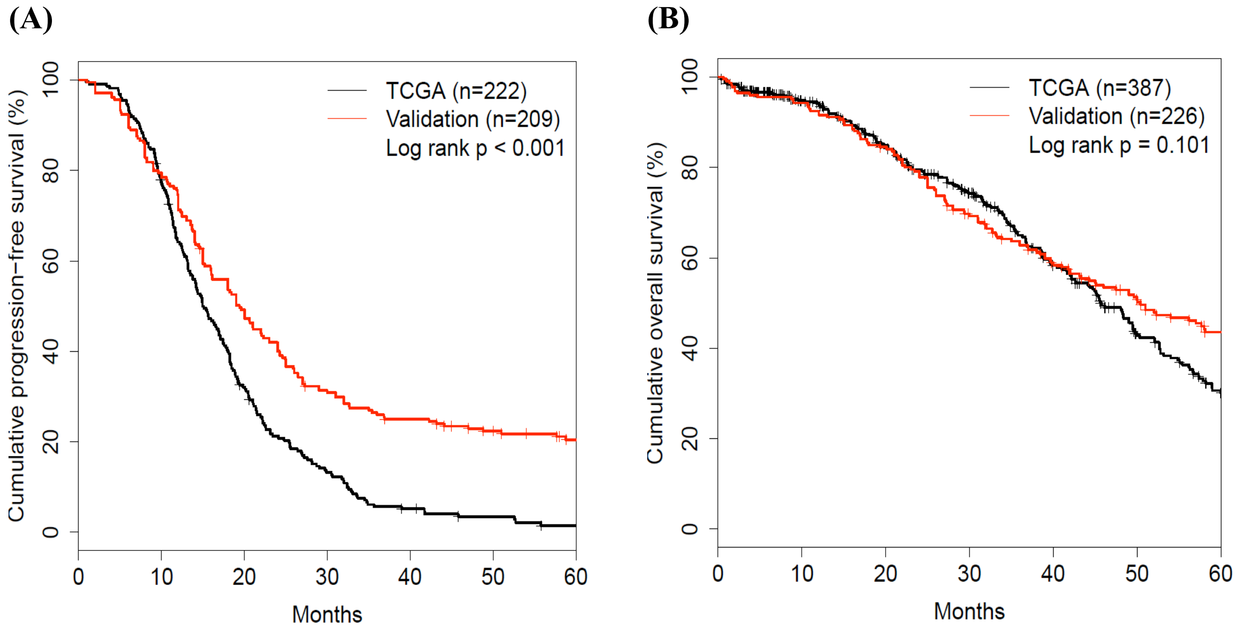
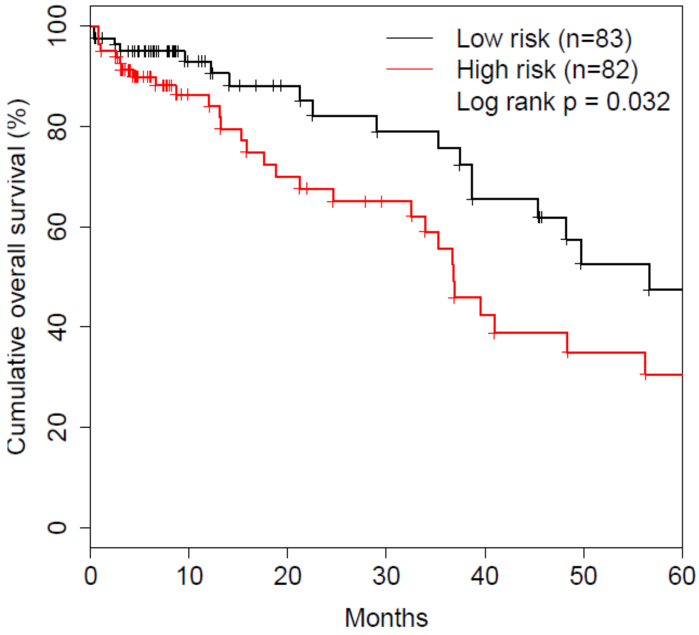
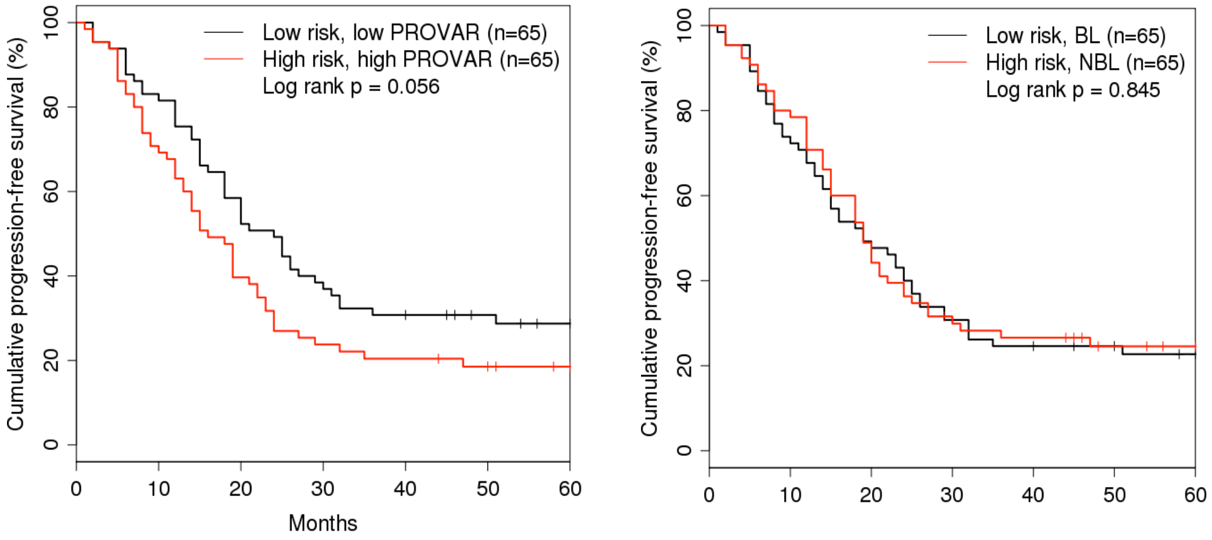


Supplemental Figure 1. Kaplan-Meier curves comparing progression-free survival (A) and overall survival (B) for the training and validation sets.

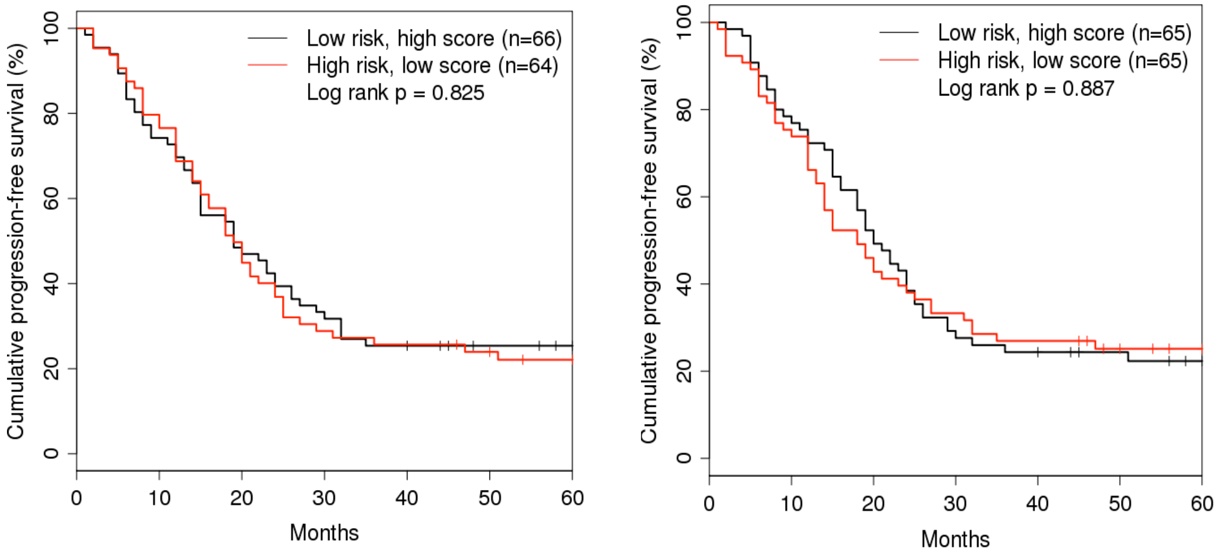


Supplemental Figure 2. Kaplan-Meier curves comparing overall survival in the 165 TCGA samples that were not used to construct the model. The same cutoff was used as in the analysis of PFS.

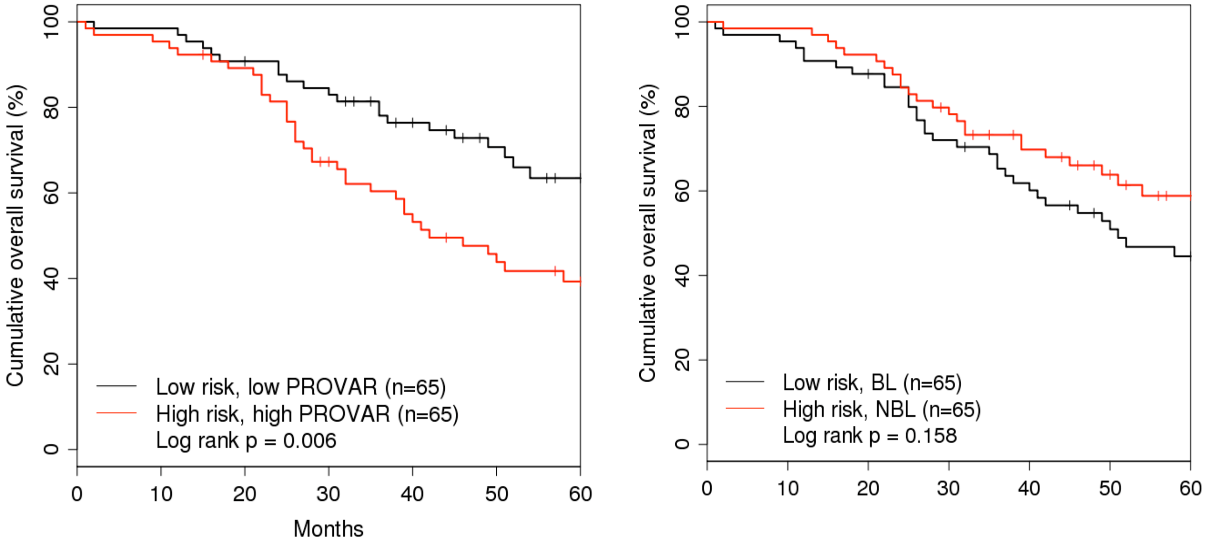
(A) PROVAR: PFS **(B) Konstantinopoulos: PFS**



(C) Kang: PFS **(D) Verhaak: PFS**

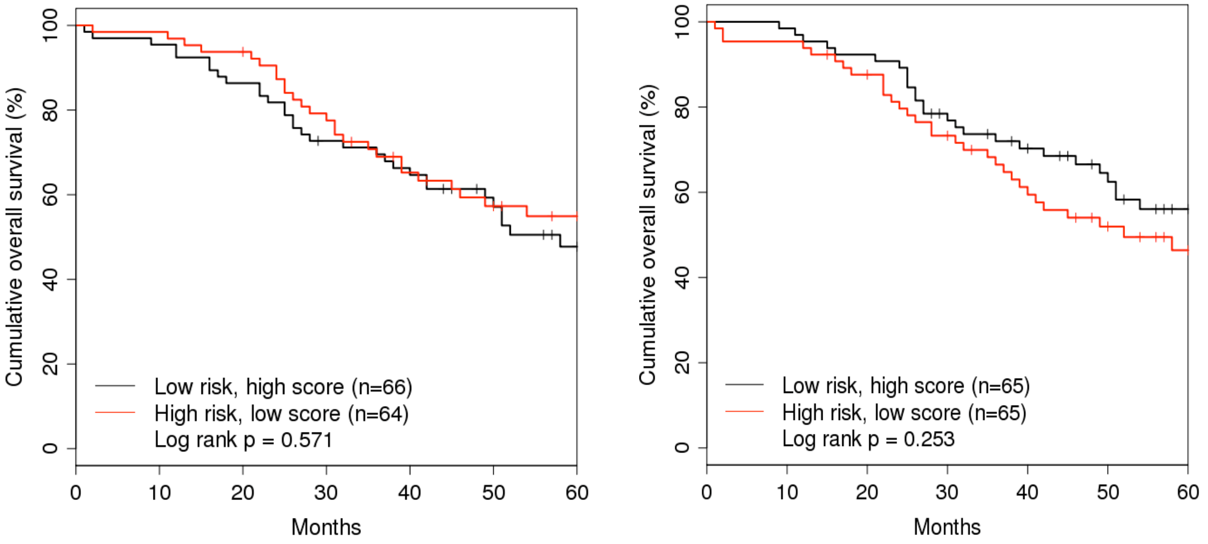


Supplemental Figure 3A. Kaplan-Meier curves of progression-free survival in the subset of validation samples (n=130) after classifying patients into two groups by median split.



