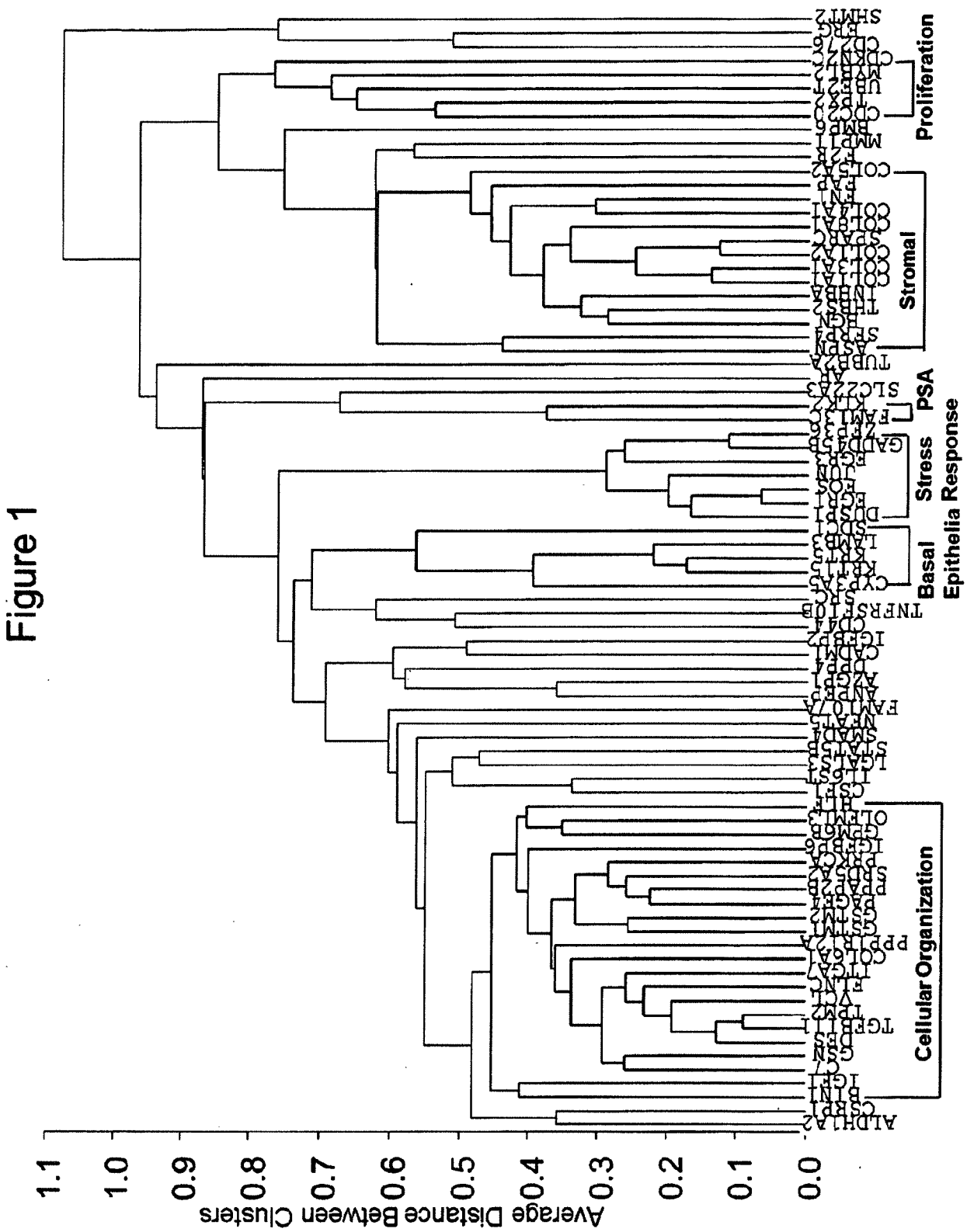


Figure 1
Average Distance Between Clusters
1.1
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Cellular Organization
Basal
Stress
PSA
Stromal
Proliferation
Epithelia Response

