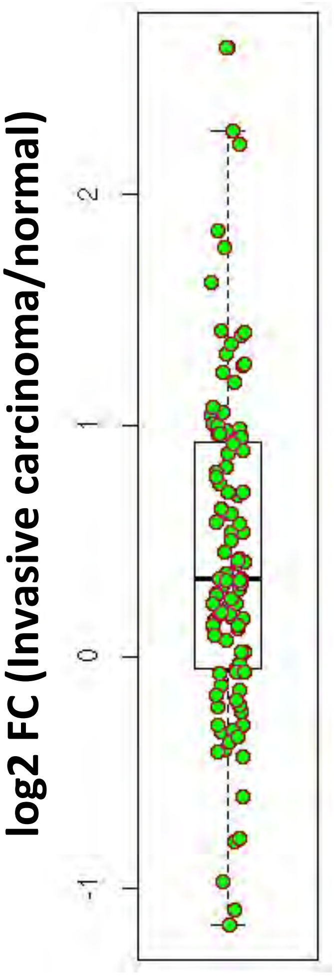
Pathiraja, et al.
Supp. Fig. S1

A

TRIM24 expression in TCGA BRCA



Paired Samples

- Fold change > 0 for 78 of 106 (73%) patients with paired profiles
- 40 out of 106 (37.8%) patients have fold change > 1.5

B

Top 30% vs. Bottom 70%

TRIM24 =>	High Exp	Low Exp
LumA	107	325
LumB	77	117
Basal	66	74
Her2	31	36

p-value: 1.32e-07

TRIM24 =>	High Exp	Low Exp
LumA	107	325
Not LumA	174	227

p-value: 1.46e-08; **Odds ratio**: 0.43

TRIM24 =>	High Exp	Low Exp
Lum B	77	117
Not LumB	204	435

p-value: 0.047; **odds ratio**: 1.40

TRIM24 =>	High Exp	Low Exp
Basal	66	74
Not Basal	215	478

p-value: 3.8e-04; **Odds ratio**: 1.98

TRIM24 =>	High Exp	Low Exp
Her2	31	36
Not Her2	250	516

p-value: 0.03; **Odds ratio**: 1.78

Key:
LumA: ER+, PR+, HER2-
LumB: ER+, PR+, HER2+
HER2: ER-, PR-, HER2+
Basal: ER-, PR-, HER2-

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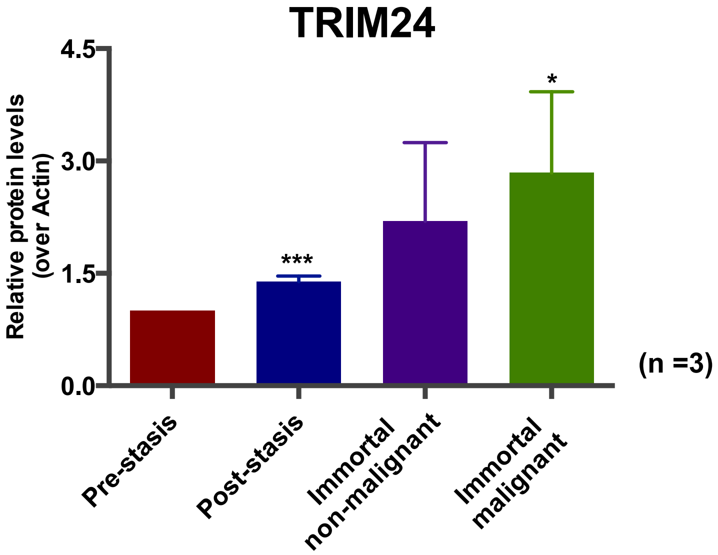
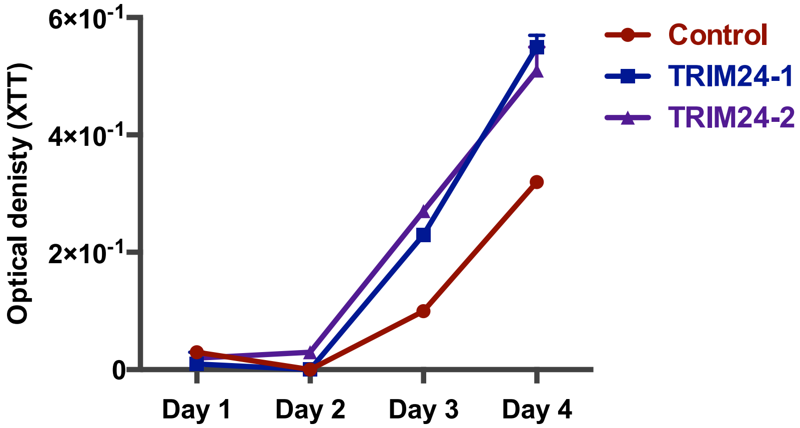
Supp. Fig. S2

A



B



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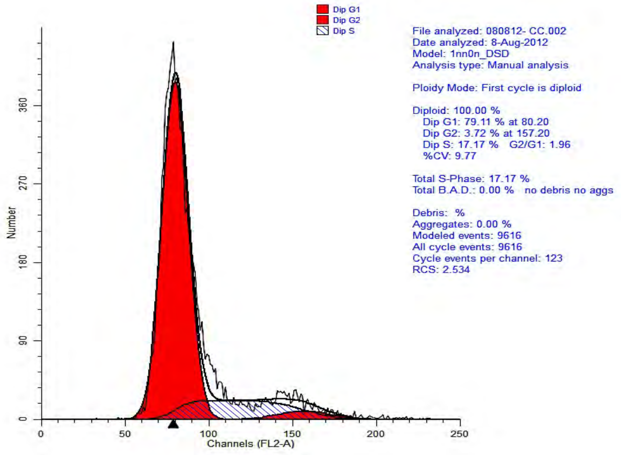
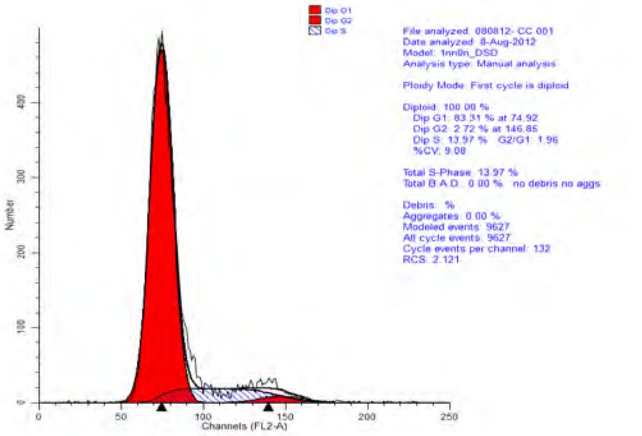
Supp. Fig. S3

Control

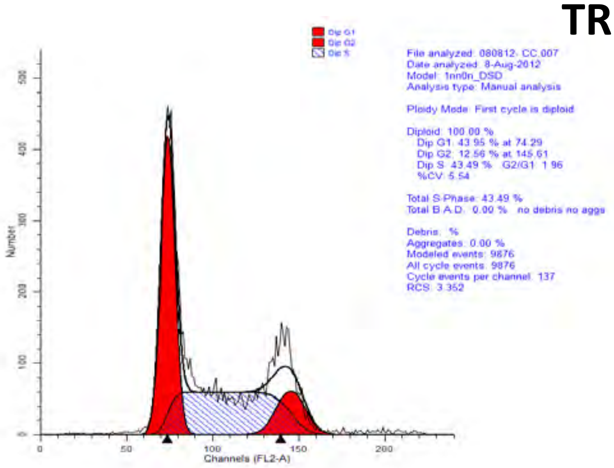


```
File analyzed: 080812- CC.002
Date analyzed: 8-Aug-2012
Model: 1nn0n_DSD
Analysis type: Manual analysis

Ploidy Mode: First cycle is diploid

Diploid: 100.00 %
  Dip G1: 79.11 % at 80.20
  Dip G2: 3.72 % at 157.20
  Dip S: 17.17 %   G2/G1: 1.96
  %CV: 9.77

Total S-Phase: 17.17 %
Total B.A.D.: 0.00 %   no debris no aggs

Debris:  %
Aggregates: 0.00 %
Modeled events: 9616
All cycle events: 9616
Cycle events per channel: 123
RCS: 2.534
```

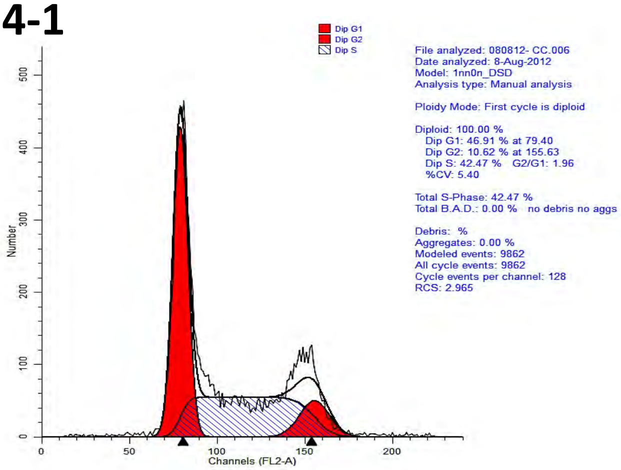


```
File analyzed: 080812- CC.001
Date analyzed: 8-Aug-2012
Model: 1nn0n_DSD
Analysis type: Manual analysis

Ploidy Mode: First cycle is diploid

Diploid: 100.00 %
  Dip G1: 83.31 % at 74.92
  Dip G2: 2.72 % at 146.85
  Dip S: 13.97 %   G2/G1: 1.96
  %CV: 9.08

Total S-Phase: 13.97 %
Total B.A.D.: 0.00 %   no debris no aggs

Debris:  %
Aggregates: 0.00 %
Modeled events: 9627
All cycle events: 9627
Cycle events per channel: 132
RCS: 2.121
```

TRIM24-1

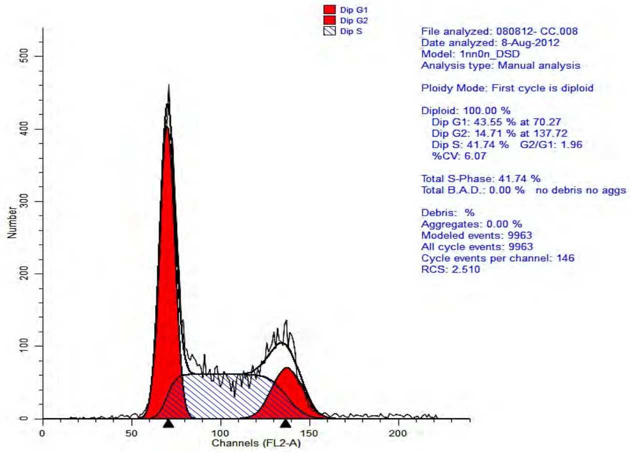


```
File analyzed: 080812- CC.007
Date analyzed: 8-Aug-2012
Model: 1nn0n_DSD
Analysis type: Manual analysis

Ploidy Mode: First cycle is diploid

Diploid: 100.00 %
  Dip G1: 43.95 % at 74.29
  Dip G2: 12.56 % at 145.61
  Dip S: 43.49 %   G2/G1: 1.96
  %CV: 5.54

Total S-Phase: 43.49 %
Total B.A.D.: 0.00 %   no debris no aggs

Debris:  %
Aggregates: 0.00 %
Modeled events: 9876
All cycle events: 9876
Cycle events per channel: 137
RCS: 3.352
```

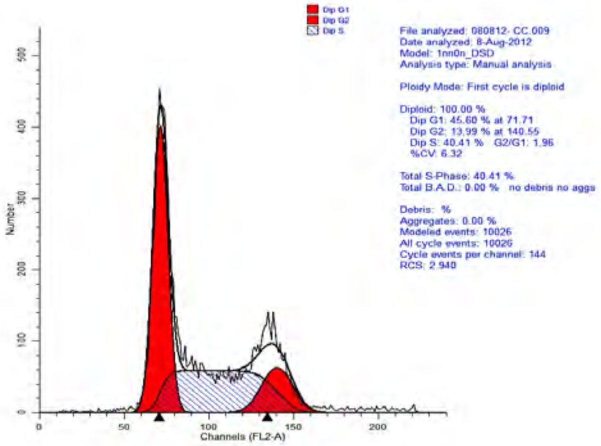


```
File analyzed: 080812- CC.006
Date analyzed: 8-Aug-2012
Model: 1nn0n_DSD
Analysis type: Manual analysis

Ploidy Mode: First cycle is diploid

Diploid: 100.00 %
  Dip G1: 46.91 % at 79.40
  Dip G2: 10.62 % at 155.63
  Dip S: 42.47 %   G2/G1: 1.96
  %CV: 5.40

Total S-Phase: 42.47 %
Total B.A.D.: 0.00 %   no debris no aggs

Debris:  %
Aggregates: 0.00 %
Modeled events: 9862
All cycle events: 9862
Cycle events per channel: 128
RCS: 2.965
```

TRIM24-2



```
File analyzed: 080812- CC.008
Date analyzed: 8-Aug-2012
Model: 1nn0n_DSD
Analysis type: Manual analysis

Ploidy Mode: First cycle is diploid

Diploid: 100.00 %
  Dip G1: 43.55 % at 70.27
  Dip G2: 14.71 % at 137.72
  Dip S: 41.74 %   G2/G1: 1.96
  %CV: 6.07

Total S-Phase: 41.74 %
Total B.A.D.: 0.00 %   no debris no aggs

Debris:  %
Aggregates: 0.00 %
Modeled events: 9963
All cycle events: 9963
Cycle events per channel: 146
RCS: 2.510
```



```
File analyzed: 080812- CC.009
Date analyzed: 8-Aug-2012
Model: 1nn0n_DSD
Analysis type: Manual analysis

Ploidy Mode: First cycle is diploid

Diploid: 100.00 %
  Dip G1: 45.60 % at 71.71
  Dip G2: 13.99 % at 140.55
  Dip S: 40.41 %   G2/G1: 1.96
  %CV: 6.32

Total S-Phase: 40.41 %
Total B.A.D.: 0.00 %   no debris no aggs

Debris:  %
Aggregates: 0.00 %
Modeled events: 10026
All cycle events: 10026
Cycle events per channel: 144
RCS: 2.940
```

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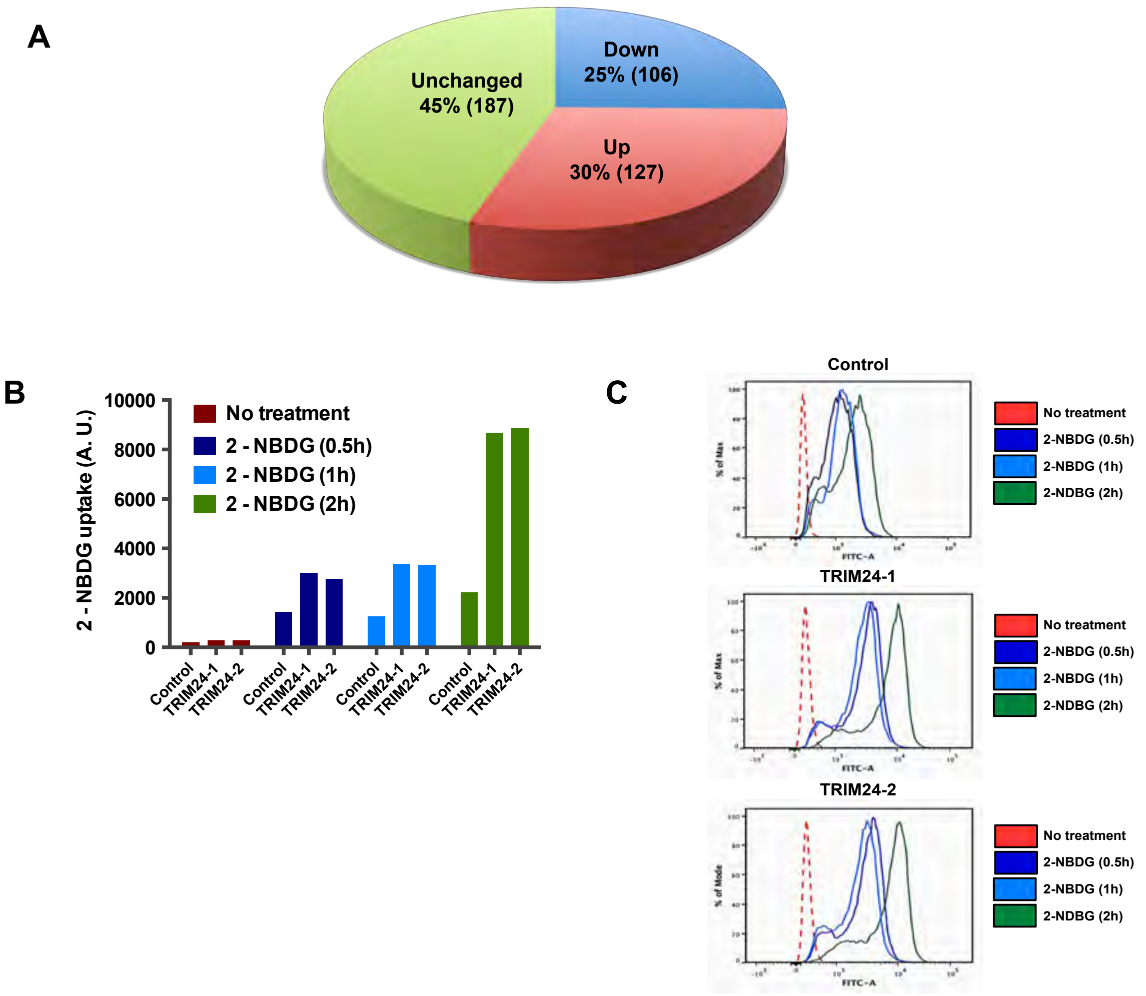
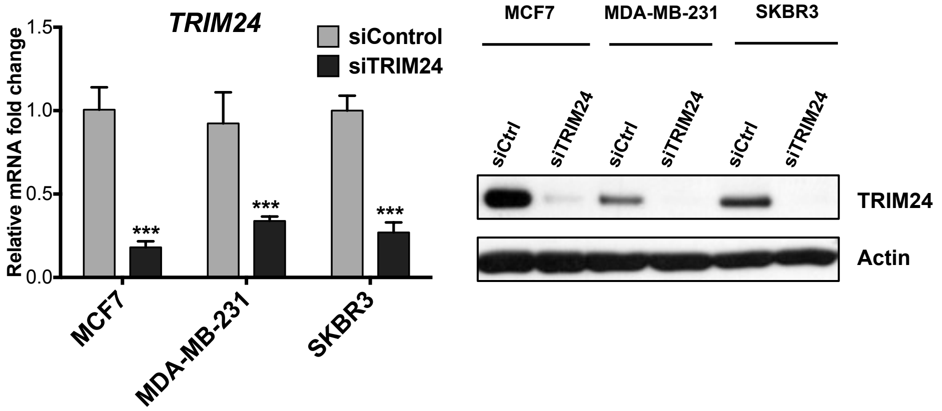
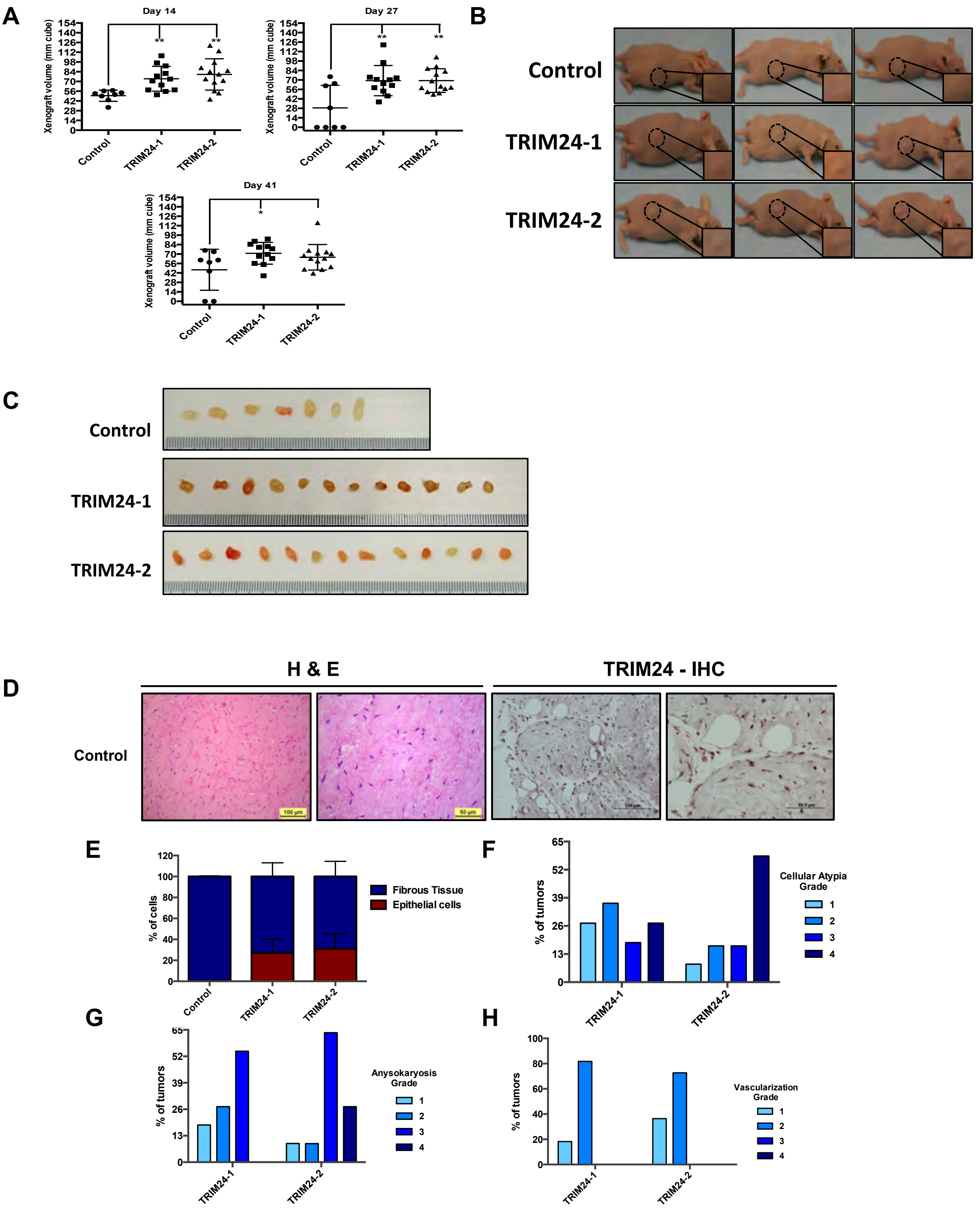
Supp. Fig. S4



Pathiraja, et al.
Supp. Fig. S5



Pathiraja, et al.
Supp. Fig. S6



T1

	Status	All red score	Status	All red score	Status	All red score	Status	All red score	Status	All red score	Status	All red score
position	ER status	ER	PR status	PR	P53 status	P53	Ki67 status	ki67	HER2	HER2	TRIM24	Trim24 status
A11	0	0	0	0	0	0	0	0	0	0	0	0
A13	1	3	1	4	0	1	0	1	1	2	1	0
A15	1	3	1	3	0	1	0	1	0	0	3	1
A7	1	4	1	6	0	1	0	2	0	0	3	1
A9	0	1	1	4	0	1	0	2	0	0	1	0
B10	1	6	0	1	1	7	0	1	1	2	6	2
B12	1	8	1	7	0	0	0	2	1	2	6	2
B14	0	0	0	0	1	7	1	5	1	3	5	1
B2	0	0	0	0	0	0	1	8	0	0	2	0
B4	1	7	1	8	0	0	0	2	0	1	4	1
B6	0	0	0	0	1	8	1	3	1	3	4	1
B8	0	0	1	8	0	1	0	2	1	2	6	2
C1	1	4	0	1	1	5	1	5	1	3	6	2
C11	0	1	0	0	0	1	1	3	1	2	2	0
C13	1	6	0	1	1	4	1	5	1	3	5	1
C15	1	4	0	1	1	3	1	3	1	3	4	1
C3	0	0	0	0	0	1	1	8	1	2	3	1
C5	0	0	0	0	0	0	1	7	1	2	1	0
C7	1	8	1	7	0	1	1	4	1	2	4	1
C9	0	0	0	0	1	4	0	2	1	2	5	1
D10	0	0	0	0	1	7	0	1	1	3	6	2
D12	1	4	0	0	1	3	0	2	1	2	6	2
D14	1	8	0	0	0	0	1	5	1	3	6	2
D2	0	0	0	0	1	8	1	8	0	0	2	0
D4	1	8	1	8	0	1	1	3	1	2	6	2
D6	1	3	0	0	0	0	1	3	1	2	6	2
D8	1	8	1	8	0	1	1	7	1	2	8	2
E1	1	3	0	1	1	6	1	6	1	2	2	0
E11	1	8	0	0	0	2	1	6	1	2	4	1
E13	1	8	1	5	0	2	1	3	1	3	8	2
E15	1	7	0	2	1	6	1	4	1	2	3	1
E3	1	6	1	3	0	0	0	1	0	1	2	0
E5	0	0	0	0	0	1	1	7	1	3	3	1
E7	1	8	1	7	0	0	1	7	1	3	6	2
E9	1	4	1	3	1	8	1	6	1	3	4	1
F10	1	6	0	0	1	6	1	5	1	2	6	2
F12	0	0	0	0	1	8	1	8	1	2	6	2
F14	1	8	0	2	0	0	0	2	1	2	4	1
F2	0	0	0	0	1	8	1	8	1	3	6	2
F4	0	0	0	0	0	1	0	1	1	3	6	2
F6	0	0	1	5	0	0	1	6	1	2	3	1
F8	0	0	1	6	0	1	1	4	1	3	6	2
G1	0	2	1	3	1	5	1	7	1	3	5	1
G11	0	0	0	0	1	7	0	1	0	0	2	0
G13	0	0	1	6	0	1	0	1	0	1	0	0
G15	1	7	1	3	1	3	1	4	1	2	4	1
G3	0	0	0	0	1	5	1	4	1	2	3	1
G5	0	1	0	0	1	6	1	7	1	3	4	1
G7	0	0	0	0	0	0	1	5	0	1	3	1
G9	1	5	1	5	1	7	1	4	1	3	5	1
H10	1	8	1	8	0	0	1	5	1	2	6	2
H12	0	0	1	8	0	0	1	4	0	0	4	1
H14	1	7	1	8	1	3	1	8	1	3	6	2
H2	0	0	0	0	1	4	1	3	1	2	3	1
H4	0	0	0	0	1	4	0	1	0	0	3	1
H6	0	0	0	0	1	6	0	1	0	1	3	1
H8	0	0	0	0	0	2	1	6	0	1	1	0
I1	0	0	0	2	1	4	1	5	1	3	3	1
I11	0	0	0	0	1	4	1	5	0	0	1	0
I13	0	0	0	0	0	0	0	2	0	0	2	0
I15	0	0	0	0	0	1	1	6	1	3	3	1
I3	0	0	0	0	0	1	0	0	0	0	1	0
I5	1	8	1	7	0	0	0	1	1	2	7	2
I7	0	0	0	0	0	1	1	5	1	3	3	1
I9	0	0	0	1	1	3	1	6	1	2	4	1
J10	0	0	0	0	0	0	1	7	1	2	5	1
J12	0	0	0	0	0	1	1	8	1	2	4	1
J14	0	0	0	0	0	0	1	6	1	2	3	1
J2	0	0	0	0	1	8	1	8	0	1	2	0
J4	0	0	0	0	1	3	1	7	0	1	2	0
J6	0	0	0	2	0	0	1	4	0	1	1	0
J8	0	0	0	0	1	6	1	5	0	0	3	1

