FIG. 1A

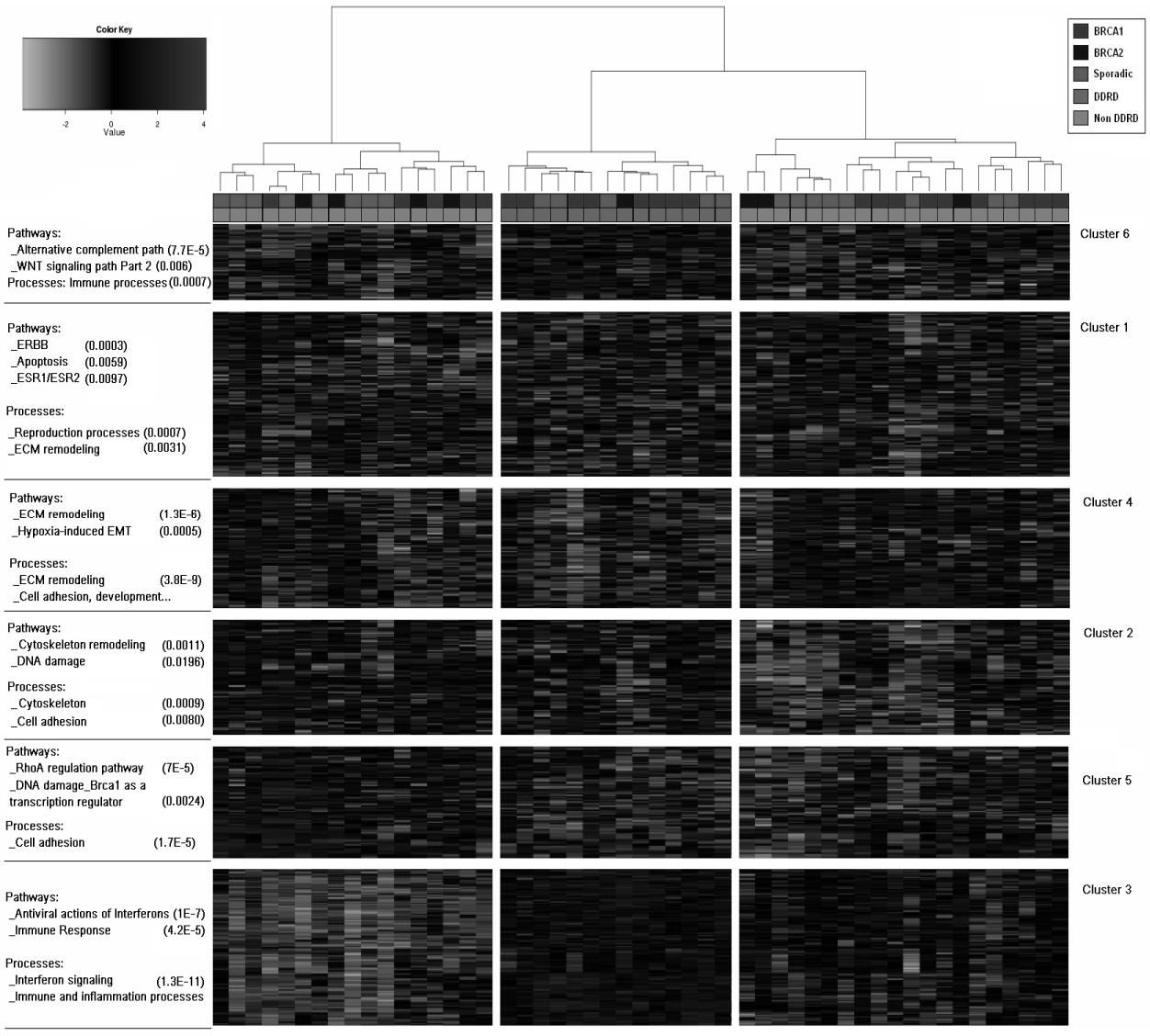

Color Key
-2
0
2
4
Value
BRCA1
BRCA2
Sporadic
DDRD
Non DDRD
Pathways:
_Alternative complement path (7.7E-5)
_WNT signaling path Part 2 (0.006)
Processes: Immune processes (0.0007)
Cluster 6
Pathways:
_ERBB (0.0003)
_Apoptosis (0.0059)
_ESR1/ESR2 (0.0097)
Processes:
_Reproduction processes (0.0007)
_ECM remodeling (0.0031)
Cluster 1
Pathways:
_ECM remodeling (1.3E-6)
_Hypoxia-induced EMT (0.0005)
Processes:
_ECM remodeling (3.8E-9)
_Cell adhesion, development...
Cluster 4