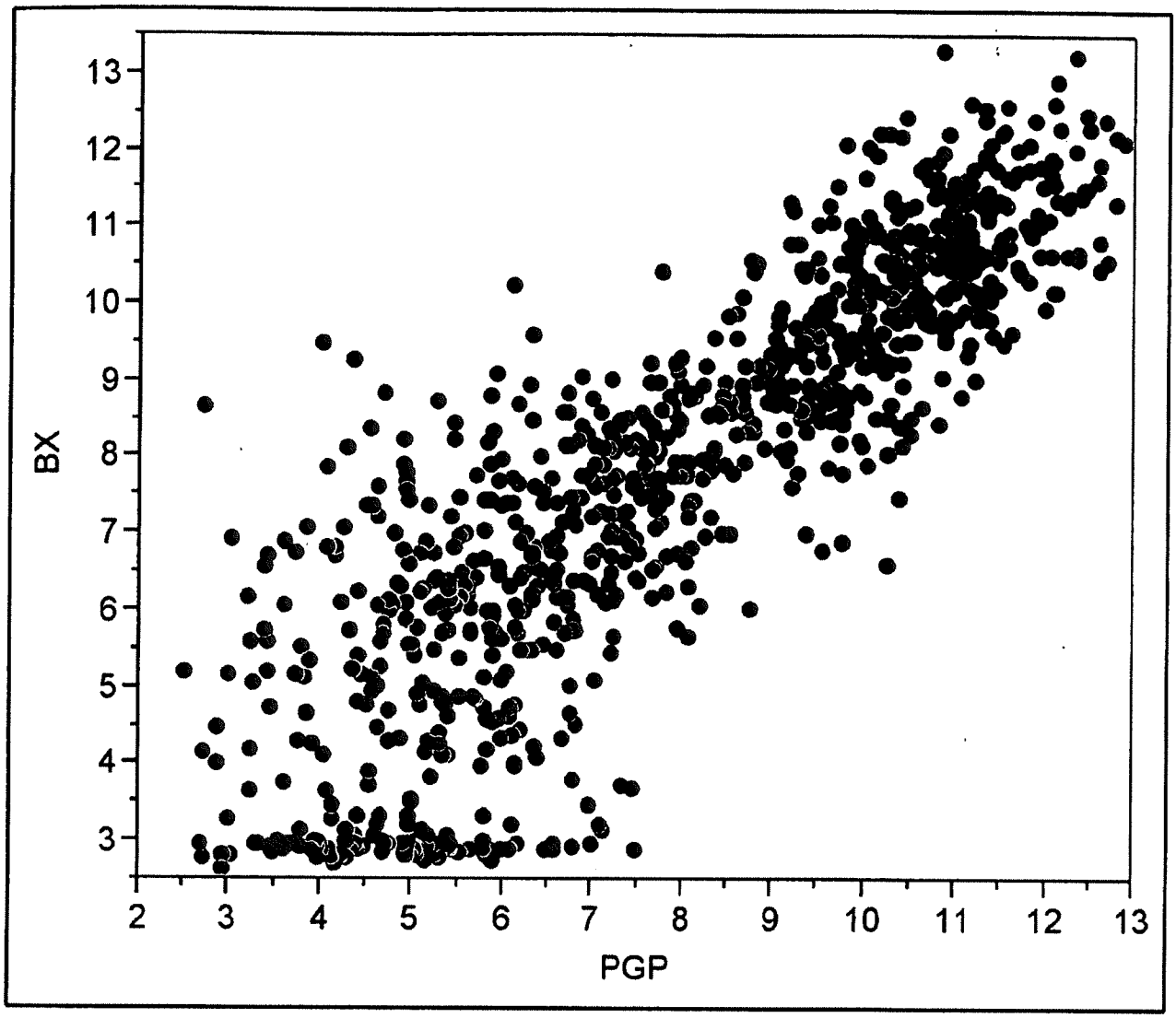


FIG. 2A

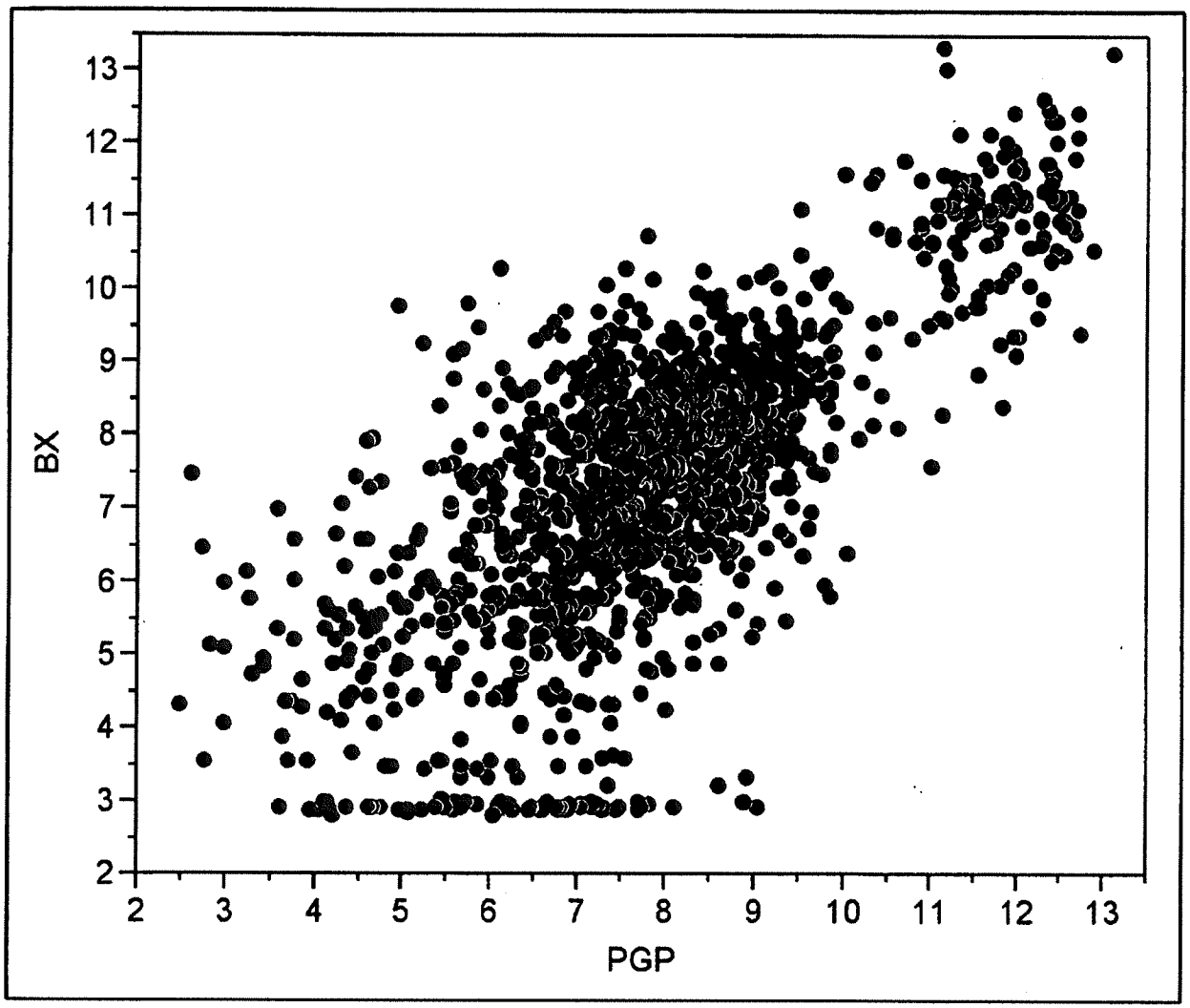


FIG. 2B

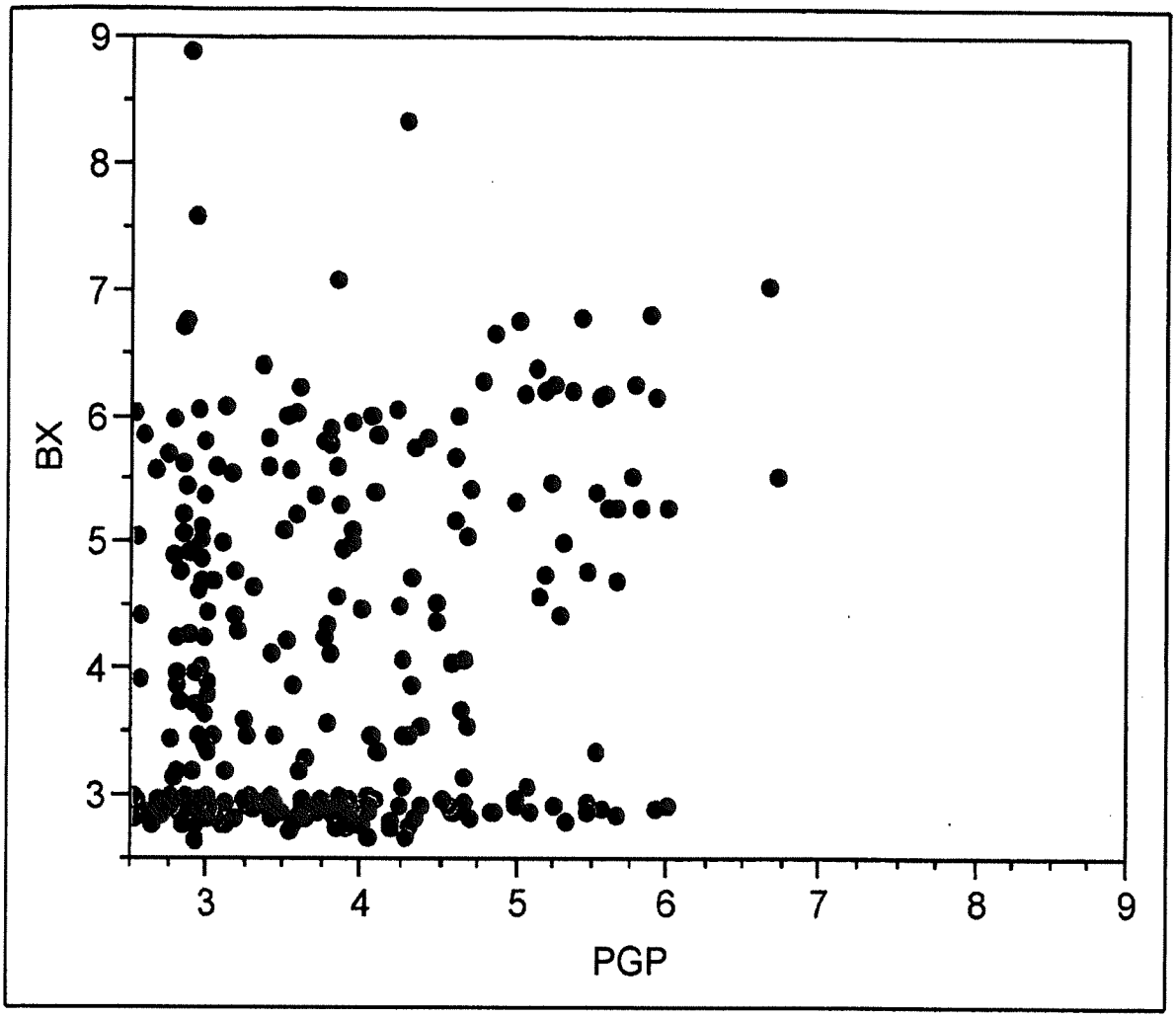


FIG. 2C

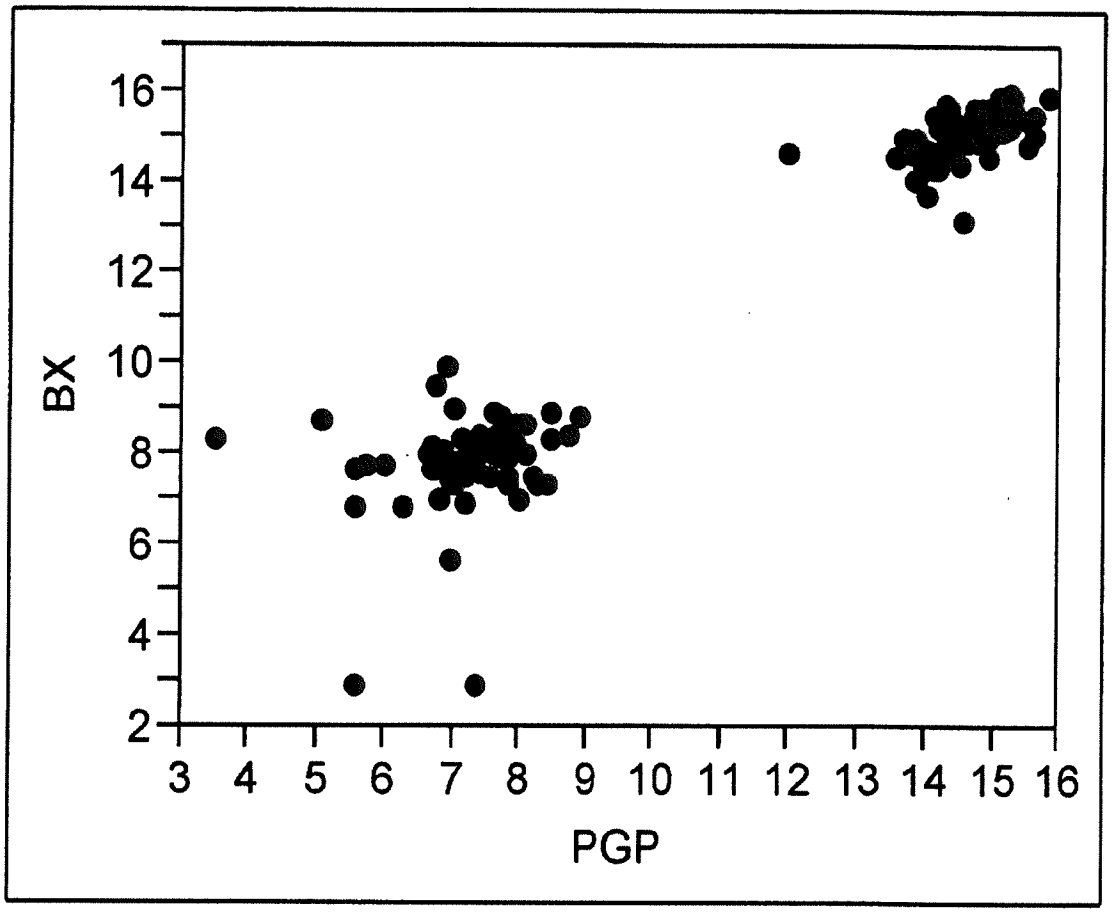


FIG. 2D

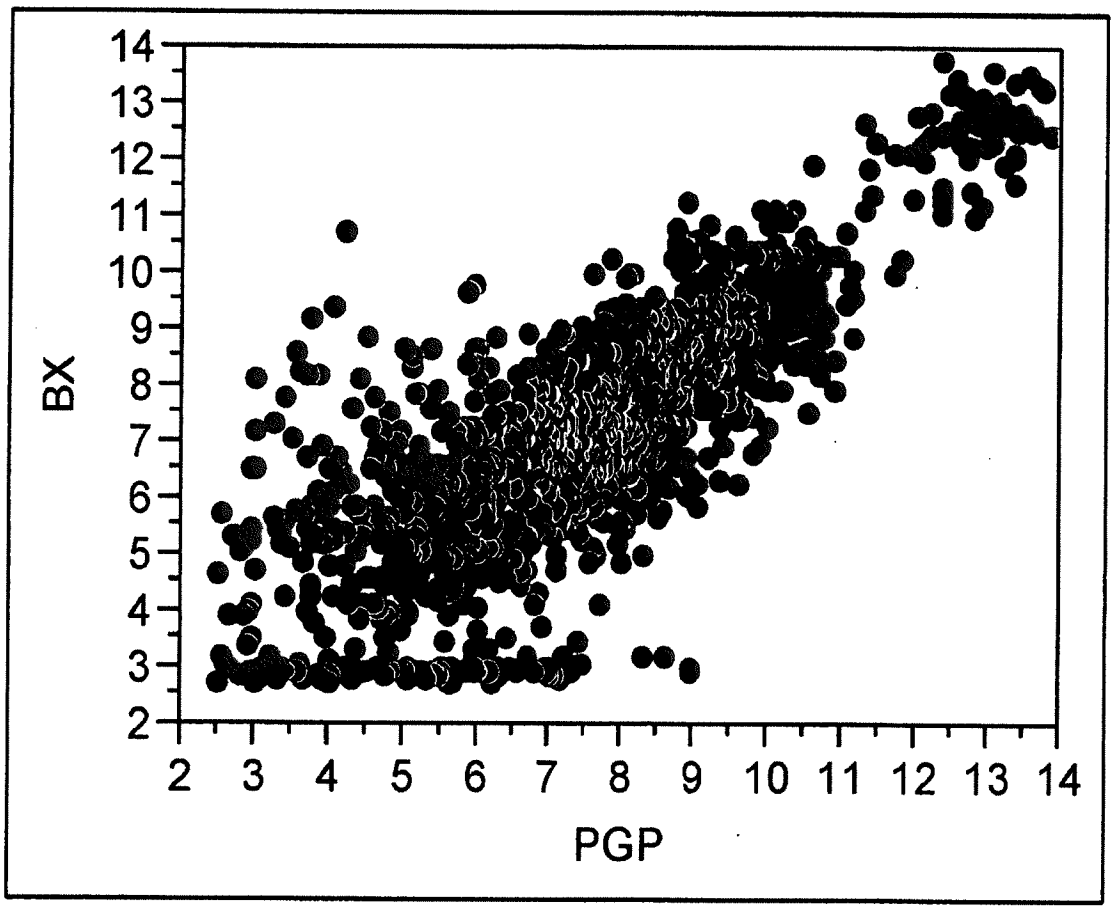


FIG. 2E

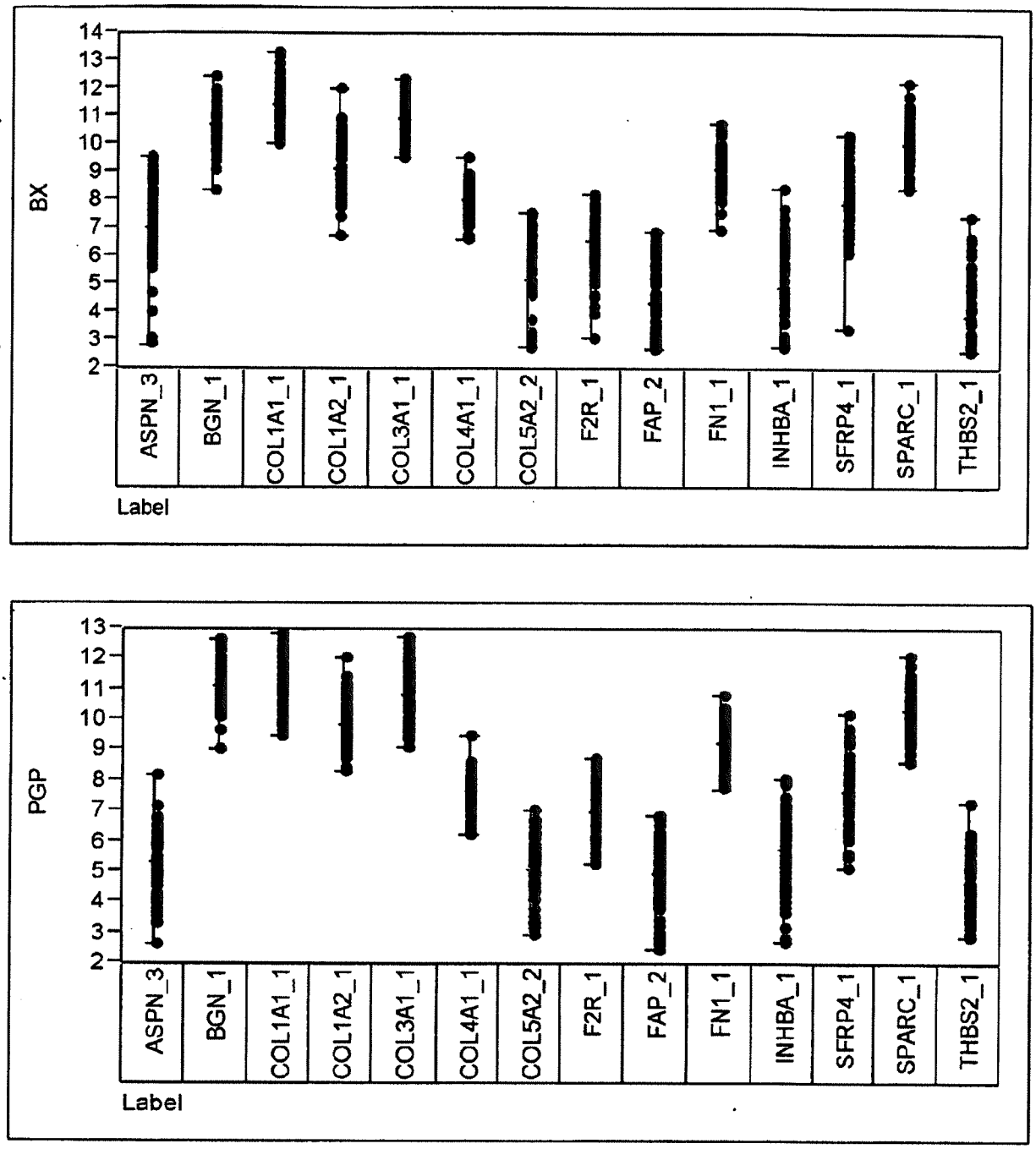