TRIM24 Analysis

			TRIM24		Total		
		low	medium	High			
ER status	low	15	22	6	43	Chi-square	11.87
	high	3	12	14	29	P-value	0.0026
					72		
	Total	18	34	20			

Key

TRIM24	ER/PR	HER2
low (0-2)	low(0-3)	low (0-1)
medium (3-5)	high (3-8)	High (2-3)
high (6-8)		

			TRIM24		Total		
		low	medium	High			
PR status	low	14	24	10	48	Chi-square	3.74
	high	4	10	10	24	P-value	0.1541
					72		
	Total	18	34	20			

			TRIM24		Total		
		low	medium	High			
HER2 status	low	14	8	0	22	Chi-square	28.51
	high	4	26	20	50	P-value	<.0001
					72		
	Total	18	34	20			

			TRIM24		Total		
		low	medium	High			
P53	low	12	16	12	40	Chi-square	2.05
	high	6	18	8	32	P-value	0.3588
					72		
	Total	18	34	20			

			TRIM24		Total		
		low	medium	High			
Ki67	low	8	7	7	22	Chi-square	3.41
	high	10	27	13	50	P-value	0.1818
					72		
	Total	18	34	20			

ER Analysis

			ER		Total		
		low	medium	High			
PR status	low	34	7	7	48	Chi-square	17.87
	high	5	6	13	24	P-value	0.0002
					72		
	Total	39	13	20			

Key

ER	PR	HER2
low (0)	low(0-3)	low (0-1)
Medium (1-4)	high (3-8)	High (2-3)
High (5-8)		

			ER		Total		
		low	medium	High			
HER2 status	low	**17**	**3**	**2**	22	Chi-square	7.45
	high	**22**	**10**	**18**	50	P-value	0.0241
					72		
	Total	39	13	20			

			ER		Total		
		low	medium	High			
P53	low	21	6	13	40	Chi-square	1.23
	high	18	7	7	32	P-value	0.5406
					72		
	Total	39	13	20			

			ER		Total		
		low	medium	High			
Ki67	low	11	5	6	22	Chi-square	0.49
	high	28	8	14	50	P-value	0.7827
					72		
	Total	39	13	20			

T2

Upregulated genes

	Control			TRIM24				
Gene	**A**	**B**	**C**	**A**	**B**	**C**	**t-test**	**Fold change**
TRIM39	0.00	167.49	132.51	605.68	572.34	591.15	0.00	5.9
PDE4DIP	0.00	219.12	80.88	833.22	376.66	408.42	0.05	5.4
GLS2	236.96	35.30	27.74	518.79	374.78	469.60	0.01	4.5
PRKCI	91.91	92.75	115.34	397.29	440.82	450.99	0.00	4.3
PRKCH	75.47	97.49	127.04	369.65	389.17	473.85	0.00	4.1
CAMKK2	117.28	87.50	95.22	462.87	391.28	374.84	0.00	4.1
SgK494	0.00	202.37	97.63	525.91	415.23	285.19	0.03	4.1
TESK2	0.00	84.47	215.53	370.71	330.23	496.93	0.02	4.0
MYC	84.91	106.26	108.84	336.89	370.51	392.51	0.00	3.7
MAPKAPK5	70.14	94.23	135.63	331.82	317.40	397.15	0.00	3.5
STRADA	21.47	168.55	109.99	285.93	384.41	290.46	0.01	3.2
ME3	17.33	172.80	109.87	310.73	288.43	353.48	0.01	3.2
FGFR2	100.45	114.59	84.96	273.19	277.81	358.25	0.00	3.0
TTL	84.61	111.39	104.00	293.80	305.09	309.23	0.00	3.0
DDX5	90.50	124.69	84.81	357.23	258.22	290.89	0.00	3.0
TRIM26	44.07	142.46	113.47	260.31	272.90	327.49	0.01	2.9
CEBPA	90.19	111.15	98.66	266.75	298.82	274.99	0.00	2.8
TRIM37	85.26	113.30	101.44	292.72	278.46	264.67	0.00	2.8
TRIM39	84.33	116.55	99.12	296.83	235.94	284.93	0.00	2.7
MTOR	57.47	135.06	107.47	218.24	306.41	280.85	0.01	2.7
PIK3CA	63.52	93.07	143.41	254.09	241.62	309.69	0.01	2.7
BIRC3	98.26	102.09	99.65	288.82	256.61	243.06	0.00	2.6
PTPN11	80.24	120.97	98.80	238.57	259.67	286.49	0.00	2.6
PFKFB2	57.89	122.72	119.40	216.86	265.92	299.32	0.01	2.6
EPHA1	86.47	88.62	124.92	274.97	203.83	302.21	0.01	2.6
TTK	103.65	88.67	107.68	238.36	225.32	295.02	0.00	2.5
YES1	80.08	109.47	110.45	240.24	247.23	272.17	0.00	2.5
NEK6	99.98	87.87	112.15	256.38	207.41	255.11	0.00	2.4
NADK	80.59	132.86	86.55	193.31	240.18	272.71	0.01	2.4
STK38L	108.16	97.62	94.22	229.55	233.62	228.09	0.00	2.3
CDKN2A	189.02	74.63	36.35	217.37	229.33	240.38	0.05	2.3
ERN1	78.27	133.34	88.39	265.59	213.98	203.27	0.01	2.3
SDHD	96.31	83.77	119.92	210.35	205.87	264.55	0.00	2.3
TNK2	88.53	97.96	113.52	201.61	234.60	243.05	0.00	2.3
LGR5	162.81	64.29	72.90	176.33	251.31	206.28	0.04	2.1
COX6C	96.44	102.71	100.85	207.39	198.92	224.80	0.00	2.1
TSC1	80.94	107.44	111.62	220.08	174.18	231.16	0.01	2.1
STK38	71.10	105.05	123.85	198.54	203.43	215.53	0.00	2.1
TRIM59	73.62	115.41	110.97	207.78	203.48	203.30	0.00	2.1
PIP4K2A	80.18	116.42	103.40	211.78	196.78	182.02	0.00	2.0
BRCA1	61.92	123.09	115.00	190.10	195.23	195.77	0.01	1.9
SIX4	117.49	84.35	98.17	166.19	214.52	202.52	0.01	1.9
SIK3	97.85	116.82	85.33	189.45	199.08	193.78	0.00	1.9
MASTL	63.29	121.37	115.34	197.64	184.52	198.17	0.01	1.9
ADRBK1	98.21	95.03	106.76	176.92	204.95	197.93	0.00	1.9

MAP3K5	101.84	103.09	95.07	208.56	139.72	227.76	0.03	1.9
SUFU	112.01	99.86	88.12	168.24	211.29	196.43	0.00	1.9
RPIA	104.92	102.65	92.43	152.23	192.15	221.93	0.01	1.9
EZH2	78.28	98.23	123.49	211.74	164.89	187.48	0.01	1.9
BRD3	66.22	104.59	129.19	194.66	160.63	189.77	0.02	1.8
PFKFB3	100.47	114.40	85.13	186.71	186.88	170.40	0.00	1.8
TRIM8	110.66	97.48	91.86	160.42	184.29	189.82	0.00	1.8
GNAQ	114.66	96.08	89.26	192.33	166.22	174.53	0.00	1.8
DLAT	88.02	116.26	95.71	157.99	208.15	163.98	0.01	1.8
SUZ12	96.47	92.31	111.22	162.27	156.41	208.20	0.01	1.8
RPS6KB1	109.51	99.07	91.42	167.09	187.02	165.46	0.00	1.7
TUBB	97.55	95.46	106.99	175.70	162.12	179.90	0.00	1.7
CSK	74.68	117.18	108.14	149.28	207.10	160.90	0.03	1.7
AURKB	86.51	111.06	102.43	161.71	188.84	164.13	0.00	1.7
HPRT1	103.22	87.37	109.41	171.22	164.29	179.41	0.00	1.7
ACLY	88.10	95.11	116.79	171.95	156.01	185.87	0.00	1.7
VEGFA	96.71	95.72	107.56	161.44	162.53	182.52	0.00	1.7
SDHB	88.47	96.21	115.32	159.71	157.81	183.03	0.00	1.7
SNX16	110.81	94.84	94.35	175.13	151.39	174.28	0.00	1.7
PIK3R4	76.17	113.25	110.58	159.56	168.70	163.27	0.01	1.6
EXOSC10	103.90	92.24	103.86	182.68	151.99	153.98	0.00	1.6
DDR1	117.47	98.22	84.31	163.14	146.66	177.28	0.01	1.6
TIAM1	139.77	86.31	73.93	163.60	150.38	173.17	0.04	1.6
CSNK1D	75.44	119.51	105.05	149.96	171.24	160.75	0.01	1.6
DNMT3A	119.72	82.23	98.05	151.03	154.57	177.99	0.01	1.6
NRAS	83.60	121.47	94.93	163.56	167.72	152.35	0.01	1.6
MELK	87.94	104.29	107.77	137.44	163.73	174.99	0.01	1.6
GSG2	88.51	106.43	105.06	160.65	153.49	164.00	0.00	1.6
KRAS	72.02	113.59	114.40	163.79	159.94	150.47	0.02	1.6
PAK2	87.05	101.44	111.51	143.84	161.38	161.67	0.00	1.6
PANK4	85.52	100.27	114.21	162.11	159.11	147.79	0.00	1.6
GMPS	88.50	103.49	108.01	157.02	147.45	161.72	0.00	1.6
CHEK1	95.68	101.35	102.97	166.56	147.35	150.39	0.00	1.6
PDP1	104.21	84.35	111.44	147.34	148.89	165.52	0.01	1.5
SGK1	111.61	97.68	90.71	170.02	146.22	142.16	0.01	1.5
MAPK8	106.53	101.84	91.63	144.52	149.29	163.98	0.00	1.5
RIOK1	100.31	106.32	93.37	142.94	154.84	156.08	0.00	1.5
BUB1B	103.13	90.63	106.24	167.40	138.12	140.39	0.01	1.5
HIPK1	106.47	97.06	96.47	151.93	148.97	146.76	0.00	1.5
DYRK1A	95.03	110.40	94.57	126.29	173.39	144.49	0.03	1.5
SDHA	115.02	87.55	97.43	159.51	137.58	146.76	0.01	1.5
HK1	69.60	108.27	122.13	139.79	145.81	156.05	0.05	1.5
LGR4	92.55	101.35	106.10	174.12	134.23	128.84	0.04	1.5
PRKAR2A	108.79	96.03	95.18	138.54	153.30	143.89	0.00	1.5
SRPK1	77.14	124.73	98.13	134.12	147.25	151.52	0.04	1.4
MARK2	112.57	85.94	101.49	128.35	137.62	167.43	0.03	1.4
BRD8	95.25	113.48	91.27	129.06	142.60	159.09	0.02	1.4
INPP4A	123.68	92.94	83.37	162.34	131.32	135.13	0.05	1.4
GPR172A	110.01	92.75	97.24	150.82	140.09	134.87	0.00	1.4
PAFAH1B2	97.27	92.88	109.85	131.99	140.01	151.57	0.01	1.4

NLK	114.80	83.74	101.46	146.56	140.69	133.29	0.01	1.4
MAP3K7	111.10	103.76	85.14	139.29	139.75	138.50	0.01	1.4
CS	119.50	92.02	88.48	157.98	128.22	130.72	0.05	1.4
P2RY2	90.52	92.84	116.64	137.82	134.08	145.78	0.01	1.4
KIAA1524	106.11	94.53	99.36	146.37	145.96	124.19	0.01	1.4
AK3	88.50	112.84	98.65	133.79	134.47	146.39	0.01	1.4
BRD2	92.84	105.03	102.13	138.39	148.03	127.62	0.01	1.4
ABL1	100.00	104.92	95.08	116.72	158.40	134.39	0.04	1.4
SH3BP5	85.21	107.66	107.13	137.75	138.42	132.58	0.01	1.4
BRD7	88.56	108.28	103.16	116.82	138.78	148.61	0.04	1.4
C17orf75	102.12	94.30	103.58	120.93	145.56	131.93	0.01	1.3
PI4K2B	81.40	114.94	103.65	137.73	127.26	131.01	0.04	1.3
MDH2	106.64	99.58	93.78	132.61	136.44	125.99	0.00	1.3
SMARCB1	89.38	105.81	104.81	115.12	141.11	135.71	0.03	1.3
BRD9	109.05	100.42	90.53	144.25	128.72	120.62	0.02	1.3
MAPK14	89.74	110.37	99.89	133.47	127.90	127.64	0.01	1.3
VHL	111.08	98.47	90.45	136.91	135.91	112.84	0.04	1.3
CSNK2B	87.32	101.10	111.58	120.88	135.08	131.34	0.02	1.3
MAPK9	93.30	103.48	103.23	116.71	134.68	136.63	0.02	1.3
FH	88.01	103.30	108.69	116.95	122.93	134.12	0.04	1.3
RIPK2	107.86	93.78	98.36	128.03	118.96	127.05	0.01	1.3
RB1	100.30	99.01	100.69	127.90	127.04	119.56	0.00	1.2
MAPK6	89.31	101.11	109.58	112.56	134.50	123.49	0.05	1.2
MAP2K4	106.21	87.45	106.34	113.59	124.80	128.78	0.04	1.2
TGFBR1	106.30	96.83	96.87	123.82	125.83	116.76	0.01	1.2
MET	100.36	97.04	102.60	117.81	120.36	123.81	0.00	1.2
ACO1	91.31	106.02	102.67	116.76	121.04	122.48	0.01	1.2
GPI	98.78	108.12	93.10	125.55	118.94	111.49	0.04	1.2
RAF1	100.61	102.72	96.68	114.38	109.57	131.47	0.05	1.2
CDK4	101.71	103.23	95.06	113.55	113.40	125.26	0.02	1.2
CDK1	94.53	104.79	100.68	113.34	112.18	125.61	0.03	1.2
PTEN	104.69	102.38	92.93	118.46	113.63	114.01	0.02	1.2
Down-Regulated Genes								
CANT1	102.26	102.13	95.61	74.26	77.76	72.82	0.00	0.7
RPS6KA4	89.61	112.76	97.63	67.81	80.92	74.18	0.03	0.7
ATIC	92.36	103.75	103.90	69.51	72.44	77.62	0.00	0.7
RPS6KC1	97.65	110.53	91.82	63.45	84.16	71.48	0.03	0.7
PRKAR1A	99.04	100.29	100.67	68.68	72.59	76.65	0.00	0.7
RIPK1	100.25	95.01	104.74	63.70	69.64	83.27	0.01	0.7
BRCA2	94.16	106.10	99.74	68.15	71.34	77.11	0.00	0.7
PDXK	95.39	105.72	98.89	73.37	69.33	73.59	0.00	0.7
LATS2	109.68	106.83	83.49	76.02	66.31	71.03	0.03	0.7
AURKA	94.64	113.24	92.13	71.74	65.29	75.09	0.02	0.7
SPTAN1	94.90	102.35	102.74	68.42	69.69	72.68	0.00	0.7
CAMK2D	85.56	115.08	99.36	69.50	65.52	74.53	0.03	0.7
BMPR1A	109.26	103.28	87.46	65.26	71.55	69.21	0.01	0.7
TKT	94.42	106.27	99.31	65.99	67.99	70.86	0.00	0.7
SGK196	86.59	112.34	101.08	72.34	66.83	65.30	0.01	0.7
LIMK2	101.43	93.63	104.94	69.47	68.76	64.83	0.00	0.7
FBXW7	106.32	104.96	88.72	72.23	65.27	65.31	0.01	0.7

SRPK2	94.96	101.78	103.26	71.26	63.48	65.17	0.00	0.7
SMAD4	106.16	95.81	98.03	58.31	63.28	74.85	0.00	0.7
PIP5K1A	97.04	106.67	96.29	65.90	68.32	62.03	0.00	0.7
CARS	109.98	104.43	85.59	63.52	60.63	65.80	0.01	0.6
BRD1	120.83	90.76	88.41	65.75	63.12	60.99	0.03	0.6
PDK1	103.94	109.44	86.61	73.79	60.17	53.65	0.01	0.6
H6PD	124.34	78.77	96.89	54.75	70.57	60.73	0.05	0.6
RUNX1	110.51	88.95	100.54	60.45	62.33	62.23	0.00	0.6
PIKFYVE	105.65	89.69	104.66	65.22	53.00	66.37	0.00	0.6
PRKD2	114.02	96.97	89.01	59.53	57.54	66.06	0.01	0.6
NF2	104.52	97.14	98.34	60.72	64.47	57.76	0.00	0.6
JUN	110.79	105.36	83.84	60.50	58.71	62.61	0.01	0.6
BMPR2	102.34	97.17	100.49	61.37	54.70	63.72	0.00	0.6
CCND1	107.49	97.78	94.73	58.79	58.02	61.48	0.00	0.6
CDH1	93.28	106.31	100.41	58.32	61.00	58.15	0.00	0.6
TRIB1	114.51	88.92	96.56	58.70	54.87	63.68	0.01	0.6
ABL2	110.03	101.83	88.14	54.74	62.36	58.45	0.00	0.6
NPM1	96.75	104.96	98.29	54.00	54.00	56.62	0.00	0.5
ETNK2	95.16	87.67	117.17	44.66	52.02	66.98	0.01	0.5
JAK1	70.16	104.17	125.66	55.93	54.15	51.56	0.05	0.5
PLXNB2	107.81	99.81	92.38	53.14	49.49	57.30	0.00	0.5
NEK7	106.05	94.44	99.51	50.83	55.51	53.60	0.00	0.5
HERC4	101.72	105.21	93.07	53.40	50.35	53.23	0.00	0.5
RIOK3	114.66	102.70	82.64	52.09	41.01	62.60	0.01	0.5
ATF2	93.99	107.22	98.78	38.01	56.30	58.19	0.00	0.5
APC	93.07	133.46	73.47	54.11	50.09	48.61	0.05	0.5
PIK3R1	71.49	110.08	118.43	55.74	41.38	52.83	0.03	0.5
TNIK	92.42	118.61	88.97	48.05	40.12	59.52	0.01	0.5
CXCR7	96.52	94.33	109.15	52.16	52.47	38.81	0.00	0.5
GNAS	99.34	98.90	101.76	48.50	47.80	48.36	0.00	0.5
PKN1	104.60	88.72	106.68	45.31	46.34	47.45	0.00	0.5
LPAR1	93.72	116.63	89.65	36.29	49.87	48.58	0.00	0.4
PIK3C2B	101.12	103.81	95.08	56.94	39.02	38.43	0.00	0.4
IRAK2	85.32	108.56	106.12	42.10	56.71	35.03	0.00	0.4
TGFBR2	87.37	113.03	99.60	37.35	40.70	43.57	0.00	0.4
CALM3	88.83	102.81	108.35	36.49	43.15	36.87	0.00	0.4
HRAS	69.46	116.39	114.15	38.16	35.63	41.85	0.02	0.4
IDH1	106.85	109.69	83.46	37.03	29.78	47.63	0.00	0.4
MAGI2	133.29	92.11	74.60	43.31	45.01	21.11	0.03	0.4
FLT3	122.76	113.11	64.13	26.59	47.37	34.56	0.03	0.4
PRKCQ	101.45	100.14	98.41	32.96	35.88	39.27	0.00	0.4
ILK	96.77	106.34	96.88	29.07	34.35	42.80	0.00	0.4
INPP4B	92.55	107.86	99.59	36.86	29.67	37.83	0.00	0.3
PLK2	97.54	92.11	110.35	30.90	32.64	37.50	0.00	0.3
AURKC	122.94	116.51	60.55	21.30	37.95	41.54	0.03	0.3
FLNB	105.10	95.84	99.05	32.87	31.05	28.04	0.00	0.3
EPHB6	121.89	96.25	81.86	26.40	39.20	25.74	0.01	0.3
NTRK1	119.13	109.76	71.12	25.80	22.99	41.93	0.01	0.3
TGFBR3	149.12	84.11	66.77	36.91	32.88	17.99	0.05	0.3
TRIM5	119.21	101.99	78.80	22.75	26.84	35.36	0.00	0.3

HKDC1	98.24	135.77	65.98	26.60	33.17	20.75	0.02	0.3
TBX22	130.75	120.46	48.79	28.32	33.64	18.41	0.05	0.3
HOXB7	118.67	96.82	84.51	24.45	31.31	19.46	0.00	0.3
MST1R	104.36	103.37	92.27	22.22	24.91	26.15	0.00	0.2
MYLK4	69.48	137.18	93.33	30.10	26.81	14.67	0.02	0.2
MRGPRX3	118.30	93.42	88.28	25.62	22.83	16.65	0.00	0.2
ALK	104.07	102.73	93.20	22.54	20.08	21.98	0.00	0.2
INSR	99.84	92.06	108.09	13.64	17.95	29.07	0.00	0.2
LRP1B	119.97	126.32	53.71	0.00	15.43	33.78	0.03	0.2
EPHA4	128.80	106.80	64.40	20.46	14.91	12.69	0.01	0.2
ERBB4	98.24	135.77	65.98	10.64	18.96	10.37	0.01	0.1
ROBO1	103.32	95.99	100.69	14.48	12.90	11.55	0.00	0.1
STK32A	84.10	121.76	94.14	10.12	16.23	7.89	0.00	0.1
MAP2K6	98.31	109.99	91.70	10.65	15.81	6.92	0.00	0.1
RPS6KA6	143.73	83.17	73.10	14.01	10.05	7.98	0.02	0.1
ANGPTL4	120.81	95.40	83.79	9.35	12.90	7.06	0.00	0.1
FYN	82.16	118.31	99.54	8.37	8.39	9.18	0.00	0.1
PRKD1	74.75	114.38	110.87	6.07	9.01	9.87	0.00	0.1
SMO	120.56	92.82	86.62	0.00	15.95	0.00	0.00	0.1
AKT3	88.61	105.97	105.42	3.84	4.88	5.35	0.00	0.0
TP53	110.82	99.07	90.11	4.99	3.59	2.62	0.00	0.0
CDK14	118.73	90.53	90.74	3.55	5.53	1.73	0.00	0.0
ROS1	92.87	100.01	107.11	2.13	1.90	3.86	0.00	0.0
HCK	100.78	126.35	72.87	0.00	0.00	0.00	0.00	0.0

T3

Upregulated Genes

Term	Count	%	PValue
GO:0006468~protein amino acid phosphorylation	52	41.2698413	4.83E-37
GO:0016310~phosphorylation	55	43.6507937	1.13E-36
GO:0006793~phosphorus metabolic process	57	45.2380952	1.61E-34
GO:0006796~phosphate metabolic process	57	45.2380952	1.61E-34
GO:0007242~intracellular signaling cascade	38	30.1587302	2.28E-12
GO:0043549~regulation of kinase activity	19	15.0793651	7.45E-10
GO:0042325~regulation of phosphorylation	21	16.6666667	1.28E-09
GO:0051338~regulation of transferase activity	19	15.0793651	1.44E-09
GO:0019220~regulation of phosphate metabolic process	21	16.6666667	2.55E-09
GO:0051174~regulation of phosphorus metabolic process	21	16.6666667	2.55E-09
GO:0045859~regulation of protein kinase activity	18	14.2857143	3.28E-09
GO:0006084~acetyl-CoA metabolic process	8	6.34920635	4.92E-09
GO:0007243~protein kinase cascade	18	14.2857143	9.35E-09
GO:0009060~aerobic respiration	8	6.34920635	1.23E-08
GO:0046356~acetyl-CoA catabolic process	7	5.55555556	2.53E-08
GO:0006099~tricarboxylic acid cycle	7	5.55555556	2.53E-08
GO:0006732~coenzyme metabolic process	12	9.52380952	5.32E-08
GO:0009109~coenzyme catabolic process	7	5.55555556	5.66E-08
GO:0051187~cofactor catabolic process	7	5.55555556	1.75E-07
GO:0042127~regulation of cell proliferation	23	18.2539683	4.02E-07
GO:0046777~protein amino acid autophosphorylation	9	7.14285714	4.86E-07
GO:0042981~regulation of apoptosis	23	18.2539683	5.78E-07
GO:0051186~cofactor metabolic process	12	9.52380952	6.22E-07
GO:0043067~regulation of programmed cell death	23	18.2539683	6.83E-07
GO:0010941~regulation of cell death	23	18.2539683	7.27E-07
GO:0000075~cell cycle checkpoint	9	7.14285714	8.24E-07
GO:0044093~positive regulation of molecular function	19	15.0793651	1.41E-06
GO:0043085~positive regulation of catalytic activity	17	13.4920635	5.66E-06
GO:0043066~negative regulation of apoptosis	14	11.1111111	7.11E-06
GO:0043648~dicarboxylic acid metabolic process	6	4.76190476	8.17E-06
GO:0043069~negative regulation of programmed cell death	14	11.1111111	8.27E-06
GO:0060548~negative regulation of cell death	14	11.1111111	8.52E-06
GO:0006091~generation of precursor metabolites and energy	13	10.3174603	1.06E-05
GO:0018107~peptidyl-threonine phosphorylation	5	3.96825397	1.25E-05
GO:0006917~induction of apoptosis	13	10.3174603	1.33E-05
GO:0012502~induction of programmed cell death	13	10.3174603	1.37E-05
GO:0045333~cellular respiration	8	6.34920635	1.54E-05

GO:0051726~regulation of cell cycle	13	10.3174603	1.86E-05
GO:0018210~peptidyl-threonine modification	5	3.96825397	2.39E-05
GO:0010033~response to organic substance	19	15.0793651	2.46E-05
GO:0019318~hexose metabolic process	10	7.93650794	3.02E-05
GO:0006915~apoptosis	17	13.4920635	3.47E-05
GO:0006006~glucose metabolic process	9	7.14285714	3.92E-05
GO:0012501~programmed cell death	17	13.4920635	4.14E-05
GO:0042770~DNA damage response, signal transduction	7	5.55555556	5.14E-05
GO:0043065~positive regulation of apoptosis	14	11.1111111	5.49E-05
GO:0043068~positive regulation of programmed cell death	14	11.1111111	5.90E-05
GO:0010942~positive regulation of cell death	14	11.1111111	6.18E-05
GO:0008219~cell death	18	14.2857143	8.34E-05
GO:0016265~death	18	14.2857143	9.08E-05
GO:0005996~monosaccharide metabolic process	10	7.93650794	9.33E-05
GO:0006007~glucose catabolic process	6	4.76190476	1.15E-04
O:0007167~enzyme linked receptor protein signaling pathwa	12	9.52380952	1.24E-04
GO:0033674~positive regulation of kinase activity	10	7.93650794	1.26E-04
GO:0000165~MAPKKK cascade	9	7.14285714	1.43E-04

Down-regulated Genes

Term	Count	%	PValue
GO:0016310~phosphorylation	50	54.9450549	5.39E-37
GO:0006468~protein amino acid phosphorylation	47	51.6483516	1.07E-36
GO:0006793~phosphorus metabolic process	50	54.9450549	5.99E-33
GO:0006796~phosphate metabolic process	50	54.9450549	5.99E-33
GO:0007242~intracellular signaling cascade	31	34.0659341	1.56E-10
GO:0007167~enzyme linked receptor protein signaling pathw	17	18.6813187	6.50E-10
GO:0042325~regulation of phosphorylation	19	20.8791209	1.07E-09
GO:0051174~regulation of phosphorus metabolic process	19	20.8791209	2.01E-09
GO:0019220~regulation of phosphate metabolic process	19	20.8791209	2.01E-09
GO:0007243~protein kinase cascade	17	18.6813187	2.03E-09
GO:0042127~regulation of cell proliferation	22	24.1758242	2.66E-08
GO:0051094~positive regulation of developmental process	14	15.3846154	3.07E-08
GO:0044093~positive regulation of molecular function	18	19.7802198	2.19E-07
GO:0045597~positive regulation of cell differentiation	12	13.1868132	2.95E-07
GO:0045859~regulation of protein kinase activity	14	15.3846154	3.77E-07
GO:0043549~regulation of kinase activity	14	15.3846154	5.57E-07
GO:0010033~response to organic substance	19	20.8791209	8.33E-07
GO:0051338~regulation of transferase activity	14	15.3846154	8.86E-07
GO:0001932~regulation of protein amino acid phosphorylati	10	10.989011	1.96E-06

