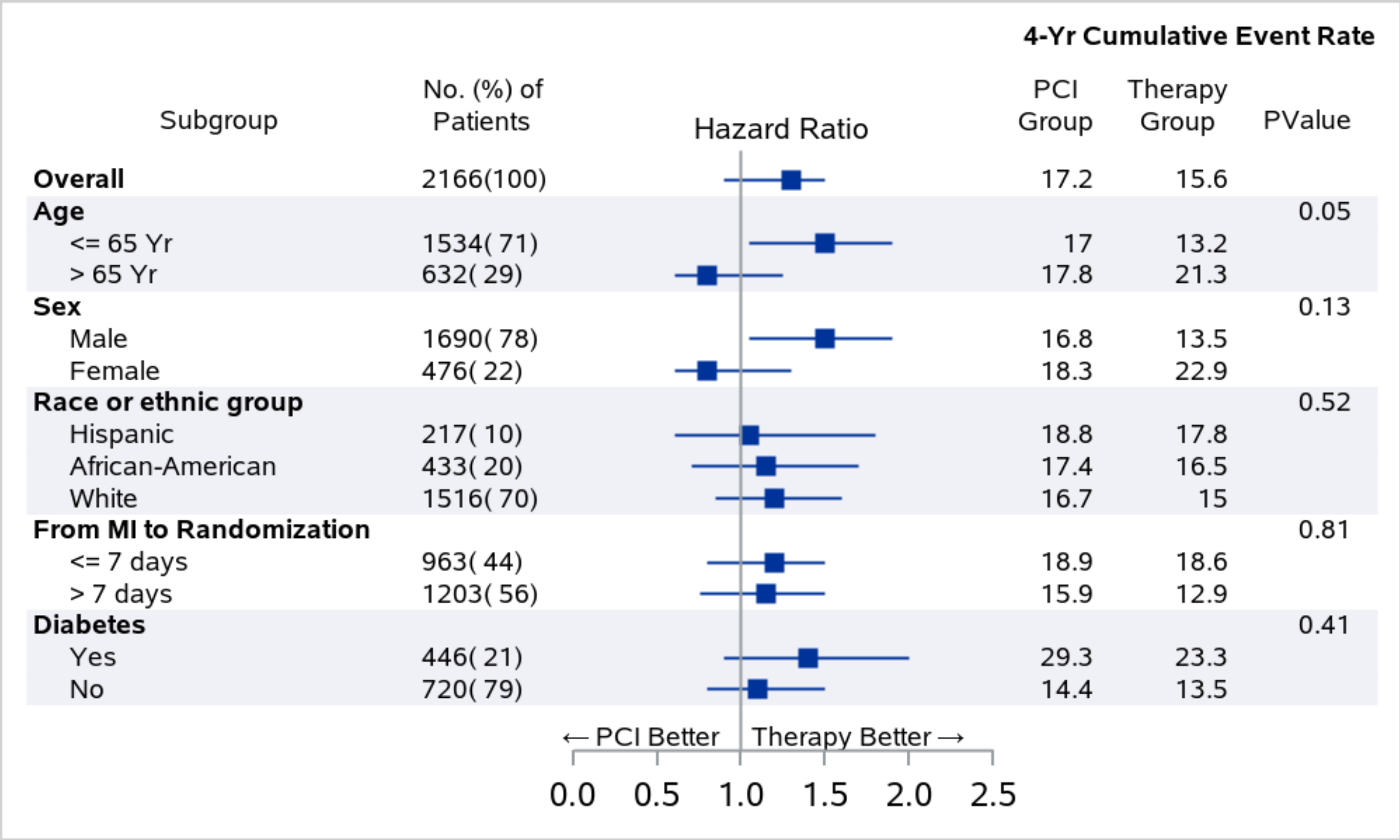


# Forest Plot with Labeled Limits

## Code

```
title "Impact of Treatment on Mortality by Study";
title2 h=8pt 'Odds Ratio and 95% CL';
ods graphics / attrpriority=none;
proc sgplot data=forest noautolegend nocycleattrs;
  styleattrs datasymbols=(squarefilled diamondfilled);
  highlow y=study high=ucl low=lcl / group=grp highlabel=ucl lowlabel=lcl;
  scatter y=study x=or / group=grp;
  yaxistable study / y=study location=inside position=left;
  yaxistable or wt / y=study location=inside position=right nomissingchar;
  refline 0.01 1 100 / axis=x noclip;
  refline 0.1 10 / axis=x lineattrs=(pattern=shortdash) transparency=0.5 noclip;
  text y=study x=xlbl text=lbl / position=center contributeoffsets=none;
  xaxis type=log max=100 minor display=(nolabel) valueattrs=(size=7);
  yaxis display=none fitpolicy=none reverse valueshalign=left
    colorbandsattrs=Graphdatadefault(transparency=0.8)
    colorbands=even valueattrs=(size=7);
run;
```

# Subgrouped Forest Plot



# Subgrouped Forest Plot

## Code

```
title j=r h=7pt '4-Yr Cumulative Event Rate';
