Probe Name	P-value	Common	Genbank	Description
mwghuman30K#B:3667	0.049	TXNDC5	NM_030810	Thioredoxin domain containing 5
mwghuman30K#A:06694	0.049	PILRA	NM_013439	Paired immunoglobin-like type 2 receptor alpha
mwghuman30K#A:06347	0.049	HLA-E	NM_005516	Major histocompatibility complex, class I, E
mwghuman30K#B:2443	0.049		XM_036173	kiaa1067; kiaa1067
mwghuman30K#A:09174	0.049	ITPA	NM_033453	Inosine triphosphatase (nucleoside triphosphate pyrophosphatase)
mwghuman30K#B:1847	0.0482	DMN	NZ_145728	Desmuslin*
mwghuman30K#A:07569	0.0429	GTPBP2	NM_019096	GTP binding protein 2
mwghuman30K#A:09053	0.0429	MFGE8	NM_005928	Milk fat globule-EGF factor 8 protein
mwghuman30K#A:06363	0.0365	IDH1	NM_005896	Isocitrate dehydrogenase 1 (NADP+), soluble
mwghuman30K#B:9466	0.0365	MRPS5	NM_031902	Mitochondrial ribosomal protein S5
mwghuman30K#A:04768	0.0307	LGALS7	NM_002307	Lectin, galactoside-binding, soluble, 7 (galectin 7)
mwghuman30K#B:5919	0.0295	KCNIP2	AF347114	Kv channel interacting protein 2
mwghuman30K#A:04955	0.0295	CHST4	NM_005769	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4
mwghuman30K#C:4262	0.0295		AL451139.11.67295.95669.1	ensembl genscan prediction
mwghuman30K#B:5235	0.023	OSIL; A170; p62B	U46752	Human phosphotyrosine independent ligand
mwghuman30K#A:03491	0.023	NFKBIB	NM_002503	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta
mwghuman30K#A:00049	0.023	MTCH2	NM_014342	Mitochondrial carrier homolog 2 (C. elegans)
mwghuman30K#A:04349	0.0136	ARFRP1	NM_003224	ADP-ribosylation factor related protein 1
mwghuman30K#C:0720	0.0136	BABI-L	AJ131063	Birch pollen allergen specific immunoglobulin gamma chain**
mwghuman30K#B:4873	0.0136	TUBA1B	NM_006082	Tubulin alpha 1b***
mwghuman30K#B:7713	0.00371		AJ242956_2	partial n-myc exon 3
mwghuman30K#B:0031	0.000756	PLXNB2	AB002313	Plexin B2

* This marker was previously known as kiaa0353; dmn (XM_031031).
** This marker was previously known as Immunoglobulin kappa variable 1-5 (IGKC; AJ131063).
*** This marker was previously known as similar to tubulin alpha 6; loc143712 (XM_084610).