Pathways:
_Cytoskeleton remodeling (0.0011)
_DNA damage (0.0196)
Processes:
_Cytoskeleton (0.0009)
_Cell adhesion (0.0080)
Cluster 2
Pathways:
_RhoA regulation pathway (7E-5)
_DNA damage_Brca1 as a transcription regulator (0.0024)
Processes:
_Cell adhesion (1.7E-5)
Cluster 5
Pathways:
_Antiviral actions of Interferons (1E-7)
_Immune Response (4.2E-5)
Processes:
_Interferon signaling (1.3E-11)
_Immune and inflammation processes
Cluster 3

FIG. 1B

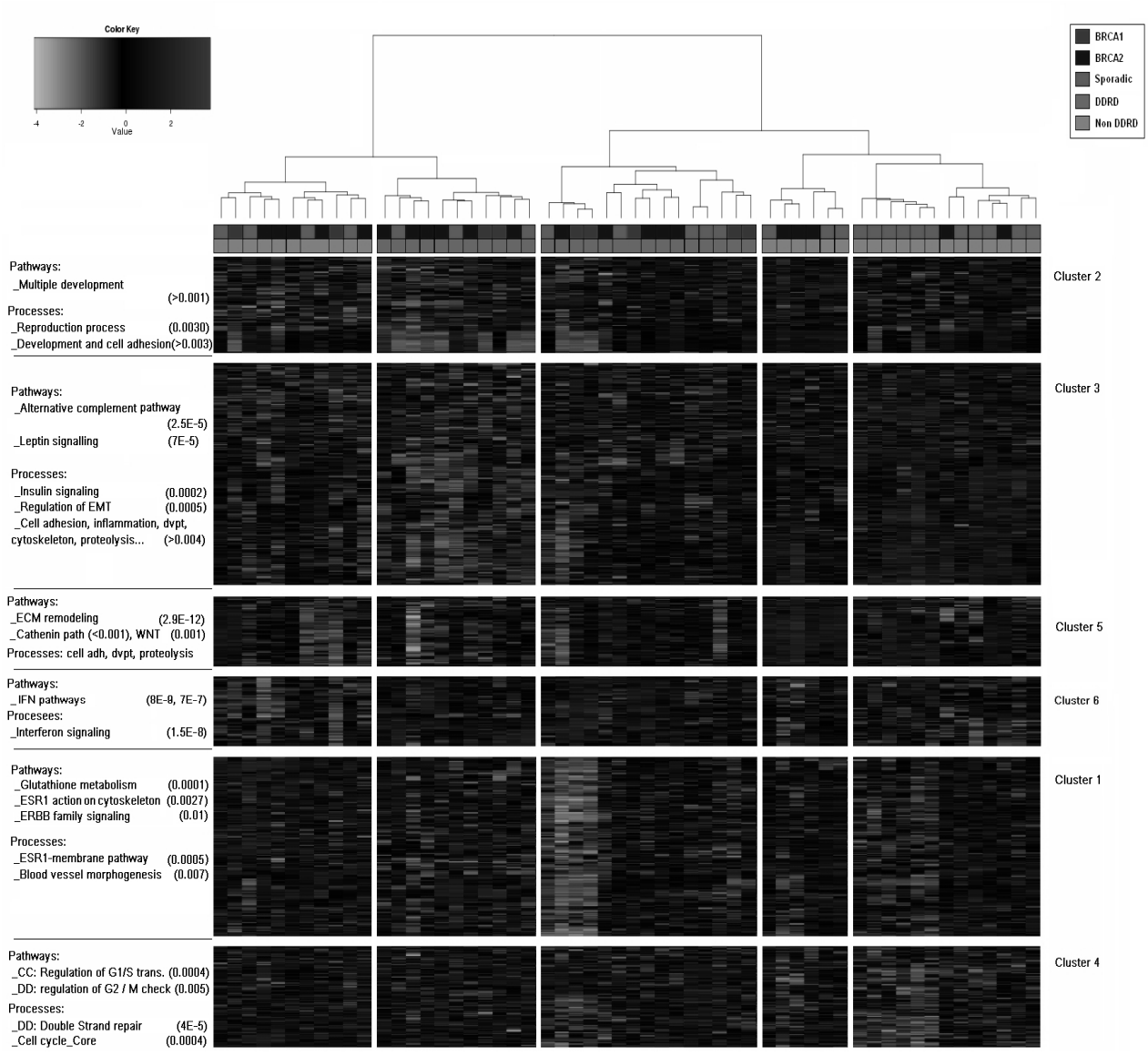
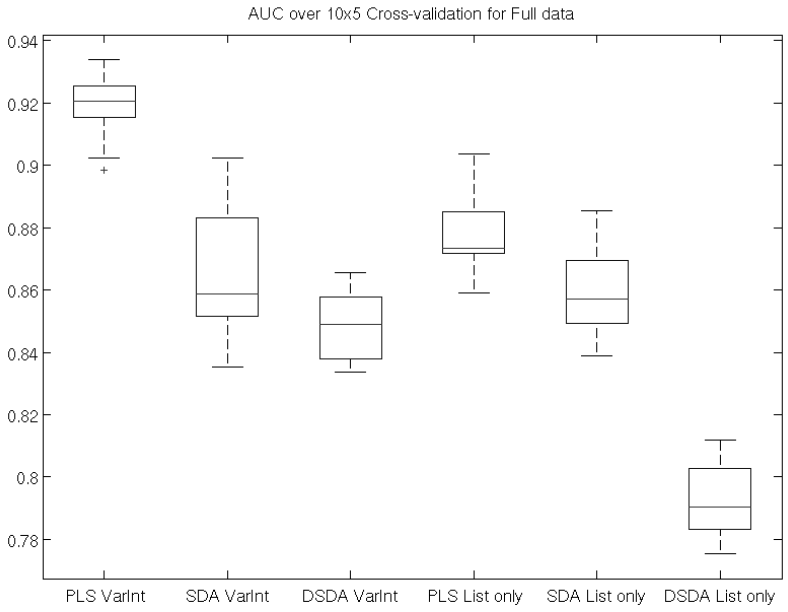

