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/*****
/* To produce a more graphical plot, use GPLOT statement */
*****/

options ls=80;
libname amy '.';

/*using SYMBOL statement to assign different symbols for original data
from different treatment groups */

symbol1 color=black value=star interpol=none;
symbol2 color=red value=circle interpol=none;
symbol3 color=green value=dot interpol=none;
symbol4 color=blue value=square interpol=none;

/*using GOPTIONS to create the output in pdf file */

goptions device=pdfc gsfmode=append gsfname=grafout;
  filename grafout 'all_glm.pdf';
data amy.all_treat;
  set amy.allgene;
  if treat ne ' ';

/*creating a SAS data set called "bygene" to run the same program for
different genes instead of writing different SAS files */

data bygene;
  set amy.all_treat;
  expression = arg1;
  gene='Arg1  ';
  output;
  expression = arg2;
  gene='Arg2  ';
  output;
  expression = vcaml;
  gene='Vcaml  ';
  output;
  expression = pglyrp;
  gene='Pglyrp  ';
  output;
  expression = ccl8;
  gene='Ccl8  ';
  output;
  expression = gatm;
  gene='Gatm  ';
  output;
  expression = scycial1;
  gene='Scycial1';
  output;
  expression = chia;
  gene='Chia  ';
  output;
  expression = chi313;
  gene='Chi313  ';
  output;
  expression = ccla3;

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    gene='Ccla3      ';
    output;
proc sort data=bygene;
    by gene treat;
run;

/*ploting target genes vs housekeeping genes from different treatment
group using GPLOT statement */

proc gplot data=amy.all_treat;
    plot arg1*g6pt1=treat arg2*g6pt1=treat vcaml*g6pt1=treat
pglyrp*g6pt1=treat ccl8*g6pt1=treat gatm*g6pt1=treat
scycial1*g6pt1=treat chia*g6pt1=treat chi313*g6pt1=treat
ccla3*g6pt1=treat;
run;

/*using GLM statement to fit the data with general linear models such
as regression, producing a predicted data set "pred" */

proc glm data=bygene;
    class treat;
    model expression = g6pt1 treat/solution ss3;
    output out=outpred p=pred;
    by gene;
run;
proc sort data=outpred;
    by gene treat pred;
run;

/*using ORDER statement to change the tick marks of the graphs, and
using HSIZE and VSIZE to change the size of the graph */

axis1 label=none order=(14 16 18 20 22 24 26 28 30 32 34);
axis2 order=(14 16 18 20 22 24 26 28 30 32 34);
goptions hsize=6in vsize=6in;

/*using SYMBOL statement to assign different symbols for predicted data
from different treatment groups */

symbol5 color=black interpol=join line=1;
symbol6 color=red interpol=join line=3;
symbol7 color=green interpol=join line=5;
symbol8 color=blue interpol=join line=7;
run;

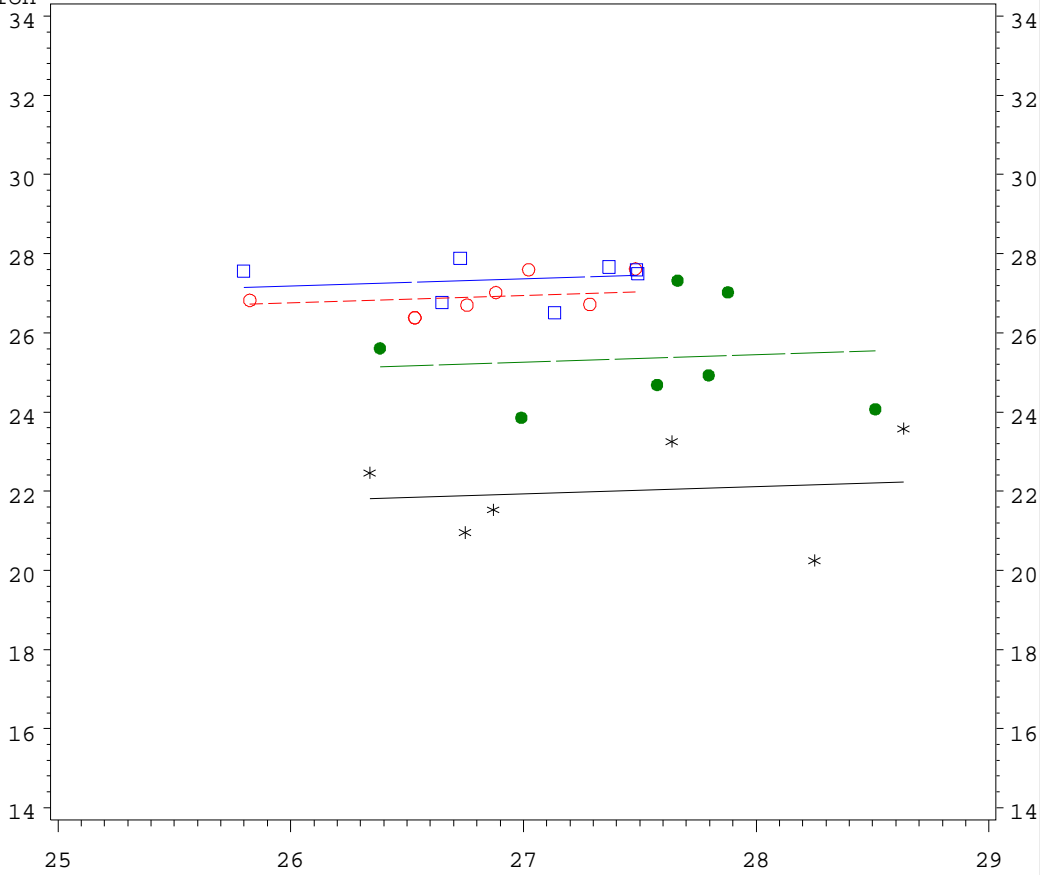
/*ploting the predicted and original data on the same graph */