(A) PROVAR: OS

(B) Konstantinopoulos: OS

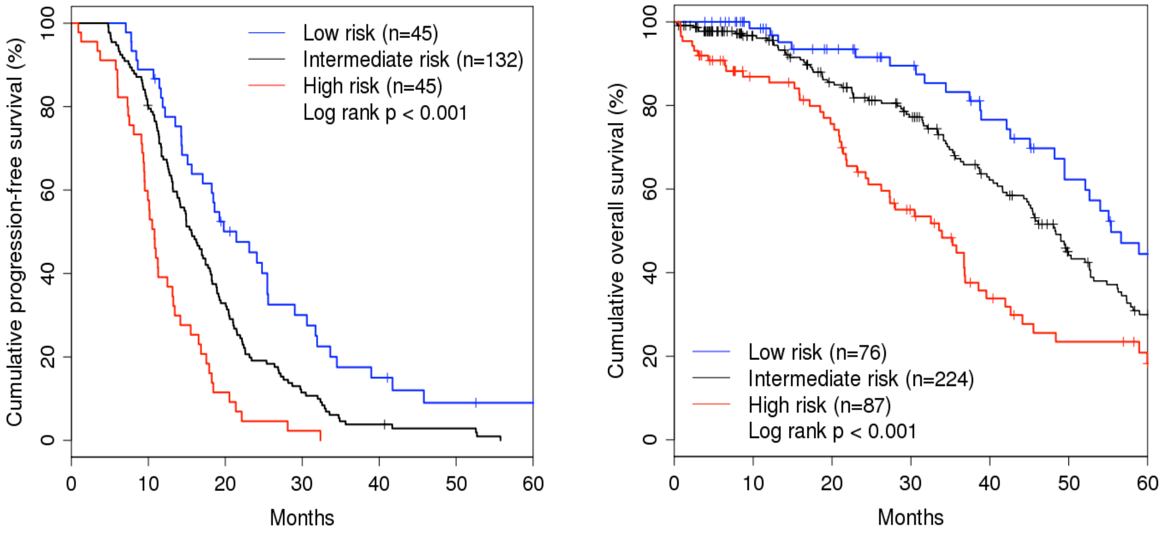


(C) Kang: OS

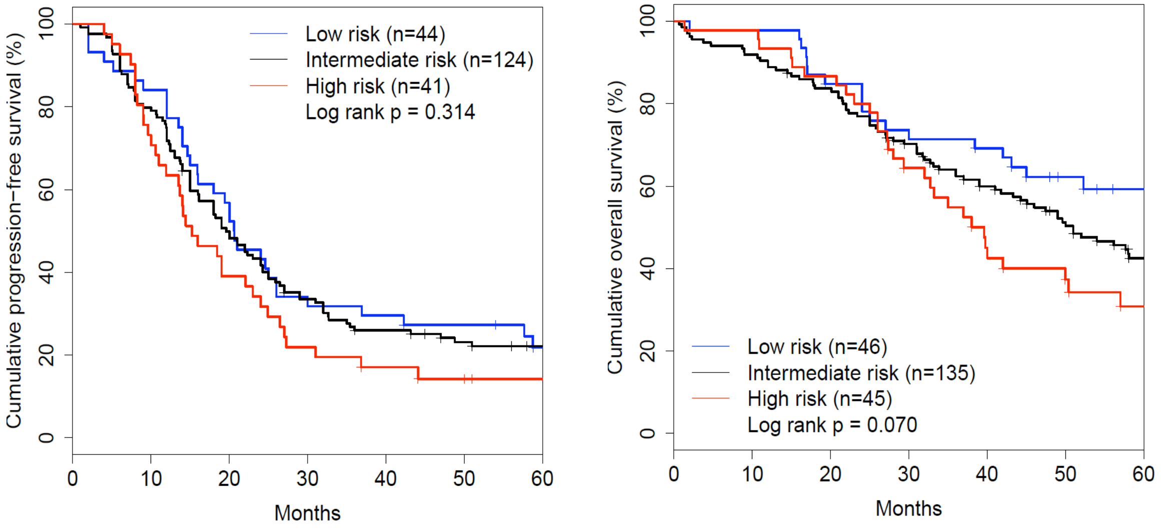
(D) Verhaak: OS

Supplemental Figure 3B. Kaplan-Meier curves of overall survival in the subset of validation samples (n=130) after classifying patients into two groups by median split. Note that the outcome difference seen in (B) Konstantinopoulos: OS is inverted, with low risk patients performing worse than high risk patients.

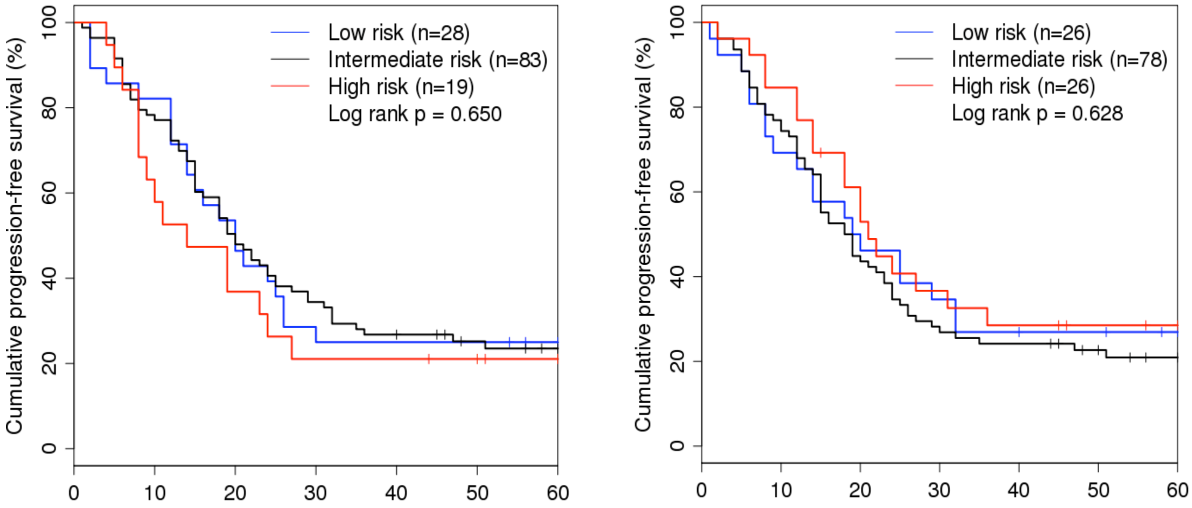
(A) TCGA: PFS **(B) TCGA: OS**



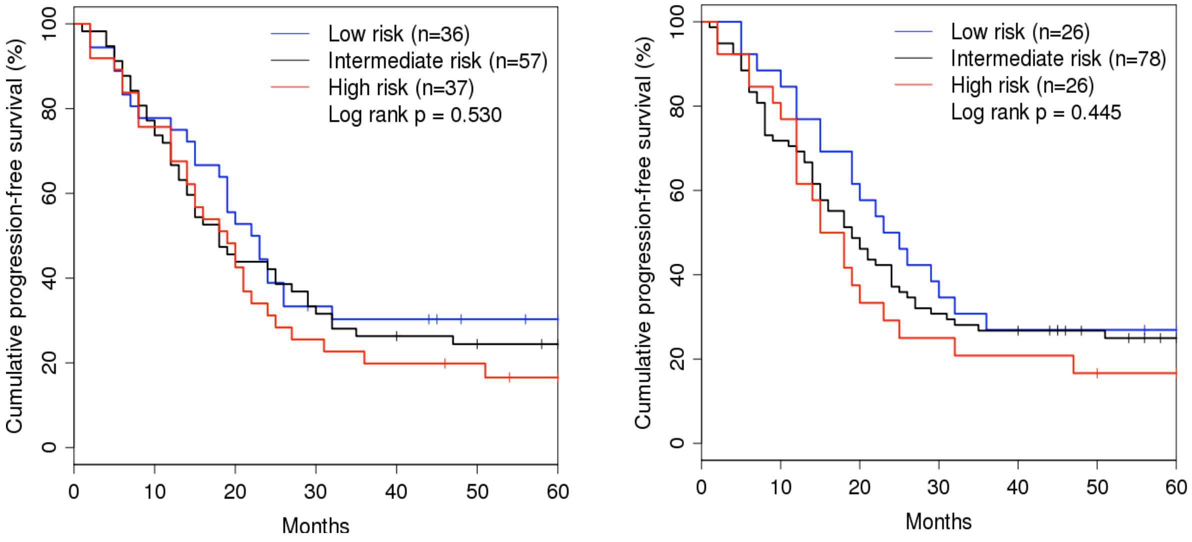
(C) Validation: PFS **(D) Validation: OS**



Supplemental Figure 4A. Kaplan-Meier curves for the training set (TCGA) and the validation set after classifying patients into three groups at the 20- and 80-percentiles, using PROVAR.

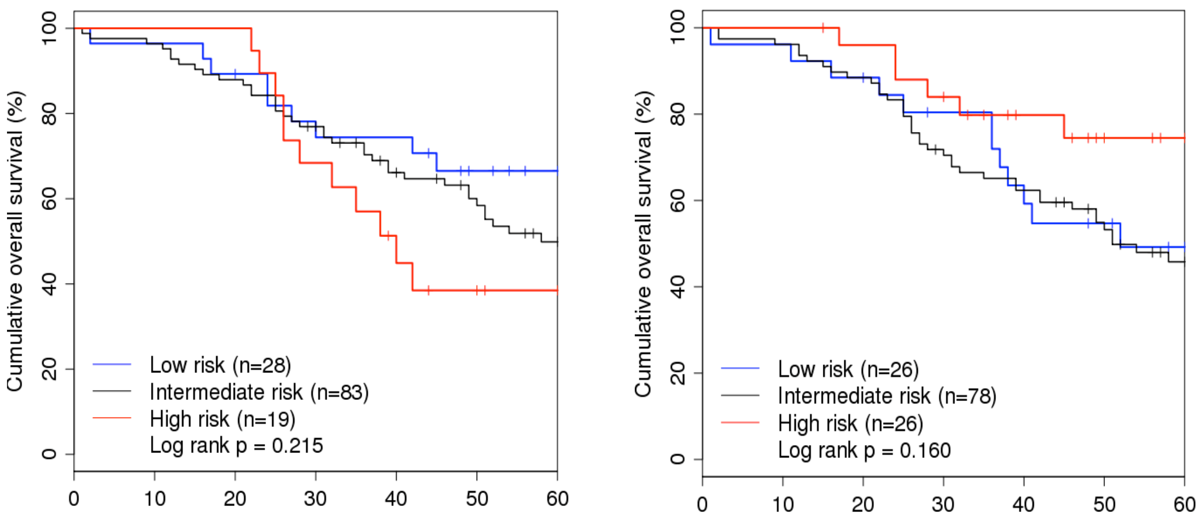


(A) PROVAR: PFS **(B) Konstantinopoulos: PFS**



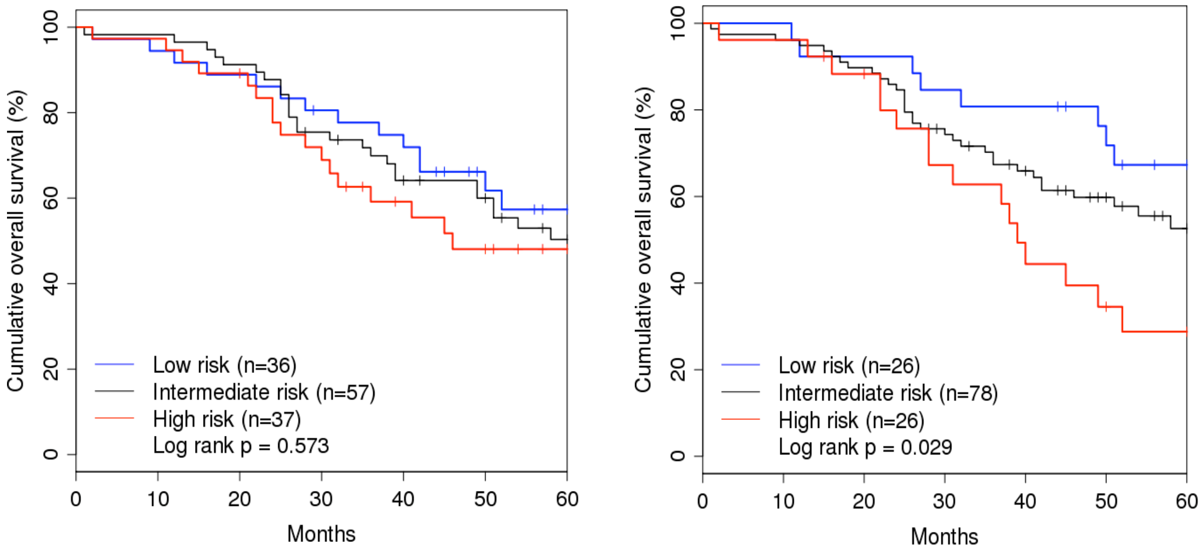
(C) Kang: PFS **(D) Verhaak: PFS**

Supplemental Figure 4B. Kaplan-Meier curves for progression-free survival in the subset of validation samples (n=130) after classifying patients into three groups at the 20- and 80-percentiles. Due to many ties, sample sizes of high and low risk groups are not 20% of the entire sample size with Kang's model.



(A) PROVAR: OS

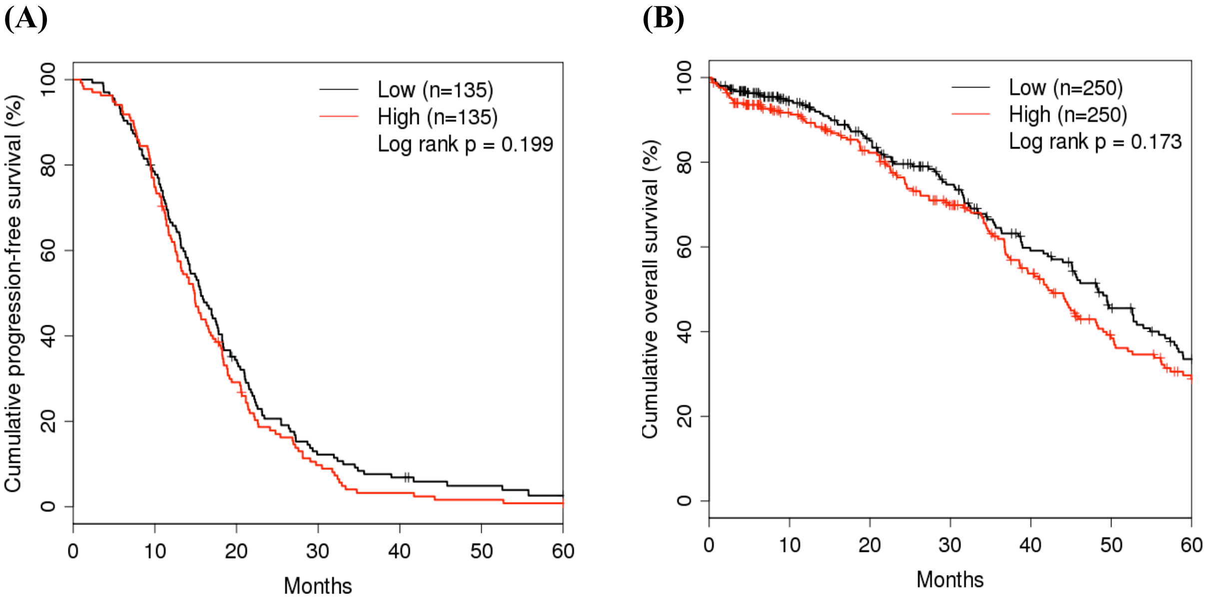
(B) Konstantinopoulos: OS



(C) Kang: OS

(D) Verhaak: OS

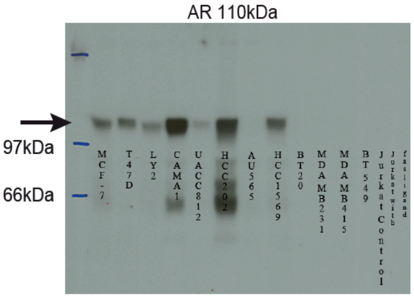
Supplemental Figure 4C. Kaplan-Meier curves for overall survival in the subset of validation samples (n=130) after classifying patients into three groups at the 20- and 80-percentiles. Due to many ties, sample sizes of high and low risk groups are not 20% of the entire sample size with Kang's model.