Color Key
-4
-2
0
2
Value
BRCA1
BRCA2
Sporadic
DDRD
Non DDRD
Pathways:
_Multiple development (>0.001)
Processes:
_Reproduction process (0.0030)
_Development and cell adhesion(>0.003)
Cluster 2
Pathways:
_Alternative complement pathway (2.5E-5)
_Leptin signalling (7E-5)
Processes:
_Insulin signaling (0.0002)
_Regulation of EMT (0.0005)
_Cell adhesion, inflammation, dvpt, cytoskeleton, proteolysis... (>0.004)
Cluster 3
Pathways:
_ECM remodeling (2.9E-12)
_Cathenin path (<0.001), WNT (0.001)
Processes: cell adh, dvpt, proteolysis
Cluster 5
Pathways:
_IFN pathways (8E-9, 7E-7)
Procesees:
_Interferon signaling (1.5E-8)
Cluster 6
Pathways:
_Glutathione metabolism (0.0001)
_ESR1 action on cytoskeleton (0.0027)
_ERBB family signaling (0.01)
Processes:
_ESR1-membrane pathway (0.0005)
_Blood vessel morphogenesis (0.007)
Cluster 1
Pathways:
_CC: Regulation of G1/S trans. (0.0004)
_DD: regulation of G2 / M check (0.005)
Processes:
_DD: Double Strand repair (4E-5)
_Cell cycle_Core (0.0004)
Cluster 4

FIG. 2

A.


AUC over 10x5 Cross-validation for Full data
0.94
0.92
0.9
0.88
0.86
0.84
0.82
0.8
0.78
PLS VarInt
SDA VarInt
DSDA VarInt
PLS List only
SDA List only
DSDA List only

B.