proc sgplot data=forest_subgroup_2 nowall noborder nocycleattrs dattrmap=attrmap noautolegend;
  format text $txt.;
  styleattrs axisextent=data;
  refline ref / lineattrs=(color=cxf0f0f7) DiscreteThickness=1;
  highlow y=obsid low=low high=high;
  scatter y=obsid x=mean / markerattrs=(symbol=squarefilled);
  scatter y=obsid x=mean / markerattrs=(size=0) x2axis;
  refline 1 / axis=x;
  text x=x1 y=obsid text=text / position=bottom contributeoffsets=none strip;
  yaxistable subgroup / location=inside position=left textgroup=id
    labelattrs=(size=7) textgroupid=text indentweight=indentWt;
  yaxistable countpct / location=inside position=left labelattrs=(size=7)
    valueattrs=(size=7);
  yaxistable PCIGroup group pvalue / location=inside position=right pad=(right=15px)
    labelattrs=(size=7) valueattrs=(size=7);
  yaxis reverse display=none colorbands=odd type=discrete colorbandsattrs=(transparency=1);
  xaxis display=(nolabel) values=(0.0 0.5 1.0 1.5 2.0 2.5);
  x2axis label='Hazard Ratio' display=(noline noticks novalues) labelattrs=(size=8);
run;
```