FIGURE 1

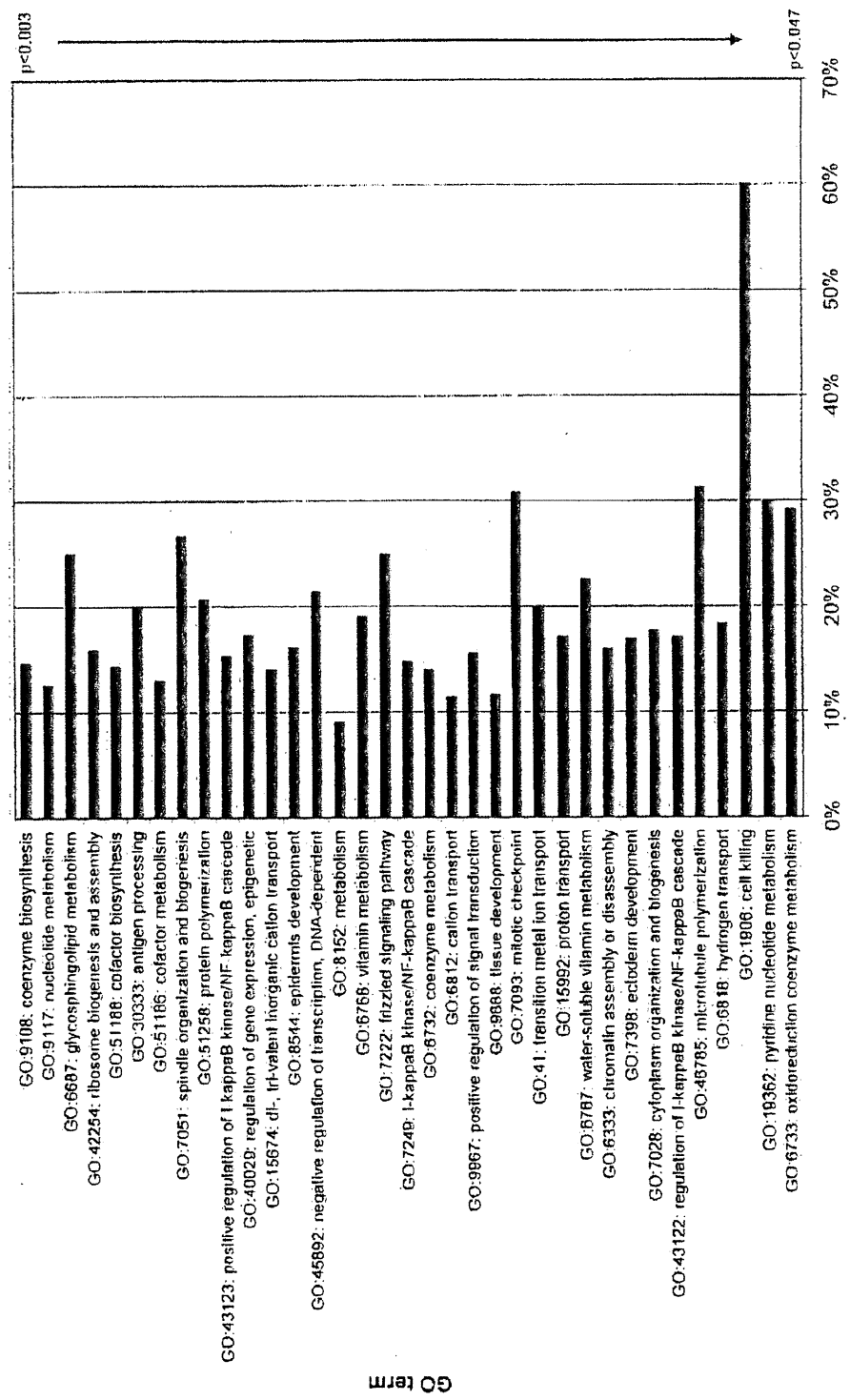

GO classification of differentially expressed genes
GO:9108: coenzyme biosynthesis
GO:9117: nucleotide metabolism
GO:6687: glycosphingolipid metabolism
GO:42254: ribosome biogenesis and assembly
GO:51188: cofactor biosynthesis
GO:30333: antigen processing
GO:51186: cofactor metabolism
GO:7051: spindle organization and biogenesis
GO:51258: protein polymerization
GO:43123: positive regulation of I kappaB kinase/NF-kappaB cascade
GO:40029: regulation of gene expression, epigenetic
GO:15674: di-, tri-valent inorganic cation transport
GO:8544: epidermis development
GO:45892: negative regulation of transcription, DNA-dependent
GO:8152: metabolism
GO:6766: vitamin metabolism
GO:7222: frizzled signaling pathway
GO:7249: I-kappaB kinase/NF-kappaB cascade
GO:6732: coenzyme metabolism
GO:6812: cation transport
GO:9967: positive regulation of signal transduction
GO:9888: tissue development
GO:7093: mitotic checkpoint
GO:41: transition metal ion transport
GO:15992: proton transport
GO:6787: water-soluble vitamin metabolism
GO:6333: chromatin assembly or disassembly
GO:7398: ectoderm development
GO:7028: cytoplasm organization and biogenesis
GO:43122: regulation of I-kappaB kinase/NF-kappaB cascade
GO:46785: microtubule polymerization
GO:6818: hydrogen transport
GO:1906: cell killing
GO:19362: pyridine nucleotide metabolism
GO:6733: oxidoreduction coenzyme metabolism
GO term
p<0.003
p<0.047
0%
10%
20%
30%
40%
50%
60%
70%
% genes involved in process