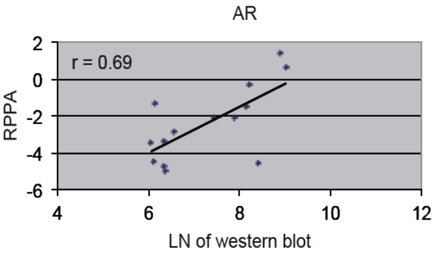


Supplemental Figure 5. Kaplan-Meier curves for PFS and OS in the TCGA set, which were generated using a new prediction index based on the genes matching the nine proteins consisting of PROVAR and the same coefficient weights.

(1)

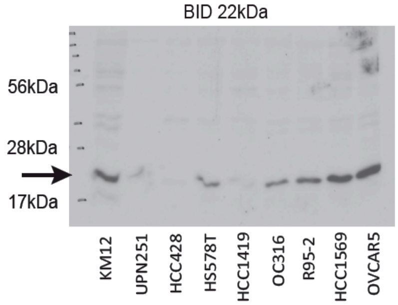
Androgen receptor (AR)

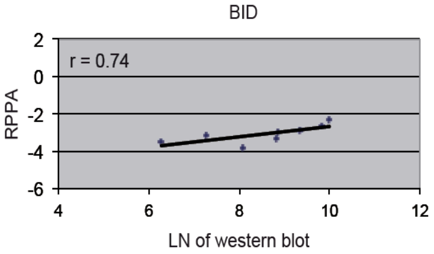




(2)

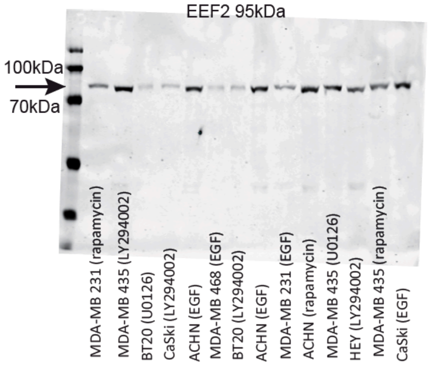
BH3-interacting domain death agonist (BID)

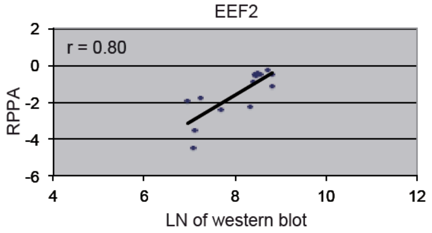




(3)

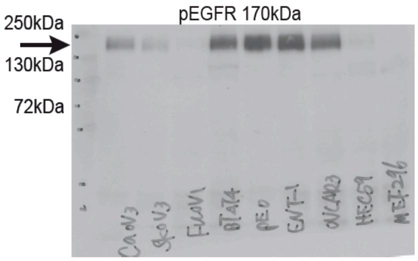
Eukaryotic translation elongation factor 2 (EEF2)

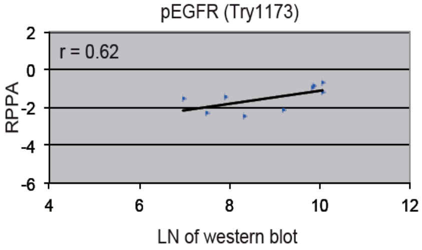




(4)

phospholylated Epidermal growth factor receptor (pEGFR Try1173)

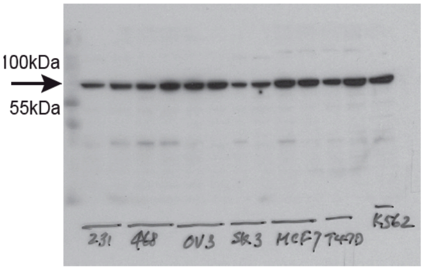




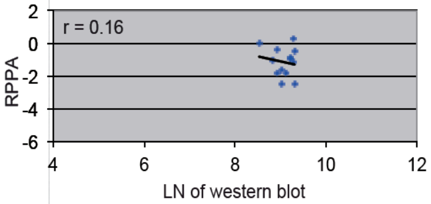
(5)

70kDa heat-shock protein (HSP70)

HSP70 72-73kDa



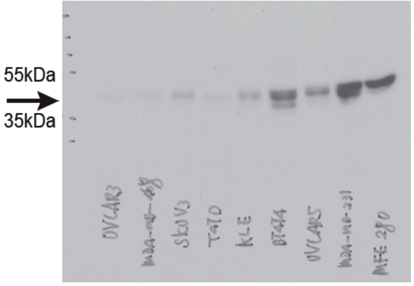
HSP70



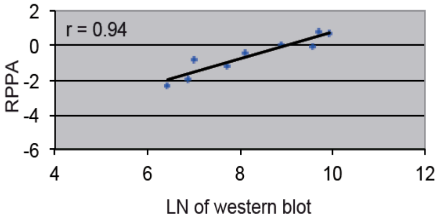
(6)

phosphorylated Dual specificity mitogen-activated protein kinase kinase 1 (pMEK1 Ser217+Ser221)

pMEK1 45kDa



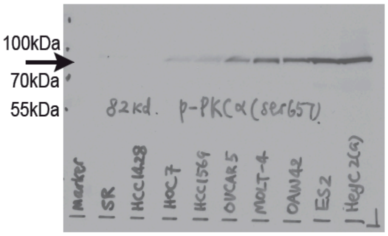
pMEK1



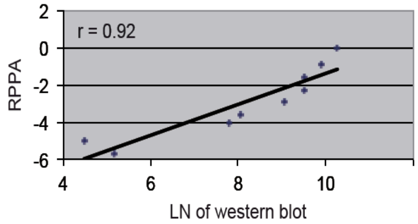
(7)

phospholylated Protein kinase C alpha (pPKCα Ser675)

pPKCα 82kDa

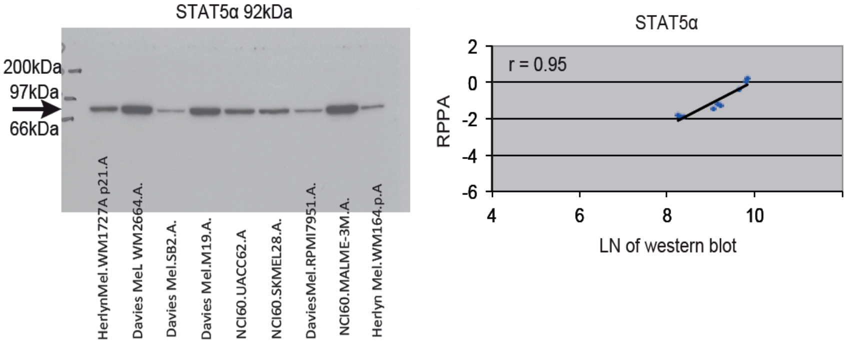


pPKCα (Ser675)



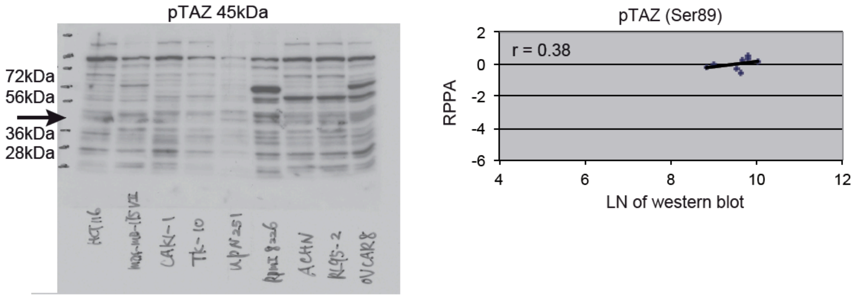
(8)

Signal transducer and activator of transcription 5A (STAT5α)

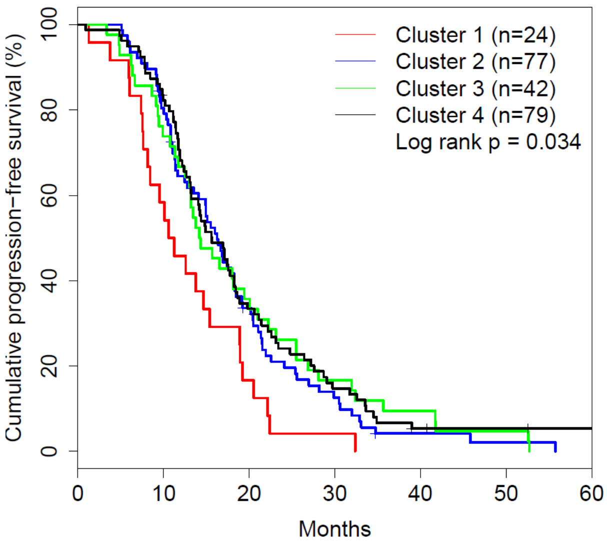


(9)

phosphorylated Tafazzin (pTAZ Ser89)

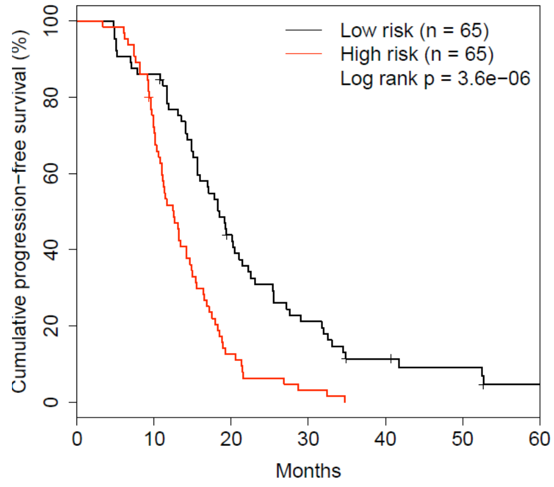


Supplemental Figure 6. Western blot analysis for the nine proteins. Plots on the left show the representative bands from western blot experiments, and plots on the right illustrate correlations between RPPA and western blotting data. Seven markers except pTAZ and HSP70 showed monospecific bands with high correlation coefficients between RPPA and western blot based protein expressions. Although HSP70 had a low correlation coefficient, it showed a distinct monospecific band. The low correlation was thought to be purely due to a narrow dynamic range of expression levels. Despite the relatively poor validation, pTAZ antibody was used for RPPA, because pTAZ is one of markers that we believe may represent damaged tumor samples, and thus pTAZ antibody, more than being a specifically pTAZ targeting antibody, is a marker for damaged tumor samples. Also Table 2 shows pTAZ has a fairly significant association with progression-free survival, which has led us to retain pTAZ in our protein pool.

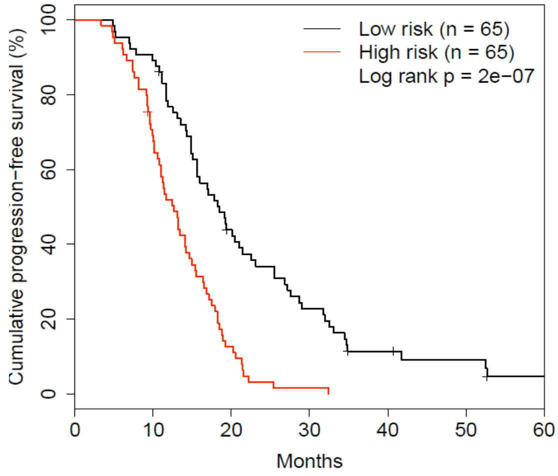


Supplemental Figure 7. Kaplan-Meier curves comparing progression-free survival in the four clusters of samples obtained from hierarchical clustering using RPPA data as illustrated in Figure 4. In Supplemental Table 2, are provided the sample size of each cluster and a comparison with existing molecular subtypes.

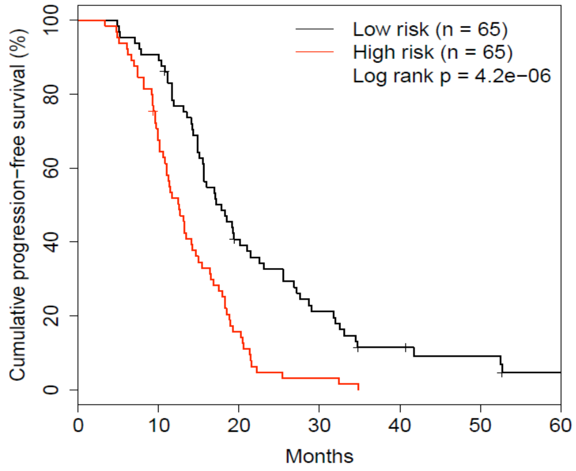
(A)TCGA:PROVAR



(B)TCGA:PROVAR+(age,stage,grade,surgery status)

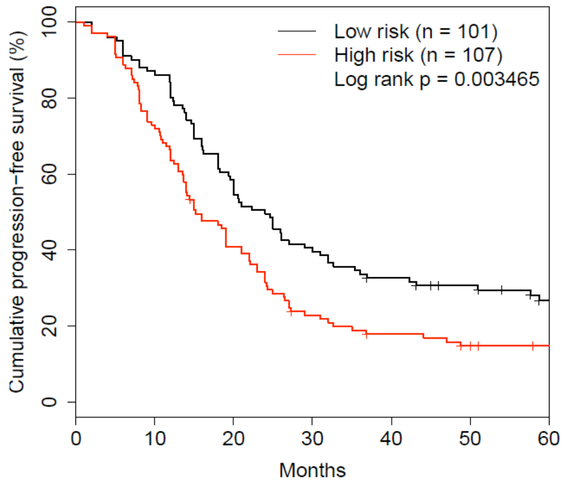


(C)TCGA:PROVAR+(age,stage,grade,surgery status)+*BRCA* mutation

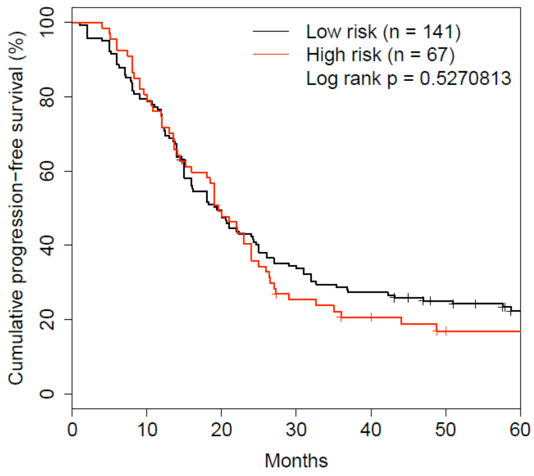


Time (mo)	Differences in survival rates between low and high risk groups		
	Model (A)	Model (B)	Model (C)
12	0.250	0.249	0.249
15	0.329	0.297	0.297
18	0.329	0.297	0.234
21	0.280	0.312	0.281
24	0.246	0.310	0.279
27	0.213	0.277	0.246
30	0.180	0.212	0.180

(D)Validation:PROVAR



(E)Validation:PROVAR+(age,stage,grade, surgery status)



Supplemental Figure 8. Kaplan-Meier curves for three models with the followings as covariates: (i) PROVAR only, (ii) PROVAR + age, stage, grade, surgery status, (iii) PROVAR + age, stage, grade, surgery status + *BRCA*1/2 germline/somatic mutation. A total of 130 TCGA samples had complete data for analysis. Because mutation status was not available, the first two models were considered for 208 validation samples. For each model, Cox regression coefficients were estimated using 130 TCGA samples. Patients were classified into two risk groups according to their risk scores (that is, predicted values derived from multivariate Cox regressions) with cutoff points at the median risk score in each model. The embedded table in this figure shows difference in survival rates between two risk groups for three models at certain times in the TCGA data.