GO:0007169~transmembrane receptor protein tyrosine kinas	11	12.0879121	2.06E-06
GO:0051130~positive regulation of cellular component organ	10	10.989011	2.85E-06
GO:0008284~positive regulation of cell proliferation	14	15.3846154	2.91E-06
GO:0009725~response to hormone stimulus	13	14.2857143	4.81E-06
GO:0051098~regulation of binding	9	9.89010989	7.25E-06
GO:0007166~cell surface receptor linked signal transduction	29	31.8681319	1.27E-05
GO:0009719~response to endogenous stimulus	13	14.2857143	1.30E-05
GO:0051101~regulation of DNA binding	8	8.79120879	1.45E-05
GO:0045860~positive regulation of protein kinase activity	10	10.989011	1.55E-05
GO:0033674~positive regulation of kinase activity	10	10.989011	2.05E-05
GO:0008285~negative regulation of cell proliferation	12	13.1868132	2.38E-05
GO:0030097~hemopoiesis	10	10.989011	2.43E-05
GO:0051347~positive regulation of transferase activity	10	10.989011	2.77E-05
GO:0043085~positive regulation of catalytic activity	14	15.3846154	3.33E-05
GO:0032388~positive regulation of intracellular transport	5	5.49450549	4.21E-05
GO:0048534~hemopoietic or lymphoid organ development	10	10.989011	5.18E-05
GO:0006275~regulation of DNA replication	6	6.59340659	5.30E-05
GO:0007569~cell aging	5	5.49450549	6.19E-05
GO:0044092~negative regulation of molecular function	11	12.0879121	6.64E-05
GO:0043408~regulation of MAPKKK cascade	7	7.69230769	8.05E-05
GO:0002520~immune system development	10	10.989011	8.21E-05
GO:0007568~aging	7	7.69230769	8.47E-05
GO:0042493~response to drug	9	9.89010989	8.64E-05
GO:0007369~gastrulation	6	6.59340659	9.51E-05
GO:0043388~positive regulation of DNA binding	6	6.59340659	9.51E-05
GO:0032386~regulation of intracellular transport	6	6.59340659	1.02E-04
GO:0051050~positive regulation of transport	9	9.89010989	1.08E-04
GO:0030334~regulation of cell migration	8	8.79120879	1.22E-04
GO:0031399~regulation of protein modification process	10	10.989011	1.36E-04
GO:0051259~protein oligomerization	8	8.79120879	1.47E-04
GO:0051092~positive regulation of NF-kappaB transcription f	5	5.49450549	1.47E-04
GO:0051099~positive regulation of binding	6	6.59340659	1.59E-04
GO:0042306~regulation of protein import into nucleus	5	5.49450549	1.94E-04
GO:0010627~regulation of protein kinase cascade	9	9.89010989	2.30E-04
GO:0018108~peptidyl-tyrosine phosphorylation	5	5.49450549	2.31E-04
GO:0031346~positive regulation of cell projection organizatio	5	5.49450549	2.52E-04
GO:0040012~regulation of locomotion	8	8.79120879	2.68E-04
GO:0018212~peptidyl-tyrosine modification	5	5.49450549	2.73E-04
GO:0051270~regulation of cell motion	8	8.79120879	2.77E-04
GO:0032880~regulation of protein localization	7	7.69230769	2.93E-04

T4

Up-regulated Genes

Term	Count	%	P-Value	Benjamini	GENES
Citrate cycle (TCA cycle)	9	7.1	2.1E-08	0.000002	SDHA, SDHB, ACO1, SDHD, CS, ACLY, DLAT, MDH2, FH
Pathways in cancer	22	17.5	3.3E-08	0.0000016	CEBPA, FGFR2, VHL, TGFBR1, MET, RAF1, RB1, CDK4, BIRC3, PTEN, SUFU, NRAS, CDKN2A, KRAS, VEGFA, MAPK9, PIK3CA, MAPK8, MTOR, ABL1, MYC, FH
ErbB signaling pathway	12	9.5	1.1E-07	0.0000036	NRAS, KRAS, PAK2, MAP2K4, RAF1, MAPK9, PIK3CA, MAPK8, RPS6KB1, MTOR, ABL1, MYC
Chronic myeloid leukemia	11	8.7	2.7E-07	0.0000064	NRAS, CDKN2A, KRAS, TGFBR1, RAF1, PIK3CA, RB1, ABL1, CDK4, MYC, PTPN11
Renal cell carcinoma	10	7.9	0.0000015	0.000029	NRAS, KRAS, PAK2, VHL, MET, VEGFA, RAF1, PIK3CA, FH, PTPN11
Pancreatic cancer	10	7.9	0.000002	0.000031	CDKN2A, KRAS, TGFBR1, VEGFA, RAF1, MAPK9, PIK3CA, MAPK8, RB1, CDK4
Bladder cancer	8	6.3	0.0000041	0.000055	NRAS, CDKN2A, KRAS, VEGFA, RAF1, RB1, CDK4, MYC
Neurotrophin signaling pathway	12	9.5	0.0000042	0.00005	NRAS, MAP3K5, KRAS, MAPK14, RAF1, MAPK9, RIPK2, PIK3CA, MAPK8, ABL1, CSK, PTPN11
Glioma	9	7.1	0.0000067	0.000071	NRAS, CDKN2A, KRAS, RAF1, PIK3CA, RB1, MTOR, CDK4, PTEN
Insulin signaling pathway	12	9.5	0.0000097	0.000092	NRAS, PRKAR2A, KRAS, TSC1, PRKCI, HK1, RAF1, MAPK9, PIK3CA, MAPK8, RPS6KB1, MTOR
Melanoma	9	7.1	0.000017	0.00014	NRAS, CDKN2A, KRAS, MET, RAF1, PIK3CA, RB1, CDK4, PTEN
Acute myeloid leukemia	8	6.3	0.000037	0.00029	CEBPA, NRAS, KRAS, RAF1, PIK3CA, RPS6KB1, MTOR, MYC
MAPK signaling pathway	15	11.9	0.000087	0.00063	FGFR2, MAPKAPK5, TGFBR1, NLK, MAP2K4, RAF1, MAP3K7, NRAS, MAP3K5, KRAS, PAK2, MAPK14, MAPK9, MAPK8, MYC
Non-small cell lung cancer	7	5.6	0.00022	0.0015	NRAS, CDKN2A, KRAS, RAF1, PIK3CA, RB1, CDK4
Fc epsilon RI signaling pathway	8	6.3	0.00025	0.0016	NRAS, KRAS, MAPK14, MAP2K4, RAF1, MAPK9, PIK3CA, MAPK8
T cell receptor signaling pathway	9	7.1	0.00034	0.002	MAP3K7, NRAS, KRAS, PAK2, MAPK14, RAF1, MAPK9, PIK3CA, CDK4
Colorectal cancer	8	6.3	0.00039	0.0022	KRAS, TGFBR1, MET, RAF1, MAPK9, PIK3CA, MAPK8, MYC
Prostate cancer	8	6.3	0.00056	0.003	FGFR2, NRAS, KRAS, RAF1, PIK3CA, RB1, MTOR, PTEN
Epithelial cell signaling in Helicobacter pylori infection	7	5.6	0.00077	0.0038	MAPK14, MET, MAP2K4, MAPK9, MAPK8, CSK, PTPN11
Cell cycle	9	7.1	0.0009	0.0043	CDK1, CDKN2A, BUB1B, TTK, CHEK1, RB1, ABL1, CDK4, MYC
GnRH signaling pathway	8	6.3	0.001	0.0045	NRAS, KRAS, GNAQ, MAPK14, MAP2K4, RAF1, MAPK9, MAPK8
mTOR signaling pathway	6	4.8	0.0015	0.0063	TSC1, VEGFA, STRADA, PIK3CA, RPS6KB1, MTOR
Endometrial cancer	6	4.8	0.0015	0.0063	NRAS, KRAS, RAF1, PIK3CA, MYC, PTEN
Progesterone-mediated oocyte maturation	7	5.6	0.0026	0.011	CDK1, KRAS, MAPK14, RAF1, MAPK9, PIK3CA, MAPK8
Gap junction	7	5.6	0.0031	0.012	CDK1, NRAS, TUBB, KRAS, GNAQ, CSNK1D, RAF1
NOD-like receptor signaling pathway	6	4.8	0.0032	0.012	MAP3K7, MAPK14, MAPK9, RIPK2, MAPK8, BIRC3

Down-regulated Genes

Term	Count	%	P-Value	Benjamini	GENES
Neurotrophin signaling pathway	12	13.186813	1.45E-07	1.23E-05	PDK1, IRAK2, RPS6KA6, HRAS, RPS6KA4, JUN, NTRK1, CAMK2D, TP53, CALM3, AKT3, PIK3R1
Endometrial cancer	8	8.7912088	1.97E-06	8.36E-05	HRAS, CCND1, ILK, TP53, CDH1, AKT3, PIK3R1, APC
Pathways in cancer	16	17.582418	3.75E-06	1.06E-04	HRAS, FLT3, TGFBR2, TP53, SMAD4, BRCA2, CDH1, SMO, CCND1, JUN, NTRK1, JAK1, RUNX1, PIK3R1, AKT3, APC
Pancreatic cancer	8	8.7912088	1.80E-05	3.83E-04	CCND1, TGFBR2, SMAD4, TP53, JAK1, BRCA2, AKT3, PIK3R1
Chronic myeloid leukemia	8	8.7912088	2.36E-05	4.02E-04	HRAS, CCND1, TGFBR2, SMAD4, TP53, RUNX1, AKT3, PIK3R1
Colorectal cancer	8	8.7912088	4.97E-05	7.03E-04	CCND1, JUN, TGFBR2, SMAD4, TP53, AKT3, PIK3R1, APC
Glioma	7	7.6923077	8.44E-05	0.001023812	HRAS, CCND1, CAMK2D, TP53, CALM3, AKT3, PIK3R1
Thyroid cancer	5	5.4945055	3.34E-04	0.003540472	HRAS, CCND1, NTRK1, TP53, CDH1
Apoptosis	7	7.6923077	5.04E-04	0.004745506	IRAK2, RIPK1, NTRK1, PRKAR1A, TP53, AKT3, PIK3R1
ErbB signaling pathway	7	7.6923077	5.04E-04	0.004745506	HRAS, ERBB4, JUN, CAMK2D, ABL2, AKT3, PIK3R1
Acute myeloid leukemia	6	6.5934066	5.48E-04	0.004649785	HRAS, CCND1, FLT3, RUNX1, AKT3, PIK3R1
MAPK signaling pathway	11	12.087912	9.84E-04	0.00757819	RPS6KA6, HRAS, RPS6KA4, JUN, NTRK1, TGFBR2, TP53, FLNB, AKT3, MAP2K6, ATF2
Melanoma	6	6.5934066	0.0013855	0.009772924	HRAS, CCND1, TP53, CDH1, AKT3, PIK3R1
T cell receptor signaling pathway	7	7.6923077	0.0015755	0.010256427	PDK1, PRKCQ, HRAS, FYN, JUN, AKT3, PIK3R1
Phosphatidylinositol signaling system	6	6.5934066	0.0016686	0.011895322	PIK3C2B, PIKFYVE, CALM3, INPP4B, PIP5K1A, PIK3R1
Fc epsilon RI signaling pathway	6	6.5934066	0.0021095	0.01880995	PDK1, HRAS, FYN, AKT3, MAP2K6, PIK3R1
Non-small cell lung cancer	5	5.4945055	0.003568	0.019191213	HRAS, CCND1, TP53, AKT3, PIK3R1
Axon guidance	7	7.6923077	0.0038681	0.02325531	EPHA4, HRAS, EPHB6, LIMK2, ROBO1, FYN, PLXNB2
Fc gamma R-mediated phagocytosis	6	6.5934066	0.0049704	0.025122413	LIMK2, HCK, PIKFYVE, PIP5K1A, AKT3, PIK3R1
GnRH signaling pathway	6	6.5934066	0.0056712	0.037135172	HRAS, JUN, CAMK2D, CALM3, GNAS, MAP2K6
Focal adhesion	8	8.7912088	0.0088645	0.049605821	HRAS, CCND1, FYN, JUN, ILK, FLNB, AKT3, PIK3R1
Adherens junction	5	5.4945055	0.0124913	0.049066116	FYN, TGFBR2, SMAD4, CDH1, INSR
Bladder cancer	4	4.3956044	0.0129372	0.073016493	HRAS, CCND1, TP53, CDH1
Prostate cancer	5	5.4945055	0.0203068	0.071758939	HRAS, CCND1, TP53, AKT3, PIK3R1
Insulin signaling pathway	6	6.5934066	0.0208056	0.083465575	HRAS, PRKAR1A, CALM3, INSR, AKT3, PIK3R1
Inositol phosphate metabolism	4	4.3956044	0.0253083	0.096635656	PIK3C2B, PIKFYVE, INPP4B, PIP5K1A
Toll-like receptor signaling pathway	5	5.4945055	0.0306084	0.096883875	JUN, RIPK1, AKT3, MAP2K6, PIK3R1
Wnt signaling pathway	6	6.5934066	0.0318513	0.132025268	CCND1, JUN, CAMK2D, SMAD4, TP53, APC

Long-term potentiation	4	4.3956044	0.0455713	0.136841201	RPS6KA6, HRAS, CAMK2D, CALM3

T5

Pathways postively enriched with TRIM24

Negative - below

NAME	SIZE	FDR q-val	ES	NES	NOM p-val	FWER p-val	RANK AT MAX	LEADING EDGE
KEGG_OOCYTE_MEIOSIS	87	0.06407774	0.52151257	1.8744404	0	0.495	2107	tags=40%, list=20%, signal=50%
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	35	0.06433764	0.6259229	1.8780497	0.00381679	0.485	2554	tags=66%, list=25%, signal=87%
REACTOME_KINESINS	18	0.06713493	0.83313584	1.8781717	0.00191939	0.485	973	tags=72%, list=9%, signal=80%
PID_AURORA_B_PATHWAY	34	0.06794949	0.7155593	1.8576249	0.00763359	0.543	1499	tags=65%, list=14%, signal=75%
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLES	28	0.0684518	0.7171073	1.882034	0.00389105	0.474	1823	tags=75%, list=18%, signal=91%
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADA	149	0.07023305	0.49986956	1.8580425	0.00185529	0.543	2162	tags=44%, list=21%, signal=54%
REACTOME_GLUCOSE_TRANSPORT	36	0.070659	0.63171184	1.8839049	0.00185874	0.469	1823	tags=56%, list=18%, signal=67%
REACTOME_TRANSCRIPTION	131	0.07192238	0.5535502	1.9142996	0.00546448	0.38	2460	tags=60%, list=24%, signal=78%
REACTOME_MITOTIC_G2_G2_M_PHASES	68	0.07214313	0.56096804	1.847535	0.00546448	0.567	1560	tags=44%, list=15%, signal=52%
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	25	0.07262644	0.75148666	1.8585649	0.00195313	0.542	1823	tags=80%, list=18%, signal=97%
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	60	0.07322135	0.61327076	1.8851805	0	0.466	2136	tags=55%, list=21%, signal=69%
KEGG_RNA_DEGRADATION	43	0.07602149	0.5983397	1.9153907	0	0.376	2554	tags=58%, list=25%, signal=77%
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_	25	0.07689999	0.71516156	1.8855654	0.00189753	0.464	1823	tags=72%, list=18%, signal=87%
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEU	25	0.078276835	0.75012314	1.8890096	0	0.45	1823	tags=80%, list=18%, signal=97%
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	88	0.0798239	0.5532845	1.8321847	0.00570342	0.602	2445	tags=63%, list=23%, signal=81%
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	39	0.08047694	0.6861041	1.8974146	0.00387597	0.428	2513	tags=79%, list=24%, signal=104%
REACTOME_MEIOSIS	62	0.081455134	0.5950874	1.9161471	0	0.376	3052	tags=69%, list=29%, signal=98%
BIOCARTA_ATRBRCA_PATHWAY	19	0.08189245	0.76268107	1.890015	0	0.447	1955	tags=79%, list=19%, signal=97%
REACTOME_MEIOTIC_RECOMBINATION	37	0.08225334	0.64033824	1.8254842	0.00187617	0.62	3052	tags=78%, list=29%, signal=110%
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	29	0.083246626	0.72805715	1.9221653	0.00195313	0.36	1823	tags=72%, list=18%, signal=88%
REACTOME_MRNA_3_END_PROCESSING	21	0.08412655	0.6913187	1.8157525	0.00585938	0.646	2513	tags=71%, list=24%, signal=94%
REACTOME_RNA_POL_II_TRANSCRIPTION	79	0.08625827	0.55333495	1.8029414	0.01094891	0.674	2513	tags=61%, list=24%, signal=79%
REACTOME_METABOLISM_OF_NON_CODING_RNA	40	0.086275935	0.6659836	1.8163214	0.00575816	0.644	2460	tags=73%, list=24%, signal=95%
REACTOME_TELOMERE_MAINTENANCE	41	0.08643117	0.6809423	1.8053694	0.01328273	0.665	2077	tags=66%, list=20%, signal=82%
REACTOME_HIV_LIFE_CYCLE	100	0.08865291	0.5444222	1.805871	0.00948767	0.664	2445	tags=60%, list=23%, signal=78%
REACTOME_MEIOTIC_SYNAPSIS	38	0.089806385	0.6271161	1.9236449	0	0.357	2529	tags=66%, list=24%, signal=87%
PID_PLK1_PATHWAY	39	0.09298865	0.7054155	1.9397254	0.00365631	0.311	569	tags=54%, list=5%, signal=57%
PID_BARD1PATHWAY	27	0.09308295	0.7055288	1.7913538	0.00592885	0.708	1937	tags=63%, list=19%, signal=77%
REACTOME_MITOTIC_M_M_G1_PHASES	139	0.094886385	0.6783716	1.9275595	0.00372439	0.348	1507	tags=58%, list=14%, signal=66%
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_RE	28	0.095086835	0.6797084	1.7862389	0.00568182	0.724	2513	tags=71%, list=24%, signal=94%
PID_E2F_PATHWAY	64	0.09586132	0.53454643	1.7817421	0.00727273	0.731	1391	tags=39%, list=13%, signal=45%
REACTOME_G2_M_CHECKPOINTS	31	0.096607305	0.74741536	1.7747201	0.01325758	0.75	1423	tags=71%, list=14%, signal=82%
KEGG_CELL_CYCLE	104	0.096872516	0.5586234	1.777332	0.01296296	0.741	1486	tags=45%, list=14%, signal=52%
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	47	0.097130485	0.5405905	1.7687203	0.00749064	0.763	1313	tags=36%, list=13%, signal=41%
REACTOME_CELL_CYCLE_MITOTIC	258	0.09823454	0.6341808	2.0153189	0.00365631	0.155	1507	tags=51%, list=14%, signal=58%
PID_ATM_PATHWAY	30	0.09938273	0.62878406	1.7688948	0.00558659	0.763	2299	tags=63%, list=22%, signal=81%
REACTOME_G0_AND_EARLY_G1	18	0.09997691	0.744877	1.763292	0.00764818	0.778	1391	tags=61%, list=13%, signal=70%
REACTOME_MRNA_PROCESSING	110	0.10061881	0.5523103	1.7504597	0.01526718	0.813	2554	tags=59%, list=25%, signal=77%
PID_P53REGULATIONPATHWAY	50	0.10128432	0.51185733	1.7545682	0.00383877	0.804	1691	tags=42%, list=16%, signal=50%
REACTOME_CELL_CYCLE_CHECKPOINTS	93	0.10151619	0.63477147	1.7593431	0.01498127	0.787	2338	tags=63%, list=22%, signal=81%
REACTOME_DEADENYLATION_OF_MRNA	16	0.101887636	0.6787476	1.7514621	0.00410678	0.81	2389	tags=75%, list=23%, signal=97%
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_T	25	0.102042675	0.7110379	1.7388387	0.01333333	0.834	2077	tags=76%, list=20%, signal=95%
REACTOME_MITOTIC_G1_G1_S_PHASES	112	0.10254448	0.59615666	1.7406121	0.01679105	0.83	1499	tags=45%, list=14%, signal=52%
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	26	0.10291234	0.7647587	1.7552145	0.01330799	0.802	1423	tags=73%, list=14%, signal=84%
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_	89	0.10314614	0.44948667	1.7423247	0.00513699	0.828	1554	tags=30%, list=15%, signal=35%
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	53	0.10343303	0.49065134	1.7442812	0.00178571	0.825	2029	tags=47%, list=19%, signal=58%
PID_ATR_PATHWAY	36	0.104035236	0.7386535	1.9400655	0.00184843	0.311	1423	tags=67%, list=14%, signal=77%
REACTOME_G1_S_TRANSITION	92	0.10675577	0.6184406	1.7310522	0.02052239	0.851	1595	tags=50%, list=15%, signal=59%
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	22	0.10905583	0.6760333	1.7259576	0.02067669	0.861	1391	tags=59%, list=13%, signal=68%
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	68	0.11119936	0.6387584	1.7213694	0.02385321	0.871	2228	tags=60%, list=21%, signal=76%
PID_FANCONI_PATHWAY	36	0.117885515	0.73211044	1.9411031	0.00188324	0.308	1955	tags=72%, list=19%, signal=89%
REACTOME_PACKAGING_OF_TELOMERE_ENDS	18	0.118495315	0.68107355	1.6903661	0.02457467	0.916	2352	tags=72%, list=23%, signal=93%
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETERO	33	0.11935501	0.51551384	1.6913769	0.00549451	0.914	2029	tags=48%, list=19%, signal=60%
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	97	0.119671956	0.55975544	1.7101259	0.02681992	0.886	2554	tags=60%, list=25%, signal=78%
REACTOME_DNA_STRAND_ELONGATION	26	0.120333225	0.76699644	1.6859914	0.01904762	0.919	1247	tags=69%, list=12%, signal=78%
KEGG_VIBRIO_CHOLERAE_INFECTION	45	0.120374754	0.51593	1.6964225	0.01289135	0.908	3008	tags=53%, list=29%, signal=75%
REACTOME_DNA_REPAIR	89	0.12055682	0.5142796	1.6922164	0.02616822	0.914	1937	tags=49%, list=19%, signal=60%
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	22	0.12056231	0.65992707	1.6944016	0.02573529	0.909	2299	tags=64%, list=22%, signal=82%
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	63	0.12074049	0.5043358	1.683728	0.01841621	0.925	2445	tags=57%, list=23%, signal=74%
REACTOME_SYNTHESIS_OF_DNA	77	0.1209472	0.64069414	1.6996429	0.02578269	0.905	1595	tags=51%, list=15%, signal=59%
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COM	53	0.12102578	0.505388	1.7043699	0.00914077	0.898	1313	tags=36%, list=13%, signal=41%
REACTOME_S_PHASE	92	0.121185385	0.61691564	1.6974783	0.03142329	0.907	1595	tags=49%, list=15%, signal=57%
REACTOME_CHROMOSOME_MAINTENANCE	74	0.121254615	0.6744589	2.0221937	0	0.145	2077	tags=64%, list=20%, signal=79%
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	182	0.121795036	0.44952235	1.7008208	0.00550459	0.902	2177	tags=41%, list=21%, signal=51%
REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_AC	18	0.12293223	0.6063839	1.7045463	0.00787402	0.898	2029	tags=56%, list=19%, signal=69%
REACTOME_HIV_INFECTION	172	0.12411085	0.5002294	1.676016	0.02420857	0.934	1909	tags=44%, list=18%, signal=53%
REACTOME_MITOTIC_PROMETAPHASE	69	0.12437699	0.7036969	1.9513204	0.00189036	0.286	1507	tags=64%, list=14%, signal=74%
PID_FOXOPATHWAY	45	0.124811955	0.48527598	1.6734878	0.0088968	0.939	1691	tags=40%, list=16%, signal=48%
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	18	0.12513752	0.6940431	1.6767459	0.01934236	0.934	2460	tags=72%, list=24%, signal=94%
REACTOME_DNA_REPLICATION	158	0.13021842	0.6848052	1.9630483	0.00368324	0.254	1507	tags=58%, list=14%, signal=66%
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	21	0.13126844	0.77417374	1.6624975	0.01934236	0.942	867	tags=67%, list=8%, signal=73%
KEGG_DNA_REPLICATION	32	0.13128528	0.71137786	1.6606499	0.03780719	0.944	2042	tags=72%, list=20%, signal=89%
PID_MYC_ACTIVPATHWAY	68	0.13238217	0.51319	1.6634464	0.03825137	0.942	2818	tags=51%, list=27%, signal=70%
REACTOME_RNA_POL_I_TRANSCRIPTION	35	0.13567908	0.54072607	1.6540781	0.03096539	0.95	2445	tags=60%, list=23%, signal=78%
BIOCARTA_MPR_PATHWAY	29	0.13573524	0.53412044	1.6523368	0.01834862	0.95	2064	tags=52%, list=20%, signal=64%
PID_NFAT_3PATHWAY	47	0.13881032	0.45721254	1.6474698	0.01621622	0.952	1586	tags=34%, list=15%, signal=40%
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	17	0.14737275	0.65242016	1.6372324	0.02985075	0.962	2107	tags=76%, list=20%, signal=96%
REACTOME_EXTENSION_OF_TELOMERES	23	0.14907688	0.71080786	1.6337173	0.03738318	0.963	1247	tags=57%, list=12%, signal=64%
KEGG_BASAL_TRANSCRIPTION_FACTORS	27	0.15401207	0.5408654	1.6271219	0.02123552	0.967	2387	tags=59%, list=23%, signal=77%
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	72	0.1632321	0.44447088	1.6120628	0.01067616	0.977	2137	tags=43%, list=21%, signal=54%
BIOCARTA_G2_PATHWAY	23	0.1646114	0.6010924	1.6125305	0.03136531	0.977	2451	tags=65%, list=24%, signal=85%
REACTOME_CELL_CYCLE	309	0.16471994	0.6169384	2.0326982	0.00361011	0.129	2077	tags=55%, list=20%, signal=67%
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	51	0.16534413	0.49104476	1.604849	0.03683241	0.979	2445	tags=55%, list=23%, signal=71%
KEGG_MISMATCH_REPAIR	22	0.16576818	0.6484285	1.6131997	0.03512015	0.976	1247	tags=45%, list=12%, signal=52%
KEGG_NUCLEOTIDE_EXCISION_REPAIR	40	0.16580872	0.51853645	1.6027012	0.03795067	0.979	1313	tags=43%, list=13%, signal=48%
REACTOME_M_G1_TRANSITION	66	0.16619298	0.6319666	1.6057734	0.05639098	0.979	1595	tags=52%, list=15%, signal=60%
PID_CDC42_PATHWAY	60	0.16620177	0.44910452	1.6146843	0.01298701	0.976	2300	tags=42%, list=22%, signal=53%
PID_FOXM1PATHWAY	38	0.1672106	0.5534771	1.6065508	0.05128205	0.979	1293	tags=45%, list=12%, signal=51%
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	110	0.16791742	0.51663864	1.5992283	0.04135338	0.982	1909	tags=45%, list=18%, signal=54%
REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION_INDE	16	0.16929969	0.65791976	1.5962929	0.03512015	0.982	2299	tags=69%, list=22%, signal=88%