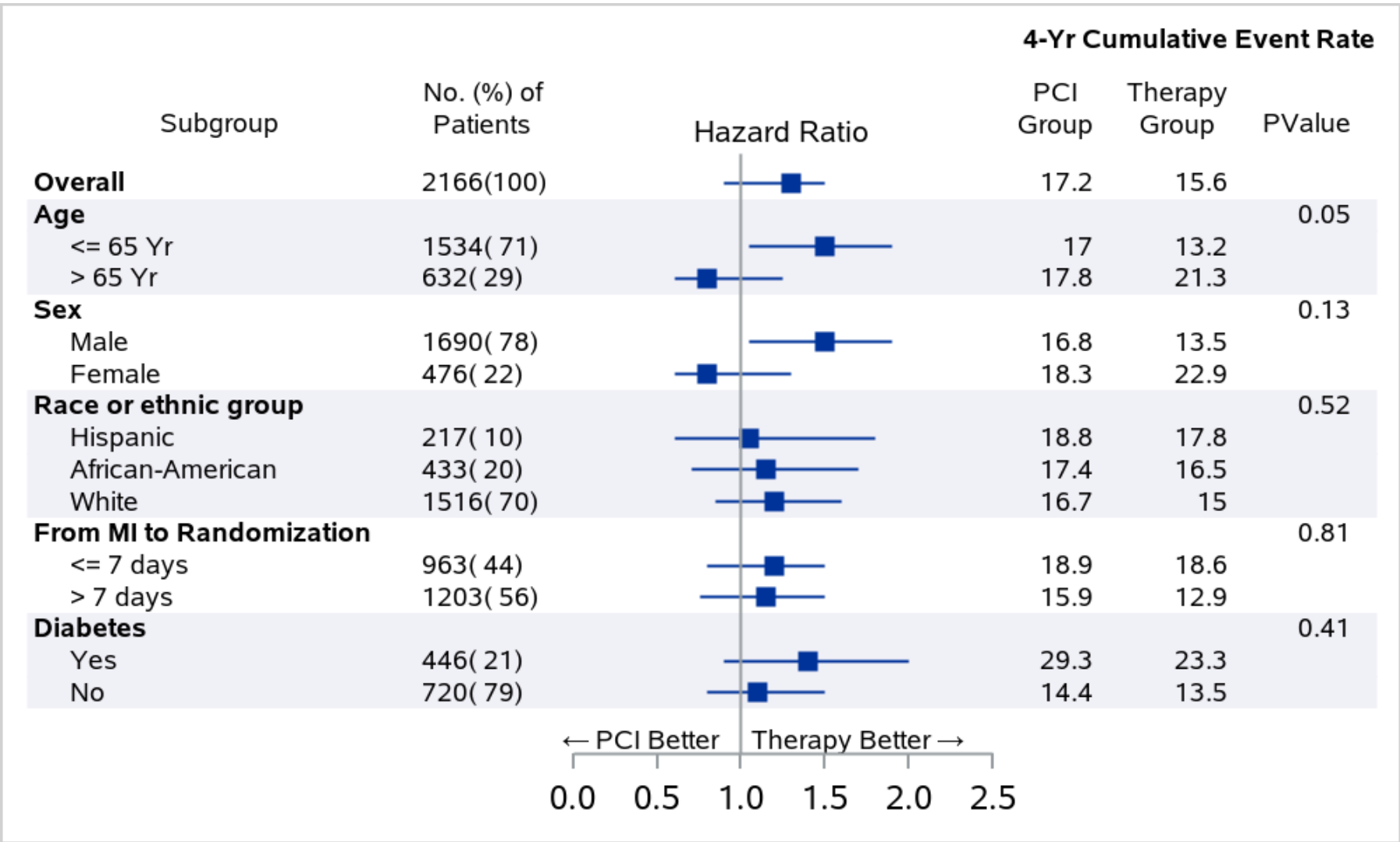
# Subgrouped Forest Plot

## Subgroup control

```
yaxistable subgroup / location=inside position=left textgroup=id  
labelattrs=(size=7) textgroupid=text indentweight=indentWt;
```