proc gplot data=outpred;
    plot expression*g6pt1=treat/vaxis=axis2;
    plot2 pred*g6pt1=treat/vaxis=axis1;
    by gene;
run;

```

gene=Arg1

expression

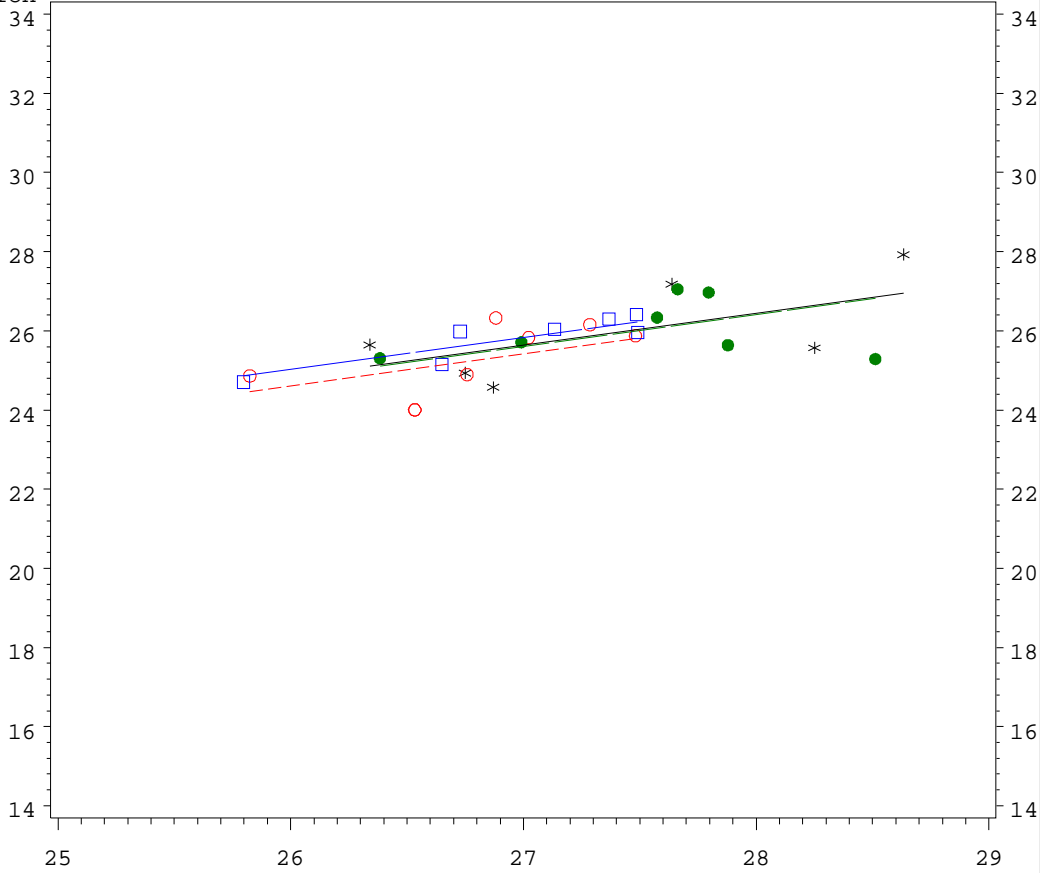