REACTOME_LAGGING_STRAND_SYNTHESIS	17	0.17240992	0.7154413	1.5917407	0.04460967	0.985	1247	tags=59%, list=12%, signal=67%
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	57	0.1811984	0.60192	1.58256	0.07063197	0.988	2228	tags=58%, list=21%, signal=73%
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_	57	0.19812818	0.59770286	1.5670825	0.0742115	0.99	2228	tags=58%, list=21%, signal=73%
KEGG_SPLICEOSOME	81	0.20513706	0.51304084	1.5594462	0.06433824	0.991	2554	tags=56%, list=25%, signal=73%
KEGG_HOMOLOGOUS_RECOMBINATION	25	0.20534082	0.6054251	1.5575466	0.06179775	0.991	2042	tags=52%, list=20%, signal=65%
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	59	0.2193444	0.56081754	1.5450006	0.0873606	0.995	1800	tags=44%, list=17%, signal=53%
REACTOME_RNA_POL_I_PROMOTER_OPENING	16	0.22835203	0.6499947	1.5367987	0.06857143	0.997	3038	tags=81%, list=29%, signal=115%
PID_PI3KCIAKTPATHWAY	31	0.23155028	0.4581829	1.5327475	0.03018109	0.997	1293	tags=32%, list=12%, signal=37%
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	55	0.23914647	0.5846298	1.5236588	0.0988806	0.997	2913	tags=64%, list=28%, signal=88%
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU	70	0.24074456	0.51165193	1.524294	0.07933579	0.997	2913	tags=60%, list=28%, signal=83%
BIOCARTA_PROTEASOME_PATHWAY	26	0.24789473	0.65029293	1.5158061	0.09477756	0.997	2912	tags=77%, list=28%, signal=107%
PID_TELOMERASEPATHWAY	62	0.26376665	0.41596246	1.5031215	0.02973978	0.997	2221	tags=40%, list=21%, signal=51%
PID_INSULIN_GLUCOSE_PATHWAY	21	0.26954383	0.4841086	1.4975495	0.06578948	0.997	802	tags=29%, list=8%, signal=31%
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	50	0.27322116	0.5779377	1.4884555	0.11359404	0.998	1595	tags=42%, list=15%, signal=49%
REACTOME_SIGNALING_BY_WNT	58	0.27351007	0.5156448	1.4931153	0.08679245	0.998	2959	tags=57%, list=28%, signal=79%
BIOCARTA_ACTINY_PATHWAY	17	0.27414975	0.59575063	1.4894589	0.06903353	0.998	2228	tags=59%, list=21%, signal=75%
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	53	0.27478662	0.5972967	1.49072	0.10841122	0.998	2913	tags=68%, list=28%, signal=94%
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	77	0.2910182	0.41678193	1.4718512	0.07195572	0.998	2203	tags=38%, list=21%, signal=47%
SA_G1_AND_S_PHASES	15	0.29140112	0.5932573	1.4732578	0.08812261	0.998	2790	tags=53%, list=27%, signal=73%
PID_ECADHERIN_NASCENTAJ_PATHWAY	33	0.29209745	0.4702026	1.4746785	0.05321101	0.998	3008	tags=52%, list=29%, signal=72%
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	104	0.2930664	0.5425524	2.0442512	0.00187617	0.117	2381	tags=51%, list=23%, signal=65%
KEGG_PYRIMIDINE_METABOLISM	71	0.2938467	0.45504412	1.468083	0.0754717	0.999	1902	tags=41%, list=18%, signal=50%
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	200	0.29591098	0.40078443	1.4633963	0.09464286	0.999	2197	tags=37%, list=21%, signal=46%
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	39	0.29715347	0.5048912	1.4642608	0.08969466	0.999	1493	tags=44%, list=14%, signal=51%
REACTOME_RNA_POL_I_TRANSCRIPTION_INITIATION	18	0.3022849	0.5227506	1.4578091	0.08364312	0.999	2445	tags=50%, list=23%, signal=65%
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	50	0.30503663	0.5514066	1.4544494	0.13197026	0.999	2228	tags=52%, list=21%, signal=66%
REACTOME_INSULIN_RECEPTOR_RECYCLING	17	0.31322733	0.5596978	1.4476588	0.11132438	0.999	1791	tags=35%, list=17%, signal=43%
PID_AURORA_A_PATHWAY	29	0.31582433	0.4882126	1.4442364	0.08671587	0.999	1477	tags=38%, list=14%, signal=44%
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	55	0.32016093	0.5122438	1.439924	0.12037037	0.999	2913	tags=56%, list=28%, signal=78%
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	49	0.32273537	0.5413635	1.4333602	0.13457943	0.999	2913	tags=57%, list=28%, signal=79%
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	45	0.3228216	0.5721276	1.434911	0.13644859	0.999	1800	tags=44%, list=17%, signal=54%
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	44	0.3243196	0.46860102	1.4356334	0.09829868	0.999	1493	tags=43%, list=14%, signal=50%
REACTOME_MRNA_SPLICING	70	0.3312156	0.4874268	1.4230144	0.11685824	0.999	2554	tags=51%, list=25%, signal=68%
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_C	33	0.33272928	0.473773	1.4254011	0.09640832	0.999	1478	tags=39%, list=14%, signal=46%
KEGG_PROTEASOME	40	0.33353868	0.59199905	1.4232576	0.15789473	0.999	2913	tags=65%, list=28%, signal=90%
KEGG_PROTEIN_EXPORT	17	0.33893797	0.5817911	1.416839	0.12398374	1	2853	tags=53%, list=27%, signal=73%
BIOCARTA_G1_PATHWAY	27	0.34162378	0.4681821	1.4117543	0.09009009	1	1423	tags=30%, list=14%, signal=34%
PID_AJDISS_2PATHWAY	45	0.34311327	0.40989354	1.4125097	0.06944445	1	3527	tags=56%, list=34%, signal=84%
PID_MYC_PATHWAY	22	0.34561014	0.45364535	1.4077361	0.086629	1	680	tags=23%, list=7%, signal=24%
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	19	0.34577858	0.49901304	1.4041791	0.10638298	1	1793	tags=47%, list=17%, signal=57%
REACTOME_GLOBAL_GENOMIC_NER_GG_NER	29	0.34756723	0.48890918	1.4047921	0.11742424	1	1247	tags=41%, list=12%, signal=47%
BIOCARTA_CK1_PATHWAY	15	0.3479081	0.5118231	1.4013877	0.10826772	1	2766	tags=47%, list=27%, signal=63%
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	45	0.35084054	0.56106424	1.3978455	0.16165413	1	1800	tags=44%, list=17%, signal=54%
REACTOME_TRNA_AMINOACYLATION	31	0.37214202	0.5217424	1.3826948	0.15384616	1	3089	tags=61%, list=30%, signal=87%
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	45	0.37400493	0.54963934	1.3656354	0.18441065	1	2913	tags=60%, list=28%, signal=83%
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRI	18	0.37430072	0.5648612	1.3685796	0.16666667	1	2036	tags=56%, list=20%, signal=69%
REACTOME_PERK_REGULATED_GENE_EXPRESSION	24	0.37467763	0.46723077	1.3828405	0.10157618	1	2514	tags=54%, list=24%, signal=71%
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	44	0.3750727	0.5564403	1.371387	0.1741573	1	2913	tags=61%, list=28%, signal=85%
REACTOME_ARMS_MEDIATED_ACTIVATION	15	0.3753402	0.48257846	1.374439	0.09345795	1	2255	tags=47%, list=22%, signal=59%
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	22	0.3754832	0.47460604	1.3663086	0.1183432	1	1793	tags=41%, list=17%, signal=49%
REACTOME_RNA_POL_III_TRANSCRIPTION	28	0.37562057	0.45738953	1.3633449	0.12241054	1	1853	tags=43%, list=18%, signal=52%
REACTOME_CHOLESTEROL_BIOSYNTHESIS	18	0.37569618	0.5541837	1.361744	0.18518518	1	3123	tags=67%, list=30%, signal=95%
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	63	0.37603804	0.4071886	1.3755872	0.12619503	1	3073	tags=52%, list=30%, signal=74%
KEGG_STEROID_BIOSYNTHESIS	15	0.37648335	0.53507626	1.3721179	0.15568863	1	3123	tags=53%, list=30%, signal=76%
PID_ERBB1_INTERNALIZATION_PATHWAY	37	0.37652174	0.39843115	1.3688426	0.09289618	1	2255	tags=43%, list=22%, signal=55%
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	28	0.37823007	0.524143	1.375938	0.1425819	1	2497	tags=54%, list=24%, signal=70%
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	43	0.37838438	0.55780923	1.3775302	0.17293233	1	2913	tags=60%, list=28%, signal=84%
KEGG_BASE_EXCISION_REPAIR	31	0.38186806	0.49267802	1.352313	0.1716418	1	1247	tags=42%, list=12%, signal=48%
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	80	0.38435823	0.4009764	1.3523368	0.13898917	1	2296	tags=40%, list=22%, signal=51%
REACTOME_REGULATION_OF_APOPTOSIS	50	0.3862315	0.49620178	1.3527935	0.1929499	1	2244	tags=46%, list=22%, signal=58%
REACTOME_APOPTOSIS	127	0.38678256	0.37421468	1.3539026	0.11408199	1	2913	tags=47%, list=28%, signal=65%
REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	31	0.40441602	0.4418654	1.3305327	0.15339805	1	3073	tags=55%, list=30%, signal=78%
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	43	0.4053378	0.52874136	1.3343809	0.20637898	1	2913	tags=56%, list=28%, signal=77%
REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	17	0.40604326	0.4561101	1.3310748	0.13068181	1	2782	tags=53%, list=27%, signal=72%
PID_MET_PATHWAY	67	0.40620127	0.36202857	1.3354335	0.09323584	1	2266	tags=31%, list=22%, signal=40%
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_END	41	0.4065068	0.53687423	1.3323131	0.21780303	1	2913	tags=59%, list=28%, signal=81%
PID_WNT_NONCANONICAL_PATHWAY	26	0.40673724	0.429522	1.3365818	0.11688311	1	2248	tags=54%, list=22%, signal=69%
BIOCARTA_TEL_PATHWAY	18	0.4072894	0.4645813	1.3227246	0.1743295	1	3403	tags=61%, list=33%, signal=91%
BIOCARTA_CREB_PATHWAY	23	0.40891138	0.42187116	1.3060098	0.1534196	1	3048	tags=52%, list=29%, signal=74%
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	45	0.40926826	0.5283949	1.3230946	0.21797323	1	2913	tags=60%, list=28%, signal=83%
REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	19	0.40937328	0.4895233	1.3245395	0.17366412	1	1791	tags=32%, list=17%, signal=38%
PID_ERBB1_DOWNSTREAM_PATHWAY	92	0.40971002	0.33505103	1.3069867	0.11231884	1	2300	tags=38%, list=22%, signal=48%
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	37	0.4112394	0.43226117	1.3249519	0.13926499	1	1798	tags=43%, list=17%, signal=52%
BIOCARTA_ATM_PATHWAY	20	0.41172582	0.45732266	1.3072299	0.13405797	1	874	tags=30%, list=8%, signal=33%
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	20	0.4117397	0.55478823	1.3171179	0.20267686	1	1758	tags=50%, list=17%, signal=60%
BIOCARTA_CCR3_PATHWAY	21	0.4118096	0.4359449	1.3099475	0.14310955	1	2521	tags=43%, list=24%, signal=56%
BIOCARTA_MITOCHONDRIA_PATHWAY	19	0.41287872	0.46041512	1.3022697	0.1452514	1	1469	tags=32%, list=14%, signal=37%
PID_AR_TF_PATHWAY	46	0.4132813	0.38345143	1.3105483	0.14003591	1	862	tags=20%, list=8%, signal=21%
BIOCARTA_TNFR1_PATHWAY	28	0.4133558	0.41317487	1.3176546	0.12255773	1	979	tags=25%, list=9%, signal=28%
REACTOME_APOPTOTIC_EXECUTION_PHASE	46	0.41346845	0.3811402	1.307575	0.12939002	1	2871	tags=50%, list=28%, signal=69%
KEGG_P53_SIGNALING_PATHWAY	59	0.41406474	0.36936128	1.3144804	0.12190813	1	1115	tags=22%, list=11%, signal=25%
PID_P73PATHWAY	71	0.41575417	0.3428265	1.3105645	0.10238908	1	735	tags=18%, list=7%, signal=20%
REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BI	16	0.4157672	0.47826782	1.2992668	0.19960861	1	1948	tags=56%, list=19%, signal=69%
PID_PRLSIGNALINGEVENTSPATHWAY	20	0.41816697	0.4434418	1.3106145	0.17680608	1	2068	tags=40%, list=20%, signal=50%
REACTOME_MRNA_CAPPING	24	0.42045453	0.4527907	1.2952356	0.1741683	1	1478	tags=42%, list=14%, signal=48%
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	46	0.42577276	0.5150407	1.2907393	0.25	1	2913	tags=57%, list=28%, signal=78%
PID_WNT_CANONICAL_PATHWAY	16	0.42583096	0.45459422	1.2893248	0.165692	1	1293	tags=31%, list=12%, signal=36%
SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCTES	62	0.4289762	0.32782248	1.2862085	0.09205777	1	1712	tags=26%, list=16%, signal=31%
PID_RAC1_PATHWAY	44	0.43415093	0.3770038	1.2818105	0.16337523	1	2300	tags=41%, list=22%, signal=52%
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	25	0.4434244	0.4281423	1.2752316	0.15799257	1	1469	tags=36%, list=14%, signal=42%
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPT	23	0.45613068	0.41908595	1.26664	0.15355805	1	1756	tags=39%, list=17%, signal=47%
PID_MTOR_4PATHWAY	58	0.4570946	0.3420726	1.2647	0.15798923	1	2020	tags=28%, list=19%, signal=34%
PID_AR_PATHWAY	49	0.4676001	0.35596374	1.257681	0.15653776	1	2138	tags=41%, list=21%, signal=51%

REACTOME_ADAPTIVE_IMMUNE_SYSTEM	412	0.47013575	0.3189989	1.254965	0.19494584	1	2255	tags=31%, list=22%, signal=38%
REACTOME_ENOS_ACTIVATION_AND_REGULATION	16	0.4739411	0.4434454	1.2515316	0.1953125	1	1075	tags=31%, list=10%, signal=35%
KEGG_THYROID_CANCER	29	0.47957233	0.36091068	1.24131	0.15009381	1	1625	tags=28%, list=16%, signal=33%
KEGG_RNA_POLYMERASE	21	0.479858	0.4868234	1.2424982	0.25925925	1	1853	tags=43%, list=18%, signal=52%
REACTOME_ELONGATION_ARREST_AND_RECOVERY	29	0.48025876	0.43740997	1.2451053	0.21960784	1	1798	tags=45%, list=17%, signal=54%
REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_ABSENCE	21	0.48066488	0.48836106	1.2434884	0.23856859	1	1478	tags=43%, list=14%, signal=50%
BIOCARTA_MAL_PATHWAY	17	0.48251304	0.43099785	1.2452904	0.19851577	1	2068	tags=41%, list=20%, signal=51%
BIOCARTA_P53_PATHWAY	16	0.4930932	0.44211826	1.2280332	0.21280603	1	2847	tags=56%, list=27%, signal=77%
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	24	0.49460116	0.4875279	1.2301192	0.2756654	1	2036	tags=46%, list=20%, signal=57%
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	23	0.4947044	0.42166618	1.2286333	0.21350364	1	1990	tags=22%, list=19%, signal=27%
REACTOME_G1_PHASE	32	0.49633506	0.4014409	1.2306517	0.23649907	1	3012	tags=50%, list=29%, signal=70%
BIOCARTA_PTDINS_PATHWAY	20	0.5088557	0.3938643	1.2182064	0.19428572	1	2886	tags=45%, list=28%, signal=62%
KEGG_PURINE_METABOLISM	125	0.51348424	0.30410093	1.2141192	0.18038529	1	700	tags=16%, list=7%, signal=17%
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GO	16	0.5177159	0.4393636	1.2104529	0.23314066	1	2327	tags=31%, list=22%, signal=40%
REACTOME_PI_METABOLISM	34	0.5267114	0.37901545	1.2041165	0.22968198	1	2681	tags=41%, list=26%, signal=55%
BIOCARTA_IGF1MTOR_PATHWAY	19	0.54641885	0.40023994	1.1923712	0.22178988	1	2886	tags=53%, list=28%, signal=73%
REACTOME_FORMATION_OF_THE_HIV1_EARLY_ELONGATION_COMPLEX	27	0.5584334	0.42561477	1.1844033	0.26284584	1	1478	tags=37%, list=14%, signal=43%
PID_P75NTRPATHWAY	62	0.5710281	0.30141145	1.176566	0.19202898	1	2131	tags=27%, list=20%, signal=34%
REACTOME_ER_PHAGOSOME_PATHWAY	55	0.576122	0.46538186	1.1725123	0.34269664	1	2913	tags=51%, list=28%, signal=70%
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_2_PROMO	19	0.5783453	0.43341458	1.1657321	0.28927204	1	1853	tags=37%, list=18%, signal=45%
BIOCARTA_BARRESTIN_SRC_PATHWAY	15	0.5785551	0.4291831	1.1641988	0.2694497	1	2020	tags=47%, list=19%, signal=58%
BIOCARTA_RACCYCD_PATHWAY	26	0.5793706	0.3644484	1.169503	0.26802218	1	2886	tags=46%, list=28%, signal=64%
REACTOME_METABOLISM_OF_NUCLEOTIDES	56	0.57939506	0.36124998	1.1566855	0.3074074	1	1920	tags=38%, list=18%, signal=46%
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	21	0.58055556	0.4086638	1.1660726	0.27482268	1	2447	tags=48%, list=24%, signal=62%
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	104	0.5814603	0.32838845	1.1570625	0.29227942	1	2913	tags=41%, list=28%, signal=57%
PID_MAPKTRKPATHWAY	33	0.58223414	0.33009687	1.1539708	0.22463769	1	2349	tags=39%, list=23%, signal=51%
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	59	0.58257335	0.3110025	1.1664822	0.22780569	1	2046	tags=32%, list=20%, signal=40%
BIOCARTA_CASPASE_PATHWAY	22	0.58326226	0.43138164	1.1589965	0.30291972	1	258	tags=18%, list=2%, signal=19%
BIOCARTA_CELLCYCLE_PATHWAY	21	0.5836944	0.42676988	1.1573721	0.3032015	1	2847	tags=48%, list=27%, signal=65%
REACTOME_MEMBRANE_TRAFFICKING	97	0.58400863	0.3046184	1.160075	0.23854962	1	2183	tags=32%, list=21%, signal=40%
PID_PI3KPLCTRKPATHWAY	32	0.58755004	0.33350873	1.1498392	0.25411335	1	2886	tags=44%, list=28%, signal=60%
PID_CASPASE_PATHWAY	48	0.5930302	0.31615478	1.136209	0.29180887	1	258	tags=13%, list=2%, signal=13%
KEGG_N_GLYCAN_BIOSYNTHESIS	34	0.59380704	0.36819413	1.137152	0.30632412	1	2449	tags=41%, list=24%, signal=54%
KEGG_ADHERENS_JUNCTION	70	0.59468913	0.3231919	1.1449805	0.28884825	1	2020	tags=26%, list=19%, signal=32%
BIOCARTA_CHREBP2_PATHWAY	36	0.59488976	0.35601097	1.1379507	0.30291262	1	2959	tags=39%, list=28%, signal=54%
PID_LKB1_PATHWAY	32	0.5974001	0.3283687	1.1380702	0.2605364	1	1128	tags=19%, list=11%, signal=21%
ST_G_ALPHA_S_PATHWAY	15	0.5974425	0.39773527	1.1311129	0.2911153	1	2020	tags=40%, list=19%, signal=50%
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	183	0.59775025	0.2617805	1.1323675	0.24878837	1	1942	tags=21%, list=19%, signal=25%
REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	15	0.5989119	0.40269738	1.1387385	0.29577464	1	2959	tags=53%, list=28%, signal=74%
KEGG_ONE_CARBON_POOL_BY_FOLATE	15	0.599297	0.423642	1.1399012	0.3203125	1	701	tags=27%, list=7%, signal=29%
SIG_REGULATION_OF_THE_ACTIN_CYTOSKELETON_BY_RHO_GTPASES	32	0.5995167	0.35835466	1.1411194	0.28675136	1	2392	tags=34%, list=23%, signal=44%
REACTOME_MICRORNA_MIRNA_BIOGENESIS	18	0.6012417	0.41939822	1.1213828	0.34179688	1	2251	tags=44%, list=22%, signal=57%
REACTOME_FORMATION_OF_TRANSCRIPTION_COUPLED_NER_TC_NER_REPAIR	24	0.6019405	0.38350514	1.1276168	0.31384015	1	1493	tags=38%, list=14%, signal=44%
BIOCARTA_SPPA_PATHWAY	20	0.6019786	0.37979877	1.1223581	0.31393299	1	2020	tags=35%, list=19%, signal=43%
REACTOME_LIGAND_GATED_ION_CHANNEL_TRANSPORT	20	0.6020008	0.38097987	1.1195972	0.3321918	1	6450	tags=100%, list=62%, signal=262%
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	33	0.6036612	0.43904623	1.1172614	0.40582526	1	1498	tags=36%, list=14%, signal=42%
PID_LIS1PATHWAY	28	0.6044827	0.36347014	1.1224225	0.2977099	1	3003	tags=50%, list=29%, signal=70%
BIOCARTA_STATHMIN_PATHWAY	16	0.6065201	0.44171384	1.122751	0.35037878	1	1680	tags=25%, list=16%, signal=30%
PID_EPHA2_FWDPATHWAY	16	0.6068591	0.38829112	1.1239624	0.29791272	1	2848	tags=44%, list=27%, signal=60%
PID_RB_1PATHWAY	62	0.6101667	0.30095232	1.1112653	0.2951389	1	2847	tags=44%, list=27%, signal=60%
REACTOME_SIGNALLING_TO_ERKS	33	0.61198425	0.3236589	1.1116728	0.31588784	1	2828	tags=45%, list=27%, signal=62%
ST_G_ALPHA_I_PATHWAY	34	0.6161176	0.33097687	1.1017622	0.31858408	1	2886	tags=41%, list=28%, signal=57%
REACTOME_INTERFERON_SIGNALING	126	0.616849	0.34346092	1.1066182	0.34358048	1	2199	tags=30%, list=21%, signal=38%
REACTOME_DARPP_32_EVENTS	20	0.6178579	0.37045437	1.1022269	0.32329318	1	3077	tags=40%, list=30%, signal=57%
SIG_CHEMOTAXIS	43	0.61942416	0.31911415	1.1041256	0.32389382	1	2438	tags=33%, list=23%, signal=42%
ST_PHOSPHOINOSITIDE_3_KINASE_PATHWAY	31	0.62016654	0.3274032	1.1023945	0.31283906	1	1712	tags=26%, list=16%, signal=31%
REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	69	0.624886	0.2760696	1.0868604	0.29695886	1	2006	tags=25%, list=19%, signal=30%
REACTOME_SIGNALING_BY_FGFR1_MUTANTS	24	0.6256609	0.35858333	1.0837582	0.35650623	1	564	tags=13%, list=5%, signal=13%
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	46	0.62623566	0.3434038	1.0847915	0.34432235	1	2068	tags=30%, list=20%, signal=38%
PID_HEDGEHOG_GLIPATHWAY	42	0.62636954	0.30529347	1.087382	0.3256705	1	3192	tags=45%, list=31%, signal=65%
KEGG_COLORECTAL_CANCER	61	0.6281471	0.28631723	1.0917737	0.30072463	1	535	tags=13%, list=5%, signal=14%
BIOCARTA_FAS_PATHWAY	29	0.6288894	0.35253444	1.0874047	0.34900543	1	2879	tags=48%, list=28%, signal=67%
PID_ECADHERIN_KERATINOCYTE_PATHWAY	19	0.6289714	0.3716037	1.0780008	0.3514563	1	1990	tags=26%, list=19%, signal=32%
KEGG_WNT_SIGNALING_PATHWAY	128	0.6297566	0.2607478	1.0882246	0.31118882	1	2959	tags=37%, list=28%, signal=51%
REACTOME_REGULATORY_RNA_PATHWAYS	19	0.629907	0.39598498	1.0922339	0.3625731	1	2251	tags=42%, list=22%, signal=54%
PID_SMAD2_3PATHWAY	15	0.6301358	0.4237554	1.0934883	0.34714004	1	2274	tags=53%, list=22%, signal=68%
REACTOME_BASE_EXCISION_REPAIR	18	0.6301563	0.45541197	1.089372	0.38076922	1	1884	tags=39%, list=18%, signal=47%
REACTOME_PROTEIN_FOLDING	38	0.63030773	0.36658296	1.0800052	0.3752345	1	2036	tags=37%, list=20%, signal=46%
KEGG_LONG_TERM_POTENTIATION	60	0.63135195	0.2849505	1.0780694	0.31118882	1	2451	tags=32%, list=24%, signal=41%
BIOCARTA_WNT_PATHWAY	24	0.63657695	0.34452492	1.0726992	0.36074767	1	3247	tags=46%, list=31%, signal=66%
PID_NETRIN_PATHWAY	28	0.63944936	0.3512579	1.0699525	0.38623327	1	2244	tags=32%, list=22%, signal=41%
REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PAT	16	0.6446399	0.4569175	1.0634086	0.41020793	1	1247	tags=31%, list=12%, signal=35%
PID_BETACATENIN_NUC_PATHWAY	67	0.64598817	0.28583315	1.0640128	0.34362933	1	889	tags=15%, list=9%, signal=16%
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	16	0.6464673	0.41840586	1.0611794	0.4090909	1	1187	tags=31%, list=11%, signal=35%
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	31	0.64691025	0.34833524	1.0595555	0.39499035	1	3337	tags=45%, list=32%, signal=66%
BIOCARTA_EIF4_PATHWAY	22	0.64786386	0.36728635	1.0643877	0.36520076	1	2886	tags=41%, list=28%, signal=56%
REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSION_BY_REV_ERBA	19	0.65316546	0.40480113	1.0550503	0.41984734	1	611	tags=21%, list=6%, signal=22%
KEGG_SELENOAMINO_ACID_METABOLISM	19	0.6608738	0.3712349	1.0483633	0.38666666	1	3337	tags=58%, list=32%, signal=85%
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	23	0.66302973	0.3324784	1.0485827	0.37523106	1	2609	tags=35%, list=25%, signal=46%
PID_HIVNEFPATHWAY	35	0.6654351	0.33649364	1.0447251	0.39317775	1	1115	tags=20%, list=11%, signal=22%
ST_FAS_SIGNALING_PATHWAY	56	0.6711593	0.28796542	1.0405208	0.39045936	1	2068	tags=29%, list=20%, signal=35%
REACTOME_METABOLISM_OF_RNA	210	0.67146784	0.33000836	1.0390186	0.4593573	1	2180	tags=37%, list=21%, signal=46%
BIOCARTA_CHEMICAL_PATHWAY	21	0.67946774	0.3251586	1.0337266	0.40257353	1	2029	tags=33%, list=19%, signal=41%
REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION	18	0.68912125	0.37906724	1.0275477	0.42193308	1	2866	tags=56%, list=28%, signal=77%
BIOCARTA_HIVNEF_PATHWAY	54	0.6986539	0.28608215	1.0214273	0.42408377	1	1259	tags=20%, list=12%, signal=23%
PID_P38ALPHABETADOWNSTREAMPATHWAY	35	0.7022964	0.2916178	1.0181601	0.4489051	1	3005	tags=46%, list=29%, signal=64%
REACTOME_UNFOLDED_PROTEIN_RESPONSE	68	0.70255977	0.2827321	0.99970853	0.44781783	1	2760	tags=46%, list=27%, signal=62%
KEGG_LYSINE_DEGRADATION	37	0.70486593	0.30981395	0.9998011	0.42911154	1	2174	tags=30%, list=21%, signal=37%
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMO	21	0.70532644	0.35810524	1.0125734	0.45300752	1	1853	tags=38%, list=18%, signal=46%
PID_S1P_META_PATHWAY	15	0.705336	0.3476084	1.0008602	0.4494382	1	1979	tags=33%, list=19%, signal=41%
REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	41	0.70533675	0.30678266	1.015187	0.43333334	1	2773	tags=39%, list=27%, signal=53%
REACTOME_SIGNALING_BY_BMP	19	0.70534074	0.39330217	1.0059751	0.47206166	1	2502	tags=47%, list=24%, signal=62%
REACTOME_PURINE_METABOLISM	27	0.70555043	0.3415163	1.0137758	0.45167285	1	679	tags=22%, list=7%, signal=24%

KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	19	0.7064448	0.34273946	1.0041679	0.4581105	1	3778	tags=42%, list=36%, signal=66%
PID_ERBB1_RECEPTOR_PROXIMAL_PATHWAY	34	0.7065465	0.3016492	1.0080081	0.45212767	1	3029	tags=50%, list=29%, signal=70%
KEGG_PROSTATE_CANCER	84	0.70696884	0.24520151	1.0013285	0.45913044	1	2886	tags=36%, list=28%, signal=49%
PID_RETINOIC_ACID_PATHWAY	28	0.7076546	0.31329688	1.0060858	0.44787645	1	2886	tags=43%, list=28%, signal=59%
REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_E	18	0.70886123	0.35967836	1.0081521	0.41967872	1	1977	tags=39%, list=19%, signal=48%
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION	16	0.7089152	0.35767385	1.001625	0.45167285	1	3083	tags=56%, list=30%, signal=80%
BIOCARTA_HSP27_PATHWAY	15	0.710075	0.3554067	1.0087749	0.44322345	1	1115	tags=20%, list=11%, signal=22%
PID_NECTIN_PATHWAY	28	0.71940273	0.33748394	0.9897298	0.4681648	1	1928	tags=32%, list=19%, signal=39%
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	24	0.7218646	0.3085464	0.9871965	0.48428836	1	2281	tags=29%, list=22%, signal=37%
PID_S1P_S1P2_PATHWAY	22	0.72188413	0.3362593	0.9832866	0.46095237	1	2020	tags=36%, list=19%, signal=45%
REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	30	0.7227308	0.3044514	0.98539096	0.48021582	1	2866	tags=47%, list=28%, signal=64%
REACTOME_EGFR_DOWNREGULATION	22	0.723682	0.30993477	0.98112196	0.47495362	1	876	tags=18%, list=8%, signal=20%
BIOCARTA_RHO_PATHWAY	29	0.72402203	0.32073298	0.98346	0.48181817	1	2438	tags=41%, list=23%, signal=54%
PID_PS1PATHWAY	39	0.72544223	0.27610815	0.9777518	0.47689465	1	3293	tags=51%, list=32%, signal=75%
REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION	21	0.7259715	0.36612472	0.97868913	0.47674417	1	611	tags=19%, list=6%, signal=20%
KEGG_ERBB_SIGNALING_PATHWAY	79	0.74188924	0.24498089	0.9628762	0.49373883	1	2255	tags=29%, list=22%, signal=37%
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	127	0.7421879	0.25160673	0.9666894	0.48846152	1	3073	tags=39%, list=30%, signal=54%
PID_NCADHERINPATHWAY	32	0.74233854	0.30300635	0.9679316	0.4973638	1	2266	tags=31%, list=22%, signal=40%
REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	84	0.7432774	0.24441256	0.96346325	0.48969072	1	2881	tags=37%, list=28%, signal=51%
REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOA	19	0.7445462	0.39709613	0.96024287	0.518591	1	2760	tags=53%, list=27%, signal=71%
PID_CDC42_REG_PATHWAY	23	0.74474525	0.3359954	0.9640271	0.4943182	1	3081	tags=43%, list=30%, signal=62%
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	88	0.74905497	0.23445822	0.9566969	0.53723407	1	1869	tags=24%, list=18%, signal=29%
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	66	0.75012237	0.351146	0.9548724	0.53497165	1	1800	tags=29%, list=17%, signal=35%
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	27	0.7524733	0.291854	0.95236933	0.5391791	1	2281	tags=26%, list=22%, signal=33%
REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	45	0.75404793	0.27078316	0.94768023	0.5344538	1	1197	tags=13%, list=11%, signal=15%
PID_NOTCH_PATHWAY	49	0.7563331	0.26054302	0.9477843	0.5254237	1	3225	tags=41%, list=31%, signal=59%
PID_REG_GR_PATHWAY	81	0.75843877	0.24059041	0.9480019	0.53457	1	2028	tags=27%, list=19%, signal=33%
PID_HDAC_CLASSI_PATHWAY	57	0.76253104	0.25299186	0.9418471	0.5397412	1	2451	tags=33%, list=24%, signal=43%
REACTOME_RECYCLING_PATHWAY_OF_L1	24	0.7719672	0.30004677	0.93192786	0.55765593	1	1017	tags=17%, list=10%, signal=18%
SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES	48	0.7734897	0.25686187	0.93247235	0.5631769	1	2020	tags=23%, list=19%, signal=28%
REACTOME_SIGNALING_BY_HIPPO	16	0.7756752	0.3603243	0.9326494	0.54189944	1	1952	tags=38%, list=19%, signal=46%
PID_NEPHRIN_NEPH1_PATHWAY	30	0.7776866	0.27446365	0.9329449	0.55454546	1	420	tags=13%, list=4%, signal=14%
PID_SYNDECAN_2_PATHWAY	31	0.77953833	0.28645918	0.92551124	0.535461	1	808	tags=16%, list=8%, signal=17%
PID_P38_MK2PATHWAY	20	0.781291	0.30815217	0.92588985	0.55597013	1	2075	tags=35%, list=20%, signal=44%
KEGG_GLIOMA	58	0.78424484	0.24143703	0.9217637	0.57363015	1	3077	tags=41%, list=30%, signal=58%
REACTOME_IRON_UPTAKE_AND_TRANSPORT	27	0.78519994	0.30801824	0.9161795	0.55140185	1	1791	tags=22%, list=17%, signal=27%
PID_FASPATHWAY	36	0.7872196	0.28952718	0.9189748	0.54884547	1	808	tags=17%, list=8%, signal=18%
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM	24	0.78726864	0.3274122	0.9163768	0.54291046	1	1791	tags=25%, list=17%, signal=30%
PID_HDAC_CLASSII_PATHWAY	31	0.78829384	0.26396388	0.91717947	0.59562844	1	1788	tags=26%, list=17%, signal=31%
PID_S1P_S1P3_PATHWAY	25	0.79603416	0.3096512	0.90936136	0.55451125	1	2379	tags=32%, list=23%, signal=41%
REACTOME_SIGNALING_BY_FGFR_MUTANTS	36	0.79985577	0.26717052	0.9061354	0.60231024	1	564	tags=8%, list=5%, signal=9%
PID_PDGFRBPATHWAY	114	0.8035931	0.23338224	0.90301794	0.6	1	2300	tags=30%, list=22%, signal=38%
KEGG_PANCREATIC_CANCER	70	0.8072041	0.23661192	0.8999346	0.6347518	1	2137	tags=27%, list=21%, signal=34%
REACTOME_SIGNALLING_TO_RAS	24	0.808078	0.28476313	0.8982412	0.58845437	1	2255	tags=38%, list=22%, signal=48%
KEGG_ENDOMETRIAL_CANCER	50	0.8109268	0.23511077	0.8873077	0.63833636	1	420	tags=8%, list=4%, signal=8%
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	323	0.8116993	0.19246796	0.8882175	0.69953054	1	2794	tags=26%, list=27%, signal=34%
REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	70	0.8140947	0.25406635	0.88828367	0.5745856	1	1719	tags=21%, list=17%, signal=25%
REACTOME_SIGNALLING_BY_NGF	187	0.81420237	0.1976035	0.8789282	0.70034844	1	2020	tags=21%, list=19%, signal=26%
BIOCARTA_PYK2_PATHWAY	22	0.8143584	0.27789527	0.8775469	0.64695007	1	2020	tags=32%, list=19%, signal=39%
PID_VEGFR1_2_PATHWAY	67	0.8144096	0.2459865	0.892271	0.5886525	1	2943	tags=39%, list=28%, signal=54%
REACTOME_ION_CHANNEL_TRANSPORT	51	0.814411	0.24720077	0.8828636	0.6151203	1	3998	tags=49%, list=38%, signal=79%
REACTOME_NETRIN1_SIGNALING	30	0.81533796	0.28566134	0.89031184	0.61202186	1	1909	tags=23%, list=18%, signal=28%
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	38	0.8155505	0.34813416	0.87561363	0.6147705	1	2049	tags=29%, list=20%, signal=36%
REACTOME_PKB_MEDIATED_EVENTS	21	0.81611544	0.29555857	0.8792101	0.61382115	1	2881	tags=48%, list=28%, signal=66%
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINAT	15	0.81628096	0.3265066	0.89266634	0.58601135	1	2371	tags=33%, list=23%, signal=43%
REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	49	0.8163097	0.2353736	0.88843805	0.6549165	1	2006	tags=22%, list=19%, signal=28%
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	114	0.81679565	0.2048745	0.8829143	0.6694915	1	2266	tags=25%, list=22%, signal=32%
REACTOME_CTLA4_INHIBITORY_SIGNALING	21	0.81691283	0.30188623	0.8801107	0.6159555	1	2959	tags=38%, list=28%, signal=53%
SA_CASPASE_CASCADE	18	0.81945413	0.33521935	0.8670959	0.62711865	1	258	tags=11%, list=2%, signal=11%
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	59	0.82086986	0.23273306	0.8688836	0.6861702	1	2398	tags=29%, list=23%, signal=37%
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	224	0.82106036	0.23810458	0.8714116	0.5976231	1	2137	tags=24%, list=21%, signal=29%
REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	48	0.82164705	0.25890774	0.8671886	0.63320464	1	3434	tags=48%, list=33%, signal=71%
REACTOME_PLATELET_SENSITIZATION_BY_LDL	15	0.8227986	0.31232384	0.8639501	0.61877394	1	2054	tags=33%, list=20%, signal=41%
KEGG_LONG_TERM_DEPRESSION	62	0.8232144	0.22543378	0.8689279	0.6783831	1	2959	tags=29%, list=28%, signal=40%
PID_ERBB2ERBB3PATHWAY	41	0.82828367	0.24157166	0.8595718	0.70075756	1	2266	tags=34%, list=22%, signal=43%
REACTOME_PYRUVATE_METABOLISM	16	0.82984465	0.32903108	0.85607576	0.6060606	1	1712	tags=25%, list=16%, signal=30%
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	40	0.8303611	0.24969915	0.8507241	0.70254403	1	2203	tags=33%, list=21%, signal=41%
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	166	0.830364	0.22509289	0.8571438	0.6300885	1	1815	tags=17%, list=17%, signal=21%
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_	17	0.83164394	0.3334303	0.8460311	0.6443515	1	1782	tags=35%, list=17%, signal=43%
REACTOME_NOD1_2_SIGNALING_PATHWAY	25	0.8319363	0.29703107	0.8536823	0.6494662	1	1816	tags=28%, list=17%, signal=34%
BIOCARTA_STRESS_PATHWAY	24	0.8319711	0.28288203	0.85118514	0.6760563	1	1378	tags=21%, list=13%, signal=24%
BIOCARTA_TGFB_PATHWAY	18	0.8330918	0.3285379	0.8465525	0.6419295	1	1784	tags=22%, list=17%, signal=27%
BIOCARTA_AT1R_PATHWAY	27	0.83418953	0.25485384	0.85129297	0.6732852	1	2085	tags=30%, list=20%, signal=37%
PID_AR_NONGENOMIC_PATHWAY	30	0.83548576	0.25366488	0.84655327	0.6772983	1	2020	tags=33%, list=19%, signal=41%
REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECU	24	0.83593607	0.26078534	0.8422869	0.6847826	1	2436	tags=29%, list=23%, signal=38%
PID_REELINPATHWAY	29	0.83735484	0.26288623	0.840207	0.68233085	1	1650	tags=21%, list=16%, signal=25%
PID_SMAD2_3NUCLEARPATHWAY	73	0.8432349	0.21455282	0.82503843	0.7703436	1	2088	tags=25%, list=20%, signal=31%
BIOCARTA_GPCR_PATHWAY	29	0.84358907	0.25578827	0.82209253	0.71428573	1	1869	tags=28%, list=18%, signal=34%
REACTOME_DAG_AND_IP3_SIGNALING	25	0.84381765	0.27110645	0.8233027	0.70912546	1	3077	tags=40%, list=30%, signal=57%
BIOCARTA_CARM_ER_PATHWAY	27	0.8442996	0.27290013	0.8351601	0.6479401	1	689	tags=15%, list=7%, signal=16%
PID_BMPPATHWAY	33	0.84444124	0.26904854	0.82973075	0.69114876	1	2502	tags=39%, list=24%, signal=52%
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	23	0.8448186	0.29454243	0.8308434	0.6629002	1	2137	tags=30%, list=21%, signal=38%
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_	31	0.84504634	0.24845402	0.8253461	0.7211009	1	2281	tags=23%, list=22%, signal=29%
REACTOME_NEPHRIN_INTERACTIONS	17	0.84510696	0.30200845	0.8199445	0.70610684	1	1203	tags=18%, list=12%, signal=20%
PID_INTEGRIN_A4B1_PATHWAY	29	0.8458725	0.27478042	0.8315551	0.6761905	1	1909	tags=28%, list=18%, signal=34%
KEGG_ENDOCYTOSIS	142	0.84652364	0.1890844	0.8258276	0.82470787	1	2099	tags=23%, list=20%, signal=29%
REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPORTERS	15	0.8467136	0.3057155	0.81641537	0.69926196	1	4860	tags=73%, list=47%, signal=137%
REACTOME_PLC_BETA_MEDIATED_EVENTS	35	0.84716344	0.2490875	0.826866	0.71090907	1	2650	tags=34%, list=25%, signal=46%
KEGG_INSULIN_SIGNALING_PATHWAY	120	0.84810275	0.20175338	0.8169675	0.70961887	1	1694	tags=17%, list=16%, signal=20%
PID_NFKAPPABCANONICALPATHWAY	22	0.84817046	0.29932374	0.8316188	0.65162456	1	2382	tags=32%, list=23%, signal=41%
BIOCARTA_ARF_PATHWAY	16	0.8518282	0.29214635	0.812141	0.6986817	1	3496	tags=50%, list=34%, signal=75%
REACTOME_RNA_POL_III_TRANSCRIPTION_TERMINATION	15	0.8527627	0.3183491	0.81028795	0.6955684	1	1853	tags=33%, list=18%, signal=40%
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	34	0.8536469	0.28455803	0.80840355	0.62068963	1	3781	tags=50%, list=36%, signal=78%

REACTOME_SIGNALING_BY_NOTCH	76	0.8577613	0.20214413	0.8019043	0.8318426	1	3249	tags=41%, list=31%, signal=59%
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	75	0.85882074	0.21672735	0.79180175	0.7307692	1	2142	tags=28%, list=21%, signal=35%
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	31	0.85902727	0.24123463	0.7970657	0.7372014	1	1902	tags=23%, list=18%, signal=28%
PID_EPHBFWDPATHWAY	39	0.8595773	0.23944049	0.79536694	0.7571942	1	2255	tags=26%, list=22%, signal=33%
REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	31	0.85993564	0.2480436	0.80196804	0.7311828	1	3071	tags=35%, list=30%, signal=50%
KEGG_NON_SMALL_CELL_LUNG_CANCER	51	0.8600103	0.21502937	0.79788554	0.80144405	1	2990	tags=39%, list=29%, signal=55%
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_T	116	0.8604033	0.18675753	0.7936117	0.7862969	1	3078	tags=32%, list=30%, signal=45%
ST_P38_MAPK_PATHWAY	33	0.86057675	0.23784351	0.8029335	0.7561437	1	2020	tags=30%, list=19%, signal=37%
BIOCARTA_FMLP_PATHWAY	32	0.8608759	0.23937525	0.7892049	0.77715355	1	2020	tags=31%, list=19%, signal=39%
KEGG_SMALL_CELL_LUNG_CANCER	81	0.8609025	0.20759414	0.79193264	0.8168761	1	1259	tags=15%, list=12%, signal=17%
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	32	0.86190885	0.243937	0.7981542	0.7614679	1	3008	tags=44%, list=29%, signal=61%
REACTOME_AMYLOIDS	34	0.8673487	0.25156447	0.7826166	0.6939891	1	2077	tags=29%, list=20%, signal=37%
REACTOME_SIGNALING_BY_ROBO_RECEPTOR	25	0.8687075	0.2466458	0.7832041	0.79501915	1	2512	tags=32%, list=24%, signal=42%
REACTOME_METABOLISM_OF_CARBOHYDRATES	196	0.869379	0.18894184	0.7771059	0.82222223	1	1567	tags=15%, list=15%, signal=18%
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	18	0.8707975	0.2814244	0.7776562	0.7278106	1	3065	tags=50%, list=29%, signal=71%
REACTOME_METABOLISM_OF_MRNA	173	0.8710022	0.25338143	0.7746267	0.6731141	1	2180	tags=32%, list=21%, signal=40%
REACTOME_CELL_CELL_COMMUNICATION	98	0.8716814	0.2073635	0.7784921	0.787307	1	1378	tags=15%, list=13%, signal=17%
REACTOME_OPIOID_SIGNALLING	63	0.8782945	0.20020103	0.76132685	0.8263889	1	3077	tags=37%, list=30%, signal=52%
REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	22	0.8783217	0.2503943	0.7582788	0.79888266	1	3820	tags=50%, list=37%, signal=79%
KEGG_HUNTINGTONS_DISEASE	147	0.8792135	0.23279735	0.76809555	0.6731141	1	2451	tags=27%, list=24%, signal=34%
REACTOME_SIGNAL_AMPLIFICATION	24	0.8792961	0.24086837	0.7591631	0.82363635	1	2280	tags=33%, list=22%, signal=43%
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	27	0.8796161	0.23036925	0.7634129	0.8106618	1	1920	tags=22%, list=18%, signal=27%
REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	15	0.87967944	0.30859756	0.76184046	0.7013233	1	3153	tags=47%, list=30%, signal=67%
PID_IL1PATHWAY	29	0.8797341	0.24768522	0.766327	0.7764505	1	726	tags=14%, list=7%, signal=15%
PID_PI3KCIPATHWAY	39	0.88182306	0.2483783	0.7634423	0.739823	1	2646	tags=31%, list=25%, signal=41%
KEGG_INOSITOL_PHOSPHATE_METABOLISM	40	0.8851689	0.21873315	0.7522316	0.8457249	1	2646	tags=33%, list=25%, signal=43%
REACTOME_SHC_RELATED_EVENTS	15	0.89222413	0.2605252	0.7443586	0.79477614	1	2255	tags=33%, list=22%, signal=42%
BIOCARTA_41BB_PATHWAY	16	0.89254236	0.26915297	0.7456024	0.80633146	1	2199	tags=31%, list=21%, signal=40%
KEGG_O_GLYCAN_BIOSYNTHESIS	18	0.89929235	0.26543957	0.7379467	0.7826923	1	3725	tags=61%, list=36%, signal=95%
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	20	0.9073158	0.26841727	0.73090273	0.79880476	1	611	tags=15%, list=6%, signal=16%
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	21	0.9158724	0.25545067	0.7231212	0.8330134	1	3434	tags=52%, list=33%, signal=78%
KEGG_MELANOGENESIS	83	0.919698	0.17066115	0.6867682	0.9498328	1	2676	tags=25%, list=26%, signal=34%
PID_IL2_1PATHWAY	52	0.9202691	0.20020528	0.6844745	0.8842105	1	2266	tags=29%, list=22%, signal=37%
BIOCARTA_NFAT_PATHWAY	49	0.9217113	0.1957668	0.68695253	0.8926554	1	2020	tags=20%, list=19%, signal=25%
PID_HIF2PATHWAY	30	0.92218584	0.2123043	0.6790675	0.8976661	1	2451	tags=33%, list=24%, signal=43%
REACTOME_SIGNALING_BY_NOTCH1	51	0.9233177	0.18307249	0.69125295	0.95194083	1	3249	tags=39%, list=31%, signal=57%
REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	15	0.9238296	0.2718726	0.68704015	0.81037927	1	3446	tags=53%, list=33%, signal=80%
REACTOME_CIRCADIAN_CLOCK	43	0.92412096	0.21144542	0.6793141	0.9032258	1	611	tags=12%, list=6%, signal=12%
PID_TAP63PATHWAY	49	0.92553794	0.19638288	0.6912744	0.9081272	1	2451	tags=27%, list=24%, signal=35%
REACTOME_CD28_CO_STIMULATION	27	0.92580813	0.23235798	0.6872681	0.8542435	1	2137	tags=26%, list=21%, signal=33%
PID_NFKAPPABATYPICALPATHWAY	15	0.9268547	0.26178363	0.7117087	0.81835204	1	2003	tags=27%, list=19%, signal=33%
KEGG_GAP_JUNCTION	74	0.92730504	0.18662882	0.71310246	0.9001664	1	3048	tags=35%, list=29%, signal=49%
REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	29	0.92749894	0.21959862	0.691525	0.84036696	1	3725	tags=48%, list=36%, signal=75%
ST_ADRENERGIC	34	0.92753315	0.20786141	0.6723608	0.8985765	1	2020	tags=21%, list=19%, signal=25%
BIOCARTA_P38MAPK_PATHWAY	37	0.92783755	0.19753112	0.6931882	0.9172535	1	2396	tags=30%, list=23%, signal=38%
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	17	0.930012	0.28596646	0.69325876	0.76039606	1	3781	tags=53%, list=36%, signal=83%
BIOCARTA_AGR_PATHWAY	32	0.93061644	0.23195969	0.6945819	0.85607475	1	2216	tags=28%, list=21%, signal=36%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	23	0.93140745	0.2408251	0.6958055	0.86764705	1	1638	tags=17%, list=16%, signal=21%
KEGG_TGF_BETA_SIGNALING_PATHWAY	76	0.93224996	0.20425308	0.7041567	0.85294116	1	2502	tags=29%, list=24%, signal=38%
BIOCARTA_EDG1_PATHWAY	24	0.93285406	0.22899102	0.6965365	0.8465804	1	2020	tags=29%, list=19%, signal=36%
REACTOME_REGULATION_OF_HYPOXIA_INDUCIBLE_FACTOR_HIF_BY_OXYGEN	22	0.93308413	0.2348465	0.6982479	0.877551	1	2451	tags=32%, list=24%, signal=42%
REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_REC	26	0.93325406	0.20856243	0.6648727	0.90413535	1	2280	tags=27%, list=22%, signal=34%
REACTOME_L1CAM_INTERACTIONS	77	0.93386364	0.18884148	0.70122993	0.90636045	1	2634	tags=27%, list=25%, signal=36%
ST_DIFFERENTIATION_PATHWAY_IN_PC12_CELLS	41	0.93418956	0.21011631	0.704413	0.870438	1	1650	tags=20%, list=16%, signal=23%
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCH	21	0.9343719	0.24789903	0.6990494	0.8467742	1	2623	tags=38%, list=25%, signal=51%
BIOCARTA_VEGF_PATHWAY	27	0.93837595	0.21348067	0.6577987	0.89807695	1	2783	tags=37%, list=27%, signal=50%
REACTOME_OLFACTORY_SIGNALING_PATHWAY	27	0.94029725	0.22714666	0.65383106	0.8201835	1	1788	tags=11%, list=17%, signal=13%
KEGG_PENTOSE_PHOSPHATE_PATHWAY	21	0.9409768	0.22395694	0.6440631	0.91369605	1	625	tags=10%, list=6%, signal=10%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	64	0.9420931	0.21121569	0.6451983	0.83154124	1	2362	tags=33%, list=23%, signal=42%
REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRCADIAN_EXPRESSION	30	0.9441275	0.22362387	0.6453541	0.90804595	1	611	tags=13%, list=6%, signal=14%
PID_SYNDECAN_3_PATHWAY	16	0.94495654	0.22764266	0.64685106	0.91312385	1	3531	tags=50%, list=34%, signal=76%
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	163	0.94509387	0.14605778	0.6326516	0.98867315	1	3078	tags=30%, list=30%, signal=42%
REACTOME_SIGNALING_BY_CONSTITUTIVELY_ACTIVE_EGFR	16	0.9472605	0.21849562	0.63267136	0.9266055	1	2828	tags=38%, list=27%, signal=51%
PID_RET_PATHWAY	35	0.9483821	0.1870134	0.63384277	0.96037734	1	3183	tags=37%, list=31%, signal=53%
BIOCARTA_MTOR_PATHWAY	21	0.95193565	0.2088418	0.6220029	0.92621356	1	2886	tags=33%, list=28%, signal=46%
REACTOME_DOWNSTREAM_TCR_SIGNALING	27	0.9572215	0.21942073	0.61268866	0.90909094	1	1816	tags=22%, list=17%, signal=27%
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	19	0.9642563	0.212694	0.58788013	0.9509202	1	2623	tags=37%, list=25%, signal=49%
ST_WNT_CA2_CYCLIC_GMP_PATHWAY	19	0.96433336	0.19446497	0.59087175	0.95614034	1	3645	tags=42%, list=35%, signal=65%
REACTOME_CA_DEPENDENT_EVENTS	23	0.9651577	0.19928041	0.5928547	0.9649123	1	3077	tags=35%, list=30%, signal=49%
REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	21	0.9655644	0.19830573	0.5954043	0.9309091	1	8348	tags=100%, list=80%, signal=504%
PID_IL2_PI3KPATHWAY	30	0.9659084	0.17305513	0.5817594	0.9669565	1	3341	tags=40%, list=32%, signal=59%
BIOCARTA_IGF1R_PATHWAY	21	0.9663732	0.19188032	0.597362	0.95063984	1	3048	tags=38%, list=29%, signal=54%
KEGG_GLUTATHIONE_METABOLISM	35	0.9686402	0.18667205	0.5734638	0.9411765	1	1864	tags=17%, list=18%, signal=21%
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	27	0.9711653	0.17999338	0.5617665	0.96750903	1	2681	tags=26%, list=26%, signal=35%
REACTOME_TCR_SIGNALING	42	0.9716053	0.1987344	0.564803	0.91791046	1	1816	tags=19%, list=17%, signal=23%
KEGG_OXIDATIVE_PHOSPHORYLATION	97	0.98050606	0.19584201	0.53821486	0.8549618	1	3107	tags=32%, list=30%, signal=45%
BIOCARTA_ACH_PATHWAY	16	0.9923041	0.18026589	0.5009335	0.9828897	1	1259	tags=13%, list=12%, signal=14%
REACTOME_PEROXISOMAL_LIPID_METABOLISM	17	0.9930348	0.17549771	0.4744478	0.98547715	1	2421	tags=24%, list=23%, signal=31%
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	52	0.9933355	0.13871886	0.4507871	0.9925926	1	1704	tags=12%, list=16%, signal=14%
KEGG_CITRATE_CYCLE_TCA_CYCLE	28	0.9941214	0.17432939	0.4586694	0.9841584	1	3781	tags=46%, list=36%, signal=73%
KEGG_PARKINSONS_DISEASE	94	0.9942193	0.17506593	0.478785	0.92885375	1	2326	tags=21%, list=22%, signal=27%
BIOCARTA_CSK_PATHWAY	20	0.9959577	0.19375752	0.4806793	0.9576923	1	1788	tags=20%, list=17%, signal=24%
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	21	0.99668294	0.14391594	0.38640073	1	1	8913	tags=100%, list=86%, signal=694%
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	101	0.9983567	0.1468311	0.39302692	0.9814433	1	2426	tags=21%, list=23%, signal=27%