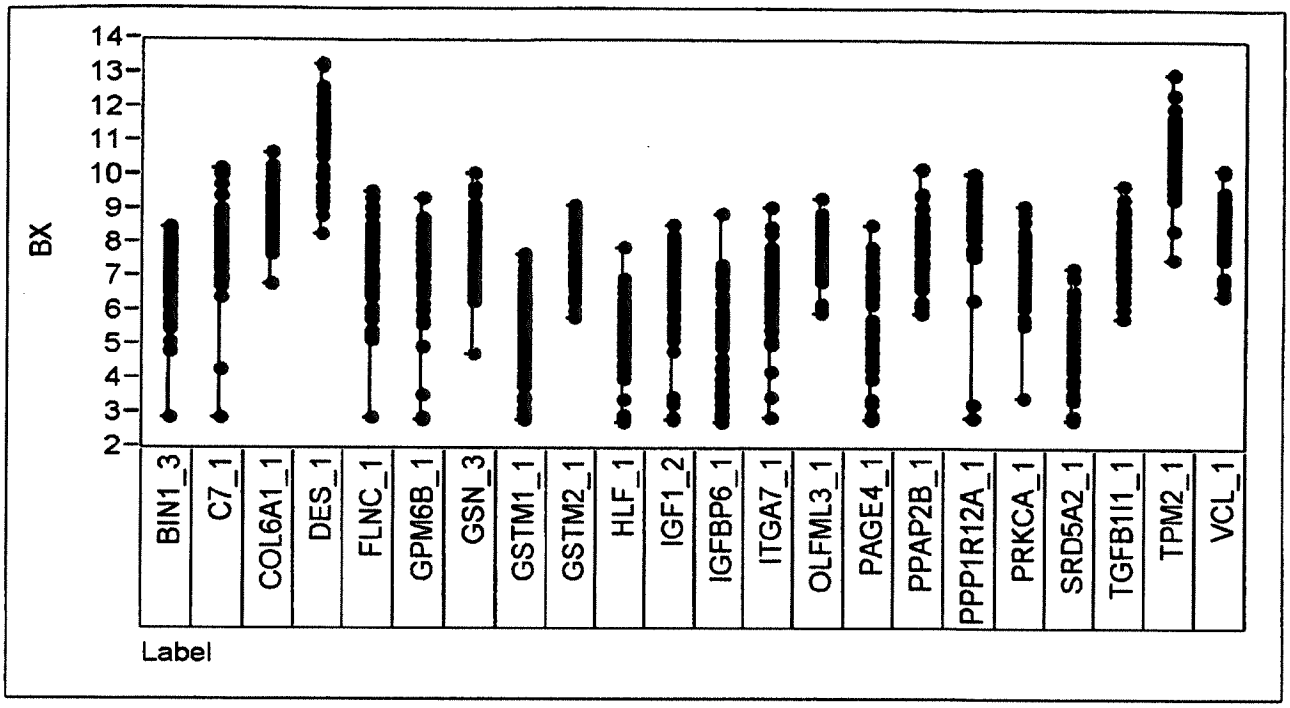

BX
14
13
12
11
10
9
8
7
6
5
4
3
2
ASPN_3
BGN_1
COL1A1_1
COL1A2_1
COL3A1_1
COL4A1_1
COL5A2_2
F2R_1
FAP_2
FN1_1
INHBA_1
SFRP4_1
SPARC_1
THBS2_1
Label
PGP
13
12
11
10
9
8
7
6
5
4
3
2
ASPN_3
BGN_1
COL1A1_1
COL1A2_1
COL3A1_1
COL4A1_1
COL5A2_2
F2R_1
FAP_2
FN1_1
INHBA_1
SFRP4_1
SPARC_1
THBS2_1
Label

FIG. 3A


BX
14
13
12
11
10
9
8
7
6
5
4
3
2
BIN1_3
C7_1
COL6A1_1
DES_1
FLNC_1
GPM6B_1
GSN_3
GSTM1_1
GSTM2_1
HLF_1
IGF1_2
IGFBP6_1
ITGA7_1
OLFML3_1
PAGE4_1
PPAP2B_1
PPP1R12A_1
PRKCA_1
SRD5A2_1
TGFB1I1_1
TPM2_1
VCL_1
Label