FIGURE 2

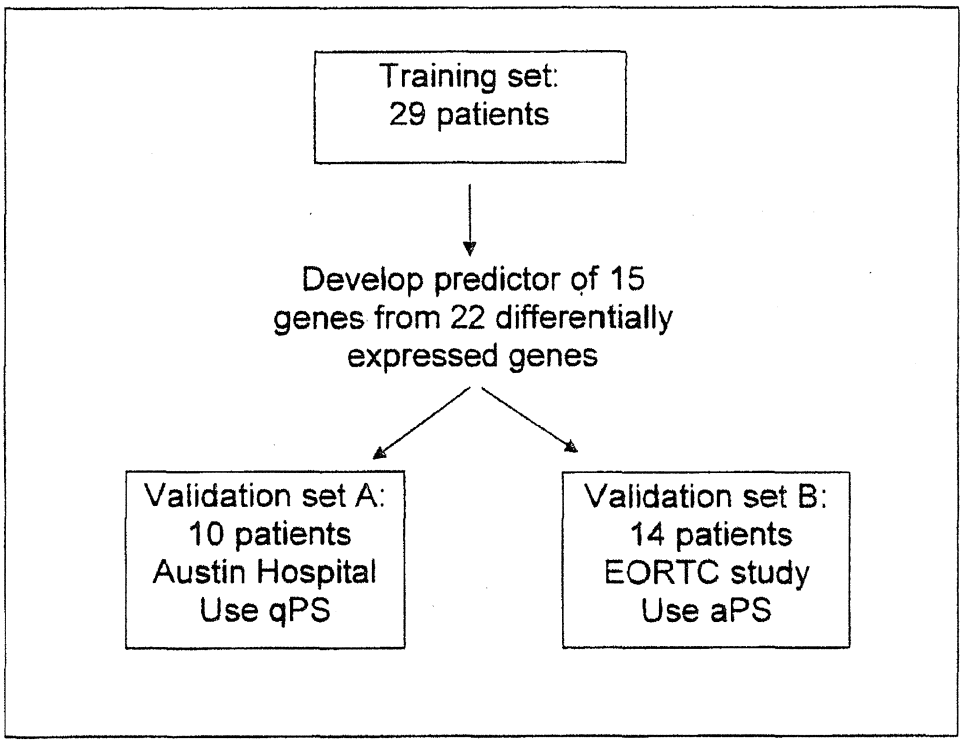

Training set:
29 patients
Develop predictor of 15
genes from 22 differentially
expressed genes
Validation set A:
10 patients
Austin Hospital
Use qPS
Validation set B:
14 patients
EORTC study
Use aPS

FIGURE 3

Cell line or tissue type	*Source*	*Weight (g)*	*Volume (mL)*	*Concentration (mg/mL)*	*Total (mg)*	*Loaded volume*
786	Kidney Ca	-	7.25	0.71	5.2	2.8
Ovcar 3	Ovarian Ca	-	5	0.82	4.1	2.4
Ovcar	Ovarian Ca	-	4.5	2.21	10	0.9
J82	Bladder Ca	-	5	1.11	5.6	1.8
AGS	Gastric Ca	-	4.5	1.2	5.4	1.7
CCRF-CEM	T-cell Leukemia	-	2.5	0.34	0.9	5
NCI-H460	Lung Ca	-	7.5	1.2	9	1.7
U251	Brain Ca	-	4	2.27	9.1	0.8
COLO	Colon Ca	-	4	1.55	6.2	1.3
M14	Mel	-	8	0.15	1.2	5
T24	Bladder Ca	-	7	1.15	8	1.7
MCF7	Breast Ca	-	4.5	2.8	12.6	0.7
PC3	Prostate Ca	-	9.5	1	9.5	2
HL60	AML	-	5	0.58	2.9	3.4
CACO6	Colon Ca	-	4.5	0.9	4.1	2.2
KATO III	Gastric Ca	-	4	0.58	2.3	3.5
C33A	Cervical Ca	-	4.5	1.41	6.3	1.4
Gastric tissue	Normal Stomach	1.5	2	0.36	0.7	5
Wilms Rhabdo	Kidney/sarcoma	9	4.5	0.3	1.4	5