treat — OA - - - OAc - - - TMA — TMAc

treat * * * OA ○ ○ ○ OAc ● ● ● TMA □ □ □ TMAc

gene=Arg2

expression

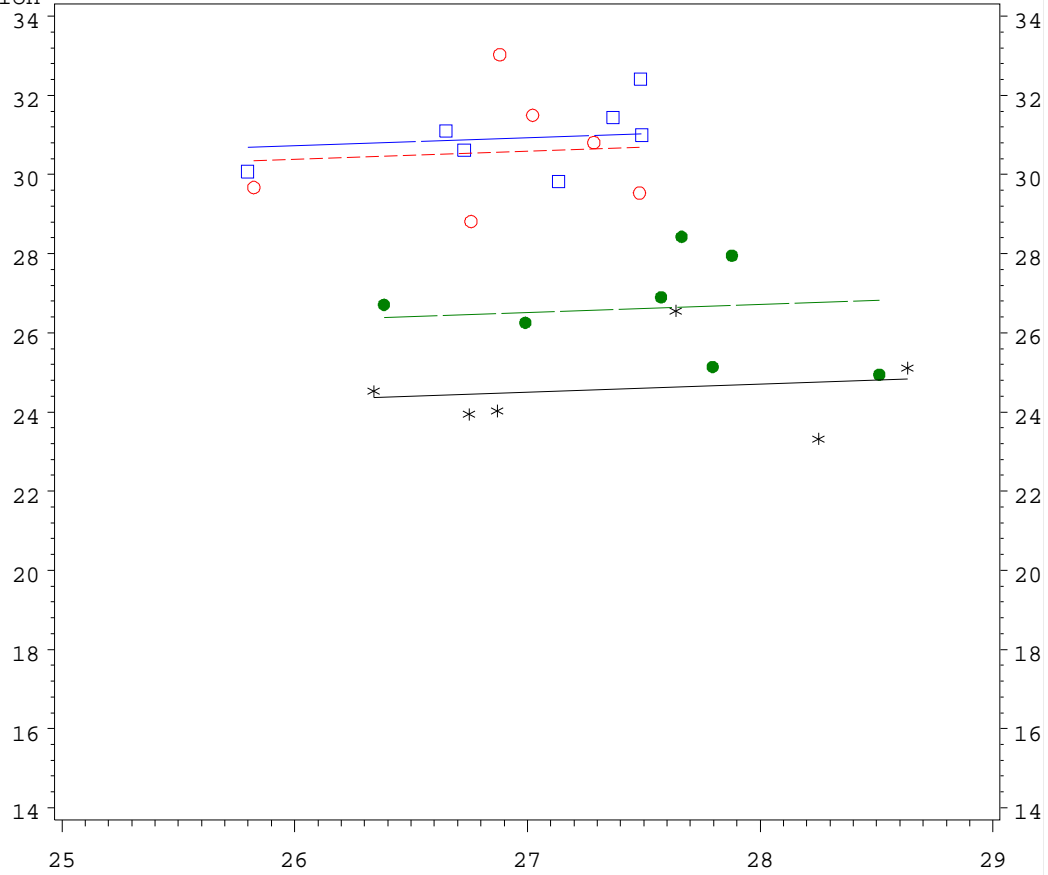


treat — OA - - - OAc — TMA — TMAc

treat * * * OA ○ ○ ○ OAc ● ● ● TMA □ □ □ TMAc