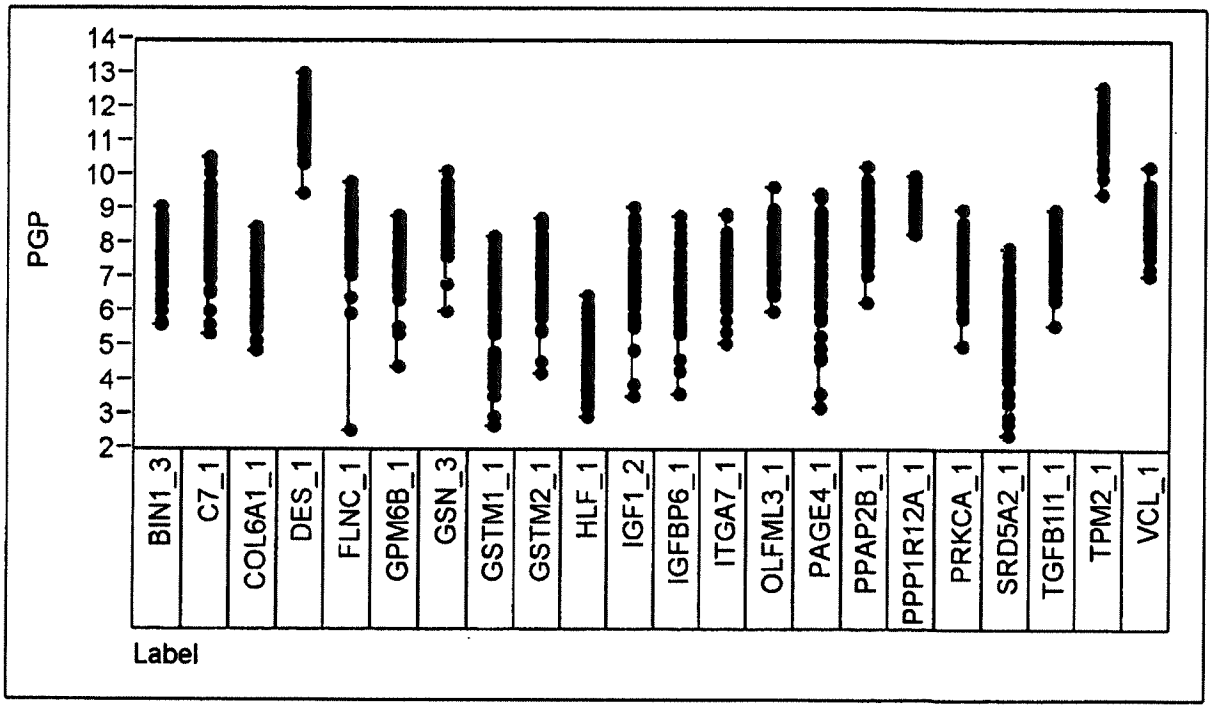
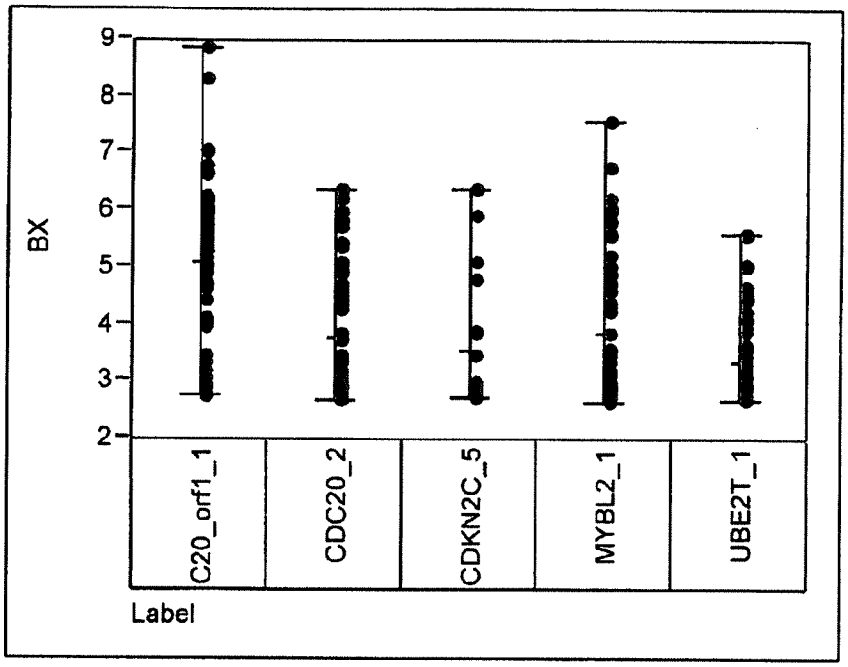

PGP
14
13
12
11
10
9
8
7
6
5
4
3
2
BIN1_3
C7_1
COL6A1_1
DES_1
FLNC_1
GPM6B_1
GSN_3
GSTM1_1
GSTM2_1
HLF_1
IGF1_2
IGFBP6_1
ITGA7_1
OLFML3_1
PAGE4_1
PPAP2B_1
PPP1R12A_1
PRKCA_1
SRD5A2_1
TGFB1I1_1
TPM2_1
VCL_1
Label

FIG. 3B


BX
9
8
7
6
5
4
3
2
C20_orf1_1
CDC20_2
CDKN2C_5
MYBL2_1
UBE2T_1
Label

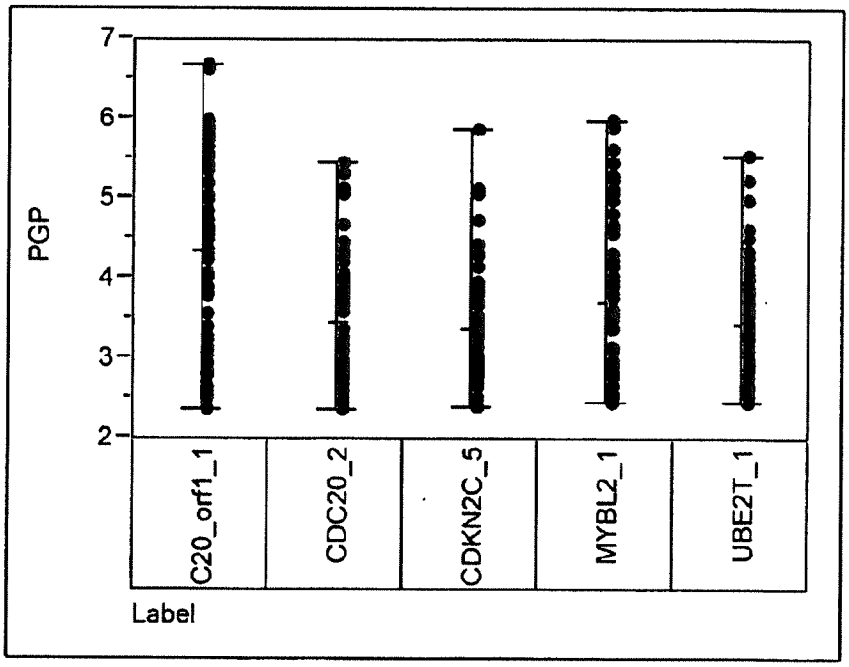
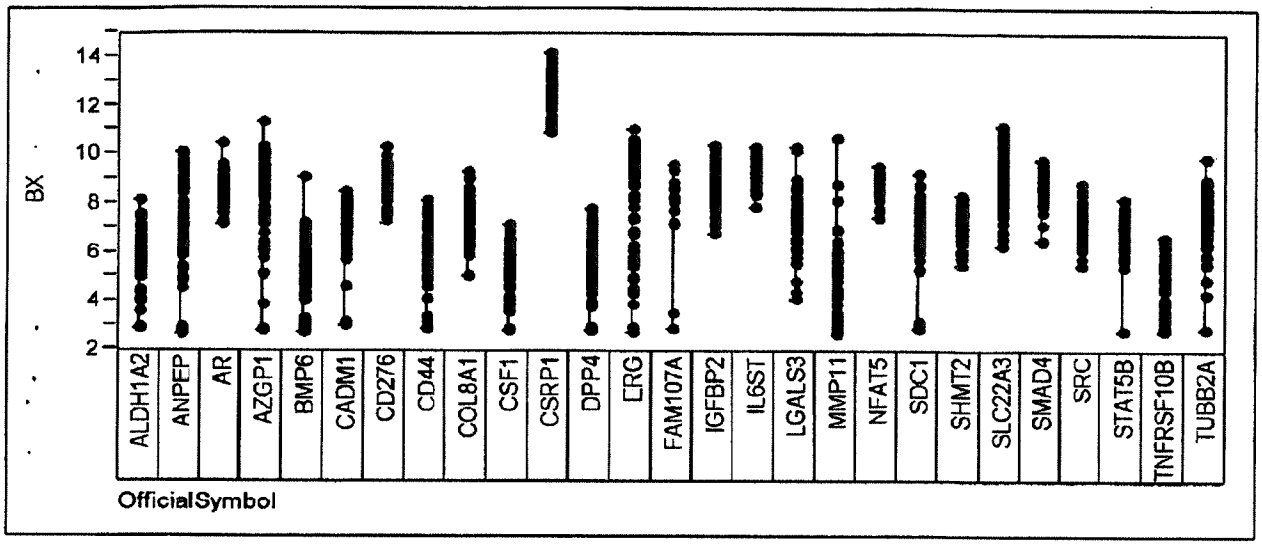