FIGURE 4

Common	Genbank	Description	Left Primer	Seq number	Right Primer	Seq number	Roche Probe #
TXNDC5	NM_030810	Thioredoxin domain containing 5	gcacttcgtcatgttcttcg	1	actttggcatcttccatgct	2	*14*
PILRA	NM_013439	Paired immunoglobin-like type 2 receptor alpha	aggggaccaaactctccatc	3	tccaggtggtagtcatgctg	4	*64*
HLA-E	NM_005516	Major histocompatibility complex, class I, E	ggaagacacatgcgtgggag	5	gtgagtcacgtgtgtctttgg	6	*80*
ITPA	NM_033453	Inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	tctggagaagttaaagcctgaag	7	aggctgacttgtcctcgaac	8	*17*
GTPBP2	NM_019096	GTP binding protein 2	gttgctcagtcacccaatg	9	ggaggtccagactctctcca	10	*47*
MFGE8	NM_005928	Milk fat globule-EGF factor 8 protein	agctacggtaacgatcagtgg	11	ccttgtaggatgccacaaact	12	*21*
IDH1	NM_005896	Isocitrate dehydrogenase 1 (NADP+), soluble	gtgacatacctggtacataactttgaa	13	gtgtgcaaaatcttcaattgactt	14	*77*
MRPS5	NM_031902	Mitochondrial ribosomal protein S5	cgtgtcttggtggctgtg	15	gcatccatccgatcagtagc	16	*17*
KCNIP2	AF347114	Kv channel interacting protein 2	aaggagagtttgtccgattcc	17	ttcatcgtccacgctgtc	18	*85*
CHST4	NM_005769	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	ggagcgagtgctttctcaag	19	tggaagaatagagccaagatgg	20	*18*
OSIL; A170;p62B	U46752	Human phosphotyrosine independent ligand	cccttggacaccatccagtat	21	atgggtgagcaaaacatcgtc	22	*72*
NFKBIB	NM_002503	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	ggctacgtcactgaggatgg	23	aggaagggttcatgctgatg	24	*76*
MTCH2	NM_014342	Mitochondrial carrier homolog 2 (C. elegans)	agggcattctaggatttttcg	25	tgacgaggtaggccagtga	26	*5*
ARFRP1	NM_003224	ADP-ribosylation factor related protein 1	gctcatgttctgggacttagga	27	cgtgacactccgcataatactt	28	*4*
	XM_084610	similar to tubulin alpha 6; loc143712	atcctagccatatgcgtga	29	ggcattgccaatctggac	30	*64*
	AJ242956_2	partial n-myc exon 3	ggcctaccataggacctcgt	31	caggcctagatgcagtagacg	32	*18*
PLXNB2	AB002313	Plexin B2	cagcaacaagctgctgtacg	33	cggatcccctgtagtaatcc	34	*39*

FIGURE 5

	Training set n=29		P value	Validation Set A n=10		P value
	Good (n=13)	**Poor** (n=16)		**Good** (n=5)	**Poor** (n=5)	
Median Age (years)	35 (19-89)	48.5 (28-74)	0.2275†	35 (24-73)	49 (43-72)	0.8125†
AJCC Stage						
IIIB	4	8	0.394‡	3	4	0.5647‡
IIIC	7	7		1	1	
IIIU	1	1		1	0	
IV	1	0		0	0	
Sex						
Male	5	8	0.4495‡	4	5	0.2723‡
Female	8	6		1	0	
Mean TTP (months)	40.3 (24-72)	4.1 (0-6)	<0.001§	52.2 (23-108)	6.6 (1-15)	<0.0256§
Tumor Infiltrating Lymphocytes						
Brisk	3	0	1‡	0	0	0.7523‡
Non Brisk	4	8		3	3	
Absent	1	1		1	0	
Not Available	5	7		1	2	
Adjuvant Interferon-α	1	1		1	0	

IIIU= Incomplete data at least IIIB
†Wilcoxon rank-sum test
‡Fisher's Exact test
§Cox proportional hazards