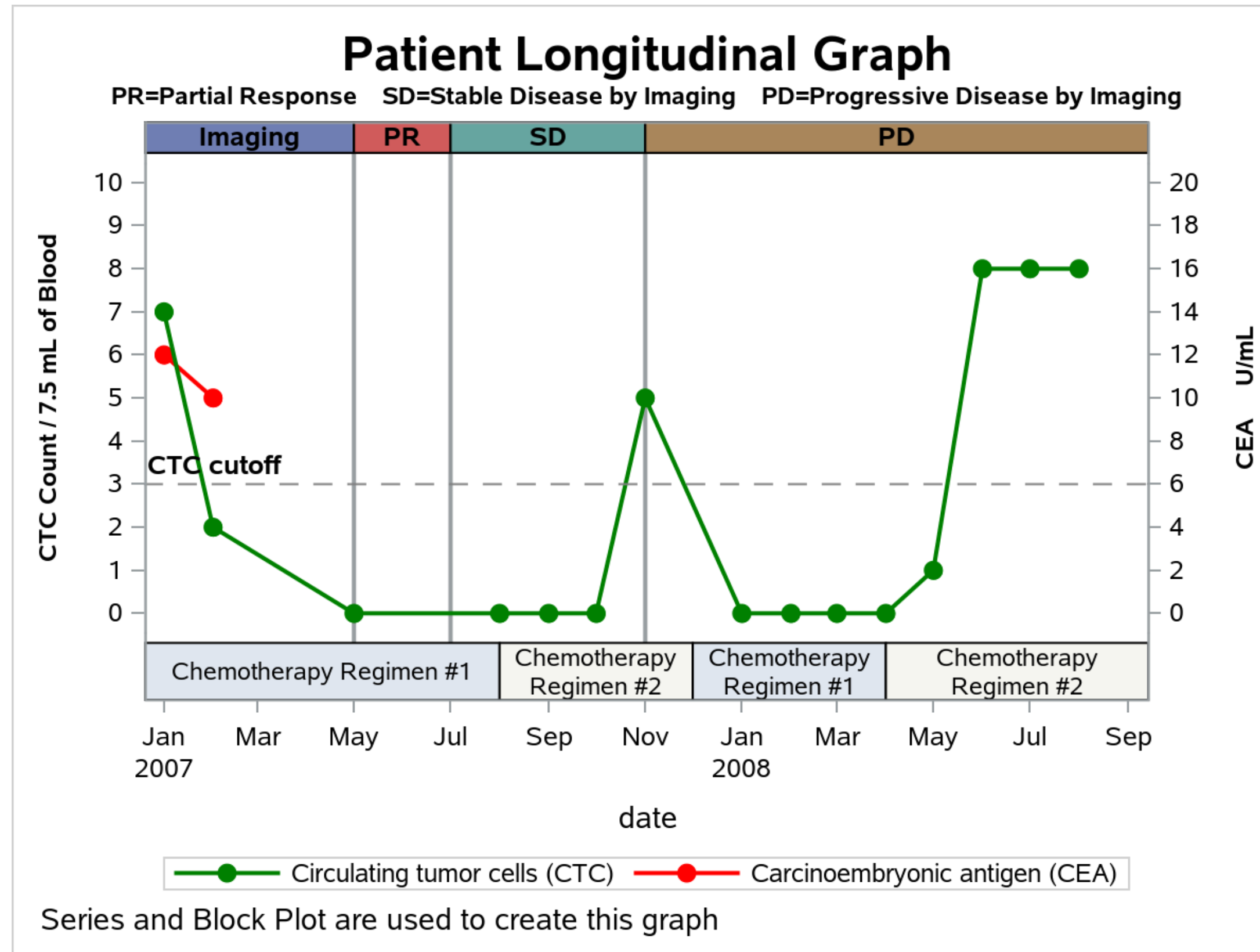
| <u>Id</u> | <u>Subgroup</u> | <u>IndentWt</u> | <u>ref</u> |
|-----------|-----------------|-----------------|------------|
| 1         | Overall         | 0               | .          |
| 1         | Age             | 0               | 2          |
| 2         | <= 65 Yr        | 1               | 3          |
| 2         | > 65 Yr         | 1               | 4          |

```
data attrmap;  
length textweight $10;  
id='text'; value='1'; textcolor='Black';  
textsize=7; textweight='bold'; output;  
id='text'; value='2'; textcolor='Black';  
textsize=5; textweight='normal'; output;  
run;
```