gene=Ccl8

expression

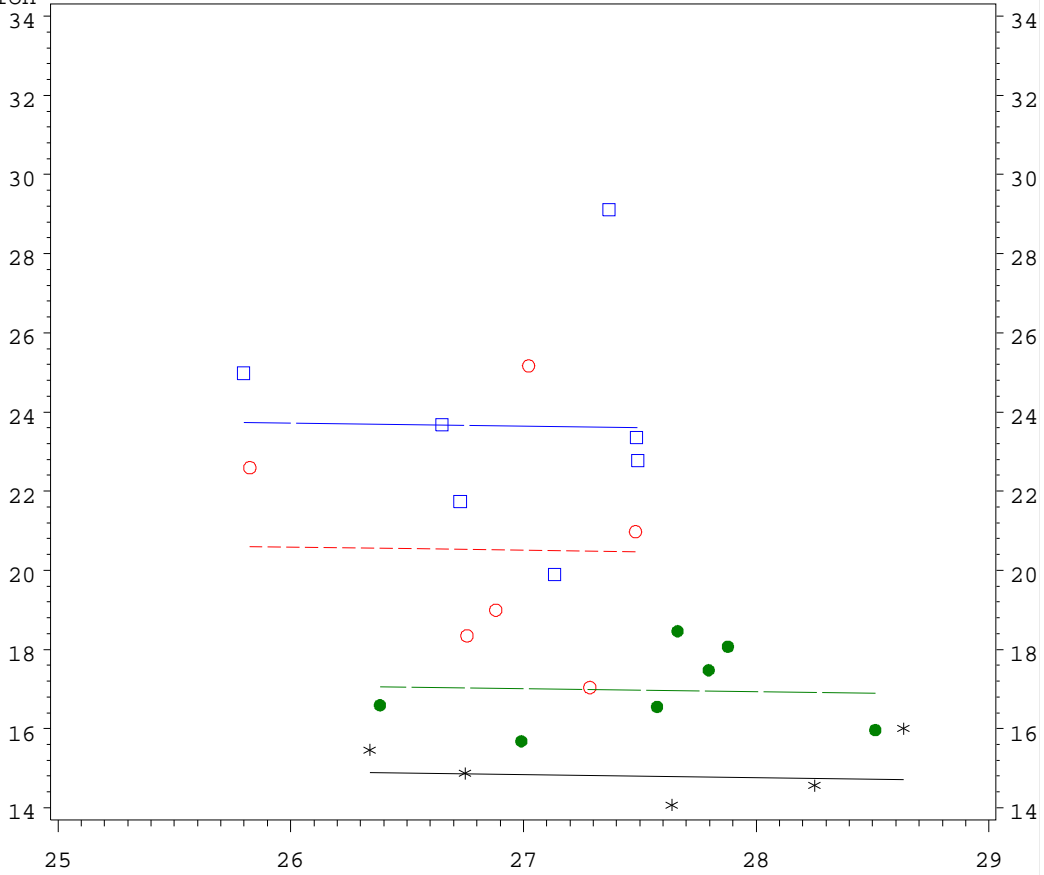


treat — OA - - - OAc - - - TMA — TMAc

treat * * * OA ○ ○ ○ OAc ● ● ● TMA □ □ □ TMAc

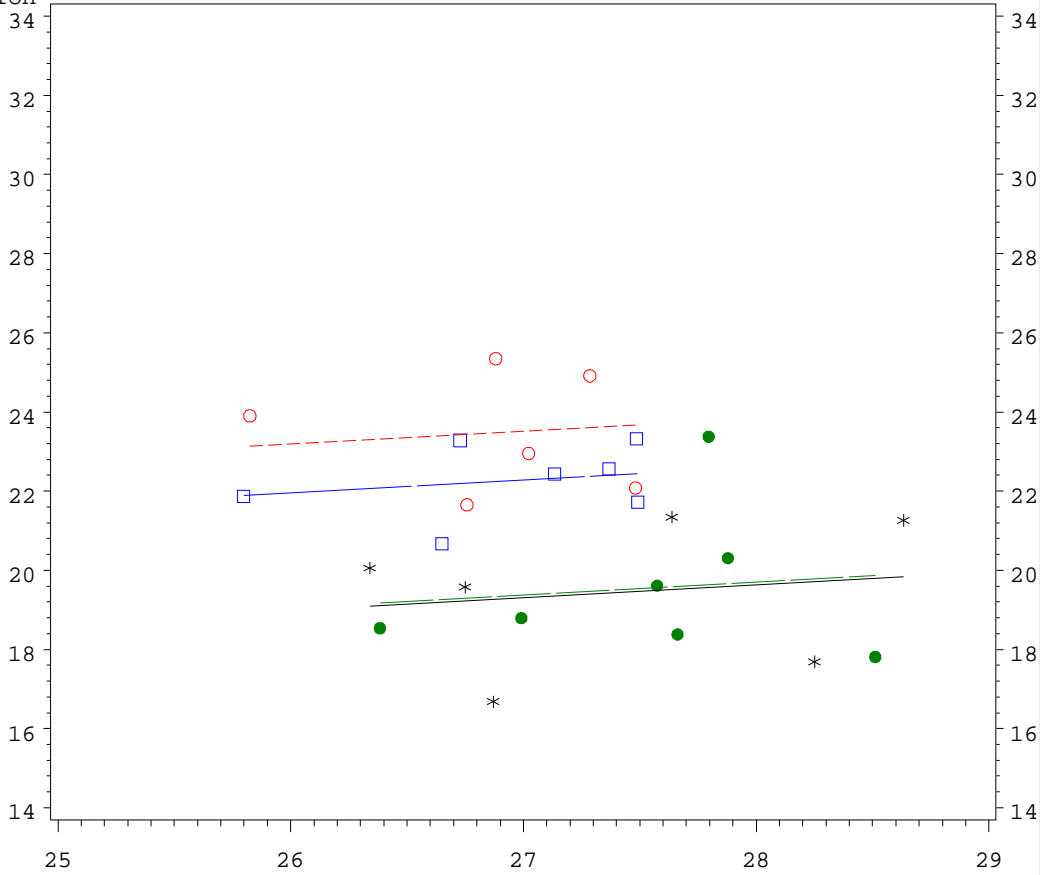
gene=Ccl3

expression