Pathways negatively enriched with TRIM24

NAME	SIZE	FDR q-val	ES	NES	NOM p-val	FWER p-val	RANK AT MAX	LEADING EDGE
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	24	0.5413832	-0.47106	-1.3795844	0.12931034	1	2824	tags=46%, list=27%, signal=63%
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	71	0.54274887	-0.3951375	-1.3857902	0.09782609	1	3445	tags=54%, list=33%, signal=79%
PID_IL12_2PATHWAY	52	0.54398227	-0.4631345	-1.3474586	0.19139785	1	3068	tags=58%, list=29%, signal=81%
KEGG_GRAFT_VERSUS_HOST_DISEASE	28	0.5442168	-0.5825915	-1.3434771	0.21581197	1	2803	tags=61%, list=27%, signal=83%
REACTOME_PI_3K_CASCADE	44	0.5447181	-0.3627366	-1.3281429	0.1313364	1	1881	tags=32%, list=18%, signal=39%

PID_IL6_7PATHWAY	46	0.54481316	-0.3922673	-1.3804728	0.10022779	1		2392	tags=41%, list=23%, signal=53%
KEGG_FOCAL_ADHESION	181	0.5448903	-0.3576089	-1.376039	0.1012931	1		2342	tags=38%, list=22%, signal=48%
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCT	85	0.5451386	-0.521822	-1.3259408	0.22970296	1		2327	tags=62%, list=22%, signal=80%
PID_IL23PATHWAY	34	0.5466097	-0.4817137	-1.3981049	0.15	1		3214	tags=59%, list=31%, signal=85%
BIOCARTA_INTRINSIC_PATHWAY	23	0.5475395	-0.5318563	-1.3862233	0.13714285	1		4331	tags=83%, list=42%, signal=141%
REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	70	0.5478431	-0.3426902	-1.3478816	0.07925408	1		2484	tags=46%, list=24%, signal=60%
KEGG_ALLOGRAFT_REJECTION	30	0.54850805	-0.5728015	-1.3436906	0.21518987	1		2803	tags=63%, list=27%, signal=86%
BIOCARTA_RELA_PATHWAY	16	0.5486015	-0.4965825	-1.3997442	0.10307018	1		1561	tags=38%, list=15%, signal=44%
PID_UPA_UPAR_PATHWAY	36	0.5486926	-0.4674975	-1.3680899	0.15486726	1		1701	tags=33%, list=16%, signal=40%
KEGG_MAPK_SIGNALING_PATHWAY	231	0.5487866	-0.2852776	-1.3513218	0.03562341	1		2719	tags=38%, list=26%, signal=50%
REACTOME_MUSCLE_CONTRACTION	40	0.54913896	-0.5335651	-1.3281718	0.18435754	1		1830	tags=33%, list=18%, signal=39%
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	22	0.54966676	-0.4373413	-1.3530182	0.11451943	1		1550	tags=23%, list=15%, signal=27%
KEGG_LEISHMANIA_INFECTION	56	0.54981273	-0.4453575	-1.3808247	0.13140312	1		2657	tags=50%, list=26%, signal=67%
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	96	0.5498968	-0.3552728	-1.3875262	0.09172259	1		1951	tags=27%, list=19%, signal=33%
BIOCARTA_GH_PATHWAY	25	0.54998296	-0.4379341	-1.4186316	0.06852248	1		2221	tags=40%, list=21%, signal=51%
BIOCARTA_TPO_PATHWAY	22	0.5502259	-0.4289018	-1.33919	0.10792951	1		2144	tags=41%, list=21%, signal=51%
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK	149	0.55044097	-0.3089211	-1.3696171	0.06435644	1		3059	tags=39%, list=29%, signal=54%
KEGG_HISTIDINE_METABOLISM	23	0.5505763	-0.4183343	-1.360944	0.12307692	1		765	tags=22%, list=7%, signal=23%
BIOCARTA_NKT_PATHWAY	25	0.5506223	-0.5161297	-1.3588872	0.17067833	1		3496	tags=68%, list=34%, signal=102%
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	80	0.5514724	-0.5751105	-1.3891852	0.19455253	1		2563	tags=70%, list=25%, signal=92%
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	29	0.5515679	-0.3985108	-1.3308388	0.140553	1		2596	tags=38%, list=25%, signal=50%
REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	27	0.55188644	-0.4320199	-1.3712354	0.11410788	1		1567	tags=30%, list=15%, signal=35%
PID_AP1_PATHWAY	67	0.5521015	-0.3861115	-1.4204513	0.07991361	1		2429	tags=43%, list=23%, signal=56%
KEGG_JAK_STAT_SIGNALING_PATHWAY	125	0.5522662	-0.3533781	-1.3624285	0.11709602	1		2833	tags=40%, list=27%, signal=54%
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	137	0.55226946	-0.3079435	-1.348118	0.06951872	1		3120	tags=34%, list=30%, signal=47%
BIOCARTA_AMI_PATHWAY	19	0.5529984	-0.5393724	-1.3930635	0.12352941	1		4715	tags=95%, list=45%, signal=173%
REACTOME_TOLL_RECEPTOR_CASCADES	98	0.5533573	-0.3329839	-1.3282994	0.10663507	1		2395	tags=42%, list=23%, signal=54%
REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLL	22	0.5539334	-0.454134	-1.4000982	0.09713025	1		2151	tags=45%, list=21%, signal=57%
BIOCARTA_NKCELLS_PATHWAY	17	0.5543452	-0.5005877	-1.3531905	0.16313559	1		2515	tags=41%, list=24%, signal=54%
KEGG_VIRAL_MYOCARDITIS	62	0.5544137	-0.4193776	-1.3334777	0.1751663	1		2700	tags=48%, list=26%, signal=65%
REACTOME_BIOLOGICAL_OXIDATIONS	97	0.5544244	-0.3286408	-1.36382	0.09	1		2316	tags=27%, list=22%, signal=34%
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	29	0.5545952	-0.4180006	-1.3315034	0.13174947	1		1579	tags=38%, list=15%, signal=45%
PID_HEDGEHOG_2PATHWAY	18	0.5548024	-0.4597193	-1.4069393	0.0831643	1		898	tags=28%, list=9%, signal=30%
REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGN	62	0.5551869	-0.3705973	-1.4219395	0.05069124	1		2335	tags=45%, list=22%, signal=58%
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	62	0.5560066	-0.3793101	-1.4113783	0.10792951	1		2335	tags=39%, list=22%, signal=50%
KEGG_BETA_ALANINE_METABOLISM	21	0.5563544	-0.4787569	-1.3895634	0.14078675	1		3841	tags=71%, list=37%, signal=113%
REACTOME_INNATE_IMMUNE_SYSTEM	196	0.557482	-0.3118425	-1.3060735	0.12864077	1		2395	tags=36%, list=23%, signal=46%
KEGG_FATTY_ACID_METABOLISM	35	0.55851203	-0.5131069	-1.4233425	0.12474849	1		2669	tags=51%, list=26%, signal=69%
REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	64	0.5587446	-0.3407099	-1.3337325	0.0952381	1		2335	tags=42%, list=22%, signal=54%
PID_FRA_PATHWAY	35	0.5588242	-0.4208154	-1.353474	0.13555555	1		3300	tags=71%, list=32%, signal=104%
PID_P38_MKK3_6PATHWAY	21	0.558928	-0.4133252	-1.3145753	0.13665944	1		2660	tags=52%, list=26%, signal=70%
BIOCARTA_AKT_PATHWAY	22	0.5596374	-0.4096229	-1.3087438	0.11827957	1		2335	tags=45%, list=22%, signal=58%
REACTOME_INFLAMMASOMES	15	0.5598382	-0.4716483	-1.3159589	0.16742082	1		1617	tags=40%, list=16%, signal=47%
BIOCARTA_DC_PATHWAY	20	0.5602223	-0.5327807	-1.4001839	0.1637931	1		3496	tags=75%, list=34%, signal=113%
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	77	0.56022334	-0.3541082	-1.2979479	0.14622642	1		3116	tags=47%, list=30%, signal=66%
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_	32	0.5606247	-0.5982679	-1.3065282	0.24448898	1		2731	tags=78%, list=26%, signal=106%
REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	26	0.56084365	-0.4445502	-1.407225	0.0945946	1		2151	tags=42%, list=21%, signal=53%
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	19	0.56126976	-0.4082676	-1.3028827	0.13755459	1		2125	tags=37%, list=20%, signal=46%
PID_ANGIOPOIETINRECEPTOR_PATHWAY	49	0.56132096	-0.4274142	-1.4251705	0.06034483	1		1951	tags=39%, list=19%, signal=47%
PID_HDAC_CLASSIII_PATHWAY	22	0.5621665	-0.4119218	-1.2988592	0.14376321	1		2665	tags=41%, list=26%, signal=55%
PID_INTEGRIN5_PATHWAY	17	0.56227285	-0.4978767	-1.3169023	0.20416667	1		3203	tags=47%, list=31%, signal=68%
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	20	0.5624958	-0.4884139	-1.4115957	0.1025641	1		1522	tags=30%, list=15%, signal=35%
REACTOME_FRS2_MEDIATED_CASCADE	30	0.5627549	-0.3901206	-1.4016398	0.07894737	1		1495	tags=30%, list=14%, signal=35%
KEGG_ACUTE_MYELOID_LEUKEMIA	55	0.5628268	-0.337231	-1.3092602	0.11694511	1		1561	tags=31%, list=15%, signal=36%
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	23	0.56527627	-0.417637	-1.2994134	0.16705883	1		2833	tags=48%, list=27%, signal=66%
REACTOME_SYNTHESIS_OF_PA	19	0.5654071	-0.4401053	-1.3100755	0.14828898	1		1256	tags=26%, list=12%, signal=30%
REACTOME_SIGNALING_BY_GPCR	469	0.5673782	-0.2909248	-1.4308473	0.02702703	1		2892	tags=32%, list=28%, signal=43%
KEGG_TYROSINE_METABOLISM	36	0.56872755	-0.4395447	-1.4252453	0.09706546	1		2669	tags=42%, list=26%, signal=56%
KEGG_AXON_GUIDANCE	108	0.5687931	-0.3222247	-1.2924994	0.11724138	1		1740	tags=24%, list=17%, signal=29%
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_M	86	0.5689007	-0.5161368	-1.2782149	0.27559054	1		2563	tags=63%, list=25%, signal=83%
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	174	0.5701685	-0.3049593	-1.2743205	0.13493976	1		2437	tags=34%, list=23%, signal=44%
PID_AVB3_INTEGRIN_PATHWAY	70	0.5714556	-0.3948417	-1.2841309	0.21336207	1		2655	tags=41%, list=26%, signal=55%
REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS	51	0.5721078	-0.3372282	-1.2785323	0.13806707	1		1277	tags=24%, list=12%, signal=27%
PID_FCER1PATHWAY	54	0.5734843	-0.4026856	-1.4262302	0.08783784	1		2397	tags=44%, list=23%, signal=57%
REACTOME_PLATELET_HOMEOSTASIS	66	0.57389444	-0.3169637	-1.2743887	0.12383178	1		2383	tags=33%, list=23%, signal=43%
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_DIFFERE	46	0.57463205	-0.367571	-1.2792177	0.17849462	1		2094	tags=41%, list=20%, signal=51%
REACTOME_SHC_MEDIATED_CASCADE	23	0.57501924	-0.4190278	-1.430986	0.07228915	1		1495	tags=30%, list=14%, signal=35%
PID_WNT_SIGNALING_PATHWAY	24	0.5750976	-0.385771	-1.284388	0.14505495	1		3555	tags=50%, list=34%, signal=76%
PID_IL27PATHWAY	25	0.5754496	-0.4613605	-1.2807032	0.23516949	1		3046	tags=48%, list=29%, signal=68%
BIOCARTA_GLEEVEC_PATHWAY	21	0.5774662	-0.4106264	-1.2851479	0.16517857	1		759	tags=24%, list=7%, signal=26%
REACTOME_SEMAPHORIN_INTERACTIONS	59	0.5775437	-0.3944427	-1.4447551	0.07399103	0.999		1775	tags=34%, list=17%, signal=41%
BIOCARTA_TH1TH2_PATHWAY	18	0.5783771	-0.5468307	-1.2866441	0.23554604	1		3496	tags=78%, list=34%, signal=117%
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	42	0.57871026	-0.3956782	-1.4326875	0.07572383	1		2297	tags=33%, list=22%, signal=43%
BIOCARTA_NTHI_PATHWAY	24	0.5814923	-0.422787	-1.267925	0.16630197	1		1574	tags=33%, list=15%, signal=39%
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	39	0.58248496	-0.3932903	-1.2658311	0.18789144	1		2678	tags=41%, list=26%, signal=55%
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	46	0.5826449	-0.4192759	-1.4340724	0.078125	1		3708	tags=50%, list=36%, signal=77%
BIOCARTA_LAIR_PATHWAY	17	0.5837818	-0.5505374	-1.4456105	0.11930586	0.999		2360	tags=41%, list=23%, signal=53%
KEGG_CELL_ADHESION_MOLECULES_CAMS	112	0.58387303	-0.4061198	-1.4396907	0.10779817	1		3042	tags=43%, list=29%, signal=60%
REACTOME_ACTIVATED_TLR4_SIGNALLING	79	0.5880653	-0.3617864	-1.4351956	0.03381642	1		2484	tags=47%, list=24%, signal=61%
KEGG_SPHINGOLIPID_METABOLISM	26	0.589705	-0.3816187	-1.2612638	0.16500995	1		627	tags=19%, list=6%, signal=20%
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	75	0.59091544	-0.6174952	-1.4462451	0.15277778	0.999		2563	tags=73%, list=25%, signal=97%
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	22	0.5932904	-0.3849448	-1.2581729	0.16880342	1		2125	tags=36%, list=20%, signal=46%
BIOCARTA_IL10_PATHWAY	17	0.5956761	-0.5394199	-1.4477	0.12471655	0.999		3185	tags=59%, list=31%, signal=85%
KEGG_ABC_TRANSPORTERS	36	0.5971319	-0.4186293	-1.4503089	0.0620985	0.999		1567	tags=25%, list=15%, signal=29%
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	17	0.59729177	-0.4758871	-1.4532632	0.07010309	0.999		2693	tags=41%, list=26%, signal=55%
REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_AR	19	0.60475	-0.5013716	-1.4540917	0.07509881	0.999		4207	tags=79%, list=40%, signal=132%
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	41	0.60759217	-0.4103668	-1.2491251	0.22535211	1		3173	tags=44%, list=30%, signal=63%
BIOCARTA_NFKB_PATHWAY	21	0.6094431	-0.4314221	-1.2500192	0.19861431	1		2335	tags=43%, list=22%, signal=55%
REACTOME_HDL_MEDIATED_LIPID_TRANSPORT	15	0.6094879	-0.5642002	-1.4558189	0.08924949	0.999		1918	tags=47%, list=18%, signal=57%
PID_INTEGRIN1_PATHWAY	61	0.6127677	-0.5370969	-1.529048	0.09307359	0.992		3345	tags=61%, list=32%, signal=89%
REACTOME_INTRINSIC_PATHWAY	15	0.6130578	-0.6061713	-1.53773	0.05555556	0.992		2886	tags=60%, list=28%, signal=83%
KEGG_AUTOIMMUNE_THYROID_DISEASE	38	0.6157489	-0.5552863	-1.480942	0.13333334	0.998		2950	tags=55%, list=28%, signal=77%
BIOCARTA_IL22BP_PATHWAY	15	0.6177552	-0.6242877	-1.5033464	0.08131868	0.996		2648	tags=60%, list=25%, signal=80%

REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADREN	19	0.6183435	-0.4896411	-1.4596084	0.07676349	0.999	2123	tags=47%, list=20%, signal=59%
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG	18	0.61844987	-0.517308	-1.456245	0.09611452	0.999	1643	tags=39%, list=16%, signal=46%
PID_LYMPHANGIOGENESIS_PATHWAY	23	0.61955637	-0.4432464	-1.2428099	0.20842105	1	2243	tags=43%, list=22%, signal=55%
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	31	0.61962664	-0.3735405	-1.2396431	0.19866072	1	1234	tags=23%, list=12%, signal=26%
KEGG_TRYPTOPHAN_METABOLISM	29	0.62199587	-0.4188716	-1.2402942	0.21748401	1	3841	tags=59%, list=37%, signal=93%
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	215	0.62320006	-0.3091188	-1.4823564	0.02762431	0.998	4086	tags=48%, list=39%, signal=77%
PID_IL4_2PATHWAY	55	0.62382185	-0.4276163	-1.530511	0.05620609	0.992	2572	tags=42%, list=25%, signal=55%
REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	130	0.6254084	-0.3399415	-1.4853116	0.03694581	0.997	3539	tags=48%, list=34%, signal=71%
REACTOME_CGMP_EFFECTS	18	0.62573785	-0.5426372	-1.5212076	0.04496788	0.994	2013	tags=44%, list=19%, signal=55%
BIOCARTA_ETS_PATHWAY	15	0.6272977	-0.5421287	-1.4740616	0.06418219	0.998	696	tags=40%, list=7%, signal=43%
PID_ALK1PATHWAY	25	0.62786615	-0.4983035	-1.4600825	0.06315789	0.999	867	tags=28%, list=8%, signal=30%
REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS	56	0.62799156	-0.4095584	-1.5382996	0.05128205	0.992	4408	tags=66%, list=42%, signal=114%
BIOCARTA_LONGEVITY_PATHWAY	15	0.62897176	-0.5298455	-1.4918061	0.08387097	0.997	3269	tags=67%, list=31%, signal=97%
REACTOME_LIPOPROTEIN_METABOLISM	25	0.6290628	-0.5118359	-1.5041622	0.07874016	0.996	2678	tags=48%, list=26%, signal=64%
REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	34	0.63036555	-0.354903	-1.2147069	0.19954649	1	2313	tags=35%, list=22%, signal=45%
KEGG_GLYCEROLIPID_METABOLISM	36	0.6315195	-0.3383188	-1.218982	0.19474836	1	1290	tags=22%, list=12%, signal=25%
BIOCARTA_TOB1_PATHWAY	19	0.63182133	-0.4425661	-1.2156498	0.27162978	1	3496	tags=63%, list=34%, signal=95%
KEGG_PPAR_SIGNALING_PATHWAY	60	0.63381934	-0.4554198	-1.5413635	0.07991803	0.989	2211	tags=35%, list=21%, signal=44%
ST_B_CELL_ANTIGEN_RECEPTOR	38	0.6343777	-0.3679514	-1.2160996	0.2274678	1	2484	tags=37%, list=24%, signal=48%
BIOCARTA_TOLL_PATHWAY	31	0.63475925	-0.3687848	-1.2191936	0.19638826	1	1562	tags=35%, list=15%, signal=42%
REACTOME_BOTULINUM_NEUROTOXICITY	15	0.6351439	-0.5188067	-1.4862208	0.06540085	0.997	1579	tags=53%, list=15%, signal=63%
REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS	70	0.63532186	-0.3543872	-1.4612439	0.03385417	0.999	3802	tags=54%, list=37%, signal=85%
REACTOME_SMOOTH_MUSCLE_CONTRACTION	19	0.63736725	-0.6057705	-1.5058098	0.08860759	0.996	1437	tags=53%, list=14%, signal=61%
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	32	0.6378049	-0.360348	-1.2082812	0.23198198	1	2827	tags=38%, list=27%, signal=51%
PID_SYNDECAN_1_PATHWAY	45	0.6378114	-0.4130927	-1.2210714	0.2638298	1	3558	tags=53%, list=34%, signal=81%
PID_ALPHASYNUCLEIN_PATHWAY	32	0.6379419	-0.3893941	-1.219476	0.22769953	1	1752	tags=34%, list=17%, signal=41%
KEGG_DILATED_CARDIOMYOPATHY	80	0.63800967	-0.3253596	-1.2051425	0.24248497	1	3304	tags=40%, list=32%, signal=58%
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	83	0.63802946	-0.400847	-1.4931555	0.05530974	0.997	2990	tags=48%, list=29%, signal=67%
REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	43	0.6384384	-0.3358693	-1.2065216	0.19438446	1	2307	tags=40%, list=22%, signal=51%
PID_RHOA_REG_PATHWAY	35	0.6392592	-0.3571461	-1.1969688	0.20386267	1	2668	tags=49%, list=26%, signal=65%
KEGG_PRION_DISEASES	33	0.6406993	-0.3593381	-1.1949155	0.24537037	1	2019	tags=33%, list=19%, signal=41%
REACTOME_NCAM1_INTERACTIONS	39	0.6408304	-0.3850394	-1.2213975	0.22494887	1	3045	tags=38%, list=29%, signal=54%
REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_ACTIVITY_	15	0.6411199	-0.5730577	-1.5088944	0.08315098	0.996	4081	tags=87%, list=39%, signal=142%
KEGG_CALCIUM_SIGNALING_PATHWAY	149	0.6411422	-0.270849	-1.229175	0.15085158	1	2798	tags=32%, list=27%, signal=43%
REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	39	0.64139044	-0.428847	-1.4661487	0.06991526	0.998	1643	tags=31%, list=16%, signal=36%
ST_ERK1_ERK2_MAPK_PATHWAY	29	0.64157104	-0.3698161	-1.2082872	0.20940171	1	2242	tags=48%, list=22%, signal=61%
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_A	49	0.64286727	-0.4566815	-1.1969746	0.2982456	1	3321	tags=61%, list=32%, signal=89%
REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING	32	0.64306253	-0.341906	-1.2268977	0.19294117	1	2015	tags=34%, list=19%, signal=42%
BIOCARTA_INTEGRIN_PATHWAY	34	0.6432572	-0.3828544	-1.2252836	0.20930232	1	1435	tags=29%, list=14%, signal=34%
PID_AMB2_NEUTROPHILS_PATHWAY	39	0.6437716	-0.4693961	-1.4621829	0.09069768	0.999	3150	tags=62%, list=30%, signal=88%
REACTOME_G_ALPHA1213_SIGNALLING_EVENTS	60	0.644122	-0.3078745	-1.2233812	0.16404495	1	2151	tags=38%, list=21%, signal=48%
SA_TRKA_RECEPTOR	15	0.6443734	-0.4168692	-1.2216179	0.23368421	1	3053	tags=47%, list=29%, signal=66%
BIOCARTA_INFLAM_PATHWAY	27	0.6445971	-0.53009	-1.5435476	0.08744395	0.989	3496	tags=70%, list=34%, signal=106%
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	42	0.64468193	-0.3579689	-1.2008517	0.2527233	1	4408	tags=57%, list=42%, signal=99%
BIOCARTA_IL7_PATHWAY	17	0.64501876	-0.4866537	-1.1975935	0.29872882	1	3269	tags=53%, list=31%, signal=77%
REACTOME_SIGNALING_BY_RHO_GTPASES	76	0.64635384	-0.2952502	-1.1986072	0.20689656	1	2479	tags=42%, list=24%, signal=55%
BIOCARTA_TID_PATHWAY	18	0.64734554	-0.4169397	-1.1832836	0.24361949	1	1561	tags=28%, list=15%, signal=33%
PID_MYC_REPRESSPATHWAY	58	0.6487673	-0.3045411	-1.1841885	0.19864559	1	2665	tags=38%, list=26%, signal=51%
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDI	40	0.64993787	-0.5004834	-1.1880835	0.3146998	1	2563	tags=63%, list=25%, signal=83%
BIOCARTA_TNFR2_PATHWAY	17	0.651283	-0.4461338	-1.1891267	0.2885906	1	3477	tags=65%, list=33%, signal=97%
REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING	24	0.65136236	-0.3778603	-1.18458	0.24835165	1	1234	tags=21%, list=12%, signal=24%
KEGG_PHENYLALANINE_METABOLISM	16	0.65272546	-0.4046997	-1.151269	0.2901879	1	2480	tags=38%, list=24%, signal=49%
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	67	0.65312016	-0.3199324	-1.1853167	0.2516129	1	3304	tags=37%, list=32%, signal=54%
REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	23	0.65341526	-0.5249937	-1.5464495	0.05508475	0.989	2013	tags=39%, list=19%, signal=48%
KEGG_RETINOL_METABOLISM	38	0.6536344	-0.4561518	-1.5097104	0.07432433	0.996	3723	tags=53%, list=36%, signal=82%
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA	15	0.6539434	-0.3857637	-1.1438916	0.30703625	1	2123	tags=40%, list=20%, signal=50%
REACTOME_SIGNALING_BY_ERBB4	75	0.6539711	-0.2797236	-1.1493894	0.225058	1	2144	tags=31%, list=21%, signal=38%
PID_INTEGRIN_A9B1_PATHWAY	22	0.6542906	-0.3967454	-1.1533129	0.30967742	1	3473	tags=64%, list=33%, signal=95%
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	52	0.6546287	-0.4125952	-1.1463385	0.34581497	1	3160	tags=44%, list=30%, signal=63%
PID_IL3_PATHWAY	22	0.6547329	-0.3474111	-1.1517918	0.23873875	1	3182	tags=41%, list=31%, signal=59%
REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	22	0.65485716	-0.3646132	-1.1544285	0.2637131	1	3174	tags=50%, list=30%, signal=72%
BIOCARTA_PDGF_PATHWAY	29	0.6557033	-0.3661637	-1.178349	0.23706897	1	2144	tags=38%, list=21%, signal=48%
PID_ARF6_PATHWAY	26	0.65578854	-0.3429992	-1.1472412	0.25917926	1	2859	tags=42%, list=27%, signal=58%
KEGG_TYPE_I_DIABETES_MELLITUS	36	0.65585065	-0.4311746	-1.1443877	0.34657836	1	2803	tags=44%, list=27%, signal=61%
REACTOME_TRANSLATION	111	0.6570132	-0.4393093	-1.1717955	0.34	1	2563	tags=54%, list=25%, signal=71%
SIG_CD40PATHWAYMAP	33	0.6572998	-0.3408825	-1.1547666	0.26593408	1	2657	tags=48%, list=26%, signal=65%
BIOCARTA_IL1R_PATHWAY	29	0.65782756	-0.3520851	-1.1559615	0.26636568	1	2564	tags=45%, list=25%, signal=59%
REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UP	64	0.6587152	-0.30055	-1.1725247	0.21002387	1	2335	tags=39%, list=22%, signal=50%
BIOCARTA_HDAC_PATHWAY	26	0.6589621	-0.3520685	-1.1610585	0.25	1	1983	tags=27%, list=19%, signal=33%
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	54	0.6590482	-0.3058065	-1.1568797	0.22792608	1	1290	tags=22%, list=12%, signal=25%
PID_IL12_STAT4PATHWAY	31	0.65937173	-0.4328154	-1.1636447	0.3106383	1	3068	tags=65%, list=29%, signal=91%
REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE	43	0.659376	-0.3180473	-1.1738058	0.20975609	1	1495	tags=23%, list=14%, signal=27%
ST_GAQ_PATHWAY	25	0.6596368	-0.3700974	-1.1594088	0.27157894	1	2579	tags=48%, list=25%, signal=64%
KEGG_PEROXISOME	65	0.6600321	-0.335429	-1.1750021	0.2584746	1	2600	tags=40%, list=25%, signal=53%
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	40	0.6606188	-0.312685	-1.165865	0.25870648	1	4408	tags=60%, list=42%, signal=104%
BIOCARTA_PGC1A_PATHWAY	20	0.660625	-0.3997104	-1.164531	0.2718254	1	2499	tags=35%, list=24%, signal=46%
PID_INTEGRIN2_PATHWAY	28	0.66062605	-0.5585262	-1.5499216	0.06768559	0.989	3339	tags=71%, list=32%, signal=105%
REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING	29	0.6610579	-0.3510473	-1.1574856	0.26004228	1	2125	tags=34%, list=20%, signal=43%
REACTOME_INTERFERON_GAMMA_SIGNALING	45	0.66224265	-0.4102501	-1.1610906	0.32079646	1	3018	tags=51%, list=29%, signal=72%
REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	15	0.6625559	-0.4009977	-1.1679133	0.2602459	1	2123	tags=47%, list=20%, signal=59%
REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	15	0.66381884	-0.4255651	-1.1659912	0.29124236	1	851	tags=20%, list=8%, signal=22%
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	23	0.6737155	-0.3415297	-1.1326206	0.3135965	1	2693	tags=30%, list=26%, signal=41%
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	39	0.67568123	-0.3486021	-1.1331412	0.30120483	1	756	tags=21%, list=7%, signal=22%
REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	26	0.6787664	-0.3564373	-1.1263536	0.32173914	1	3174	tags=46%, list=30%, signal=66%
BIOCARTA_GCR_PATHWAY	18	0.67914027	-0.372852	-1.1275747	0.29130435	1	755	tags=28%, list=7%, signal=30%
KEGG_RIBOSOME	67	0.6803679	-0.7042245	-1.5503064	0.1017964	0.989	2563	tags=82%, list=25%, signal=108%
PID_GLYPICAN_1PATHWAY	25	0.6806111	-0.3812159	-1.1282669	0.308204	1	3259	tags=64%, list=31%, signal=93%
KEGG_VEGF_SIGNALING_PATHWAY	66	0.6907506	-0.27643	-1.114587	0.25342464	1	2136	tags=32%, list=21%, signal=40%
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	76	0.69306695	-0.3092411	-1.1149173	0.32394367	1	3386	tags=39%, list=33%, signal=58%
REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	38	0.69353956	-0.3108159	-1.1160587	0.29978117	1	2776	tags=37%, list=27%, signal=50%
BIOCARTA_IL6_PATHWAY	21	0.6946696	-0.3555237	-1.1182449	0.29284164	1	2144	tags=38%, list=21%, signal=48%
PID_PDGFRAPATHWAY	20	0.6949532	-0.3809907	-1.1167861	0.30932203	1	2144	tags=40%, list=21%, signal=50%
KEGG_ECM_RECEPTOR_INTERACTION	77	0.69831127	-0.4844724	-1.5514652	0.05764967	0.988	3339	tags=60%, list=32%, signal=87%