Supplemental Table 1. The classification of patients using the nine and seven protein signatures.

		Using the seven protein signature		
		High risk group	Low risk group	Total
Using the nine protein signature	High risk group	79	32	111
	Low risk group	32	79	111
	Total	111	111	222

1. The patients in the training set were classified into two risk groups using the nine and seven protein signatures. The median was used as a cut-off for each case.
2. A chi-square test was used to compare the classification of patients under the two cases (p-value < 0.001).

Supplemental Table 2-1. A coomparison of protein expression based clusters vs. gene expression based subtypes in TCGA samples.

	Four Gene Expression Subtypes[2]					Risk Group[3]		Percentage[4]
	DIF	IMR	MES	PRO	Total	Low	High	(%)
Cluster 1[1]	5	4	15	0	24	0	24	100.0
	(6.2)	(5.6)	(6.3)	(5.9)				
Cluster 2	19	21	11	25	77	32	45	58.4
	(19.6)	(17.9)	(19.9)	(18.6)				
Cluster 3	14	10	10	8	42	23	19	45.2
	(10.8)	(9.9)	(11.0)	(10.3)				
Cluster 4	19	17	22	21	79	56	23	29.1
	(20.4)	(18.6)	(20.7)	(19.3)				
Total	57	52	58	54	222	111	111	

1. Four clusters of 222 TCGA training samples were obtained from hierarchical clustering shown in Figure 4.
2. Four subtypes of TCGA samples were obtained from TCGA Research Network, Nature 2011. (DIF: Differentiated, IMR: Immunoreactive, MES: Mesenchymal, PRO: Proliferative). There was one missing value.
3. Low and high risk group stratification was determined by PROVAR.
4. The percentage of high risk group.
5. The chi-square test was performed for testing the independence between four clusters and four subtypes (*p*-value = 0.001). Observed counts are given with expected counts in parentheses.

Supplemental Table 2-2. A comparison of protein expression based clusters vs. subtype signature activation in TCGA samples.

	Differentiated	Not Differentiated	Total
Cluster 1[1]	18 (75.0%)	6 (25.0%)	24
Cluster 2	54 (71.1%)	22 (28.9%)	76
Cluster 3	33 (78.6%)	9 (21.4%)	42
Cluster 4	58 (73.4%)	21 (26.6%)	79
Total	163 (73.8%)	58 (26.2%)	221

	Immunoreactive	Not Immunoreactive	Total
Cluster 1	17 (70.8%)	7 (29.2%)	24
Cluster 2	29 (38.2%)	47 (61.8%)	76
Cluster 3	17 (40.5%)	25 (59.5%)	42
Cluster 4	34 (43.0%)	45 (57.0%)	79
Total	97 (43.9%)	124 (56.1%)	221

	Mesenchymal	Not Mesenchymal	Total
Cluster 1	19 (79.2%)	5 (20.8%)	24
Cluster 2	19 (25.0%)	57 (75.0%)	76
Cluster 3	20 (47.6%)	22 (52.4%)	42
Cluster 4	43 (54.4%)	36 (45.6%)	79
Total	101 (45.7%)	120 (54.3%)	221

	Proliferative	Not Proliferative	Total
Cluster 1	20 (83.3%)	4 (16.7%)	24
Cluster 2	64 (84.2%)	12 (15.8%)	76
Cluster 3	30 (71.4%)	12 (28.6%)	42
Cluster 4	66 (83.5%)	13 (16.5%)	79
Total	180 (81.4%)	41 (18.6%)	221

1. Four clusters of 222 TCGA training samples were obtained from hierarchical clustering shown in - Figure 4.
2. Data on whether each subtype signature was activated in TCGA samples were obtained from Verhaak et al., 2013. There was one missing value.
3. For each subtype signature, the chi-square test was performed to see whether the signature occurred more frequently in certain clusters. The *p*-values were 0.846, 0.040, 7.7E-06, and 0.326 for

Differentiated, Immunoreactive, Mesenchymal, and Proliferative subtypes, respectively.

Supplemental Table 3. Results of functional enrichment analysis using FatiGO tool: top GO terms at level 6 and BioCarta pathways over-represented in the nine protein profile.

Terms or Pathways[1]	**Genes**[2]
GO: biological process at level 6	
positive regulation of biosynthetic process (GO:0009891)	EGFR,STAT5A
male sex differentiation (GO:0046661)	STAT5A,AR
development of primary sexual characteristics (GO:0045137)	STAT5A,AR
gland development (GO:0048732)	STAT5A,AR
BioCarta	
EGF Signaling Pathway	PRKCA,STAT5A,EGFR,MAP2K1
Bioactive Peptide Induced Signaling Pathway	PRKCA,STAT5A,MAP2K1
Growth Hormone Signaling Pathway	PRKCA,STAT5A,MAP2K1
TPO Signaling Pathway	PRKCA,STAT5A,MAP2K1
PDGF Signaling Pathway	PRKCA,STAT5A,MAP2K1
Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	PRKCA,EGFR,MAP2K1
Keratinocyte Differentiation	PRKCA,EGFR,MAP2K1
CBL mediated ligand-induced downregulation of EGF receptors	PRKCA,EGFR
Map Kinase Inactivation of SMRT Corepressor	EGFR,MAP2K1
IL 3 signaling pathway	STAT5A,MAP2K1
Mechanism of Gene Regulation by Peroxisome Proliferators via PPARa(alpha)	PRKCA,STAT5A,HSPA4

1. GO terms or pathways with a nominal *p*-value < 0.05 are shown.
2. It shows the list of protein markers involved in each term or pathway.

Supplemental Table 4. Detailed clinical information on patients in the study.

DATASET	ID	AGE	STAGE	GRADE	RESIDUAL DISEASE	OS MONTH	OS STATUS	PFS MONTH	PFS STATUS
Training	TCGA.04.1336	55	3	3	optimal	49.83	0	NA	0
Training	TCGA.04.1338	78	3	3	optimal	47.27	0	12.67	1
Training	TCGA.04.1342	80	4	2	supoptimal	18.77	1	NA	1
Training	TCGA.04.1343	72	4	3	supoptimal	12.03	1	NA	1
Training	TCGA.04.1348	44	3	3	optimal	49.43	1	19.13	1
Training	TCGA.04.1349	69	4	3	supoptimal	21.87	1	14.17	1
Training	TCGA.04.1356	62	2	3	supoptimal	49.97	1	5.20	1
Training	TCGA.04.1361	57	3	3	optimal	32.97	0	30.87	NA
Training	TCGA.04.1362	59	2	3	optimal	44.93	1	7.43	1
Training	TCGA.04.1369	53	3	2	optimal	21.40	1	10.50	1
Training	TCGA.04.1514	45	3	2	optimal	57.33	1	40.70	0
Training	TCGA.04.1517	79	3	3	supoptimal	20.27	1	11.63	1
Training	TCGA.04.1525	47	3	3	optimal	38.90	1	7.07	1
Training	TCGA.04.1542	52	3	2	optimal	60.00	0	34.50	1
Training	TCGA.04.1638	57	4	3	optimal	56.17	1	9.93	0
Training	TCGA.04.1644	48	3	3	supoptimal	49.57	1	21.13	1
Training	TCGA.04.1646	60	3	3	optimal	28.27	1	16.93	1
Training	TCGA.04.1648	57	3	2	optimal	29.03	1	13.73	NA
Training	TCGA.04.1649	74	3	3	optimal	60.00	0	55.73	NA
Training	TCGA.04.1651	53	3	3	optimal	36.73	1	33.00	NA
Training	TCGA.04.1654	69	3	2	optimal	48.37	1	26.93	NA
Training	TCGA.09.1662	58	4	3	optimal	60.00	0	34.87	1
Training	TCGA.09.1664	37	3	1	optimal	60.00	0	NA	NA
Training	TCGA.09.1665	73	3	2	optimal	42.17	1	15.60	1
Training	TCGA.09.1666	57	3	3	optimal	58.37	0	16.00	1
Training	TCGA.09.1670	57	3	3	optimal	18.23	0	18.23	1
Training	TCGA.09.1673	50	4	3	supoptimal	3.07	0	NA	1
Training	TCGA.09.1674	79	3	3	optimal	8.67	0	NA	1
Training	TCGA.09.2044	77	2	3	optimal	6.20	0	NA	0
Training	TCGA.09.2045	50	4	2	optimal	35.63	1	21.03	1
Training	TCGA.09.2049	64	3	3	supoptimal	60.00	0	31.73	1
Training	TCGA.09.2051	42	3	3	optimal	60.00	0	19.43	0
Training	TCGA.09.2054	58	3	3	optimal	21.20	1	NA	1
Training	TCGA.09.2056	62	3	3	optimal	12.63	0	NA	0
Training	TCGA.10.0925	58	3	1	optimal	55.07	1	18.60	1
Training	TCGA.10.0926	63	3	3	supoptimal	26.27	1	9.57	1
Training	TCGA.10.0931	44	3	3	optimal	33.33	1	10.00	1

Training	TCGA.10.0933	77	3	3	optimal	14.87	1	11.87	1
Training	TCGA.10.0936	69	3	3	supoptimal	37.43	1	NA	1
Training	TCGA.13.0720	48	3	3	optimal	45.17	1	9.73	1
Training	TCGA.13.0725	44	3	3	optimal	12.57	1	6.33	1
Training	TCGA.13.0793	40	4	3	optimal	29.10	0	11.70	1
Training	TCGA.13.0794	60	3	3	optimal	30.77	0	28.17	1
Training	TCGA.13.0797	49	3	3	optimal	8.83	0	NA	0
Training	TCGA.13.0799	44	3	3	optimal	7.90	0	NA	0
Training	TCGA.13.0800	52	3	3	optimal	8.23	0	NA	0
Training	TCGA.13.0801	46	3	3	optimal	8.40	0	NA	0
Training	TCGA.13.0802	79	3	3	optimal	8.30	0	NA	0
Training	TCGA.13.0804	73	3	3	optimal	35.77	1	10.97	1
Training	TCGA.13.0884	39	3	3	optimal	60.00	0	41.70	1
Training	TCGA.13.0886	67	3	3	optimal	60.00	0	NA	0
Training	TCGA.13.0887	42	3	3	optimal	60.00	0	17.10	1
Training	TCGA.13.0888	78	3	3	optimal	60.00	0	NA	0
Training	TCGA.13.0891	73	4	3	optimal	60.00	0	25.37	1
Training	TCGA.13.0894	53	3	3	optimal	50.30	1	18.83	1
Training	TCGA.13.0897	54	3	3	optimal	58.27	0	18.43	1
Training	TCGA.13.0899	60	3	3	optimal	56.93	0	18.23	1
Training	TCGA.13.0901	42	3	3	supoptimal	19.63	0	13.00	1
Training	TCGA.13.0903	42	4	3	optimal	48.03	0	NA	1
Training	TCGA.13.0906	50	3	3	optimal	45.57	0	NA	0
Training	TCGA.13.0910	58	3	3	optimal	37.60	0	NA	0
Training	TCGA.13.0911	55	4	3	optimal	28.07	0	9.27	1
Training	TCGA.13.0913	53	3	3	optimal	30.40	0	29.03	1
Training	TCGA.13.0916	49	3	3	optimal	21.43	0	NA	0
Training	TCGA.13.0920	65	3	3	optimal	14.00	0	9.90	1
Training	TCGA.13.0921	72	3	3	optimal	4.70	0	NA	0
Training	TCGA.13.1404	48	3	3	optimal	6.70	0	NA	0
Training	TCGA.13.1405	49	4	3	optimal	7.47	0	NA	0
Training	TCGA.13.1408	59	3	3	supoptimal	6.00	0	NA	1
Training	TCGA.13.1409	73	3	3	optimal	6.93	0	NA	1
Training	TCGA.13.1410	57	4	NA	supoptimal	4.77	0	NA	0
Training	TCGA.13.1411	81	3	3	supoptimal	4.27	0	NA	1
Training	TCGA.13.1412	41	4	3	optimal	5.40	0	NA	0
Training	TCGA.13.1477	49	4	2	optimal	55.37	1	7.80	1
Training	TCGA.13.1481	76	3	2	optimal	60.00	0	NA	0
Training	TCGA.13.1482	52	4	2	supoptimal	60.00	0	20.07	1
Training	TCGA.13.1483	61	3	3	supoptimal	29.80	1	9.87	1
Training	TCGA.13.1484	62	3	3	supoptimal	60.00	0	16.53	1
Training	TCGA.13.1487	74	4	NA	supoptimal	22.70	1	13.73	1
Training	TCGA.13.1488	59	4	3	supoptimal	60.00	0	11.70	1