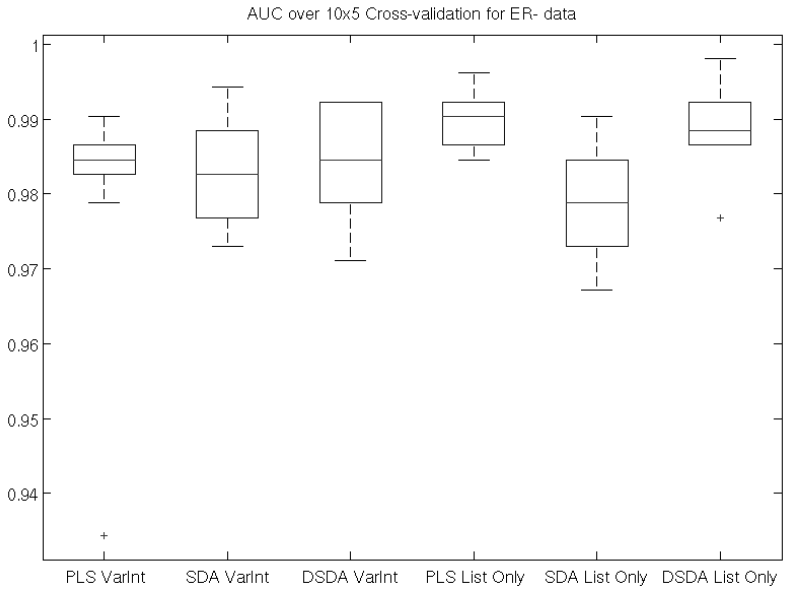
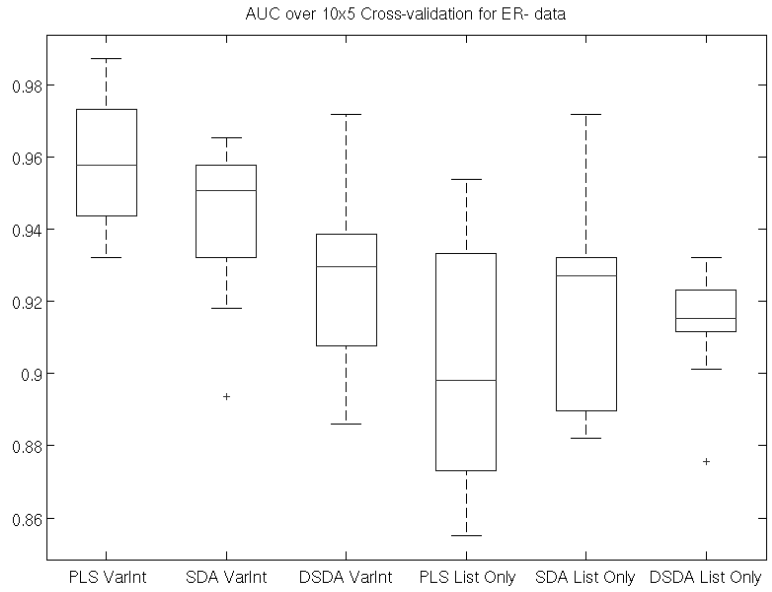

AUC over 10x5 Cross-validation for ER- data
1
0.99
0.98
0.97
0.96
0.95
0.94
PLS VarInt
SDA VarInt
DSDA VarInt
PLS List Only
SDA List Only
DSDA List Only

Fig. 2 Con't.

C.


AUC over 10x5 Cross-validation for ER- data
0.98
0.96
0.94
0.92
0.9
0.88
0.86
PLS VarInt
SDA VarInt
DSDA VarInt
PLS List Only
SDA List Only
DSDA List Only

D.

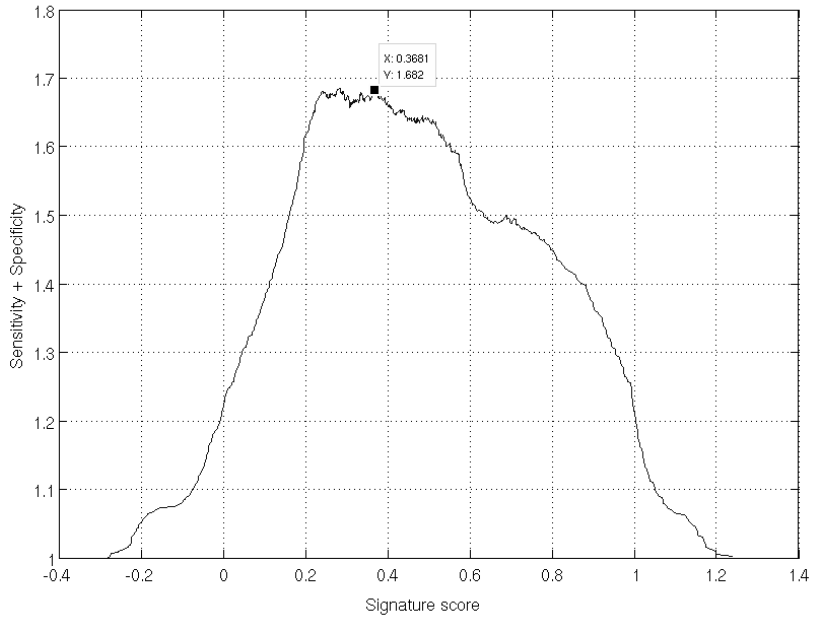

X: 0.3681
Y: 1.682
Sensitivity + Specificity
Signature score
1.8
1.7
1.6
1.5
1.4
1.3
1.2
1.1
1
-0.4
-0.2
0
0.2
0.4
0.6
0.8
1
1.2
1.4