PID_ERA_GENOMIC_PATHWAY	54	0.6992197	-0.2793837	-1.1096123	0.2880562	1	2390	tags=30%, list=23%, signal=38%
REACTOME_G_PROTEIN_ACTIVATION	21	0.70299494	-0.3487055	-1.1067581	0.33261338	1	2123	tags=33%, list=20%, signal=42%
REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR	79	0.7052843	-0.2660226	-1.1045266	0.27380952	1	1280	tags=20%, list=12%, signal=23%
KEGG_MELANOMA	66	0.7205543	-0.2660927	-1.0965896	0.33171913	1	1565	tags=27%, list=15%, signal=32%
REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_DAI	16	0.72094774	-0.3814566	-1.0937997	0.35920176	1	2484	tags=50%, list=24%, signal=66%
REACTOME_GPCR_DOWNSTREAM_SIGNALING	382	0.72197324	-0.3225404	-1.5515727	0.01851852	0.988	2847	tags=33%, list=27%, signal=44%
PID_CD40_PATHWAY	28	0.7225331	-0.3563371	-1.0944629	0.345898	1	3214	tags=54%, list=31%, signal=77%
BIOCARTA_CYTOKINE_PATHWAY	20	0.7245485	-0.3988189	-1.0827472	0.40358743	1	3496	tags=55%, list=34%, signal=83%
ST_TUMOR_NECROSIS_FACTOR_PATHWAY	27	0.7249519	-0.3587029	-1.0894536	0.3478261	1	2484	tags=44%, list=24%, signal=58%
KEGG_PROPANOATE_METABOLISM	26	0.72498715	-0.4093079	-1.090663	0.39376217	1	2884	tags=46%, list=28%, signal=64%
BIOCARTA_EPO_PATHWAY	18	0.7269514	-0.3539807	-1.0804803	0.33860046	1	696	tags=22%, list=7%, signal=24%
REACTOME_GLYCOSPHINGOLIPID_METABOLISM	24	0.72707707	-0.3554353	-1.0843624	0.34349594	1	3550	tags=46%, list=34%, signal=69%
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	88	0.7275938	-0.2863486	-1.0869315	0.32751092	1	2737	tags=36%, list=26%, signal=49%
BIOCARTA_KERATINOCYTE_PATHWAY	44	0.7276546	-0.3026682	-1.0827578	0.35402298	1	1631	tags=27%, list=16%, signal=32%
KEGG_NITROGEN_METABOLISM	22	0.72951925	-0.3374034	-1.078119	0.33982685	1	527	tags=9%, list=5%, signal=10%
BIOCARTA_MYOSIN_PATHWAY	28	0.73020536	-0.3501068	-1.0843834	0.37284482	1	1874	tags=39%, list=18%, signal=48%
PID_GMCSF_PATHWAY	33	0.7349802	-0.3034751	-1.0729924	0.3372093	1	3275	tags=42%, list=31%, signal=62%
REACTOME_SPHINGOLIPID_METABOLISM	41	0.7353642	-0.3069254	-1.0701457	0.3640082	1	2232	tags=29%, list=21%, signal=37%
REACTOME_SIGNALING_BY_FGFR	89	0.73678327	-0.2511147	-1.0735505	0.33169532	1	2144	tags=28%, list=21%, signal=35%
REACTOME_DEVELOPMENTAL_BIOLOGY	321	0.7370043	-0.2345325	-1.0707763	0.32374102	1	2260	tags=26%, list=22%, signal=32%
REACTOME_PEPTIDE_CHAIN_ELONGATION	66	0.7375271	-0.7183899	-1.5597084	0.09980431	0.987	2563	tags=85%, list=25%, signal=112%
PID_ATF2_PATHWAY	55	0.738529	-0.2775979	-1.0661504	0.35730338	1	1106	tags=20%, list=11%, signal=22%
PID_RHOA_PATHWAY	42	0.7396446	-0.311507	-1.0669869	0.38266385	1	1629	tags=26%, list=16%, signal=31%
KEGG_BUTANOATE_METABOLISM	30	0.7409131	-0.3468449	-1.0611486	0.38045737	1	2496	tags=33%, list=24%, signal=44%
KEGG_RENIN_ANGIOTENSIN_SYSTEM	16	0.7410856	-0.5462792	-1.5529585	0.05831533	0.988	2847	tags=38%, list=27%, signal=52%
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	40	0.7420012	-0.3658183	-1.0633801	0.41535434	1	3125	tags=45%, list=30%, signal=64%
REACTOME_ERK_MAPK_TARGETS	20	0.7436047	-0.3527395	-1.0613018	0.3678862	1	2221	tags=40%, list=21%, signal=51%
BIOCARTA_EGF_PATHWAY	28	0.7468152	-0.3215616	-1.0573988	0.36796537	1	2144	tags=32%, list=21%, signal=40%
PID_PTP1BPATHWAY	50	0.7517919	-0.4379496	-1.5756196	0.02386635	0.984	2859	tags=48%, list=27%, signal=66%
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	27	0.7540618	-0.4663567	-1.5818874	0.025	0.982	2123	tags=44%, list=20%, signal=56%
BIOCARTA_CTCF_PATHWAY	22	0.75688	-0.3452956	-1.0518507	0.3786611	1	2209	tags=32%, list=21%, signal=40%
REACTOME_SIGNALING_BY_SCF_KIT	66	0.7603348	-0.2622334	-1.0477079	0.36744186	1	2125	tags=29%, list=20%, signal=36%
BIOCARTA_PPARA_PATHWAY	49	0.76056165	-0.3196028	-1.0463605	0.40430108	1	1881	tags=24%, list=18%, signal=30%
BIOCARTA_IL2_PATHWAY	21	0.76229453	-0.3510092	-1.0482024	0.3847826	1	696	tags=19%, list=7%, signal=20%
REACTOME_COLLAGEN_FORMATION	49	0.76244235	-0.568419	-1.5606136	0.07659575	0.987	2958	tags=53%, list=28%, signal=74%
PID_ANTHRAXPATHWAY	16	0.7630924	-0.5391004	-1.5870569	0.02754237	0.982	1574	tags=38%, list=15%, signal=44%
KEGG_PATHWAYS_IN_CANCER	299	0.76540065	-0.2180219	-1.0417453	0.34963325	1	1777	tags=23%, list=17%, signal=27%
REACTOME_HEMOSTASIS	380	0.76820266	-0.2247469	-1.041849	0.3887468	1	2438	tags=30%, list=23%, signal=37%
BIOCARTA_CARDIACEGF_PATHWAY	17	0.76821864	-0.5691155	-1.6615808	0.0239521	0.93	3214	tags=65%, list=31%, signal=93%
REACTOME_SIGNALING_BY_PDGF	103	0.7684047	-0.2623421	-1.0352741	0.39035088	1	2811	tags=35%, list=27%, signal=47%
PID_CXCR4_PATHWAY	88	0.7685725	-0.2873356	-1.0288697	0.38428876	1	2342	tags=33%, list=22%, signal=42%
REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS	32	0.7690177	-0.2950108	-1.0389639	0.38396624	1	2776	tags=38%, list=27%, signal=51%
ST_GA12_PATHWAY	22	0.7691009	-0.3313283	-1.0324295	0.3923241	1	2302	tags=41%, list=22%, signal=52%
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	95	0.76931924	-0.2500427	-1.0362	0.3716216	1	1432	tags=21%, list=14%, signal=24%
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	17	0.76992226	-0.3645398	-1.0373148	0.4122807	1	2779	tags=47%, list=27%, signal=64%
REACTOME_BASIGIN_INTERACTIONS	23	0.77086395	-0.314843	-1.0291635	0.40384614	1	3116	tags=39%, list=30%, signal=56%
REACTOME_CELL_JUNCTION_ORGANIZATION	62	0.7708867	-0.2768465	-1.0329255	0.42753622	1	1580	tags=21%, list=15%, signal=25%
PID_A6B1_A6B4_INTEGRIN_PATHWAY	44	0.7734803	-0.2835947	-1.029324	0.4213974	1	2859	tags=45%, list=27%, signal=62%
REACTOME_REGULATION_OF_INSULIN_SECRETION	73	0.7759134	-0.254422	-1.0245311	0.39597315	1	1908	tags=22%, list=18%, signal=27%
BIOCARTA_NO2IL12_PATHWAY	15	0.7815312	-0.4950345	-1.0156984	0.4861996	1	3484	tags=67%, list=33%, signal=100%
REACTOME_GAP_JUNCTION_TRAFFICKING	16	0.78228056	-0.3550306	-1.0141267	0.43340382	1	1796	tags=31%, list=17%, signal=38%
REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	96	0.7833501	-0.2447429	-1.0161996	0.42152467	1	1908	tags=21%, list=18%, signal=25%
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	27	0.78554785	-0.3184278	-1.0114597	0.4385965	1	2845	tags=44%, list=27%, signal=61%
PID_AVB3_OPN_PATHWAY	29	0.7858879	-0.3241288	-1.0176368	0.41949153	1	696	tags=21%, list=7%, signal=22%
REACTOME_SIGNALING_BY_ILS	95	0.78591025	-0.2685388	-1.0163591	0.42542788	1	2564	tags=36%, list=25%, signal=47%
KEGG_CHEMOKINE_SIGNALING_PATHWAY	148	0.78769374	-0.2591809	-1.0181191	0.4	1	2437	tags=32%, list=23%, signal=42%
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	35	0.79134214	-0.5979724	-1.5609095	0.09030837	0.987	2932	tags=63%, list=28%, signal=87%
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	73	0.7924209	-0.5301665	-1.6033568	0.05139186	0.972	2958	tags=51%, list=28%, signal=70%
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	32	0.7931099	-0.2927794	-1.0070221	0.401766	1	1427	tags=16%, list=14%, signal=18%
PID_SHP2_PATHWAY	53	0.7986719	-0.2738186	-0.9996564	0.4701835	1	2144	tags=28%, list=21%, signal=35%
KEGG_ASTHMA	22	0.79909426	-0.6269477	-1.5870966	0.07349666	0.982	2583	tags=64%, list=25%, signal=84%
BIOCARTA_VIP_PATHWAY	21	0.8014496	-0.3306402	-1.0009992	0.4361055	1	3257	tags=57%, list=31%, signal=83%
REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	21	0.8015679	-0.3423361	-0.9996676	0.47609147	1	2486	tags=43%, list=24%, signal=56%
REACTOME_GABA_B_RECEPTOR_ACTIVATION	30	0.8015687	-0.2781311	-0.9957808	0.46495327	1	2282	tags=33%, list=22%, signal=43%
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	65	0.8018229	-0.5599576	-1.7193389	0.02195609	0.838	4102	tags=83%, list=39%, signal=136%
BIOCARTA_PAR1_PATHWAY	34	0.8021083	-0.3110012	-1.0019943	0.45238096	1	1908	tags=35%, list=18%, signal=43%
BIOCARTA_TCR_PATHWAY	38	0.8037704	-0.3013451	-0.9961276	0.44805196	1	3269	tags=53%, list=31%, signal=76%
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	76	0.8061266	-0.2504668	-0.9924758	0.4699074	1	1565	tags=22%, list=15%, signal=26%
PID_INTEGRIN_CS_PATHWAY	23	0.8177721	-0.5761822	-1.6640897	0.02484472	0.925	3321	tags=65%, list=32%, signal=96%
KEGG_RENAL_CELL_CARCINOMA	66	0.81948125	-0.2451979	-0.9830777	0.4801865	1	1881	tags=29%, list=18%, signal=35%
REACTOME_STEROID_HORMONES	23	0.8197942	-0.3328223	-0.9842662	0.48958334	1	4325	tags=48%, list=42%, signal=82%
REACTOME_MYOGENESIS	23	0.8218895	-0.3309243	-0.9808155	0.49712092	1	2657	tags=26%, list=26%, signal=35%
BIOCARTA_MAPK_PATHWAY	85	0.8221626	-0.2456415	-0.9845116	0.48617512	1	2719	tags=42%, list=26%, signal=57%
PID_KITPATHWAY	48	0.8232825	-0.2699789	-0.9777713	0.47972974	1	2524	tags=35%, list=24%, signal=47%
PID_RAS_PATHWAY	22	0.8240834	-0.295112	-0.9787	0.46680942	1	1234	tags=23%, list=12%, signal=26%
PID_EPOPATHWAY	31	0.8248873	-0.3120776	-0.9759469	0.4683258	1	3053	tags=48%, list=29%, signal=68%
REACTOME_DIABETES_PATHWAYS	110	0.82518995	-0.2246375	-0.9745578	0.47916666	1	895	tags=15%, list=9%, signal=16%
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	32	0.8255975	-0.5491858	-1.6737674	0.0371134	0.906	2990	tags=59%, list=29%, signal=83%
BIOCARTA_BIOPEPTIDES_PATHWAY	38	0.8277161	-0.2679426	-0.9709743	0.5	1	2847	tags=39%, list=27%, signal=54%
REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	21	0.8292059	-0.313602	-0.9715343	0.49278352	1	2125	tags=33%, list=20%, signal=42%
PID_NFAT_TFPATHWAY	42	0.83299434	-0.2934468	-0.9662011	0.5100671	1	1381	tags=24%, list=13%, signal=27%
REACTOME_HS_GAG_DEGRADATION	17	0.83356017	-0.5655319	-1.6040204	0.0359408	0.971	1643	tags=47%, list=16%, signal=56%
REACTOME_AXON_GUIDANCE	218	0.83387077	-0.2225365	-0.9633015	0.4965358	1	2506	tags=29%, list=24%, signal=38%
PID_ERBB4_PATHWAY	35	0.8346424	-0.2883883	-0.9642399	0.5409483	1	1881	tags=29%, list=18%, signal=35%
PID_VEGFR1_PATHWAY	25	0.83496547	-0.3203345	-0.9666514	0.49156117	1	1208	tags=24%, list=12%, signal=27%
PID_TNFPATHWAY	40	0.83565456	-0.2631595	-0.9198943	0.56207675	1	1998	tags=30%, list=19%, signal=37%
KEGG_ARGININE_AND_PROLINE_METABOLISM	45	0.83722353	-0.2552161	-0.917905	0.5663717	1	3473	tags=42%, list=33%, signal=63%
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	75	0.8375468	-0.4332658	-1.5874063	0.03719913	0.982	1673	tags=33%, list=16%, signal=39%
KEGG_GNRH_SIGNALING_PATHWAY	84	0.83755827	-0.2126367	-0.9202187	0.6033254	1	2719	tags=32%, list=26%, signal=43%
BIOCARTA_CTLA4_PATHWAY	18	0.8385422	-0.409369	-0.9209527	0.5641026	1	3022	tags=50%, list=29%, signal=70%
PID_TXA2PATHWAY	52	0.8402318	-0.2718764	-0.9213997	0.55119824	1	2859	tags=44%, list=27%, signal=61%
REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	99	0.8410352	-0.2183839	-0.9493163	0.5475	1	1495	tags=22%, list=14%, signal=26%
REACTOME_TIGHT_JUNCTION_INTERACTIONS	22	0.84103924	-0.290707	-0.9125512	0.52164006	1	480	tags=14%, list=5%, signal=14%

REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	35	0.8416429	-0.2684599	-0.9219829	0.5469729	1	2125	tags=29%, list=20%, signal=36%
PID_HIF1_TFPATHWAY	61	0.84168935	-0.2574147	-0.951382	0.537931	1	1216	tags=16%, list=12%, signal=18%
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	34	0.841798	-0.2714923	-0.9464067	0.562212	1	2662	tags=35%, list=26%, signal=47%
ST_WNT_BETA_CATENIN_PATHWAY	29	0.84225726	-0.2767129	-0.9374605	0.5445344	1	3055	tags=48%, list=29%, signal=68%
SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES	34	0.8427422	-0.2743295	-0.9141818	0.5537757	1	3086	tags=38%, list=30%, signal=54%
PID_FAK_PATHWAY	53	0.8427724	-0.2867166	-0.9409182	0.54989386	1	1951	tags=34%, list=19%, signal=42%
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	64	0.8428131	-0.2647736	-0.9520943	0.5010846	1	3289	tags=48%, list=32%, signal=70%
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	52	0.8428204	-0.2735958	-0.9472415	0.48931116	1	2738	tags=44%, list=26%, signal=60%
REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE	117	0.8429149	-0.211977	-0.9128588	0.60888886	1	2221	tags=27%, list=21%, signal=34%
BIOCARTA_IL2RB_PATHWAY	37	0.8432727	-0.2774167	-0.9495577	0.48729792	1	3269	tags=41%, list=31%, signal=59%
PID_TRKRPATHWAY	56	0.843493	-0.2254492	-0.9223447	0.6122931	1	2257	tags=29%, list=22%, signal=36%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	21	0.8435935	-0.300743	-0.9103038	0.56041664	1	2135	tags=24%, list=21%, signal=30%
PID_P53DOWNSTREAMPATHWAY	116	0.84418863	-0.2239675	-0.9415091	0.5515464	1	1833	tags=24%, list=18%, signal=29%
REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	17	0.8442029	-0.3101262	-0.9527476	0.49561402	1	2123	tags=24%, list=20%, signal=30%
PID_CERAMIDE_PATHWAY	45	0.84431684	-0.2391196	-0.9244005	0.6061269	1	1561	tags=22%, list=15%, signal=26%
REACTOME_PHOSPHOLIPID_METABOLISM	125	0.8446583	-0.2153429	-0.9376185	0.6004415	1	2369	tags=27%, list=23%, signal=35%
PID_FGF_PATHWAY	50	0.8450945	-0.2437598	-0.9228215	0.5390244	1	2336	tags=28%, list=22%, signal=36%
BIOCARTA_ALK_PATHWAY	34	0.8451176	-0.2805279	-0.9047566	0.59565216	1	1254	tags=21%, list=12%, signal=23%
REACTOME_IL_3_5_AND_GM_CSF_SIGNALING	40	0.84512454	-0.2805242	-0.9071112	0.55011135	1	3275	tags=43%, list=31%, signal=62%
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	337	0.8455833	-0.194183	-0.9081543	0.6183036	1	2369	tags=24%, list=23%, signal=30%
BIOCARTA_NO1_PATHWAY	27	0.84567845	-0.3031953	-0.9249924	0.5534591	1	1489	tags=22%, list=14%, signal=26%
ST_GA13_PATHWAY	35	0.84571177	-0.2628838	-0.9322131	0.5532359	1	2660	tags=43%, list=26%, signal=57%
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	48	0.8458646	-0.2467248	-0.9533057	0.50110376	1	2660	tags=31%, list=26%, signal=42%
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	100	0.84607834	-0.2617011	-0.9381428	0.4790287	1	3321	tags=46%, list=32%, signal=67%
ST_INTEGRIN_SIGNALING_PATHWAY	74	0.84623253	-0.246089	-0.9418344	0.55314535	1	2342	tags=35%, list=22%, signal=45%
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	175	0.8463982	-0.2230341	-0.9567232	0.5155131	1	1740	tags=22%, list=17%, signal=26%
PID_TOLL_ENDOGENOUS_PATHWAY	21	0.84649694	-0.3000286	-0.9053324	0.54385966	1	2395	tags=38%, list=23%, signal=49%
PID_ILK_PATHWAY	41	0.84657264	-0.2789894	-0.9555167	0.51918733	1	1580	tags=34%, list=15%, signal=40%
PID_THROMBIN_PAR1_PATHWAY	40	0.8466266	-0.2640012	-0.9016021	0.58719647	1	2798	tags=40%, list=27%, signal=54%
PID_CONE_PATHWAY	15	0.8472407	-0.3182351	-0.9426193	0.53539824	1	3723	tags=40%, list=36%, signal=62%
BIOCARTA_FCER1_PATHWAY	33	0.8483106	-0.2653437	-0.9250178	0.5472103	1	2499	tags=36%, list=24%, signal=48%
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAIN	39	0.8483766	-0.2783966	-0.9322398	0.536643	1	1224	tags=26%, list=12%, signal=29%
BIOCARTA_CDMAC_PATHWAY	15	0.84860563	-0.3318281	-0.9261069	0.575	1	3214	tags=47%, list=31%, signal=67%
BIOCARTA_SPRY_PATHWAY	16	0.8486662	-0.3313404	-0.953337	0.50959486	1	570	tags=19%, list=5%, signal=20%
REACTOME_POTASSIUM_CHANNELS	74	0.8488321	-0.2191492	-0.9017496	0.63744074	1	3546	tags=39%, list=34%, signal=59%
PID_ER_NONGENOMIC_PATHWAY	37	0.8489731	-0.2635498	-0.9271921	0.5704698	1	704	tags=19%, list=7%, signal=20%
KEGG_MTOR_SIGNALING_PATHWAY	45	0.8501215	-0.2493389	-0.9278725	0.5638766	1	2221	tags=33%, list=21%, signal=42%
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	24	0.8502041	-0.2818743	-0.8975322	0.5978495	1	47	tags=8%, list=0%, signal=8%
BIOCARTA_DEATH_PATHWAY	31	0.85040045	-0.2889435	-0.9325368	0.5251641	1	1561	tags=26%, list=15%, signal=30%
KEGG_BLADDER_CANCER	41	0.85073084	-0.2384404	-0.8936956	0.64665127	1	1037	tags=20%, list=10%, signal=22%
BIOCARTA_COMP_PATHWAY	15	0.8508684	-0.663784	-1.6095276	0.04233871	0.97	2609	tags=67%, list=25%, signal=89%
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	28	0.85088086	-0.3040868	-0.8959767	0.61276597	1	3269	tags=54%, list=31%, signal=78%
KEGG_BASAL_CELL_CARCINOMA	45	0.85133517	-0.2556985	-0.8981942	0.59325844	1	3802	tags=53%, list=37%, signal=84%
KEGG_LYSOSOME	105	0.8515835	-0.2548508	-0.928525	0.5327869	1	2106	tags=28%, list=20%, signal=34%
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	137	0.85303634	-0.3693899	-1.6177405	0.01842105	0.966	4170	tags=53%, list=40%, signal=88%
PID_IL8CXCR2_PATHWAY	30	0.85315186	-0.2863555	-0.8937427	0.5661605	1	867	tags=20%, list=8%, signal=22%
KEGG_PRIMARY_IMMUNODEFICIENCY	33	0.85733056	-0.3598633	-0.8869084	0.57743365	1	4004	tags=70%, list=38%, signal=113%
KEGG_CHRONIC_MYELOID_LEUKEMIA	70	0.85742617	-0.217252	-0.8833835	0.6849642	1	2335	tags=29%, list=22%, signal=37%
PID_TCRCALCIUMPATHWAY	26	0.8574835	-0.2874176	-0.8879463	0.60227275	1	3496	tags=46%, list=34%, signal=69%
BIOCARTA_PML_PATHWAY	16	0.85839295	-0.3070179	-0.8852419	0.5879733	1	1897	tags=25%, list=18%, signal=31%
BIOCARTA_ERK_PATHWAY	26	0.8587908	-0.2585931	-0.883898	0.6347826	1	2221	tags=35%, list=21%, signal=44%
REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	17	0.8595972	-0.3102311	-0.8881308	0.6028226	1	1503	tags=29%, list=14%, signal=34%
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	62	0.8629119	-0.2320163	-0.8797324	0.60264903	1	2414	tags=29%, list=23%, signal=38%
REACTOME_COMPLEMENT_CASCADE	26	0.8639752	-0.6039639	-1.6257403	0.0545809	0.961	2609	tags=58%, list=25%, signal=77%
KEGG_APOPTOSIS	76	0.86542046	-0.2265883	-0.8714653	0.63380283	1	3269	tags=42%, list=31%, signal=61%
PID_TCPTP_PATHWAY	39	0.86724305	-0.2637924	-0.8742352	0.6289593	1	2144	tags=33%, list=21%, signal=42%
PID_RXR_VDR_PATHWAY	24	0.86728007	-0.537609	-1.6344352	0.02850877	0.955	1295	tags=38%, list=12%, signal=43%
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	35	0.8673131	-0.2743956	-0.8680266	0.6048035	1	3685	tags=54%, list=35%, signal=84%
REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_LIKE_PEPTI	33	0.8676135	-0.2527525	-0.8752912	0.67170626	1	2123	tags=27%, list=20%, signal=34%
PID_LYSOPHOSPHOLIPID_PATHWAY	54	0.8677173	-0.2346007	-0.8715528	0.667426	1	1951	tags=31%, list=19%, signal=39%
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	17	0.86775887	-0.3166638	-0.8764533	0.6352201	1	1000	tags=29%, list=10%, signal=32%
PID_INTEGRIN3_PATHWAY	42	0.868696	-0.2859922	-0.8722771	0.5708245	1	3150	tags=45%, list=30%, signal=65%
WNT_SIGNALING	79	0.8690371	-0.1979735	-0.8684349	0.69859815	1	1389	tags=18%, list=13%, signal=20%
BIOCARTA_MET_PATHWAY	34	0.8708353	-0.2576326	-0.8482782	0.6717391	1	1951	tags=29%, list=19%, signal=36%
REACTOME_PI3K_CASCADE	55	0.8716805	-0.2315062	-0.8575078	0.66146994	1	1881	tags=25%, list=18%, signal=31%
PID_ECADHERIN_STABILIZATION_PATHWAY	39	0.8724881	-0.2497729	-0.8594376	0.6441441	1	1405	tags=23%, list=13%, signal=27%
REACTOME_IL_2_SIGNALING	37	0.8725593	-0.2507931	-0.848626	0.6264237	1	3275	tags=41%, list=31%, signal=59%
KEGG_NOTCH_SIGNALING_PATHWAY	35	0.87271297	-0.2522022	-0.8617312	0.6739606	1	1663	tags=20%, list=16%, signal=24%
PID_TCR_PATHWAY	55	0.87289435	-0.28518	-0.8604185	0.5804348	1	3166	tags=44%, list=30%, signal=62%
KEGG_TIGHT_JUNCTION	110	0.87307554	-0.2057253	-0.8459051	0.7028302	1	2754	tags=27%, list=26%, signal=37%
REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	34	0.87308574	-0.2519101	-0.8639572	0.6630901	1	1874	tags=32%, list=18%, signal=39%
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVA	23	0.8734688	-0.2794221	-0.8578283	0.645749	1	2221	tags=35%, list=21%, signal=44%
KEGG_DORSO_VENTRAL_AXIS_FORMATION	18	0.8736996	-0.2948175	-0.862462	0.6516854	1	529	tags=11%, list=5%, signal=12%
PID_ARF6_TRAFFICKINGPATHWAY	42	0.8744308	-0.2524337	-0.8488732	0.65367967	1	1098	tags=19%, list=11%, signal=21%
REACTOME_INFLUENZA_LIFE_CYCLE	111	0.87569356	-0.2978115	-0.8530542	0.57988167	1	2186	tags=46%, list=21%, signal=58%
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	29	0.8758716	-0.2755022	-0.8505265	0.6625259	1	2307	tags=38%, list=22%, signal=49%
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	69	0.87600034	-0.2119465	-0.8492843	0.676815	1	2707	tags=33%, list=26%, signal=45%
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	57	0.87666696	-0.2314503	-0.8513619	0.6840796	1	2335	tags=25%, list=22%, signal=31%
REACTOME_PHASE_II_CONJUGATION	42	0.87776166	-0.2363555	-0.853235	0.67777777	1	2316	tags=24%, list=22%, signal=30%
BIOCARTA_CERAMIDE_PATHWAY	21	0.8796559	-0.2642168	-0.8413958	0.7058824	1	2019	tags=29%, list=19%, signal=35%
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	23	0.89584607	-0.2551906	-0.8306493	0.6982379	1	1195	tags=17%, list=11%, signal=20%
REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	43	0.8960755	-0.2395864	-0.828	0.71365637	1	2021	tags=30%, list=19%, signal=37%
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	30	0.8975632	-0.5795682	-1.675572	0.03155819	0.903	4207	tags=90%, list=40%, signal=151%
REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	69	0.897564	-0.2095125	-0.8310301	0.75116277	1	1513	tags=20%, list=15%, signal=24%
SA_B_CELL_RECEPTOR_COMPLEXES	21	0.89843583	-0.2659849	-0.8280084	0.6967742	1	3053	tags=38%, list=29%, signal=54%
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	21	0.90269434	-0.3627673	-0.8182864	0.6498952	1	3397	tags=62%, list=33%, signal=92%
PID_DELTANP63PATHWAY	44	0.9041403	-0.2226505	-0.8187978	0.75488067	1	3285	tags=50%, list=32%, signal=73%
PID_CMYB_PATHWAY	76	0.9052415	-0.1872068	-0.8194786	0.82474226	1	1739	tags=18%, list=17%, signal=22%
BIOCARTA_IL12_PATHWAY	20	0.90659326	-0.3362388	-0.8200716	0.65957445	1	3022	tags=55%, list=29%, signal=77%
REACTOME_GPCR_LIGAND_BINDING	291	0.90797067	-0.364002	-1.720772	0	0.836	3904	tags=50%, list=38%, signal=78%
BIOCARTA_CXCR4_PATHWAY	21	0.90831935	-0.2738144	-0.8204617	0.68973213	1	2139	tags=33%, list=21%, signal=42%
REACTOME_IL1_SIGNALING	32	0.9102584	-0.2236197	-0.8066441	0.772093	1	2564	tags=34%, list=25%, signal=45%
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDI	24	0.910292	-0.2368686	-0.8053232	0.78539824	1	919	tags=17%, list=9%, signal=18%