Training	TCGA.13.1489	70	3	2	supoptimal	60.00	0	26.87	1
Training	TCGA.13.1491	55	3	3	supoptimal	53.17	1	16.93	1
Training	TCGA.13.1492	66	3	3	supoptimal	60.00	0	NA	0
Training	TCGA.13.1494	43	4	3	supoptimal	38.70	0	23.10	1
Training	TCGA.13.1495	60	3	2	optimal	49.90	0	32.57	1
Training	TCGA.13.1496	65	3	3	supoptimal	4.30	1	NA	NA
Training	TCGA.13.1498	73	3	3	supoptimal	38.13	0	17.77	1
Training	TCGA.13.1499	56	3	3	supoptimal	38.90	0	19.40	1
Training	TCGA.13.1500	71	3	3	supoptimal	14.17	1	8.43	1
Training	TCGA.13.1501	50	4	3	supoptimal	33.30	0	13.07	1
Training	TCGA.13.1504	68	3	3	supoptimal	16.80	0	NA	0
Training	TCGA.13.1505	63	3	3	optimal	4.27	0	NA	0
Training	TCGA.13.1506	45	3	3	supoptimal	4.47	0	NA	0
Training	TCGA.13.1507	77	3	3	optimal	4.83	0	NA	0
Training	TCGA.13.1509	64	4	3	optimal	4.20	0	NA	0
Training	TCGA.13.1511	52	4	3	supoptimal	3.93	0	NA	1
Training	TCGA.13.1512	49	3	3	optimal	3.13	0	NA	NA
Training	TCGA.13.1817	56	3	3	supoptimal	34.13	1	18.00	1
Training	TCGA.13.1819	59	2	3	optimal	60.00	0	14.30	1
Training	TCGA.13.2059	50	3	3	optimal	12.40	0	NA	0
Training	TCGA.13.2060	51	4	3	optimal	8.70	0	NA	0
Training	TCGA.13.2061	59	3	3	optimal	10.93	0	NA	0
Training	TCGA.13.2065	71	3	3	optimal	8.87	0	NA	0
Training	TCGA.13.2066	49	4	3	optimal	9.83	0	NA	0
Training	TCGA.20.1682	56	3	NA	supoptimal	27.87	0	NA	0
Training	TCGA.20.1683	65	3	3	optimal	25.73	0	20.60	0
Training	TCGA.20.1684	51	3	3	optimal	19.33	0	NA	0
Training	TCGA.20.1685	45	3	3	optimal	16.90	0	NA	0
Training	TCGA.20.1686	75	3	3	optimal	2.97	0	NA	0
Training	TCGA.20.1687	46	4	3	optimal	2.70	0	NA	0
Training	TCGA.23.1109	63	3	3	optimal	52.07	1	32.90	1
Training	TCGA.23.1110	42	3	3	optimal	55.27	0	10.87	0
Training	TCGA.23.1111	63	3	3	supoptimal	3.27	0	NA	NA
Training	TCGA.23.1121	52	3	3	supoptimal	6.47	0	NA	NA
Training	TCGA.23.1122	53	3	3	optimal	39.63	1	14.90	1
Training	TCGA.23.1123	59	3	3	supoptimal	33.93	1	NA	1
Training	TCGA.23.1124	63	3	3	optimal	58.93	1	21.37	1
Training	TCGA.23.1809	63	2	3	optimal	0.53	0	NA	NA
Training	TCGA.23.2077	45	3	3	optimal	60.00	0	41.07	0
Training	TCGA.23.2078	66	3	3	optimal	60.00	0	NA	0
Training	TCGA.23.2079	46	3	3	optimal	60.00	0	9.43	0
Training	TCGA.23.2081	49	4	3	optimal	60.00	0	NA	1
Training	TCGA.23.2641	85	3	3	optimal	2.80	0	NA	NA

Training	TCGA.23.2643	74	3	3	optimal	4.77	0	NA	0
Training	TCGA.23.2645	54	3	3	optimal	4.57	0	NA	NA
Training	TCGA.23.2647	49	3	3	optimal	4.50	0	NA	NA
Training	TCGA.23.2649	60	3	3	optimal	3.87	0	NA	NA
Training	TCGA.24.0966	78	3	3	supoptimal	7.73	0	NA	1
Training	TCGA.24.0970	63	3	3	supoptimal	11.80	1	9.33	1
Training	TCGA.24.0979	53	4	3	supoptimal	42.13	1	14.27	1
Training	TCGA.24.0980	53	3	3	supoptimal	7.77	1	4.83	1
Training	TCGA.24.0982	77	3	3	optimal	22.63	1	5.07	1
Training	TCGA.24.1103	50	3	3	optimal	54.83	1	22.57	1
Training	TCGA.24.1104	56	4	3	supoptimal	60.00	0	31.93	1
Training	TCGA.24.1105	36	3	3	optimal	48.07	1	15.67	1
Training	TCGA.24.1416	34	4	3	optimal	6.47	0	NA	0
Training	TCGA.24.1417	54	4	3	optimal	7.93	0	NA	0
Training	TCGA.24.1419	62	3	3	supoptimal	7.97	0	NA	0
Training	TCGA.24.1422	82	3	3	optimal	0.77	1	NA	NA
Training	TCGA.24.1423	61	3	3	optimal	6.33	0	NA	0
Training	TCGA.24.1424	67	3	3	optimal	6.10	0	NA	0
Training	TCGA.24.1427	58	3	3	supoptimal	4.87	0	NA	1
Training	TCGA.24.1428	50	3	3	optimal	17.60	0	14.93	1
Training	TCGA.24.1430	68	3	3	supoptimal	28.73	1	14.93	1
Training	TCGA.24.1431	67	3	3	optimal	19.43	1	6.63	1
Training	TCGA.24.1434	59	3	3	optimal	18.93	1	11.23	1
Training	TCGA.24.1435	57	3	3	optimal	44.13	1	16.83	1
Training	TCGA.24.1436	57	3	3	optimal	8.67	1	NA	1
Training	TCGA.24.1463	70	3	3	supoptimal	60.00	0	32.37	1
Training	TCGA.24.1464	70	3	3	supoptimal	12.63	1	10.77	1
Training	TCGA.24.1466	74	3	3	optimal	45.77	1	16.37	1
Training	TCGA.24.1467	51	3	3	optimal	60.00	0	41.73	1
Training	TCGA.24.1469	71	3	3	optimal	9.23	0	NA	0
Training	TCGA.24.1470	54	3	3	optimal	3.47	0	NA	0
Training	TCGA.24.1471	60	3	3	supoptimal	1.20	0	NA	NA
Training	TCGA.24.1474	57	3	3	optimal	22.50	1	11.03	1
Training	TCGA.24.1544	71	3	3	optimal	27.33	1	21.43	1
Training	TCGA.24.1545	69	3	3	supoptimal	58.17	1	28.70	1
Training	TCGA.24.1546	46	3	3	optimal	60.00	0	NA	NA
Training	TCGA.24.1548	57	3	3	optimal	16.43	1	6.90	1
Training	TCGA.24.1549	58	3	3	supoptimal	57.37	1	34.73	1
Training	TCGA.24.1550	49	3	3	optimal	41.63	1	29.73	1
Training	TCGA.24.1551	53	3	3	optimal	52.63	1	25.47	1
Training	TCGA.24.1552	77	3	3	optimal	41.97	1	13.43	1
Training	TCGA.24.1553	53	3	3	optimal	58.90	1	18.43	1
Training	TCGA.24.1555	50	3	3	supoptimal	60.00	0	52.57	1

Training	TCGA.24.1556	50	2	3	optimal	60.00	0	18.30	1
Training	TCGA.24.1557	49	3	3	supoptimal	40.43	1	14.90	1
Training	TCGA.24.1558	73	3	3	optimal	19.80	1	9.10	1
Training	TCGA.24.1560	51	3	4	optimal	44.70	1	4.77	1
Training	TCGA.24.1562	67	3	3	optimal	46.13	1	7.60	1
Training	TCGA.24.1563	66	3	3	optimal	48.37	1	13.20	1
Training	TCGA.24.1564	67	3	3	optimal	26.23	1	7.37	1
Training	TCGA.24.1565	74	3	3	optimal	10.40	1	4.83	1
Training	TCGA.24.1567	54	3	3	optimal	17.47	1	11.17	1
Training	TCGA.24.1603	53	3	3	supoptimal	60.00	0	33.07	1
Training	TCGA.24.1604	67	3	3	supoptimal	60.00	0	NA	1
Training	TCGA.24.1614	57	3	3	optimal	49.00	1	21.47	1
Training	TCGA.24.1616	56	3	3	optimal	38.77	1	13.50	1
Training	TCGA.24.1842	49	3	3	optimal	8.43	0	NA	0
Training	TCGA.24.1844	64	3	3	optimal	3.77	0	NA	NA
Training	TCGA.24.1845	42	3	3	optimal	3.87	0	NA	NA
Training	TCGA.24.1846	45	3	3	optimal	4.43	0	NA	NA
Training	TCGA.24.1849	80	3	3	optimal	5.83	0	NA	0
Training	TCGA.24.1850	72	3	3	optimal	5.57	0	NA	0
Training	TCGA.24.1852	55	3	3	optimal	60.00	0	33.63	1
Training	TCGA.24.1920	74	3	3	optimal	9.93	0	NA	0
Training	TCGA.24.1923	51	3	3	optimal	22.97	1	11.43	1
Training	TCGA.24.1924	65	3	3	optimal	30.63	1	10.67	1
Training	TCGA.24.1927	59	3	3	optimal	16.63	1	9.63	1
Training	TCGA.24.1930	53	3	3	optimal	60.00	0	18.10	1
Training	TCGA.24.2020	67	3	3	optimal	60.00	0	24.10	1
Training	TCGA.24.2023	54	3	3	optimal	45.47	1	35.63	1
Training	TCGA.24.2024	72	3	3	optimal	58.97	1	14.03	1
Training	TCGA.24.2026	79	3	3	supoptimal	35.30	1	NA	NA
Training	TCGA.24.2027	51	4	3	supoptimal	60.00	0	20.57	1
Training	TCGA.24.2029	75	3	3	supoptimal	14.63	1	12.40	1
Training	TCGA.24.2030	87	3	3	supoptimal	56.70	1	21.53	1
Training	TCGA.24.2033	87	3	3	supoptimal	18.73	1	11.70	1
Training	TCGA.24.2036	50	3	3	optimal	60.00	0	30.47	1
Training	TCGA.24.2038	68	3	0	optimal	45.10	1	38.97	1
Training	TCGA.24.2254	66	3	3	optimal	57.87	1	20.20	1
Training	TCGA.24.2260	74	3	3	optimal	36.67	1	22.23	1
Training	TCGA.24.2261	76	3	3	supoptimal	0.80	1	NA	1
Training	TCGA.24.2262	57	3	3	optimal	0.37	1	NA	1
Training	TCGA.24.2267	58	2	3	optimal	48.20	1	17.07	1
Training	TCGA.24.2271	55	3	3	supoptimal	32.07	1	27.57	1
Training	TCGA.24.2281	68	2	3	optimal	45.20	0	NA	0
Training	TCGA.24.2288	70	3	3	supoptimal	0.83	1	NA	1

Training	TCGA.24.2289	69	4	3	supoptimal	60.00	0	18.93	1
Training	TCGA.24.2290	56	3	3	optimal	36.73	1	10.80	1
Training	TCGA.24.2295	69	3	3	supoptimal	33.57	1	9.37	1
Training	TCGA.24.2297	56	3	3	supoptimal	56.63	1	NA	NA
Training	TCGA.24.2298	56	3	3	supoptimal	54.00	1	15.63	1
Training	TCGA.25.1312	69	4	3	optimal	1.03	1	NA	NA
Training	TCGA.25.1313	62	4	3	optimal	27.30	1	13.13	1
Training	TCGA.25.1314	42	4	3	optimal	33.43	1	9.10	1
Training	TCGA.25.1315	50	3	3	optimal	52.77	1	5.10	1
Training	TCGA.25.1316	55	3	3	optimal	42.63	1	9.20	1
Training	TCGA.25.1318	54	3	3	optimal	35.47	1	6.17	1
Training	TCGA.25.1319	73	3	3	supoptimal	60.00	0	24.33	NA
Training	TCGA.25.1320	65	3	3	optimal	38.47	1	14.10	1
Training	TCGA.25.1321	65	3	3	optimal	34.43	1	15.10	1
Training	TCGA.25.1322	62	4	3	supoptimal	3.03	1	NA	1
Training	TCGA.25.1323	72	3	3	optimal	13.17	1	12.17	1
Training	TCGA.25.1325	77	4	3	supoptimal	32.53	1	NA	NA
Training	TCGA.25.1326	61	3	3	optimal	41.60	1	13.17	1
Training	TCGA.25.1328	38	3	3	optimal	60.00	0	8.13	1
Training	TCGA.25.1329	76	3	3	supoptimal	15.23	1	NA	NA
Training	TCGA.25.1623	71	4	3	optimal	18.83	1	11.40	1
Training	TCGA.25.1625	66	3	3	optimal	28.00	1	17.53	1
Training	TCGA.25.1626	65	3	3	supoptimal	17.23	1	10.60	1
Training	TCGA.25.1627	73	3	3	optimal	13.13	1	NA	NA
Training	TCGA.25.1628	67	3	3	optimal	20.87	1	9.53	1
Training	TCGA.25.1630	73	3	3	optimal	38.73	1	NA	NA
Training	TCGA.25.1631	73	3	3	optimal	0.30	1	NA	0
Training	TCGA.25.1632	68	4	3	optimal	59.97	1	17.90	1
Training	TCGA.25.1633	64	3	3	optimal	60.00	0	20.53	1
Training	TCGA.25.1635	71	3	3	optimal	52.77	1	20.47	1
Training	TCGA.25.1878	60	3	3	optimal	60.00	0	32.37	1
Training	TCGA.25.2042	60	3	3	supoptimal	13.20	1	NA	1
Training	TCGA.25.2391	57	3	3	supoptimal	49.73	1	NA	0
Training	TCGA.25.2393	81	3	3	supoptimal	38.57	1	10.17	1
Training	TCGA.25.2396	71	3	3	optimal	3.07	1	NA	NA
Training	TCGA.25.2397	59	4	3	optimal	12.17	1	NA	NA
Training	TCGA.25.2398	71	3	3	optimal	45.63	1	19.23	1
Training	TCGA.25.2399	80	3	3	supoptimal	20.27	1	8.10	1
Training	TCGA.25.2400	76	3	3	optimal	42.60	1	19.23	1
Training	TCGA.25.2401	64	3	3	optimal	3.00	1	NA	NA
Training	TCGA.25.2404	38	3	3	optimal	29.40	1	14.17	1
Training	TCGA.25.2408	37	4	2	optimal	31.40	1	11.10	1
Training	TCGA.25.2409	71	4	3	optimal	27.33	1	10.10	1