FIG. 3

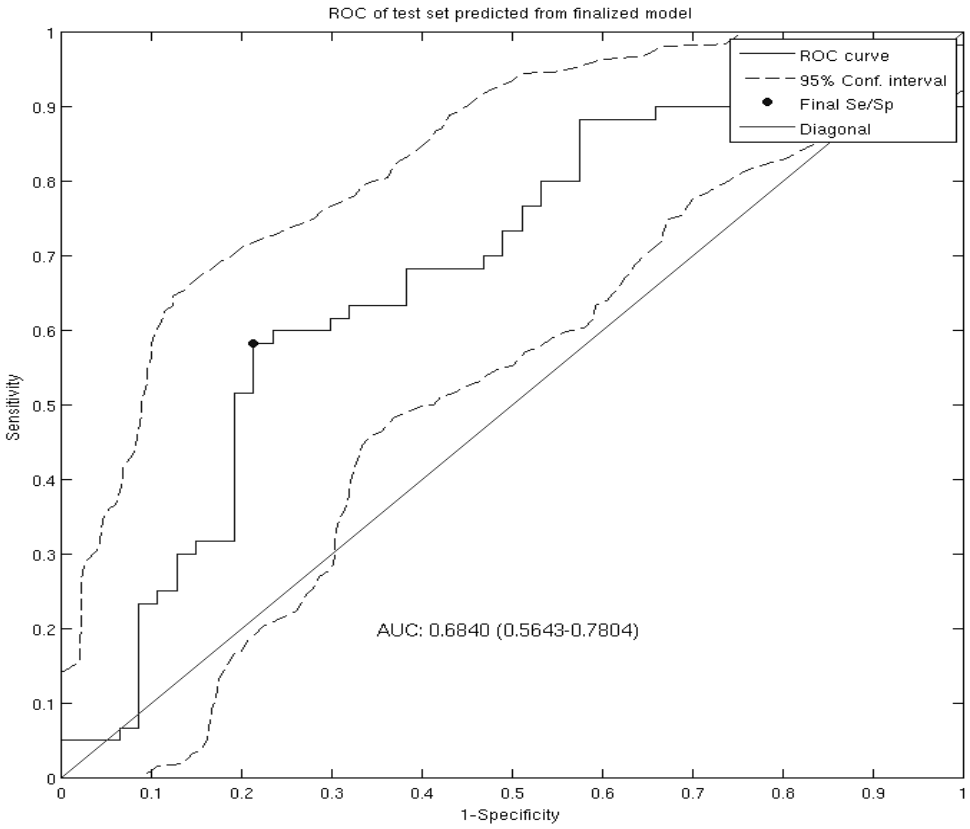

ROC of test set predicted from finalized model
ROC curve
95% Conf. interval
Final Se/Sp
Diagonal
AUC: 0.6840 (0.5643-0.7804)
Sensitivity
1-Specificity
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1