FIGURE 6

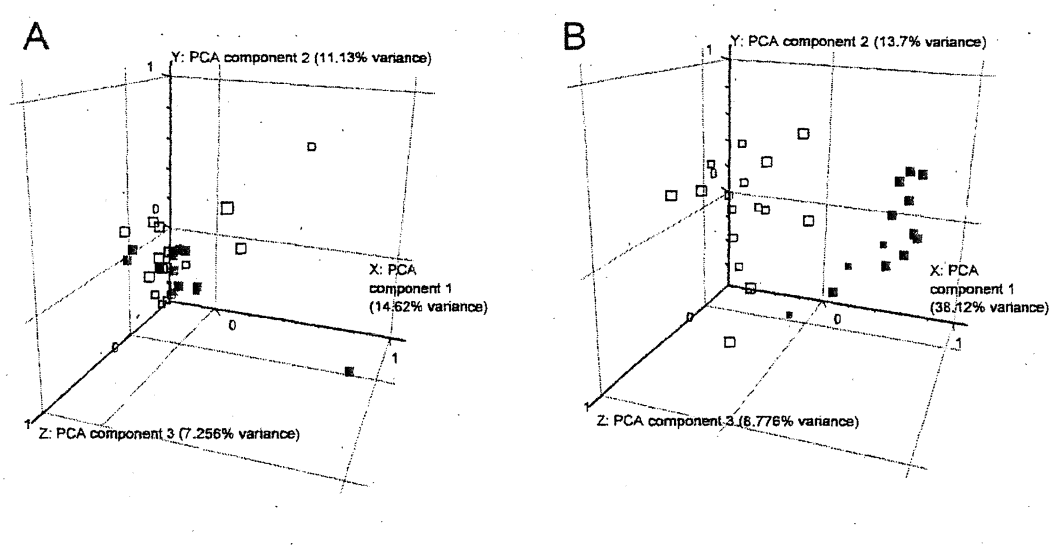

A
Y: PCA component 2 (11.13% variance)
X: PCA component 1 (14.62% variance)
Z: PCA component 3 (7.256% variance)
B
Y: PCA component 2 (13.7% variance)
X: PCA component 1 (38.12% variance)
Z: PCA component 3 (8.776% variance)