Training	TCGA.29.1688	39	3	2	supoptimal	60.00	0	6.10	1
Training	TCGA.29.1690	66	3	2	supoptimal	48.27	1	NA	1
Training	TCGA.29.1691	51	3	2	optimal	49.00	1	20.43	1
Training	TCGA.29.1693	72	3	3	supoptimal	60.00	0	23.13	1
Training	TCGA.29.1694	45	3	NA	supoptimal	39.57	1	NA	1
Training	TCGA.29.1695	62	3	2	supoptimal	40.97	1	NA	NA
Training	TCGA.29.1696	43	3	2	optimal	34.40	1	11.40	1
Training	TCGA.29.1697	62	3	3	supoptimal	31.60	1	16.63	1
Training	TCGA.29.1698	53	3	3	optimal	60.00	0	6.00	1
Training	TCGA.29.1699	57	3	3	optimal	36.87	1	NA	NA
Training	TCGA.29.1701	56	3	3	supoptimal	17.17	1	9.93	1
Training	TCGA.29.1702	84	3	3	optimal	24.27	1	9.50	1
Training	TCGA.29.1703	56	3	2	optimal	60.00	0	10.80	1
Training	TCGA.29.1705	47	3	2	supoptimal	18.50	1	9.43	1
Training	TCGA.29.1707	41	2	3	optimal	42.53	0	40.00	NA
Training	TCGA.29.1711	45	3	2	optimal	35.10	0	NA	0
Training	TCGA.29.1761	80	3	3	supoptimal	17.60	1	NA	1
Training	TCGA.29.1762	59	4	2	supoptimal	60.00	0	45.80	1
Training	TCGA.29.1764	49	3	2	supoptimal	60.00	0	26.40	1
Training	TCGA.29.1766	74	3	2	supoptimal	39.93	1	22.40	1
Training	TCGA.29.1768	50	4	3	supoptimal	31.73	1	18.23	1
Training	TCGA.29.1769	40	3	3	optimal	23.30	0	NA	0
Training	TCGA.29.1770	54	3	2	optimal	24.70	0	12.57	1
Training	TCGA.29.1771	76	3	2	supoptimal	22.83	0	19.80	1
Training	TCGA.29.1774	82	3	3	supoptimal	17.53	0	7.77	1
Training	TCGA.29.1775	51	3	2	optimal	12.53	0	11.37	1
Training	TCGA.29.1776	63	3	3	supoptimal	12.00	0	NA	1
Training	TCGA.29.1777	47	3	2	supoptimal	12.47	0	NA	1
Training	TCGA.29.1778	77	3	3	optimal	15.13	0	NA	0
Training	TCGA.29.1781	69	3	3	optimal	8.47	0	NA	0
Training	TCGA.29.1783	58	3	3	optimal	7.30	0	NA	0
Training	TCGA.29.1785	55	3	3	supoptimal	36.80	1	15.77	NA
Training	TCGA.29.2425	60	3	2	supoptimal	60.00	0	52.57	0
Training	TCGA.29.2427	60	3	3	supoptimal	60.00	0	52.70	1
Training	TCGA.29.2428	58	3	3	supoptimal	45.73	0	NA	0
Training	TCGA.29.2429	79	3	3	supoptimal	14.03	1	NA	1
Training	TCGA.29.2431	59	3	2	optimal	42.83	0	32.00	1
Training	TCGA.29.2432	61	3	3	supoptimal	21.77	1	5.77	1
Training	TCGA.29.2434	52	3	3	optimal	11.63	0	NA	0
Training	TCGA.29.2436	36	3	2	optimal	9.90	0	NA	0
Training	TCGA.30.1718	44	3	3	optimal	52.63	1	29.87	1
Training	TCGA.30.1855	61	3	3	optimal	2.50	1	NA	1
Training	TCGA.30.1856	56	3	3	optimal	15.90	1	7.30	1

Training	TCGA.30.1860	58	3	3	supoptimal	45.53	1	13.23	1
Training	TCGA.30.1861	74	3	3	optimal	35.27	1	NA	NA
Training	TCGA.30.1869	50	4	3	optimal	52.10	1	25.57	1
Training	TCGA.30.1887	67	3	2	optimal	24.60	1	NA	1
Training	TCGA.30.1891	61	3	2	optimal	30.47	1	6.03	1
Training	TCGA.30.1892	52	3	3	optimal	49.47	1	8.43	1
Training	TCGA.31.1944	47	3	3	optimal	46.20	0	22.60	1
Training	TCGA.31.1946	30	3	3	optimal	30.60	0	22.13	1
Training	TCGA.31.1950	76	3	2	optimal	19.03	0	11.63	1
Training	TCGA.31.1951	58	3	3	optimal	22.77	0	21.93	1
Training	TCGA.31.1955	43	3	3	optimal	43.10	0	30.60	1
Training	TCGA.36.1568	52	3	3	supoptimal	29.13	0	18.23	1
Training	TCGA.36.1569	52	3	3	optimal	29.47	0	NA	NA
Training	TCGA.36.1570	49	3	3	supoptimal	21.83	0	12.50	1
Training	TCGA.36.1571	53	3	3	optimal	23.17	1	12.47	1
Training	TCGA.36.1575	83	3	3	optimal	8.67	0	NA	0
Training	TCGA.36.1576	76	3	3	supoptimal	30.47	0	27.20	1
Training	TCGA.36.1577	43	2	2	optimal	26.10	0	NA	0
Training	TCGA.36.1578	63	4	3	supoptimal	28.23	0	10.33	1
Training	TCGA.36.1580	82	3	3	supoptimal	24.57	1	14.67	1
Training	TCGA.36.1581	63	2	3	optimal	25.03	0	23.40	1
Training	TCGA.36.2529	71	3	3	supoptimal	35.53	0	18.90	1
Training	TCGA.36.2530	38	3	3	supoptimal	33.47	0	21.00	1
Training	TCGA.36.2532	61	3	3	optimal	29.90	0	NA	1
Training	TCGA.36.2534	72	3	3	supoptimal	30.20	0	12.77	1
Training	TCGA.36.2537	39	3	3	supoptimal	26.27	0	14.37	1
Training	TCGA.36.2538	37	3	3	supoptimal	25.43	0	17.43	1
Training	TCGA.36.2540	26	3	1	supoptimal	24.13	0	22.17	1
Training	TCGA.36.2542	59	3	3	optimal	21.90	0	NA	0
Training	TCGA.36.2543	85	3	3	supoptimal	2.27	1	0.90	1
Training	TCGA.36.2544	58	3	3	supoptimal	21.27	0	10.83	1
Training	TCGA.36.2545	42	3	3	optimal	18.57	0	NA	0
Training	TCGA.36.2547	64	3	3	optimal	20.80	0	NA	NA
Training	TCGA.36.2548	57	3	3	supoptimal	14.37	0	13.17	1
Training	TCGA.36.2549	54	2	3	optimal	6.13	0	NA	0
Training	TCGA.36.2551	57	3	3	supoptimal	16.37	0	11.27	1
Training	TCGA.36.2552	64	2	3	optimal	11.63	0	NA	0
Training	TCGA.42.2582	49	3	3	optimal	14.50	0	NA	1
Training	TCGA.42.2587	75	3	3	supoptimal	9.20	0	NA	0
Training	TCGA.42.2588	61	4	3	supoptimal	9.57	0	3.73	1
Training	TCGA.42.2589	54	3	3	optimal	7.67	0	NA	0
Training	TCGA.42.2590	57	4	2	supoptimal	7.57	0	7.53	1
Training	TCGA.42.2591	57	3	NA	optimal	7.73	0	NA	0

Training	TCGA.57.1586	66	3	3	supoptimal	22.63	0	8.63	1
Training	TCGA.59.2348	59	3	3	supoptimal	60.00	0	NA	0
Training	TCGA.59.2351	51	3	3	optimal	60.00	0	60.00	0
Training	TCGA.59.2352	78	3	3	supoptimal	9.53	1	NA	1
Training	TCGA.59.2354	64	3	3	optimal	34.87	1	15.37	1
Training	TCGA.59.2363	40	3	3	optimal	5.47	0	NA	0
Training	TCGA.59.2372	74	3	2	optimal	45.40	1	NA	NA
Training	TCGA.61.1721	38	4	1	supoptimal	11.27	0	NA	0
Training	TCGA.61.1724	47	3	3	optimal	21.23	1	NA	1
Training	TCGA.61.1733	71	3	3	optimal	32.20	0	5.80	1
Training	TCGA.61.1736	45	3	3	supoptimal	49.47	1	25.47	1
Training	TCGA.61.1738	60	3	3	optimal	36.30	1	9.20	1
Training	TCGA.61.1740	71	3	3	supoptimal	2.47	1	NA	1
Training	TCGA.61.1741	76	3	3	supoptimal	34.13	1	16.23	1
Training	TCGA.61.1743	53	2	2	optimal	44.30	1	26.97	1
Training	TCGA.61.1895	52	3	3	optimal	1.43	0	NA	0
Training	TCGA.61.1899	81	3	3	optimal	8.53	0	NA	0
Training	TCGA.61.1900	51	3	3	optimal	5.87	0	NA	0
Training	TCGA.61.1906	55	3	3	supoptimal	34.60	1	7.87	1
Training	TCGA.61.1907	63	3	3	supoptimal	31.73	0	24.77	1
Training	TCGA.61.1910	56	2	3	optimal	37.53	0	NA	0
Training	TCGA.61.1911	55	2	3	supoptimal	43.07	0	28.10	1
Training	TCGA.61.1913	48	3	3	optimal	49.60	0	NA	0
Training	TCGA.61.1914	65	3	3	supoptimal	57.37	0	55.77	1
Training	TCGA.61.1915	50	2	3	supoptimal	60.00	0	NA	0
Training	TCGA.61.1916	53	3	2	optimal	15.83	1	10.87	NA
Training	TCGA.61.1918	45	4	3	optimal	15.97	1	13.77	1
Training	TCGA.61.1919	58	3	2	supoptimal	38.70	1	14.63	NA
Training	TCGA.61.1995	43	3	3	optimal	2.00	0	NA	1
Training	TCGA.61.2000	67	3	3	optimal	14.70	0	11.30	1
Training	TCGA.61.2003	53	3	2	optimal	4.03	0	NA	1
Training	TCGA.61.2009	65	3	3	supoptimal	40.40	0	3.37	1
Training	TCGA.61.2012	81	2	2	supoptimal	31.07	0	NA	NA
Training	TCGA.61.2017	64	3	1	optimal	46.60	0	33.53	1
Training	TCGA.61.2088	51	3	3	optimal	4.83	0	NA	0
Training	TCGA.61.2092	57	3	3	optimal	52.43	0	NA	0
Training	TCGA.61.2094	63	3	3	supoptimal	60.00	0	NA	0
Training	TCGA.61.2095	54	3	2	optimal	60.00	0	14.83	1
Training	TCGA.61.2098	62	3	2	supoptimal	60.00	0	NA	0
Training	TCGA.61.2101	55	3	2	supoptimal	56.27	1	NA	1
Training	TCGA.61.2102	74	3	3	supoptimal	6.57	1	NA	1
Training	TCGA.61.2104	53	2	2	optimal	60.00	0	56.00	NA
Training	TCGA.61.2109	40	3	3	supoptimal	20.97	1	15.50	1

Training	TCGA.61.2111	61	4	3	supoptimal	60.00	0	60.00	0
Training	TCGA.61.2113	54	2	3	supoptimal	22.53	1	9.70	NA
Training	TCGA.61.2610	61	3	3	supoptimal	52.63	1	17.43	1
Training	TCGA.61.2612	63	3	3	optimal	6.43	1	5.97	1
Training	TCGA.61.2613	73	3	3	supoptimal	31.50	1	11.93	1
Training	TCGA.61.2614	71	3	3	optimal	8.70	1	1.27	1
Validation	p89	65	3	2	supoptimal	8.97	1	NA	NA
Validation	p91	60	3	3	supoptimal	14.47	1	NA	NA
Validation	p92	39	3	3	supoptimal	17.80	1	8.23	1
Validation	p96	55	3	3	optimal	60.00	0	13.67	1
Validation	p99	59	2	3	optimal	60.00	0	NA	NA
Validation	p103	57	4	2	supoptimal	36.97	1	9.63	1
Validation	p104	67	3	2	supoptimal	39.60	1	9.03	1
Validation	p112	52	3	3	supoptimal	32.70	1	27.00	1
Validation	p113	56	3	3	supoptimal	17.77	1	11.83	1
Validation	p115	60	4	3	supoptimal	21.00	1	12.47	1
Validation	p117	48	3	2	supoptimal	16.97	1	9.00	1
Validation	p125	58	3	3	optimal	60.00	0	44.10	1
Validation	p130	69	3	2	optimal	60.00	0	32.63	1
Validation	p131	67	4	3	supoptimal	4.70	1	NA	NA
Validation	p134	57	3	2	supoptimal	39.77	1	36.83	1
Validation	p135	72	3	2	optimal	14.93	1	11.93	1
Validation	p140	58	4	3	supoptimal	3.77	1	NA	NA
Validation	p146	61	3	3	supoptimal	43.30	1	10.67	1
Validation	p169	71	3	3	supoptimal	16.23	1	NA	NA
Validation	p170	56	3	3	supoptimal	60.00	0	43.17	1
Validation	p173	63	3	2	supoptimal	47.47	1	24.23	1
Validation	p178	55	3	2	optimal	60.00	0	60.00	0
Validation	p221	46	3	3	optimal	49.60	1	21.03	1
Validation	p224	51	3	2	supoptimal	41.77	1	12.30	1
Validation	p236	57	3	3	optimal	23.40	1	12.43	1
Validation	p242	69	3	1	optimal	60.00	0	60.00	0
Validation	p244	48	3	1	optimal	60.00	0	60.00	0
Validation	p246	68	3	3	supoptimal	38.43	1	15.90	1
Validation	p250	50	3	3	optimal	57.67	1	26.43	1
Validation	p275	54	3	3	supoptimal	60.00	0	5.17	1
Validation	p278	67	3	3	supoptimal	60.00	0	20.60	1
Validation	p283	64	3	1	optimal	44.27	1	35.40	1
Validation	p292	50	3	3	supoptimal	27.23	1	7.40	1
Validation	p296	68	3	3	supoptimal	60.00	0	42.27	1
Validation	p301	58	4	3	supoptimal	30.97	1	7.13	1
Validation	p303	59	3	3	supoptimal	1.33	1	NA	NA
Validation	p310	63	3	3	supoptimal	16.90	1	NA	NA

Validation	p318	52	3	3	supoptimal	22.30	1	11.93	1
Validation	p325	48	3	1	optimal	43.10	1	20.63	1
Validation	p352	63	3	3	supoptimal	60.00	0	58.77	1
Validation	p353	67	3	3	supoptimal	57.00	1	22.07	1
Validation	p356	73	3	3	optimal	24.03	1	19.40	1
Validation	p357	49	3	3	supoptimal	25.80	1	6.23	1
Validation	p368	47	3	1	optimal	33.83	1	32.67	1
Validation	p377	69	3	3	supoptimal	20.73	1	10.60	1
Validation	p378	54	3	3	supoptimal	50.40	1	14.07	1
Validation	p382	55	3	3	supoptimal	60.00	0	27.27	1
Validation	p383	43	3	1	supoptimal	60.00	0	57.67	1
Validation	p385	78	3	3	supoptimal	33.23	1	18.43	1
Validation	p386	74	3	2	optimal	60.00	0	48.80	1
Validation	p388	58	3	3	optimal	0.63	1	NA	NA
Validation	p396	50	4	3	supoptimal	27.10	1	18.23	1
Validation	p400	71	3	3	supoptimal	21.47	1	11.47	1
Validation	p409	82	2	1	optimal	60.00	0	60.00	0
Validation	p416	54	4	3	supoptimal	60.00	0	60.00	0
Validation	p417	60	2	3	optimal	60.00	0	60.00	0
Validation	p433	71	3	3	supoptimal	32.73	1	14.43	1
Validation	p437	73	3	3	supoptimal	10.87	1	15.20	1
Validation	p439	69	4	3	supoptimal	2.30	1	NA	NA
Validation	p448	35	3	2	supoptimal	29.33	1	NA	NA
Validation	p450	64	4	3	supoptimal	33.10	1	7.83	1
Validation	p462	27	3	1	optimal	60.00	0	31.00	1
Validation	p463	54	3	3	supoptimal	60.00	0	60.00	0
Validation	p464	62	3	3	supoptimal	60.00	0	NA	NA
Validation	p474	66	4	3	supoptimal	60.00	0	60.00	0
Validation	p478	80	3	3	supoptimal	15.10	1	NA	NA
Validation	p480	70	3	3	supoptimal	1.60	1	NA	NA
Validation	p501	46	3	2	optimal	60.00	0	36.90	1
Validation	p520	57	3	2	optimal	45.07	1	24.27	1
Validation	p528	51	3	2	optimal	24.97	1	14.63	1
Validation	p533	73	3	3	optimal	56.17	1	19.60	1
Validation	p538	62	3	3	optimal	10.67	1	5.10	1
Validation	p539	61	3	3	supoptimal	49.97	1	26.47	1
Validation	p541	69	3	NA	supoptimal	8.73	1	4.30	1
Validation	p543	52	3	2	optimal	27.33	1	13.50	1
Validation	p553	54	3	3	supoptimal	21.57	1	10.73	1
Validation	p555	59	2	3	optimal	60.00	0	60.00	0
Validation	p556	69	3	3	optimal	19.30	1	13.50	1
Validation	p558	62	3	3	optimal	60.00	0	25.90	1
Validation	p563	71	3	3	supoptimal	60.00	0	60.00	0