FIG. 4

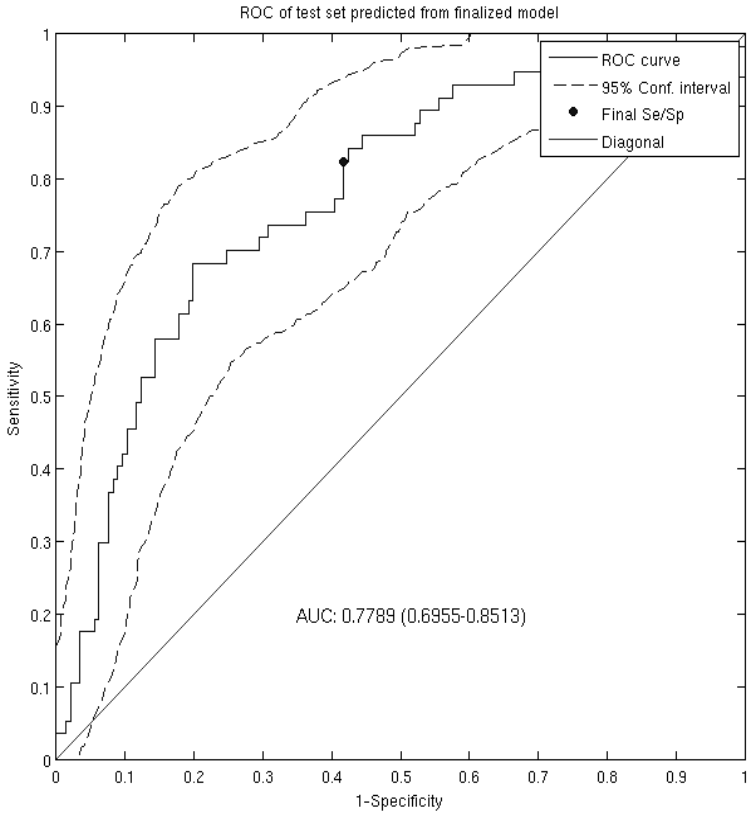

ROC of test set predicted from finalized model
ROC curve
95% Conf. interval
Final Se/Sp
Diagonal
AUC: 0.7789 (0.6955-0.8513)
Sensitivity
1-Specificity
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1

FIG. 5

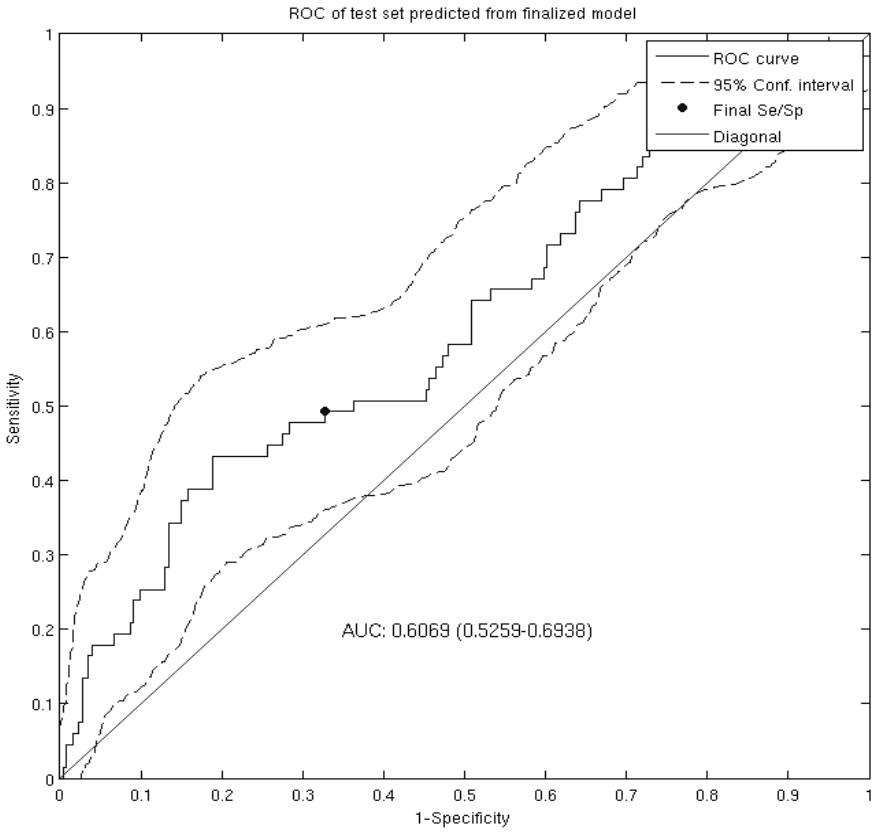

ROC of test set predicted from finalized model
ROC curve
95% Conf. interval
Final Se/Sp
Diagonal
AUC: 0.6069 (0.5259-0.6938)
Sensitivity
1-Specificity
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1