FIGURE 7

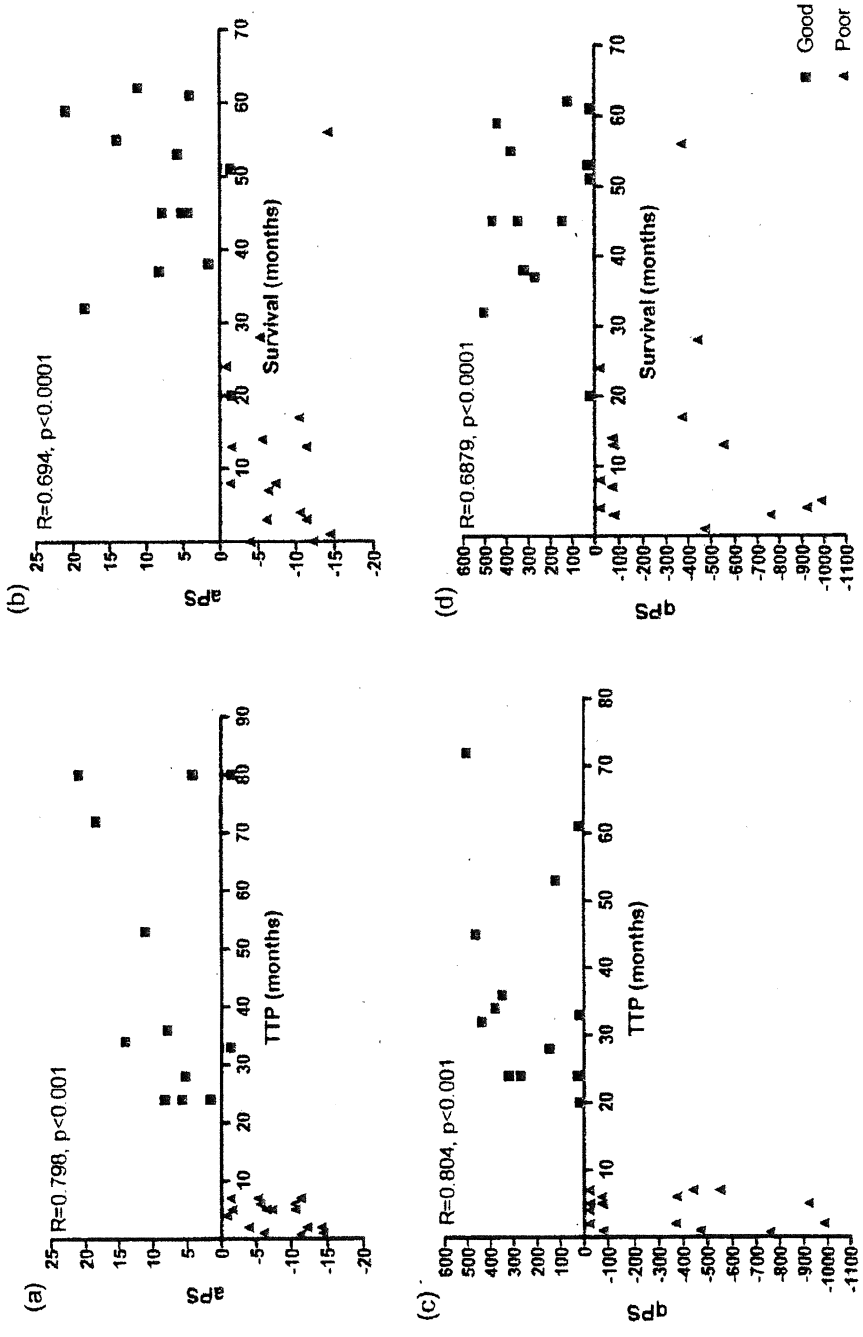

(a)
R=0.798, p<0.001
aPS
TTP (months)
(b)
R=0.694, p<0.0001
aPS
Survival (months)
(c)
R=0.804, p<0.001
qPS
TTP (months)
(d)
R=0.6879, p<0.0001
qPS
Survival (months)
Good
Poor

FIGURE 8

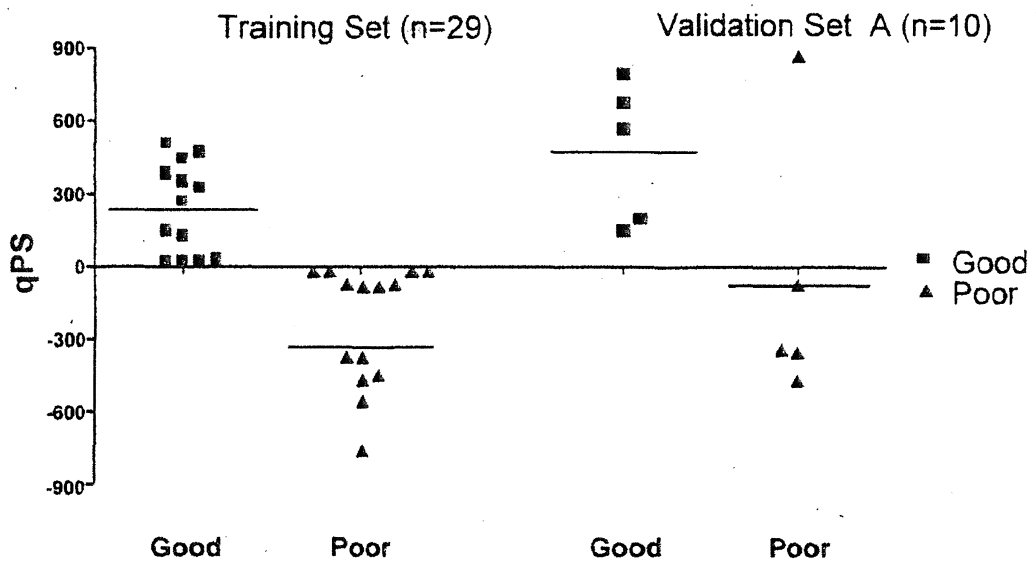

Training Set (n=29)
Validation Set A (n=10)
900
600
300
0
-300
-600
-900
qPS
Good
Poor
Good
Poor
Good
Poor

FIGURE 9

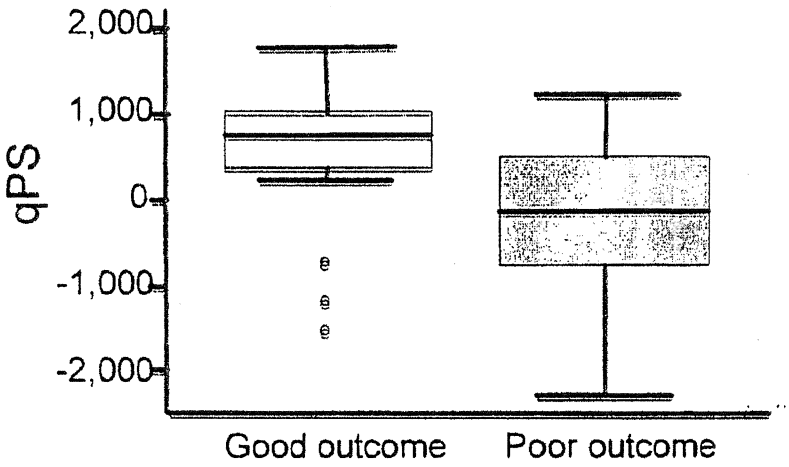


FIGURE 10