Validation	p584	68	4	3	supoptimal	29.40	1	22.30	1
Validation	p589	67	3	3	optimal	41.17	0	NA	NA
Validation	p594	45	3	3	optimal	60.00	0	60.00	0
Validation	p597	56	3	2	optimal	20.10	1	16.10	1
Validation	p606	37	3	3	optimal	31.77	1	13.77	1
Validation	p607	57	3	3	optimal	60.00	0	60.00	0
Validation	p612	56	3	3	supoptimal	58.10	1	16.13	1
Validation	p616	81	3	3	supoptimal	1.67	1	NA	NA
Validation	p621	58	2	3	supoptimal	60.00	0	15.97	1
Validation	p631	66	3	3	supoptimal	52.30	1	24.60	1
Validation	p633	57	3	3	supoptimal	29.80	0	13.67	1
Validation	p642	81	3	3	optimal	10.77	1	NA	NA
Validation	p650	60	3	3	optimal	60.00	0	24.93	1
Validation	p651	45	3	3	supoptimal	60.00	0	7.97	1
Validation	p656	64	3	3	optimal	16.63	1	8.23	1
Validation	p657	63	3	3	supoptimal	57.97	0	57.97	0
Validation	s2	68	3	2	supoptimal	49.00	1	18.00	1
Validation	s4	34	3	3	supoptimal	41.00	1	2.00	1
Validation	s6	48	3	3	optimal	32.00	1	12.00	1
Validation	s7	54	3	2	optimal	42.00	1	19.00	1
Validation	s12	74	3	3	optimal	24.00	1	8.00	1
Validation	s17	71	3	2	optimal	60.00	0	60.00	0
Validation	s18	69	3	2	optimal	60.00	0	60.00	0
Validation	s20	54	3	2	optimal	60.00	0	60.00	0
Validation	s22	77	3	2	supoptimal	15.00	0	15.00	0
Validation	s25	51	3	2	optimal	60.00	0	29.00	1
Validation	s36	58	4	2	optimal	28.00	1	23.00	1
Validation	s38	52	3	2	optimal	60.00	0	15.00	1
Validation	s41	63	3	2	optimal	60.00	0	60.00	0
Validation	s51	69	3	3	supoptimal	48.00	0	14.00	1
Validation	s54	53	3	2	optimal	54.00	0	54.00	0
Validation	s57	57	3	3	optimal	49.00	0	12.00	1
Validation	s60	71	4	2	supoptimal	60.00	0	47.00	1
Validation	s61	46	3	2	supoptimal	60.00	0	26.00	1
Validation	s62	68	3	2	supoptimal	26.00	1	11.00	1
Validation	s64	61	3	2	optimal	50.00	0	50.00	0
Validation	s66	66	3	2	optimal	31.00	1	19.00	1
Validation	s68	44	3	2	optimal	46.00	0	46.00	0
Validation	s69	65	3	2	optimal	45.00	0	45.00	0
Validation	s72	70	3	2	optimal	26.00	1	13.00	1
Validation	s77	74	3	3	supoptimal	1.00	1	1.00	1
Validation	s79	75	3	3	optimal	27.00	1	16.00	1
Validation	s80	54	3	3	supoptimal	60.00	0	12.00	1

Validation	s84	60	4	3	supoptimal	46.00	1	16.00	1
Validation	s86	43	3	3	optimal	60.00	0	60.00	0
Validation	s88	50	4	2	optimal	60.00	0	51.00	1
Validation	s90	67	3	3	supoptimal	51.00	1	29.00	1
Validation	s93	50	3	2	optimal	60.00	0	60.00	0
Validation	s94	47	4	2	optimal	57.00	0	20.00	1
Validation	s95	43	3	2	optimal	42.00	0	4.00	1
Validation	s97	69	4	2	supoptimal	28.00	0	8.00	1
Validation	s117	81	3	3	optimal	38.00	0	18.00	1
Validation	s119	59	3	3	optimal	40.00	0	40.00	0
Validation	s120	57	4	2	supoptimal	52.00	1	6.00	1
Validation	s122	52	3	2	supoptimal	25.00	1	8.00	1
Validation	s123	58	3	2	supoptimal	22.00	1	15.00	1
Validation	s125	49	4	2	supoptimal	31.00	1	10.00	1
Validation	s129	62	3	2	optimal	13.00	1	12.00	1
Validation	s130	67	3	2	supoptimal	60.00	0	25.00	1
Validation	s132	61	3	3	optimal	60.00	0	36.00	1
Validation	s134	66	3	2	optimal	60.00	0	30.00	1
Validation	s139	65	3	3	optimal	60.00	0	35.00	1
Validation	s140	56	4	3	supoptimal	28.00	1	14.00	1
Validation	s143	58	3	3	supoptimal	39.00	0	6.00	1
Validation	s144	46	4	2	supoptimal	52.00	0	26.00	1
Validation	s145	49	3	3	supoptimal	49.00	0	24.00	1
Validation	s146	64	3	3	supoptimal	44.00	0	44.00	0
Validation	s148	58	3	3	optimal	35.00	0	24.00	1
Validation	s150	56	3	2	supoptimal	35.00	0	31.00	1
Validation	s184	58	3	3	optimal	60.00	0	60.00	0
Validation	s185	84	3	3	optimal	33.00	0	20.00	1
Validation	s330	73	3	3	supoptimal	9.00	1	5.00	1
Validation	s331	53	3	3	supoptimal	30.00	0	21.00	1
Validation	s333	74	3	2	optimal	29.00	0	29.00	0
Validation	s335	65	3	3	optimal	16.00	1	12.00	1
Validation	s340	74	3	2	supoptimal	2.00	1	2.00	1
Validation	s347	50	3	3	supoptimal	48.00	0	18.00	1
Validation	s348	58	3	3	optimal	50.00	0	24.00	1
Validation	s350	56	3	3	supoptimal	24.00	1	2.00	1
Validation	s352	42	3	2	supoptimal	36.00	1	18.00	1
Validation	s356	53	4	2	optimal	58.00	0	58.00	0
Validation	s357	70	3	3	supoptimal	50.00	1	22.00	1
Validation	s358	65	3	2	optimal	52.00	0	27.00	1
Validation	s360	67	3	2	supoptimal	60.00	0	32.00	1
Validation	s362	67	3	2	supoptimal	25.00	1	14.00	1
Validation	s363	58	3	2	optimal	60.00	0	60.00	0

Validation	s365	51	3	3	optimal	37.00	1	32.00	1
Validation	s366	50	4	2	supoptimal	18.00	1	13.00	1
Validation	s367	71	3	3	optimal	49.00	1	19.00	1
Validation	s368	76	4	3	supoptimal	32.00	1	8.00	1
Validation	s462	69	3	2	supoptimal	20.00	0	20.00	1
Validation	s467	66	3	3	supoptimal	57.00	0	22.00	1
Validation	s468	51	3	2	supoptimal	22.00	1	15.00	1
Validation	s469	64	4	2	supoptimal	2.00	1	2.00	1
Validation	s470	61	3	3	optimal	60.00	0	23.00	1
Validation	s475	69	4	3	supoptimal	21.00	1	8.00	1
Validation	s476	68	3	3	supoptimal	17.00	1	14.00	1
Validation	s477	55	3	2	supoptimal	60.00	0	60.00	0
Validation	s479	63	4	2	supoptimal	40.00	1	19.00	1
Validation	s480	53	3	2	supoptimal	11.00	1	5.00	1
Validation	s481	57	3	2	supoptimal	60.00	0	60.00	0
Validation	s482	63	3	2	supoptimal	45.00	1	12.00	1
Validation	s483	76	3	3	supoptimal	60.00	0	19.00	1
Validation	s484	66	4	3	supoptimal	57.00	0	15.00	1
Validation	s486	52	3	2	supoptimal	16.00	1	2.00	1
Validation	s487	49	3	3	supoptimal	56.00	0	56.00	0
Validation	s488	53	4	3	supoptimal	56.00	0	56.00	0
Validation	s490	46	3	2	supoptimal	49.00	0	15.00	1
Validation	s491	49	3	3	supoptimal	45.00	0	45.00	0
Validation	s493	49	3	2	supoptimal	35.00	1	5.00	1
Validation	s494	62	3	3	supoptimal	15.00	1	6.00	1
Validation	s495	45	3	3	optimal	51.00	1	15.00	1
Validation	s497	56	3	3	supoptimal	22.00	1	8.00	1
Validation	s498	51	3	2	supoptimal	39.00	1	18.00	1
Validation	s499	67	3	2	supoptimal	39.00	1	7.00	1
Validation	s500	53	3	2	supoptimal	38.00	1	9.00	1
Validation	s501	51	3	3	supoptimal	42.00	1	15.00	1
Validation	s503	46	3	3	supoptimal	32.00	0	32.00	1
Validation	s507	63	4	3	optimal	60.00	0	6.00	1
Validation	s510	68	3	3	supoptimal	26.00	1	10.00	1
Validation	s511	49	3	3	supoptimal	25.00	1	5.00	1
Validation	s512	48	3	2	supoptimal	60.00	0	60.00	0
Validation	s514	47	3	3	supoptimal	36.00	1	6.00	1
Validation	s516	52	4	3	optimal	60.00	0	24.00	1
Validation	s518	33	3	3	optimal	54.00	1	25.00	1
Validation	s519	36	3	3	supoptimal	12.00	1	7.00	1
Validation	s523	71	4	2	optimal	58.00	1	6.00	1
Validation	s527	71	4	3	supoptimal	60.00	0	27.00	1
Validation	s528	61	3	3	optimal	60.00	0	60.00	0

Validation	s531	65	4	3	supoptimal	60.00	0	60.00	0
Validation	s534	45	3	2	optimal	12.00	1	7.00	1
Validation	s535	50	3	3	optimal	60.00	0	60.00	0
Validation	s542	78	4	3	supoptimal	23.00	1	4.00	1
Validation	s543	51	3	2	supoptimal	51.00	0	51.00	0
Validation	s546	55	3	3	supoptimal	60.00	0	60.00	0
Validation	s547	63	3	2	supoptimal	27.00	1	5.00	1
Validation	s549	45	3	3	supoptimal	60.00	0	60.00	0
Validation	s551	66	3	3	supoptimal	60.00	0	60.00	0
Validation	s552	67	3	2	supoptimal	25.00	1	9.00	1
Validation	s554	52	3	3	supoptimal	30.00	1	21.00	1
Validation	s558	57	4	2	optimal	60.00	0	25.00	1
Validation	s559	50	3	3	supoptimal	60.00	0	60.00	0
Validation	s565	48	4	3	supoptimal	48.00	0	48.00	0
Validation	s567	40	3	3	optimal	57.00	0	14.00	1
Validation	s573	46	3	3	supoptimal	44.00	0	20.00	1
Validation	s578	44	3	3	supoptimal	28.00	0	12.00	1

Supplemental Table 5. Antibodies used for RPPA analysis.

Antibody Name	Gene Name	Antibody Origin	Antibody Source (Company)	Catalog Number
14-3-3_epsilon	YWHAE	Mouse	Santa Cruz Biotechnology	sc-2395
4E-BP1_pS65	EIF4EBP1	Rabbit	Cell Signaling Technology	9456
4E-BP1_pT37	EIF4EBP1	Rabbit	Cell Signaling Technology	9459
4E-BP1_pT70	EIF4EBP1	Rabbit	Cell Signaling Technology	9455
4E-BP1	EIF4EBP1	Rabbit	Cell Signaling Technology	9452
53BP1	TP53BP1	Rabbit	Cell Signaling Technology	4937
A-Raf_pS299	ARAF	Rabbit	Cell Signaling Technology	4431
ACC_pS79	ACACA ACACB	Rabbit	Cell Signaling Technology	3661
ACC1	ACACA	Rabbit	Epitomics	1768-1
AIB1	NCOA3	Mouse	BD Biosciences	611105
Akt_pS473	AKT1 AKT2 AKT3	Rabbit	Cell Signaling Technology	9271
Akt_pT308	AKT1 AKT2 AKT3	Rabbit	Cell Signaling Technology	9275
Akt	AKT1 AKT2 AKT3	Rabbit	Cell Signaling Technology	9272
alpha-Catenin	CTNNA1	Mouse	Calbiochem	CA1030
AMPK_alpha	PRKAA1	Rabbit	Cell Signaling Technology	2532
AMPK_pT172	PRKAA1	Rabbit	Cell Signaling Technology	2535
ANLN	ANLN	Mouse	Atlas	CAB036211

Annexin_I	ANXA1	Rabbit	Invitrogen	71-3400
AR	AR	Rabbit	Epitomics	1852-1
ARID1A	ARID1A	Mouse	Abgent	AT1188a
ATM	ATM	Rabbit	Abcam	ab32420
B-Raf	BRAF	Mouse	Santa Cruz Biotechnology	sc-5284
Bad_pS112	BAD	Rabbit	Cell Signaling Technology	9291
Bak	BAK1	Rabbit	Epitomics	1542-1
Bax	BAX	Rabbit	Cell Signaling Technology	2772
Bcl-2	BCL2	Mouse	Dako	Dako M0887
Bcl-2	BCL2	Rabbit	Cell Signaling Technology	2872
Bcl-X	BCL2L1	Rabbit	Epitomics	1018-1
Bcl-xL	BCL2L1	Rabbit	Cell Signaling Technology	2762
Beclin	BECN1	Goat	Santa Cruz Biotechnology	sc-10086
beta-Catenin	CTNNB1	Rabbit	Cell Signaling Technology	9562
Bid	BID	Rabbit	Epitomics	1008-1
Bim	BCL2L11	Rabbit	Epitomics	1036-1
c-Jun_pS73	JUN	Rabbit	Cell Signaling Technology	9164
c-Kit	KIT	Rabbit	Epitomics	1522
c-Met_pY1235	MET	Rabbit	Cell Signaling Technology	3129
c-Met	MET	Mouse	Cell Signaling Technology	3127
c-Myc	MYC	Rabbit	Cell Signaling	9402