PGP
7
6
5
4
3
2
C20_orf1_1
CDC20_2
CDKN2C_5
MYBL2_1
UBE2T_1
Label

FIG. 3C


BX
14
12
10
8
6
4
2
ALDH1A2
ANPEP
AR
AZGP1
BMP6
CADM1
CD276
CD44
COL8A1
CSF1
CSRP1
DPP4
ERG
FAM107A
IGFBP2
IL6ST
LGALS3
MMP11
NFAT5
SDC1
SHMT2
SLC22A3
SMAD4
SRC
STAT5B
TNFRSF10B
TUBB2A
OfficialSymbol

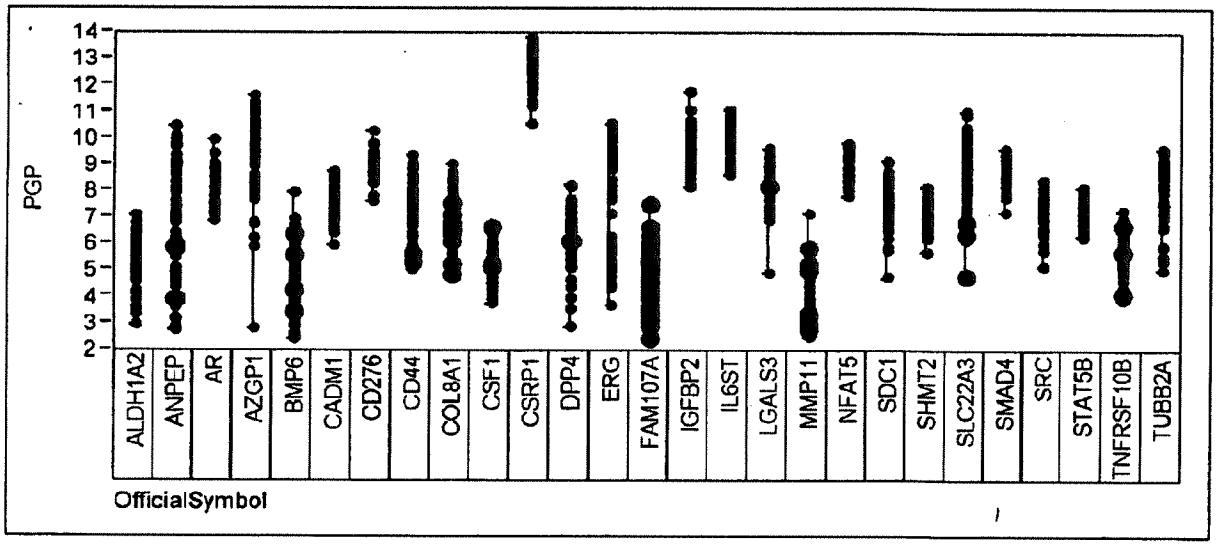

PGP
14
13
12
11
10
9
8
7
6
5
4
3
2
ALDH1A2
ANPEP
AR
AZGP1
BMP6
CADM1
CD276
CD44
COL8A1
CSF1
CSRP1
DPP4
ERG
FAM107A
IGFBP2
IL6ST
LGALS3
MMP11
NFAT5
SDC1
SHMT2
SLC22A3
SMAD4
SRC
STAT5B
TNFRSF10B
TUBB2A
OfficialSymbol

FIG. 3D

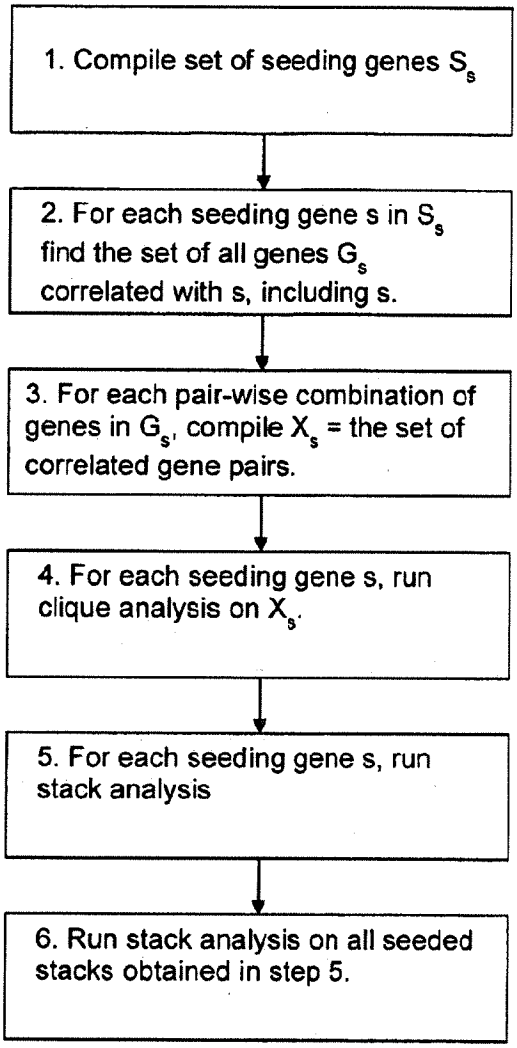

1. Compile set of seeding genes S_s
2. For each seeding gene s in S_s find the set of all genes G_s correlated with s, including s.
3. For each pair-wise combination of genes in G_s, compile X_s = the set of correlated gene pairs.
4. For each seeding gene s, run clique analysis on X_s.
5. For each seeding gene s, run stack analysis
6. Run stack analysis on all seeded stacks obtained in step 5.