gene=Chi313

expression

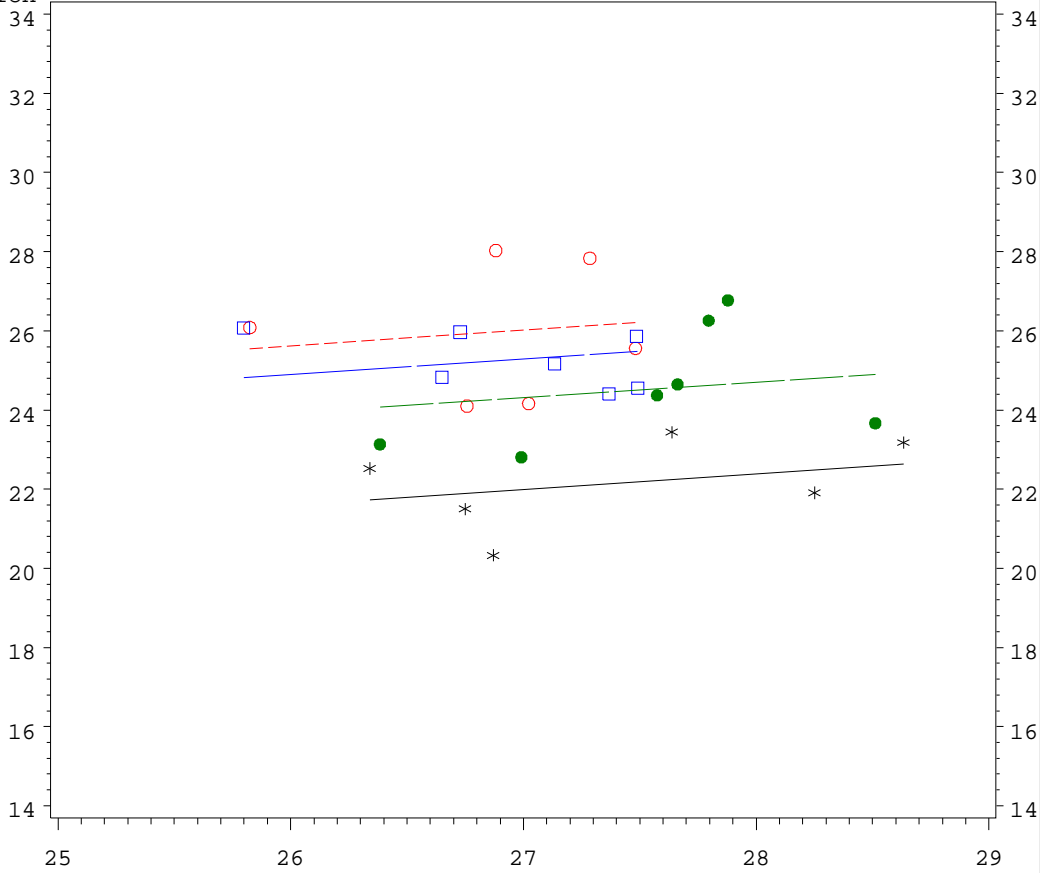


treat — OA - - - OAc — TMA — TMAc

treat * * * OA ○ ○ ○ OAc ● ● ● TMA □ □ □ TMAc

gene=Chia

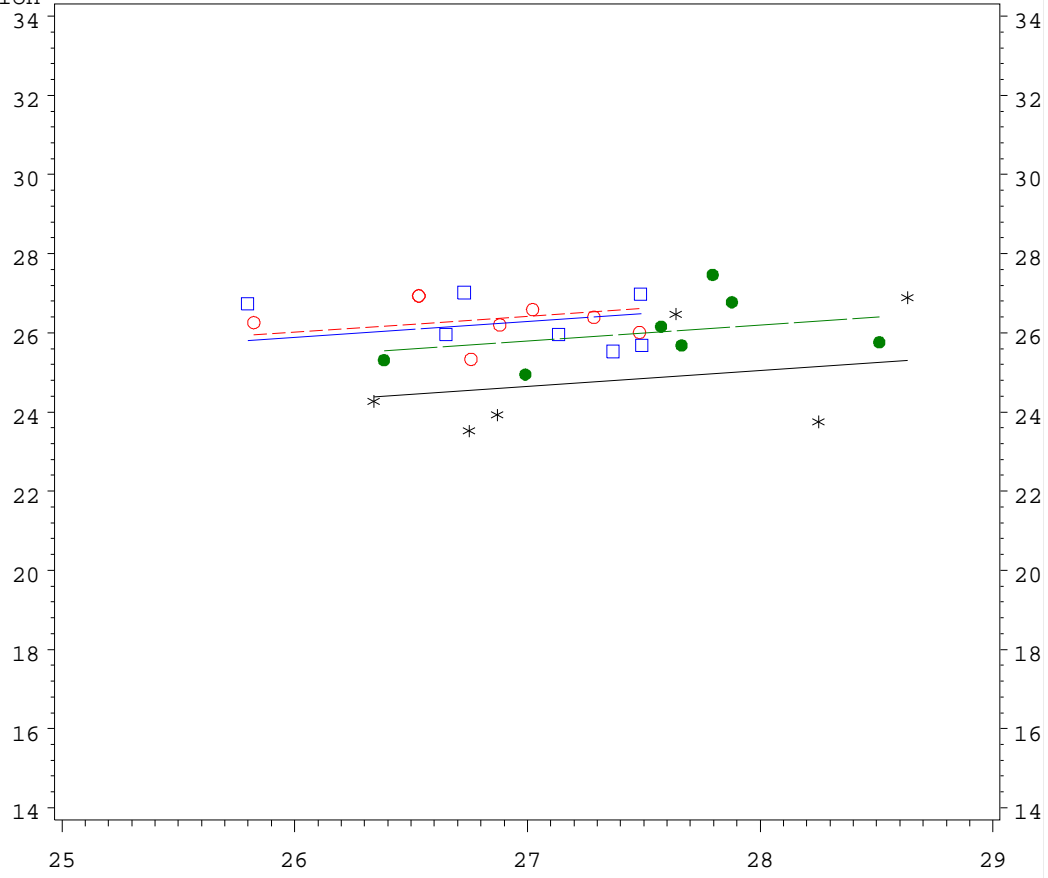
expression