FIG. 6

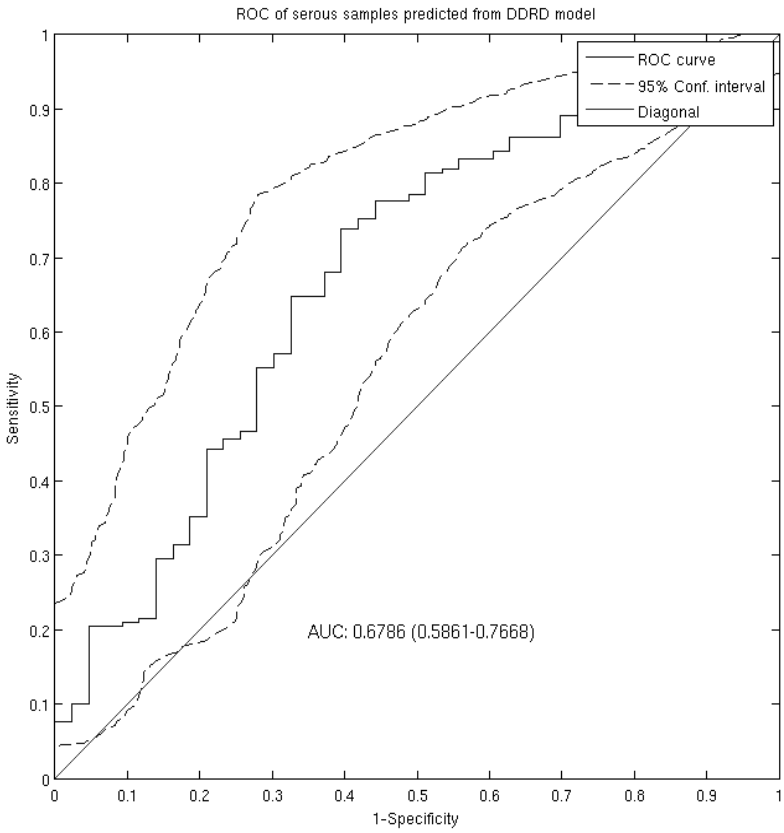

ROC of serous samples predicted from DDRD model
ROC curve
95% Conf. interval
Diagonal
AUC: 0.6786 (0.5861-0.7668)
Sensitivity
1-Specificity
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1