Figure 4

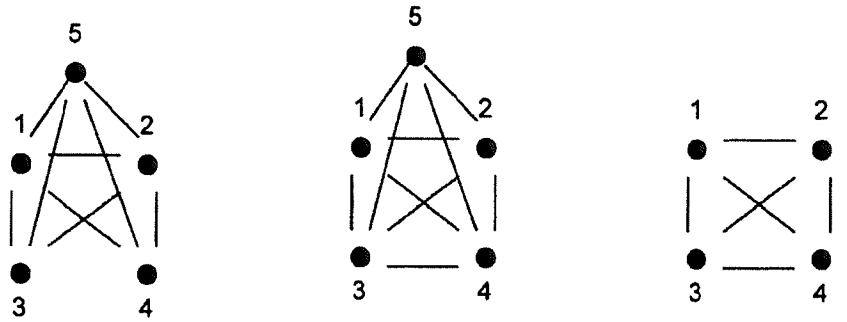


Figure 5

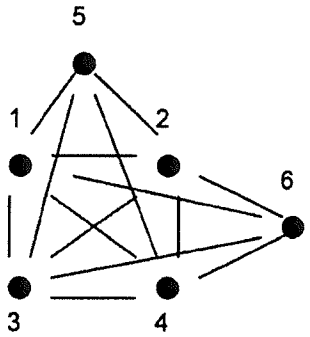


Figure 6

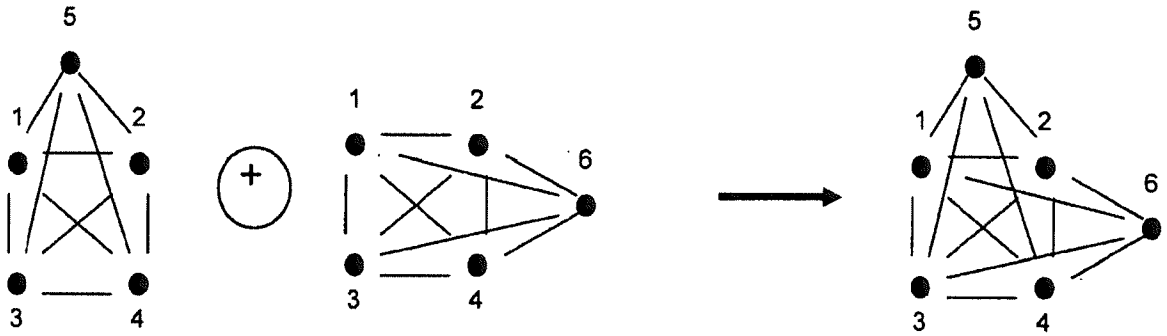


Figure 7

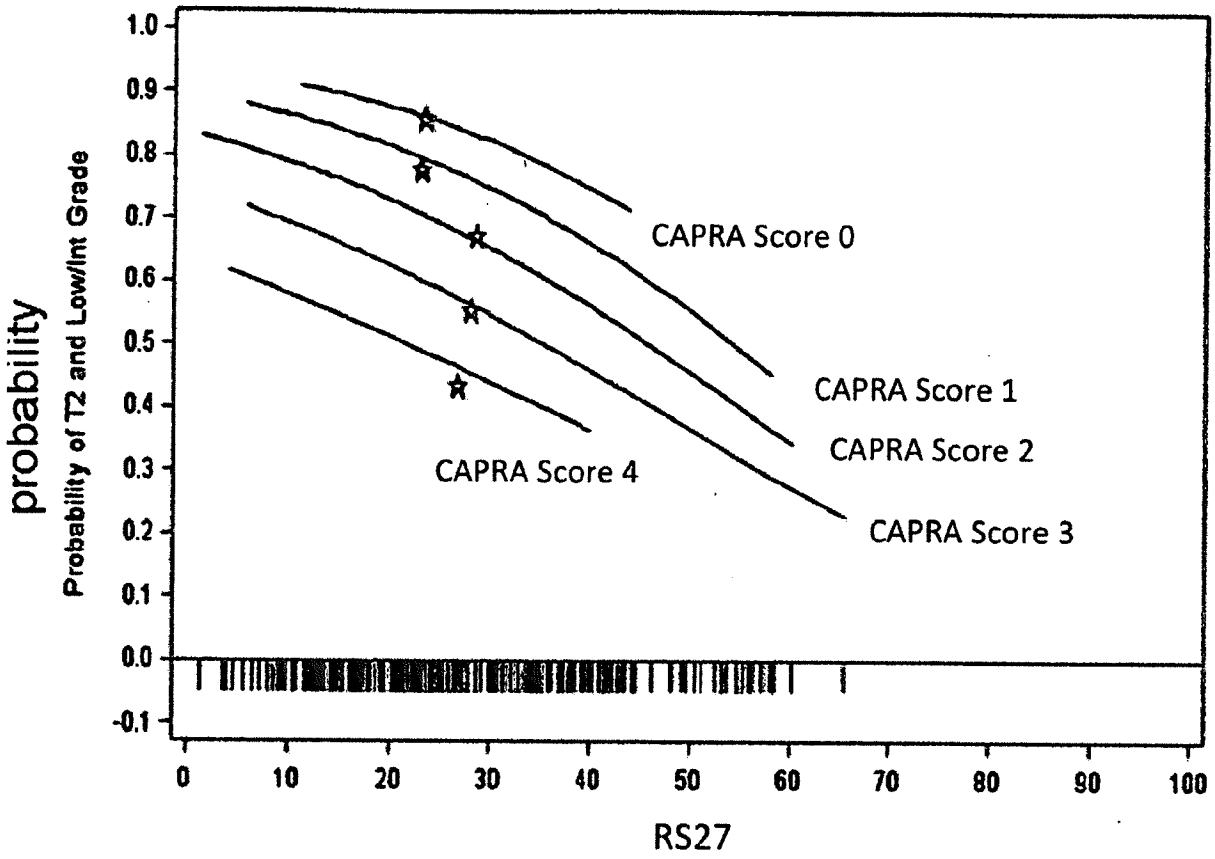

probability
Probability of T2 and Low/Int Grade
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
0
10
20
30
40
50
60
70
80
90
100
RS27
CAPRA Score 0
CAPRA Score 1
CAPRA Score 2
CAPRA Score 3
CAPRA Score 4