# Patient Longitudinal Graph



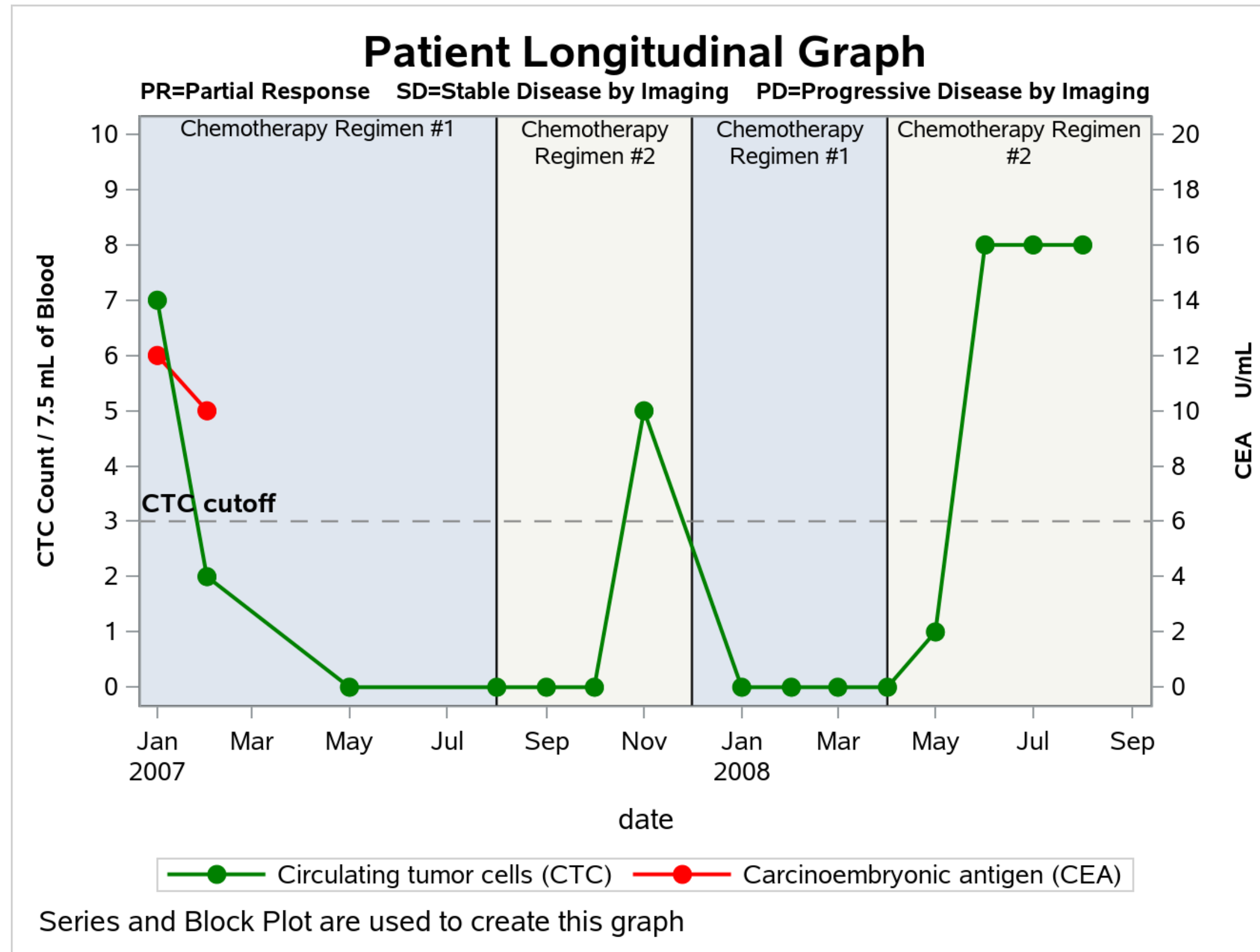


# Patient Longitudinal Graph

## Code

```
proc sgplot data=patlong;
block x=date block=blk / filltype=multicolor position=top valueattrs=(weight=bold )
    outline values nolabel;
block x=date block=therapy / filltype=alternate position=bottom
    valueattrs=(weight=normal size=8 ) outline fill values nolabel;
refline '01MAY07'd '01JUL07'd '01NOV07'd / axis=x lineattrs=(thickness=2 );
series x=date y=cea / lineattrs=(thickness=2 color=red) markers
    markerattrs=(size=9 color=red symbol=circlefilled) y2axis name="ser2"
    legendlabel="Carcinoembryonic antigen (CEA)";
series x=date y=ctc / lineattrs=(thickness=2 color=green) markers
    markerattrs=(size=9 color=green symbol=circlefilled) name="ser1"
    legendlabel="Circulating tumor cells (CTC)";
refline 3 / label="CTC cutoff" lineattrs=(pattern=dash color=gray)
    labelattrs=(weight=bold) labelpos=min labelloc=inside;
yaxis label="CTC Count / 7.5 mL of Blood" labelattrs=(weight=bold size=8)
    values=(0 to 10 by 1);
y2axis label="CEA      U/mL" labelattrs=(weight=bold size=8) values=(0 to 20 by 2);
xaxis display=(noline);
keylegend "ser1" "ser2" / location=outside border;
run;
```