treat — OA - - - OAc - - - TMA — TMAc
treat * * * OA ○ ○ ○ OAc ● ● ● TMA □ □ □ TMAc

gene=Gatm

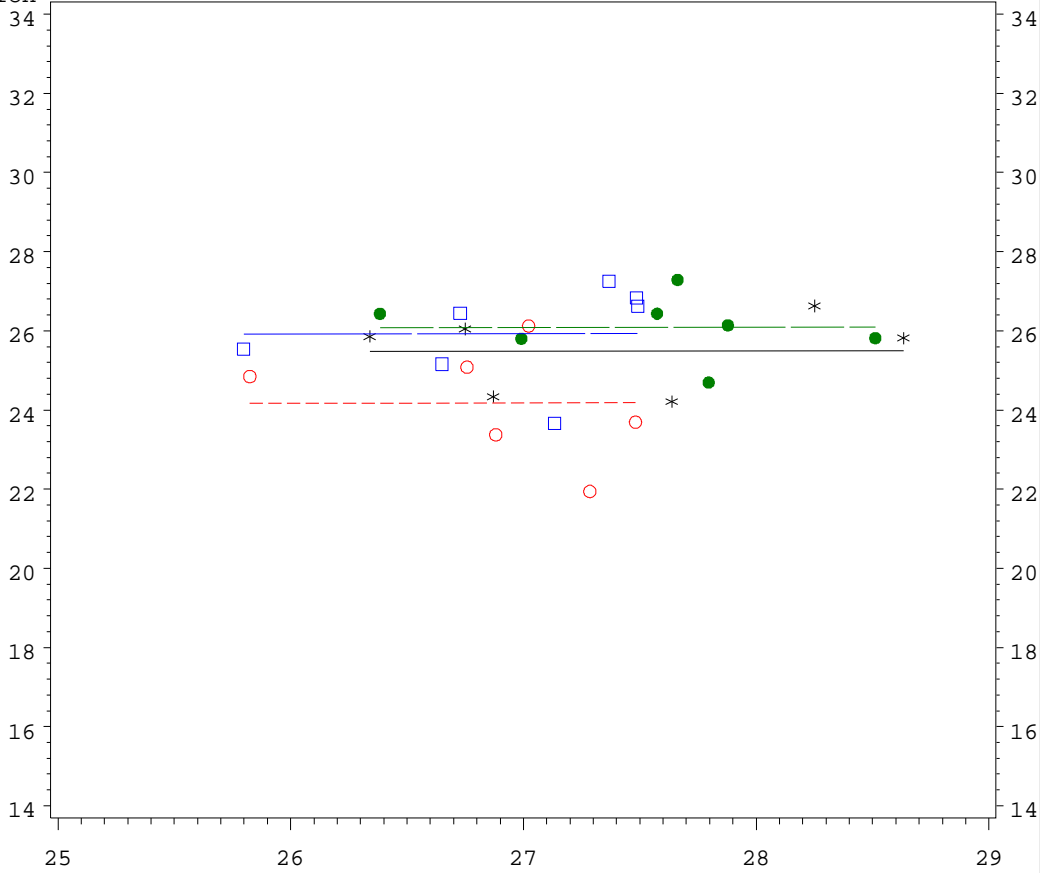
expression



treat — OA - - - OAc - - - TMA — TMAc
treat * * * OA ○ ○ ○ OAc ● ● ● TMA □ □ □ TMAc