FIGURE 8

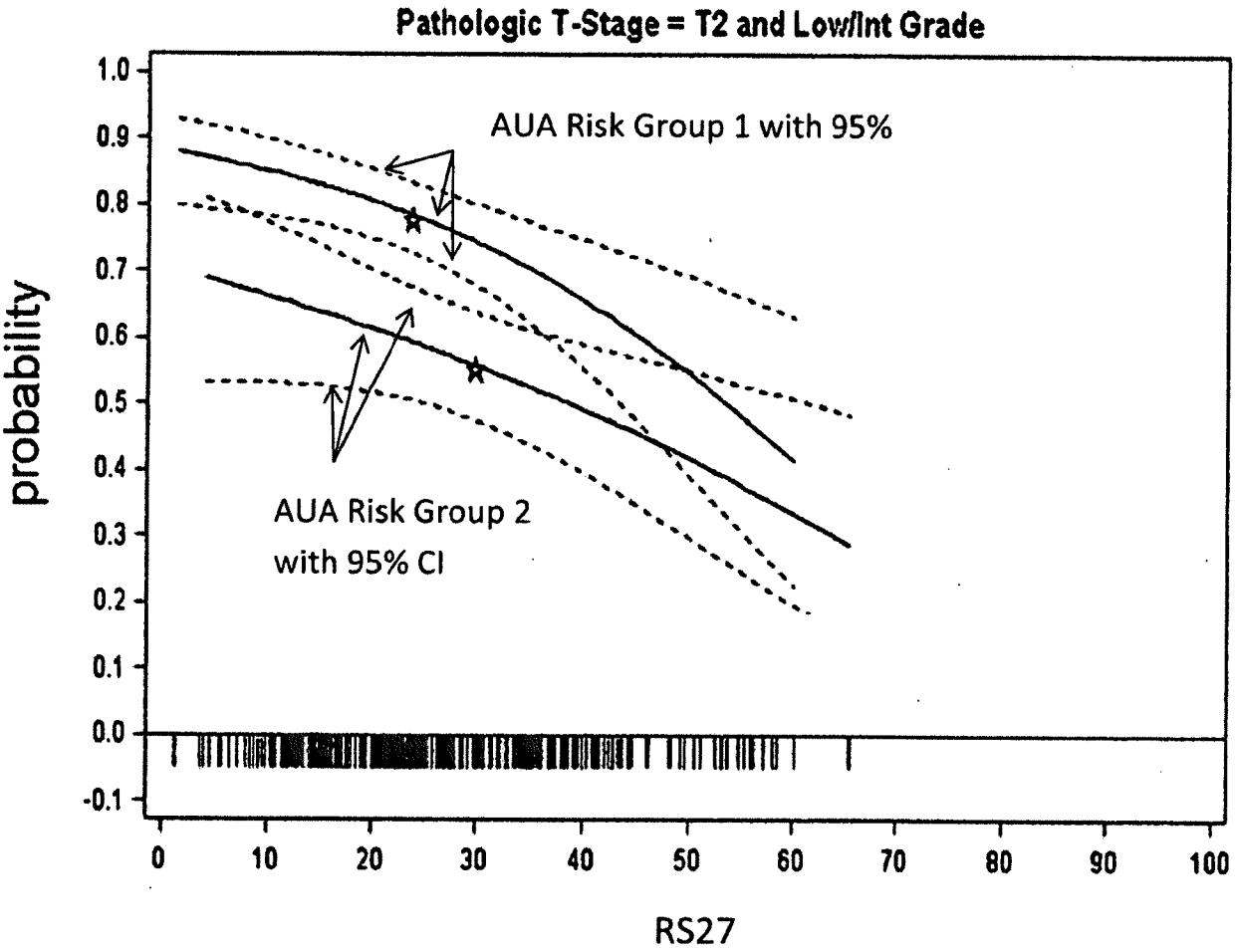

Pathologic T-Stage = T2 and Low/Int Grade
AUA Risk Group 1 with 95%
AUA Risk Group 2
with 95% CI
probability
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
0
10
20
30
40
50
60
70
80
90
100
RS27

FIGURE 9

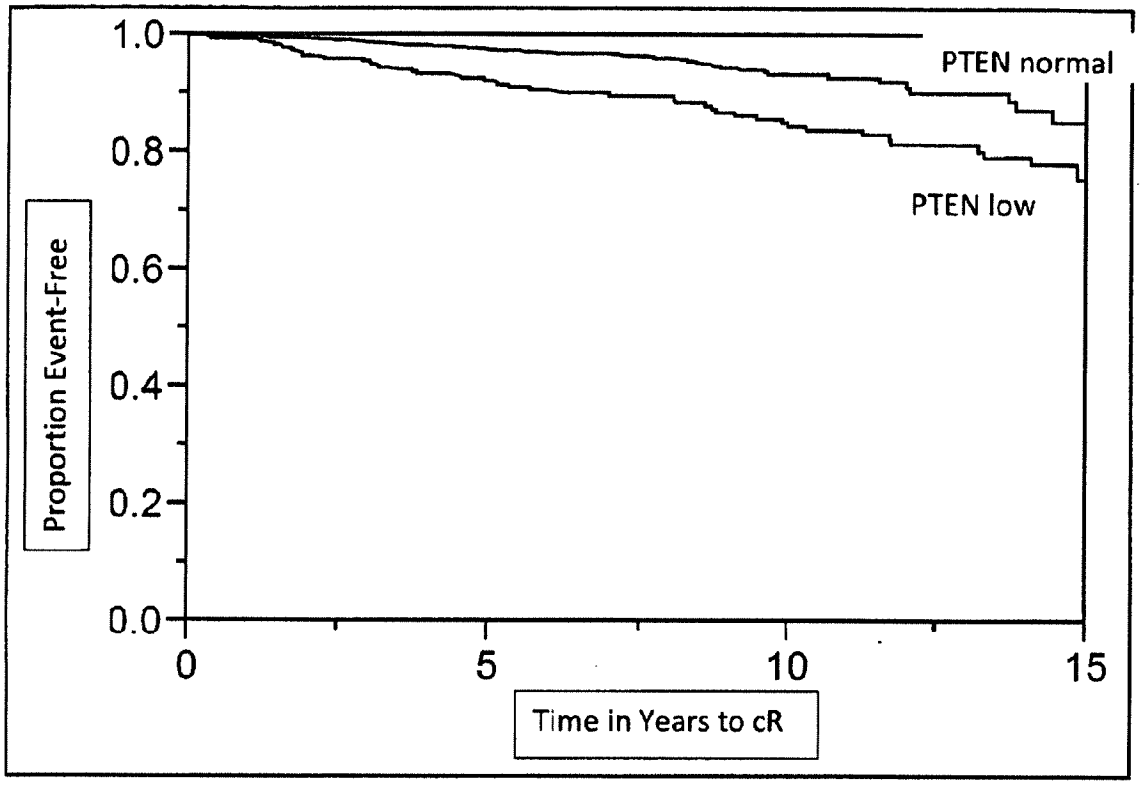

1.0
0.8
0.6
0.4
0.2
0.0
Proportion Event-Free
PTEN normal
PTEN low
0
5
10
15
Time in Years to cR

FIGURE 10

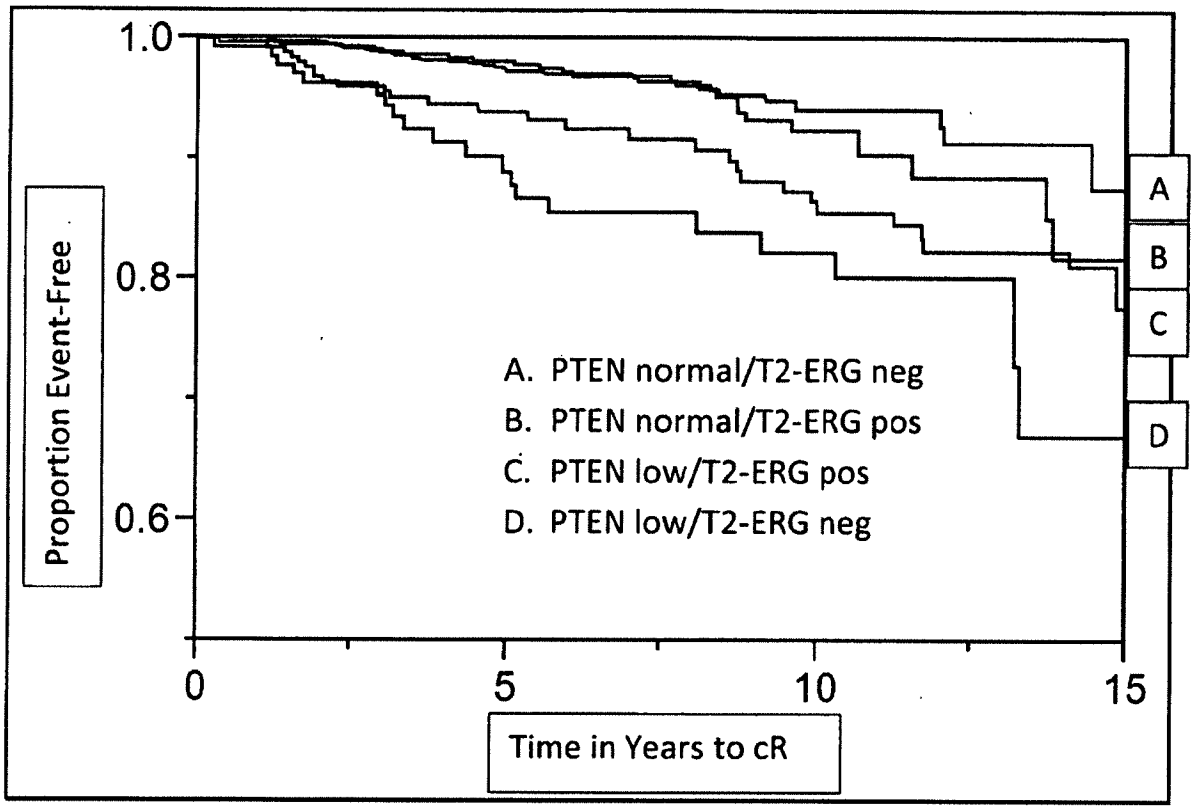

1.0
0.8
0.6
Proportion Event-Free
A. PTEN normal/T2-ERG neg
B. PTEN normal/T2-ERG pos
C. PTEN low/T2-ERG pos
D. PTEN low/T2-ERG neg
A
B
C
D
0
5
10
15
Time in Years to cR

FIGURE 11