FIG. 7

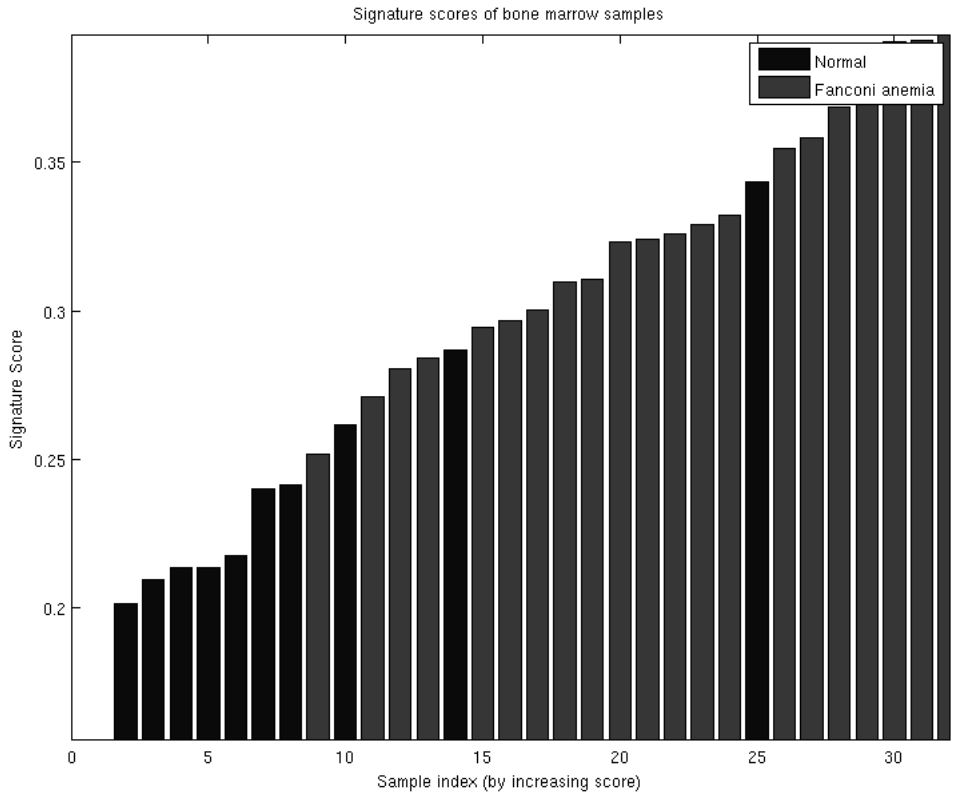
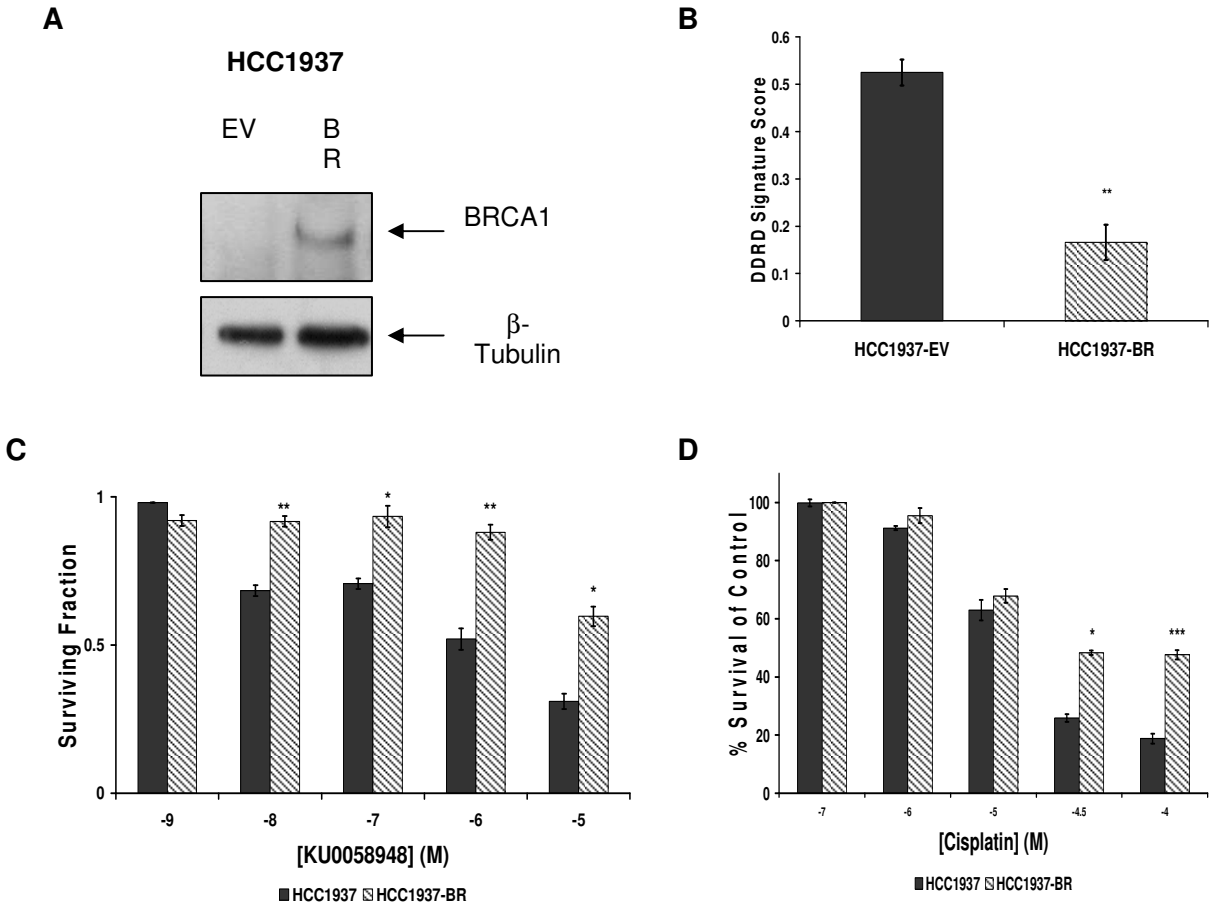

Signature scores of bone marrow samples
Normal
Fanconi anemia
Signature Score
0.35
0.3
0.25
0.2
0
5
10
15
20
25
30
Sample index (by increasing score)

FIG. 8


A
HCC1937
EV
B
R
BRCA1
β-
Tubulin
B
DDRD Signature Score
0.6
0.5
0.4
0.3
0.2
0.1
0
**
HCC1937-EV
HCC1937-BR
C
Surviving Fraction
1
0.5
0
**
*
**
*
-9
-8
-7
-6
-5
[KU0058948] (M)
HCC1937 HCC1937-BR
D
% Survival of Control
100
80
60
40
20
0
*
***
-7
-6
-5
-4.5
-4
[Cisplatin] (M)
HCC1937 HCC1937-BR