			Technology	
C-Raf_pS338	RAF1	Rabbit	Cell Signaling Technology	9427
C-Raf	RAF1	Rabbit	Millipore	05-739
Caspase-3_Active	CASP3	Rabbit	Epitomics	1476-1
Caspase-7_cleavedD198	CASP7	Rabbit	Cell Signaling Technology	9491
Caspase-8	CASP8	Mouse	Cell Signaling Technology	9746
Caspase-9_cleavedD330	CASP9	Rabbit	Cell Signaling Technology	9501
Caveolin-1	CAV1	Rabbit	Cell Signaling Technology	3238
CD20	MS4A1	Rabbit	Epitomics	1632
CD31	PECAM1	Mouse	Dako	M0823
CD49b	ITGA2	Mouse	BD Biosciences	611016
CDK1	CDC2	Rabbit	Cell Signaling Technology	9112
Chk1_pS345	CHEK1	Rabbit	Cell Signaling Technology	2348
Chk1	CHEK1	Rabbit	Cell Signaling Technology	2345
Chk2_pT68	CHEK2	Rabbit	Cell Signaling Technology	2197
Chk2	CHEK2	Mouse	Cell Signaling Technology	3440
cIAP	BIRC2	Rabbit	Millipore	07-759
Claudin-7	CLDN7	Rabbit	Novus	NB100-91714
Collagen_VI	COL6A1	Rabbit	Santa Cruz Biotechnology	SC-20649
COX-2	PTGS2	Rabbit	Epitomics	2169-1

Cyclin_B1	CCNB1	Rabbit	Epitomics	1495-1
Cyclin_D1	CCND1	Rabbit	Santa Cruz Biotechnology	SC-718
Cyclin_E1	CCNE1	Mouse	Santa Cruz Biotechnology	SC-247
Cyclin_E2	CCNE2	Rabbit	Epitomics	1142
DJ-1	PARK7	Rabbit	Abcam	ab76008
Dvl3	DVL3	Rabbit	Cell Signaling Technology	3218
E-Cadherin	CDH1	Rabbit	Cell Signaling Technology	4065
eEF2	EEF2	Rabbit	Cell Signaling Technology	2332
eEF2K	EEF2K	Rabbit	Cell Signaling Technology	3692
EGFR_pY1068	EGFR	Rabbit	Cell Signaling Technology	2234
EGFR_pY1173	EGFR	Rabbit	Epitomics	1124
EGFR_pY992	EGFR	Rabbit	Cell Signaling Technology	2235
EGFR	EGFR	Rabbit	Santa Cruz Biotechnology	SC-03
eIF4E	EIF4E	Rabbit	Cell Signaling Technology	9742
ER-alpha_pS118	ESR1	Rabbit	Epitomics	1091-1
ER-alpha	ESR1	Rabbit	Lab Vision	RM-9101-S
ERCC1	ERCC1	Mouse	Lab Vision	MS-671-PO
ERK2	MAPK1	Rabbit	Santa Cruz Biotechnology	sc-154
FAK	PTK2	Rabbit	Epitomics	1700-1
Fibronectin	FN1	Rabbit	Epitomics	1574-1
FOXO3a_pS318_S321	FOXO3	Rabbit	Cell Signaling	9465

			Technology	
FOXO3a	FOXO3	Rabbit	Cell Signaling Technology	9467
GAB2	GAB2	Rabbit	Cell Signaling Technology	3239
GATA3	GATA3	Mouse	BD Biosciences	558686
GSK3-alpha-beta_pS21_S9	GSK3A GSK3B	Rabbit	Cell Signaling Technology	9331
GSK3-alpha-beta	GSK3A GSK3B	Mouse	Santa Cruz Biotechnology	SC-7291
GSK3_pS9	GSK3A GSK3B	Rabbit	Cell Signaling Technology	9336
HER2_pY1248	ERBB2	Rabbit	Upstate (Millipore)	06-229
HER2	ERBB2	Mouse	Lab Vision	MS-325-P1
HER2_pY1248	ERBB2	Rabbit	R&D systems	AF1768
HER3_pY1289	ERBB3	Rabbit	Cell Signaling Technology	4791
HER3	ERBB3	Mouse	Lab Vision	MS-201-P1ABX
HSP70	HSPA1A	Rabbit	Cell Signaling Technology	4872
IGF-1R-beta	IGF1R	Rabbit	Cell Signaling Technology	3027
IGFBP2	IGFBP2	Rabbit	Cell Signaling Technology	3922
INPP4B	INPP4B	Goat	Santa Cruz Biotechnology	SC-12318
IRS1	IRS1	Rabbit	Upstate (Millipore)	06-248
JNK_pT183_pT185	MAPK8	Rabbit	Cell Signaling Technology	4668
JNK2	MAPK9	Rabbit	Cell Signaling	4672

			Technology	
K-Ras	KRAS	Mouse	Santa Cruz Biotechnology	sc-30 (F234)
Ku80	XRCC5	Rabbit	Cell Signaling Technology	2180
LBK1	STK11	Mouse	Abcam	ab15095
Lck	LCK	Rabbit	Cell Signaling Technology	2752
MAPK_pT202_Y204	MAPK1 MAPK3	Rabbit	Cell Signaling Technology	4377
MEK1_pS217_S221	MAP2K1	Rabbit	Cell Signaling Technology	9154
MEK1	MAP2K1	Rabbit	Epitomics	1235-1
MIG-6	ERRFI1	Mouse	Sigma	WH0054206M1
Mre11	MRE11A	Rabbit	Cell Signaling Technology	4847
MSH2	MSH2	Mouse	Cell Signaling Technology	2850
MSH6	MSH6	Rabbit	Strategic Diagnostics Inc	2203.00.02
mTOR_pS2448	FRAP1	Rabbit	Cell Signaling Technology	2971
mTOR	FRAP1	Rabbit	Cell Signaling Technology	2983
N-Cadherin	CDH2	Rabbit	Cell Signaling Technology	4061
NF-kB-p65_pS536	NFKB1	Rabbit	Cell Signaling Technology	3033
NF2	NF2	Rabbit	Strategic Diagnostics Inc	2271.00.02
Notch1	NOTCH1	Rabbit	Cell Signaling Technology	3268
Notch3	NOTCH3	Rabbit	Santa Cruz Biotechnology	sc-5593

P-Cadherin	CDH3	Rabbit	Cell Signaling Technology	2130
p21	CDKN1A	Rabbit	Santa Cruz Biotechnology	SC-397
p27_pT157	CDKN1B	Rabbit	R&D systems	AF1555
p27_pT198	CDKN1B	Rabbit	Abcam	ab64949
p27	CDKN1B	Rabbit	Epitomics	1591-1
p38_MAPK	MAPK14	Rabbit	Cell Signaling Technology	9212
p38_pT180_Y182	MAPK14	Rabbit	Cell Signaling Technology	9211
p53	TP53	Rabbit	Cell Signaling Technology	9282
p70S6K_pT389	RPS6KB1	Rabbit	Cell Signaling Technology	9205
p70S6K	RPS6KB1	Rabbit	Epitomics	1494-1
p90RSK_pT359_S363	RPS6KA1	Rabbit	Cell Signaling Technology	9344
PAI-1	SERPINE1	Mouse	BD Biosciences	612024
PARP_cleaved	PARP1	Mouse	Cell Signaling Technology	9546
Paxillin	PXN	Rabbit	Epitomics	1500-1
PCNA	PCNA	Mouse	Abcam	ab29
PDCD4	PDCD4	Rabbit	Rockland	600-401-965
PDK1_pS241	PDK1	Rabbit	Cell Signaling Technology	3061
Pea-15	PEA15	Rabbit	Cell Signaling Technology	2780
PI3K-p110-alpha	PIK3CA	Rabbit	Cell Signaling Technology	4255
PI3K-p85	PIK3R1/2	Rabbit	Upstate	06-195

			(Millipore)	
PKC-alpha_pS657	PRKCA	Rabbit	Upstate (Millipore)	06-822
PKC-alpha	PRKCA	Mouse	Upstate (Millipore)	05-154
PKC-delta_pS664	PRKCD	Rabbit	Millipore	07-875
PR	PGR	Rabbit	Epitomics	1483-1
PRAS40_pT246	AKT1S1	Rabbit	Biosource	441100G
PRDX1	PRDX1	Rabbit	Sigma/Atlas	HPA007730
PTCH	PTCH1	Rabbit	Strategic Diagnostics Inc	2113.00.02
PTEN	PTEN	Rabbit	Cell Signaling Technology	9552
Rab11	RAB11A RAB11B	Rabbit	Cell Signaling Technology	3539
Rab25	RAB25	Rabbit	Covance Custom	Covance Custom
Rad50	RAD50	Mouse	Millipore	05-525
Rad51	RAD51	Mouse	Chem Biotech	na 71
Rb_pS807_S811	RB1	Rabbit	Cell Signaling Technology	9308
Rb	RB1	Mouse	Cell Signaling Technology	9309
RBM3	RBM3	Mouse	Atlas	CAB030038
S6_pS235_S236	RPS6	Rabbit	Cell Signaling Technology	2211
S6_pS240_S244	RPS6	Rabbit	Cell Signaling Technology	2215
S6	RPS6	Rabbit	Cell Signaling Technology	2217
SCD1	SCD1	Mouse	Santa Cruz Biotechnology	sc-58420

SETD2	SETD2	Rabbit	Abcam	ab69836
Shc_pY317	SHC1	Rabbit	Cell Signaling Technology	2431
Smac	DIABLO	Mouse	Cell Signaling Technology	2954
Smad1	SMAD1	Rabbit	Epitomics	1649-1
Smad3	SMAD3	Rabbit	Epitomics	1735-1
Smad4	SMAD4	Mouse	Santa Cruz Biotechnology	sc-7866
Snail	SNAI2	Mouse	Cell Signaling Technology	3895
Src_pY416	SRC	Rabbit	Cell Signaling Technology	2101
Src_pY527	SRC	Rabbit	Cell Signaling Technology	2105
Src	SRC	Mouse	Upstate (Millipore)	05-184
STAT3_pY705	STAT3	Rabbit	Cell Signaling Technology	9131
STAT5-alpha	STAT5A	Rabbit	Epitomics	1289-1
Stathmin	STMN1	Rabbit	Epitomics	1972-1
Syk	SYK	Mouse	Santa Cruz Biotechnology	sc-1240
Tau	MAPT	Mouse	Upstate (Millipore)	05-348
TAZ_pS89	WWTR1	Rabbit	Santa Cruz Biotechnology	sc-17610
TAZ	WWTR1	Rabbit	Cell Signaling Technology	2149
Transglutaminase	TGM2	Mouse	Lab Vision	MS-224
Tuberin	TSC2	Rabbit	Epitomics	1613-1
VASP	VASP	Rabbit	Cell Signaling Technology	3112

VEGFR2	KDR	Rabbit	Cell Signaling Technology	2479
XBP1	XBP1	Goat	Santa Cruz Biotechnology	sc-32136
XIAP	XIAP	Rabbit	Cell Signaling Technology	2042
XRCC1	XRCC1	Rabbit	Cell Signaling Technology	2735
YAP_pS127	YAP1	Rabbit	Cell Signaling Technology	4911
YAP	YAP1	Rabbit	Santa Cruz Biotechnology	sc-15407
YB-1_pS102	YBX1	Rabbit	Cell Signaling Technology	2900
YB-1	YBX1	Rabbit	Strategic Diagnostics Inc	1725.00.02
ASNS	ASNS	Rabbit	Sigma	HPA029318
EGFR	EGFR	Rabbit	Cell Signaling Technology	4405
EGFR	EGFR	Rabbit	Cell Signaling Technology	2232
Rab25 sigma	Rab25		BD Biosciences	
VHL	VHL	Rabbit	Epitomics	556347 (Lot 21483)
TTF1	TTF1	Rabbit	Epitomics	2044
TTF1	TTF1	Rabbit	Cell Signaling Technology	5883
NEK7	NEK7	Rabbit		3057
P-REX1			Epitomics	
TIGAR	C12ORF5	Rabbit	abcam	S1711
Axl	AXL	Mouse	Santa Cruz Biotechnology	ab54803

E2F1	E2F1	Mouse	Cell Signaling Technology	sc-251
EZH2	EZH2	Rabbit	Cell Signaling Technology	4905
KEAP1	KEAP1	Rabbit	R&D systems	4617
LCN2a	LCN2	Goat	Sigma	AF1757
MACC1	MACC1	Rrabbit	Epitomics	HPA020081
Nrf2	NFE2L2	Rabbit	Epitomics	2178-1
p16_INK4a	CDKN2A	Rabbit	Lab Vision	1712
PARP Ab-3	PARP1	Rabbit	Abcam	RB-1680
Thymidilate Synthase	TYMS	Mouse	Abcam	ab3145
CA9-M-C	CA9	Mouse	Invitrogen	107257
Complex II_ subunit30	SDHB	Mouse	Ambion	459230 /D0803
GAPDH	GAPDH	Mouse	Novus	am4300
GYG Glycogenin1	GYG1	Mouse	Cell Signaling Technology	H00002992-M07 (Lot 09226-3B5)
GYS-R	GYS1	Rabbit	Cell Signaling Technology	3886
GYS_pS641	GYS1	Rabbit	Novus	3891
HIF-1_alpha	HIF1A	Mouse	Abcam	NB100-131 (Lot f1)
HK II	HK2	Mouse	Cell Signaling Technology	76959
LDHA	LDHA	Rabbit	Abcam	3582
LDHB	LDHB	Mouse	Abcam	ab85319
Mitochondria	MTCO2	Mouse	Invitrogen	ab3298 (Lot GR20678-1)
Oxphos complex V_subunitb	ATP5A1	Mouse	Cell Signaling Technology	A21351 (Lot 830849)

PKM2	PKM2	Rabbit	Novus	4053
PYGB	PYGB	Rabbit	Sigma	NBP1-32799 (Lot 40002)
PYGL	PYGL	Rabbit	Novus/Abnova	HPA000962 (Lot A06395)
PYGM	PYGM	Mouse		H00005837-M10 (Lot 09160-2C4)