# Background BLOCK Plot



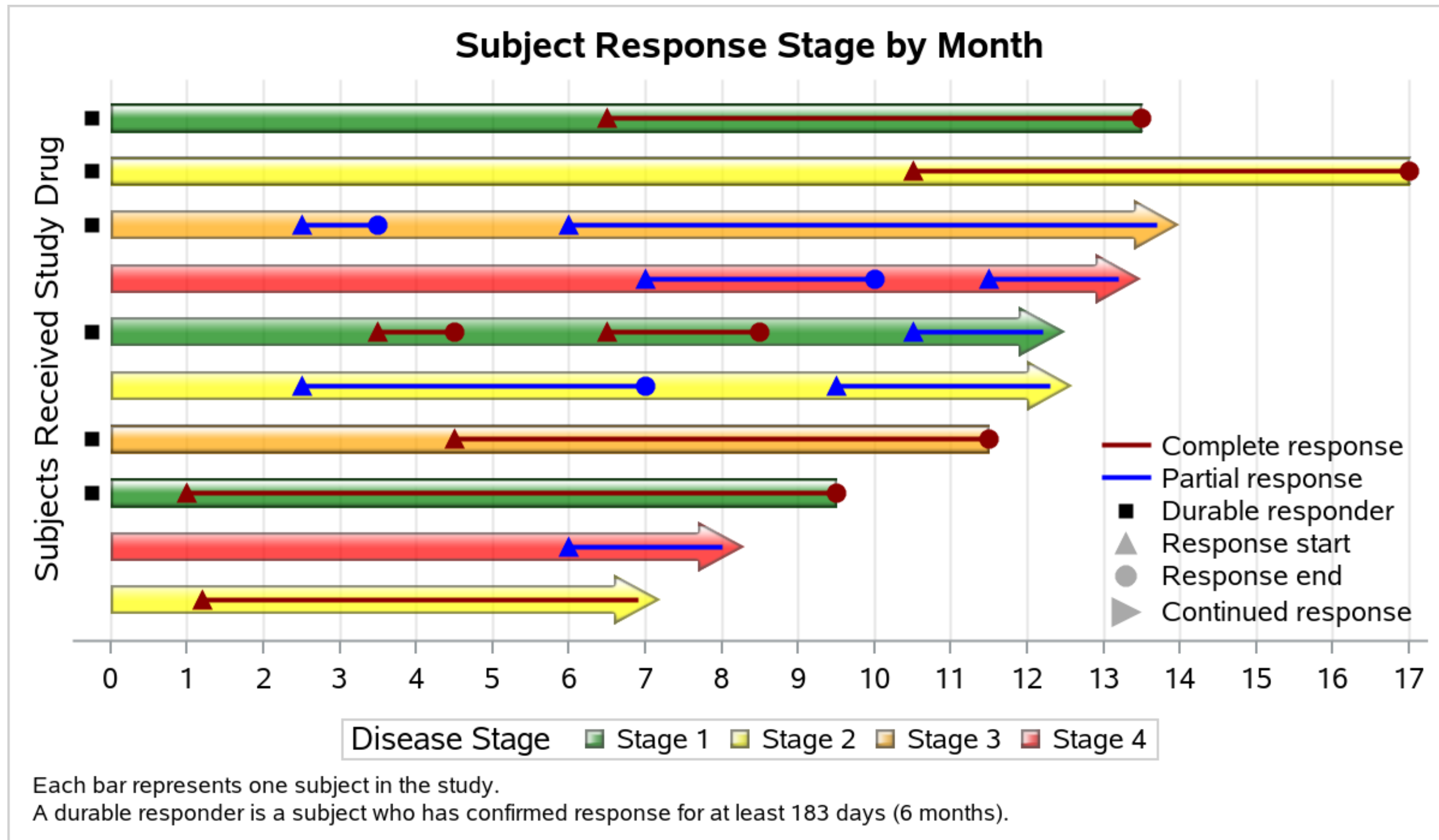


# Background BLOCK Plot

## Code

```
proc sgplot data=patlong;
block x=date block=therapy / filltype=alternate
    valueattrs=(weight=normal size=8 ) fill values nolabel;
series x=date y=cea / lineattrs=(thickness=2 color=red) markers
    markerattrs=(size=9 color=red symbol=circlefilled) y2axis
    name="ser2" legendlabel="Carcinoembryonic antigen (CEA)";
series x=date y=ctc / lineattrs=(thickness=2 color=green) markers
    markerattrs=(size=9 color=green symbol=circlefilled) name="ser1"
    legendlabel="Circulating tumor cells (CTC)";
refline 3 / label="CTC cutoff" lineattrs=(pattern=dash color=gray)
    labelattrs=(weight=bold) labelpos=min labelloc=inside;
yaxis label="CTC Count / 7.5 mL of Blood" labelattrs=(weight=bold size=8)
    values=(0 to 10 by 1);
y2axis label="CEA      U/mL" labelattrs=(weight=bold size=8)
    values=(0 to 20 by 2);
xaxis display=(noline);
keylegend "ser1" "ser2" / location=outside border;
run;
```

# Swimmer Plot



# Swimmer Plot

```
title 'Subject Response Stage by Month';
footnote J=1 h=0.8 'Each bar represents one subject in the study.';
footnote2 J=1 h=0.8 'A durable responder is a subject who has confirmed response for at least 183
days (6 months).';
proc sgplot data= swimmer datrmap=attrmap nocycleattrs noborder;
  highlow y=item low=low high=high / highcap=highcap type=bar group=stage fill nooutline
    dataskin=gloss lineattrs=(color=black) name='stage' barwidth=1 nomissinggroup