gene=Pglyrp

expression

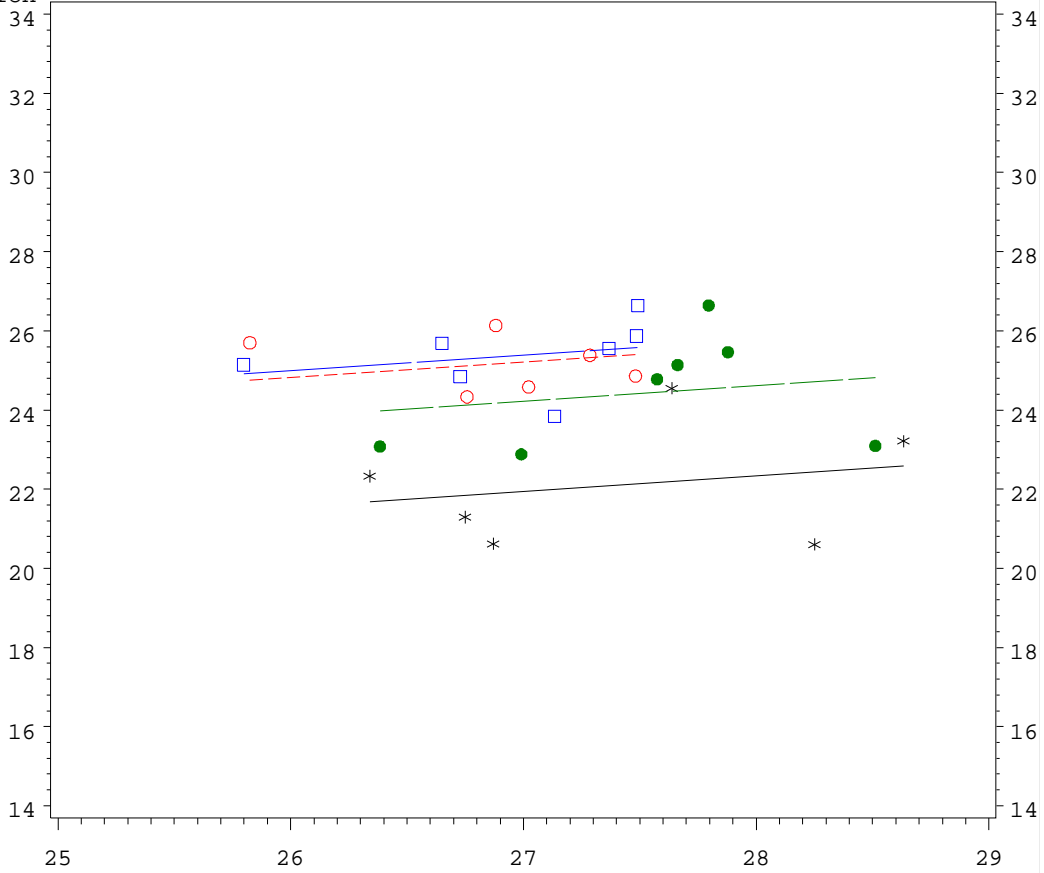


treat — OA - - - OAc - - - TMA — TMAc

treat * * * OA ○ ○ ○ OAc ● ● ● TMA □ □ □ TMAc

gene=Scycia11

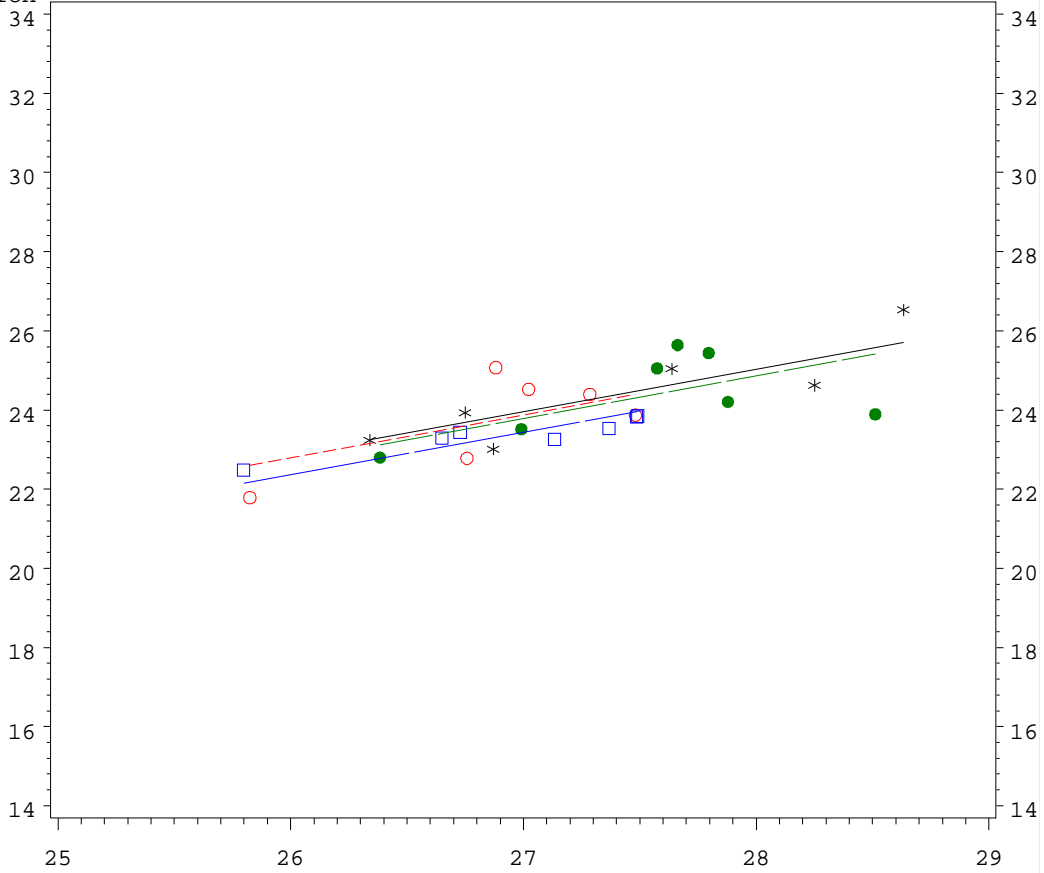
expression



treat — OA - - - OAc - - - TMA — TMAc
treat * * * OA ○ ○ ○ OAc ● ● ● TMA □ □ □ TMAc

gene=Vcam1

expression



treat — OA - - - OAc - - - TMA — TMAc

treat * * * OA ○ ○ ○ OAc ● ● ● TMA □ □ □ TMAc