    transparency=0.3 attrid=stage;
  highlow y=item low=startline high=endline / group=status lineattrs=(thickness=2 pattern=solid)
    name='status' nomissinggroup attrid=status;
  scatter y=item x=durable / markerattrs=(symbol=squarefilled size=6 color=black) name='Durable'
    legendlabel='Durable responder';
  scatter y=item x=start / markerattrs=(symbol=trianglefilled size=8) group=status attrid=status;
  scatter y=item x=end / markerattrs=(symbol=circlefilled size=8) group=status attrid=status;
  legenditem type=marker name='ResStart' / markerattrs=(symbol=trianglefilled color=darkgray size=9)
    label='Response start';
  legenditem type=marker name='ResEnd' / markerattrs=(symbol=circlefilled color=darkgray size=9)
    label='Response end';
  legenditem type=marker name='RightArrow' / markerattrs=(symbol=trianglerightfilled
    color=darkgray size=12) label='Continued response';
  xaxis display=(nolabel) values=(0 to 20 by 1) valueshint grid;
  yaxis reverse display=(noticks novalues noline) label='Subjects Received Study Drug' min=1;
  keylegend 'stage' / title='Disease Stage';
  keylegend 'status' 'Durable' 'ResStart' 'ResEnd' 'RightArrow' /
    noborder location=inside position=bottomright across=1 linelength=20;
run;
```

# Conclusion

- Remember the steps
  - Identify
  - Order
  - Add
- Think “out-of-the-box”
  - Creative use of plots
  - Annotation
- Attribute maps

# Questions?

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# Thank you for coming!

Dan.Heath@sas.com