BIOCARTA_MCALPAIN_PATHWAY	21	0.9114232	-0.2607919	-0.812428	0.71157897	1	3182	tags=43%, list=31%, signal=62%
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	37	0.91191363	-0.2204582	-0.8108473	0.74115044	1	1944	tags=24%, list=19%, signal=30%
REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_	27	0.91193104	-0.2542136	-0.8005502	0.6987448	1	4325	tags=44%, list=42%, signal=76%
PID_HNF3BPATHWAY	37	0.91201794	-0.2394548	-0.8095009	0.7022587	1	868	tags=11%, list=8%, signal=12%
REACTOME_NEURONAL_SYSTEM	228	0.9120612	-0.1663952	-0.8069708	0.8544974	1	1827	tags=17%, list=18%, signal=20%
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	17	0.9121329	-0.263698	-0.8016909	0.7286013	1	2798	tags=47%, list=27%, signal=64%
PID_TGFBRPATHWAY	48	0.91290903	-0.2286222	-0.8076756	0.76537585	1	1850	tags=25%, list=18%, signal=30%
BIOCARTA_ECM_PATHWAY	23	0.91366506	-0.2656255	-0.8021703	0.72863245	1	2144	tags=30%, list=21%, signal=38%
BIOCARTA_RAS_PATHWAY	23	0.91506875	-0.2397107	-0.7872323	0.7995825	1	1881	tags=26%, list=18%, signal=32%
REACTOME_PI3K_AKT_ACTIVATION	29	0.9151568	-0.2449474	-0.7923644	0.7827004	1	2665	tags=34%, list=26%, signal=46%
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	36	0.915643	-0.2169165	-0.7895333	0.7687366	1	1825	tags=17%, list=18%, signal=20%
REACTOME_METABOLISM_OF_PROTEINS	311	0.9163401	-0.2143652	-0.785048	0.6855346	1	2186	tags=27%, list=21%, signal=34%
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	59	0.9165248	-0.2681644	-0.7967826	0.6578366	1	2106	tags=29%, list=20%, signal=36%
REACTOME_TRAF6_MEDIATED_NFKB_ACTIVATION	17	0.91665167	-0.2739216	-0.7902317	0.7213483	1	3259	tags=53%, list=31%, signal=77%
PID_CD8TCRPATHWAY	45	0.9170343	-0.2690224	-0.7926197	0.6514161	1	3166	tags=44%, list=30%, signal=64%
REACTOME_TIE2_SIGNALING	15	0.9172243	-0.2636151	-0.7873167	0.7355555	1	2144	tags=33%, list=21%, signal=42%
PID_RAC1_REG_PATHWAY	27	0.9179706	-0.2400304	-0.793404	0.76374745	1	2668	tags=37%, list=26%, signal=50%
BIOCARTA_UCALPAIN_PATHWAY	15	0.9184573	-0.2994397	-0.7944216	0.7106918	1	2506	tags=33%, list=24%, signal=44%
REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLIS	117	0.9200419	-0.2004382	-0.7789723	0.79303277	1	2094	tags=24%, list=20%, signal=30%
REACTOME_SIGNALING_BY_ERBB2	81	0.9217407	-0.1848334	-0.7793381	0.89376444	1	2144	tags=25%, list=21%, signal=31%
PID_INSULIN_PATHWAY	38	0.92206615	-0.2186012	-0.7698088	0.81838566	1	1130	tags=16%, list=11%, signal=18%
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	51	0.9227463	-0.2412708	-0.7653666	0.6880342	1	2786	tags=39%, list=27%, signal=53%
PID_IL8CXCR1_PATHWAY	24	0.9230323	-0.2584166	-0.7718431	0.7334755	1	867	tags=17%, list=8%, signal=18%
ST_GRANULE_CELL_SURVIVAL_PATHWAY	25	0.9232113	-0.2434394	-0.7798163	0.80124223	1	2307	tags=36%, list=22%, signal=46%
SIG_IL4RECEPTOR_IN_B_LYPHOCYTES	26	0.9237592	-0.2312474	-0.7701761	0.82765955	1	2532	tags=35%, list=24%, signal=46%
BIOCARTA_NGF_PATHWAY	16	0.9239227	-0.2579828	-0.7727184	0.80982906	1	696	tags=19%, list=7%, signal=20%
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	26	0.9242301	-0.2214455	-0.7658498	0.82742316	1	3546	tags=46%, list=34%, signal=70%
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATI	24	0.9246555	-0.283568	-0.7600411	0.72077924	1	3289	tags=46%, list=32%, signal=67%
BIOCARTA_BAD_PATHWAY	24	0.92490363	-0.224071	-0.7612559	0.8189655	1	3269	tags=42%, list=31%, signal=61%
REACTOME_GAB1_SIGNALOSOME	29	0.9257987	-0.2245514	-0.7662417	0.84309626	1	2125	tags=28%, list=20%, signal=35%
REACTOME_HS_GAG_BIOSYNTHESIS	22	0.9259302	-0.2577494	-0.7728652	0.7576419	1	2550	tags=32%, list=24%, signal=42%
REACTOME_PYRIMIDINE_METABOLISM	18	0.9260641	-0.2623103	-0.7578114	0.75946546	1	1858	tags=33%, list=18%, signal=41%
KEGG_TASTE_TRANSDUCTION	30	0.9260913	-0.2252519	-0.7741349	0.7644445	1	2123	tags=20%, list=20%, signal=25%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	44	0.92660356	-0.2067272	-0.7615849	0.82570803	1	954	tags=14%, list=9%, signal=15%
ST_JNK_MAPK_PATHWAY	36	0.927082	-0.233918	-0.7557196	0.8103093	1	2912	tags=47%, list=28%, signal=65%
REACTOME_GABA_RECEPTOR_ACTIVATION	44	0.927162	-0.1938726	-0.7542377	0.8621554	1	2282	tags=23%, list=22%, signal=29%
KEGG_PYRUVATE_METABOLISM	33	0.93135095	-0.243309	-0.741357	0.7668067	1	886	tags=15%, list=9%, signal=17%
BIOCARTA_ERK5_PATHWAY	17	0.9323303	-0.2342049	-0.7179873	0.8658281	1	3269	tags=47%, list=31%, signal=68%
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GA	21	0.9326798	-0.2215418	-0.7192656	0.86946386	1	2282	tags=29%, list=22%, signal=37%
KEGG_REGULATION_OF_AUTOPHAGY	24	0.93335867	-0.2257549	-0.7414528	0.82379866	1	1778	tags=17%, list=17%, signal=20%
REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION	18	0.93366975	-0.2472621	-0.7248859	0.81006867	1	2484	tags=39%, list=24%, signal=51%
BIOCARTA_NOS1_PATHWAY	18	0.933929	-0.2414157	-0.7262019	0.8270042	1	41	tags=6%, list=0%, signal=6%
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	39	0.9340401	-0.226408	-0.7439335	0.797235	1	2515	tags=31%, list=24%, signal=40%
KEGG_STARCH_AND_SUCROSE_METABOLISM	27	0.93415153	-0.2168942	-0.7197501	0.83516484	1	3071	tags=37%, list=30%, signal=52%
KEGG_GALACTOSE_METABOLISM	22	0.9345854	-0.2486992	-0.7479173	0.7523148	1	3612	tags=50%, list=35%, signal=76%
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM	16	0.93499464	-0.2886764	-0.7447648	0.7286528	1	2418	tags=31%, list=23%, signal=41%
BIOCARTA_MTA3_PATHWAY	17	0.9351801	-0.2646928	-0.741724	0.77021277	1	1706	tags=24%, list=16%, signal=28%
REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	25	0.93526876	-0.2421194	-0.7268415	0.81996083	1	2472	tags=32%, list=24%, signal=42%
ST_T_CELL_SIGNAL_TRANSDUCTION	41	0.9358804	-0.2332192	-0.7216036	0.7461707	1	3181	tags=41%, list=31%, signal=59%
REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHO	25	0.9361126	-0.2541056	-0.7198715	0.79253113	1	2779	tags=48%, list=27%, signal=65%
REACTOME_IL_RECEPTOR_SHC_SIGNALING	24	0.936702	-0.2478649	-0.7451422	0.7626728	1	3275	tags=42%, list=31%, signal=61%
PID_P38ALPHABETAPATHWAY	28	0.9371023	-0.230796	-0.7270299	0.85809314	1	2779	tags=39%, list=27%, signal=53%
PID_ENDOTHELINPATHWAY	55	0.9372779	-0.1976213	-0.7312968	0.8551724	1	2809	tags=33%, list=27%, signal=45%
PID_BCR_5PATHWAY	58	0.93728626	-0.2044829	-0.7126021	0.8333333	1	3289	tags=43%, list=32%, signal=63%
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	99	0.93834037	-0.19849	-0.7290935	0.74613684	1	3275	tags=43%, list=31%, signal=63%
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	20	0.93865806	-0.2352684	-0.7274043	0.81978023	1	1290	tags=20%, list=12%, signal=23%
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	33	0.93911874	-0.2023028	-0.7095335	0.91206545	1	2209	tags=24%, list=21%, signal=31%
PID_CXCR3PATHWAY	39	0.93933916	-0.2084985	-0.7313793	0.8495575	1	1908	tags=23%, list=18%, signal=28%
SIG_BCR_SIGNALING_PATHWAY	43	0.94018584	-0.211385	-0.7323517	0.8098434	1	3086	tags=37%, list=30%, signal=53%
PID_S1P_S1P1_PATHWAY	20	0.94091296	-0.251104	-0.7334334	0.80827886	1	2506	tags=35%, list=24%, signal=46%
ST_MYOCYTE_AD_PATHWAY	25	0.94405246	-0.2085266	-0.6955357	0.8736617	1	2579	tags=24%, list=25%, signal=32%
BIOCARTA_IGF1_PATHWAY	20	0.94537437	-0.2241678	-0.6925491	0.89135253	1	2144	tags=30%, list=21%, signal=38%
REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	19	0.94552916	-0.2126532	-0.6960376	0.8818381	1	1109	tags=16%, list=11%, signal=18%
BIOCARTA_GSK3_PATHWAY	25	0.9462984	-0.2013658	-0.6845325	0.92699116	1	3214	tags=48%, list=31%, signal=69%
BIOCARTA_P53HYPOXIA_PATHWAY	21	0.9466769	-0.2106245	-0.6766778	0.8960177	1	2909	tags=43%, list=28%, signal=59%
KEGG_TYPE_II_DIABETES_MELLITUS	42	0.9468157	-0.1847407	-0.6967455	0.9304556	1	2953	tags=38%, list=28%, signal=53%
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	23	0.9470427	-0.207876	-0.7017182	0.8517699	1	8251	tags=100%, list=79%, signal=481%
REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	17	0.9474164	-0.2192244	-0.6854363	0.902439	1	1109	tags=18%, list=11%, signal=20%
PID_SYNDECAN_4_PATHWAY	30	0.9480903	-0.2105038	-0.6866368	0.8912037	1	3558	tags=43%, list=34%, signal=66%
REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BETA_PATHW	57	0.9481303	-0.1912411	-0.6885014	0.9199029	1	3259	tags=37%, list=31%, signal=53%
PID_HIF1APATHWAY	17	0.9481547	-0.2420046	-0.6973361	0.875	1	1835	tags=29%, list=18%, signal=36%
PID_TRAIL_PATHWAY	26	0.94863594	-0.2040997	-0.6690456	0.92671394	1	2150	tags=31%, list=21%, signal=39%
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACI	70	0.94865775	-0.1661293	-0.6767668	0.9530516	1	2857	tags=23%, list=27%, signal=31%
REACTOME_SIGNAL_TRANSDUCTION_BY_L1	32	0.9491183	-0.1954028	-0.670515	0.93492407	1	2506	tags=28%, list=24%, signal=37%
PID_IGF1_PATHWAY	27	0.94921404	-0.1937982	-0.6563926	0.9375	1	2144	tags=26%, list=21%, signal=33%
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	19	0.9492838	-0.2167529	-0.6722645	0.9076577	1	2798	tags=37%, list=27%, signal=50%
BIOCARTA_RAC1_PATHWAY	22	0.9494484	-0.2029791	-0.677978	0.9113082	1	2463	tags=32%, list=24%, signal=42%
REACTOME_SULFUR_AMINO_ACID_METABOLISM	23	0.94977486	-0.2057504	-0.6537615	0.9277344	1	2246	tags=26%, list=22%, signal=33%
BIOCARTA_BCR_PATHWAY	29	0.94978505	-0.2070373	-0.679602	0.8924731	1	2499	tags=31%, list=24%, signal=41%
PID_EPHA_FWDPATHWAY	29	0.94989383	-0.2014131	-0.6577751	0.90084386	1	1435	tags=17%, list=14%, signal=20%
REACTOME_OXYGEN_DEPENDENT_PROLINE_HYDROXYLATION_OF_HYPOXIA_IN	15	0.95021623	-0.2667204	-0.6973922	0.8390558	1	2015	tags=40%, list=19%, signal=50%
PID_HES_HEYPATHWAY	43	0.9506418	-0.1823317	-0.6651651	0.9510638	1	2623	tags=26%, list=25%, signal=34%
BIOCARTA_TFF_PATHWAY	20	0.9507958	-0.2033348	-0.6588964	0.92763156	1	2144	tags=30%, list=21%, signal=38%
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	24	0.95168227	-0.2157249	-0.6600692	0.88666666	1	2015	tags=25%, list=19%, signal=31%
PID_ARF_3PATHWAY	15	0.95247334	-0.2423787	-0.6613175	0.87598425	1	1326	tags=20%, list=13%, signal=23%
BIOCARTA_PTEN_PATHWAY	16	0.95616937	-0.2181297	-0.635584	0.91935486	1	129	tags=6%, list=1%, signal=6%
PID_RHODOPSIN_PATHWAY	19	0.95621455	-0.1951436	-0.6309617	0.95248866	1	2013	tags=21%, list=19%, signal=26%
KEGG_LINOLEIC_ACID_METABOLISM	23	0.95707935	-0.198527	-0.6226802	0.93110645	1	4408	tags=52%, list=42%, signal=90%
BIOCARTA_INSULIN_PATHWAY	21	0.95710015	-0.2000443	-0.6322228	0.9211712	1	2144	tags=29%, list=21%, signal=36%
REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	20	0.9571343	-0.1952244	-0.625012	0.9591837	1	2794	tags=35%, list=27%, signal=48%
REACTOME_STRIATED_MUSCLE_CONTRACTION	25	0.9578429	-0.3053432	-0.6265854	0.86919105	1	1830	tags=16%, list=18%, signal=19%
PID_CD8TCRDOWNSTREAMPATHWAY	52	0.9581869	-0.1939712	-0.6355928	0.8648649	1	1072	tags=13%, list=10%, signal=15%
PID_IFNGPATHWAY	35	0.9585084	-0.1948642	-0.6399235	0.9152174	1	1881	tags=20%, list=18%, signal=24%

KEGG_ALZHEIMERS_DISEASE	138	0.95918393	-0.1797653	-0.6368494	0.89375	1	2706	tags=28%, list=26%, signal=37%
REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	17	0.95933557	-0.207756	-0.6412056	0.8983402	1	8251	tags=100%, list=79%, signal=482%
PID_IL2_STAT5PATHWAY	29	0.95966154	-0.2016904	-0.6167361	0.9111111	1	2803	tags=31%, list=27%, signal=42%
PID_EPHRINBREVPATHWAY	30	0.960137	-0.1901631	-0.6131424	0.9497717	1	2779	tags=33%, list=27%, signal=45%
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	55	0.9601756	-0.2517833	-0.6103226	0.8156313	1	2694	tags=31%, list=26%, signal=41%
BIOCARTA_HER2_PATHWAY	19	0.96026635	-0.2052863	-0.6016363	0.94065934	1	2144	tags=26%, list=21%, signal=33%
PID_HNF3APATHWAY	36	0.9609799	-0.1730916	-0.6035193	0.94866073	1	696	tags=8%, list=7%, signal=9%
KEGG_OLFACTORY_TRANSDUCTION	53	0.96260804	-0.1588451	-0.6040648	0.95475113	1	8765	tags=100%, list=84%, signal=630%
BIOCARTA_HCMV_PATHWAY	16	0.9632091	-0.2095854	-0.5939847	0.9483471	1	1881	tags=25%, list=18%, signal=30%
KEGG_ETHER_LIPID_METABOLISM	24	0.9684162	-0.536034	-1.6793227	0.01652893	0.901	1256	tags=29%, list=12%, signal=33%
KEGG_STEROID_HORMONE_BIOSYNTHESIS	36	0.9712469	-0.1626338	-0.5696579	0.9506438	1	8723	tags=100%, list=84%, signal=615%
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	18	0.9726784	-0.2150783	-0.5706819	0.94273126	1	2328	tags=33%, list=22%, signal=43%
ST_INTERLEUKIN_4_PATHWAY	24	0.9731785	-0.1789952	-0.5737156	0.9527027	1	2144	tags=21%, list=21%, signal=26%
REACTOME_GLUCOSE_METABOLISM	59	0.974434	-0.1678555	-0.5549725	0.9466951	1	3182	tags=32%, list=31%, signal=46%
REACTOME_REGULATION_OF_IFNA_SIGNALING	18	0.9753254	-0.1950727	-0.5571395	0.94893616	1	8383	tags=100%, list=81%, signal=513%
KEGG_CARDIAC_MUSCLE_CONTRACTION	60	0.98121786	-0.1610573	-0.5231097	0.9690522	1	3127	tags=30%, list=30%, signal=43%
REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	15	0.9827331	-0.2008589	-0.5244379	0.9717172	1	2472	tags=33%, list=24%, signal=44%
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMI	71	0.98346645	-0.1996173	-0.4959228	0.88645416	1	2694	tags=27%, list=26%, signal=36%
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPT	18	0.98398423	-0.1955613	-0.5266373	0.960499	1	2779	tags=39%, list=27%, signal=53%
REACTOME_GLUCONEOGENESIS	28	0.98442185	-0.1705915	-0.4995998	0.9793388	1	3182	tags=36%, list=31%, signal=51%
REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND	62	0.9857973	-0.1243341	-0.5018296	0.9976744	1	3231	tags=27%, list=31%, signal=40%
REACTOME_GLYCOLYSIS	25	0.9955174	-0.1401194	-0.4095187	0.99782133	1	8955	tags=100%, list=86%, signal=714%
KEGG_ARACHIDONIC_ACID_METABOLISM	44	1	-0.5109065	-1.8251216	0.0043956	0.581	1862	tags=32%, list=18%, signal=39%
KEGG_HEMATOPOIETIC_CELL_LINEAGE	75	1	-0.542672	-1.7855005	0.01856148	0.694	3526	tags=67%, list=34%, signal=100%
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	210	1	-0.4740979	-1.7685441	0.00959233	0.745	3209	tags=52%, list=31%, signal=74%
REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION	18	1	-0.5741548	-1.7515368	0.01138952	0.783	1495	tags=39%, list=14%, signal=45%
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	212	1	-0.3859918	-1.7313335	0.00539084	0.815	3904	tags=50%, list=38%, signal=78%
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	92	1	-0.4321774	-1.7220203	0.00977995	0.834	2553	tags=36%, list=25%, signal=47%

T6

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Date: November 12, 2013

THE UNIVERSITY OF TEXAS
MD Anderson Cancer Center
Making Cancer History®

To: Dr. M. Barton, S. Jiang, K. Thakkar

HISTOPATHOLOGY REPORT AND DIAGNOSIS

Group		CONTROL						Summary	TRIM24-1											
Animal ID		2506	2508	2509	2510	2549	2550		2513	2515	2516	2517	2518	2519	2520	2531	2532	2533	2534	2535
Specie		Mouse	Mouse	Mouse	Mouse	Mouse	Mouse		Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse
Genotype/Strain		C57/129	C57/129	C57/129	C57/129	C57/129	C57/129		C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129
Sex																				
Age																				
Tumor weight (grams) or size (mm)																				
bservations																				
Block No.	Organ Morphologic Diagnosis	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Incidence or Average Score of lesions	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade
	Xenograft tissue sample on the slide	P	P	P	P	P	P	6	P	P	P	P	P	P	P	P	P	P	P	P
	Dx: Fibrous tissue	P	P			P		3												
	Dx: Epithelial cells intermixed with fibrous tissue			P	P		P	3	P	P	P	P	P	P	P	P	P	P	P	P
	Epithelial cells (percent of epithelial cells from the total tumor mass)	0	0	1	1	0	1	0.5	5	25	35	30	40	40	30	35	20	35	1	2
	Fibrous tissue (percent fibrous tissue and collagen deposition from the total tumor mass)	100	100	99	99	100	99	99.5	95	75	65	70	60	60	70	65	80	65	99	98
	Cellular atypia of neoplastic epithelial cells (grade 0-4)			0	0		0	0	2	1	4	2	3	4	2	4	2	3	0	1
	Anysokaryosis (grade 0-4)			0	0		0	0	1	1	3	2	3	3	2	3	3	3	0	2
	Mitotic rate (total number of mitotic epithelial cells within the xenograft tumor)			0	0		0	0	1	0	3	0	2	2	0	0	0	1	0	1
	Vascularization (grade 1-4)	1	1	1	1	1	1	1	1	2	2	1	2	2	2	2	2	2	2	2
	Grade of malignancy (grade 0-3)	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**1**	**3**	**2**	**2**	**3**	**2**	**3**	**2**	**2**	**0**	**1**
	Inflammation	P	P	P	P	P		5	P	P	P	P	P	P	P	P	P	P	P	P
	Infiltration of Neutrophilis and/or Macrophages	1	1	1	1	2		1.2	3	2	3	3	2	3	2	2	4	4	3	2
	Infiltration of Lymphocytes	0	0	0	0	0		0	1	1	2	1	2	2	1	3	3	1	0	0
	Additional Observations			there are 3 small nests of epithelial cells composed of 7-18 epithelial cells	there is a single small nest of 11 epithelial cells		there is a single small nest of 13 epithelial cells						There is evidence of infiltration of neoplastic epithelial cells into surrounding tissue at the periphery of the tumor		there is minimal infiltration of neoplastic epithelial cells at the periphery of tumor mass		There is evidence of infiltration of neoplastic epithelial cells into surrounding tissue at the periphery of the tumor	There is minimal infiltration of neoplastic epithelial cells at the periphery of the tumor mass	I think this is a sampling error and probably should be excluded from this group analysis	

*Note: No tissue was obtained for 2 more Control mice

LEGEND
N = Normal tissue or No significant lesion observed
P = The lesion is present

Cellular Atypia
0 = normal cells
ninimal atypia (minimal nuclear hyperchromasia and pleomorphism)
2 = mild atypia (mild nuclear hyperchromasia and pleomorphism)
oderate atypia (moderate nuclear hyperchromasia and pleomorphism)
marked atypia (marked nuclear hyperchromasia and pleomorphism)

Anisokaryosis
0 = normal (uniform) size of nuclei
1 = 1-fold variation in the size of nuclei
2 = 2-fold variation in the size of nuclei
3 = 3-fold variation in the size of nuclei
4 = 4- or more folds variation in the size of nuclei

Grade of Malignancy
0 = no evidence of neoplasia or malignancy
lls with mild cellular atypia, mild nuclear hyperchromatism and pleomorphism, 1-2 folds anysokaryosis, and no evidence of invasion/infiltration
e moderate cellular atypia, moderate nuclear hyperchromatism and pleomorphism, and 2-3 fold anysokaryosis, and no or minimal evidence of invasion/infiltration
have marked cellular atypia, marked nuclear hyperchromatism and pleomorphism, and 4 or more folds anysokaryosis, and presence of invasion/infiltration

GRADING/SCORING OF OTHER HISTOLOGICAL LESIONS
Grade 0 = no histologic lesion
esion is **minimal**, rare, occasional (or affects **less than 10%** of the tissue)
ion is **mild**, slight, infrequent, random, sporadic (or affects **10-20%** of tissue)
esion is **moderate**, frequent, typical, common (or affects **20-40%** of tissue)
sion is **marked**, extensive, numerous, severe (or affects **40-100%** of tissue)

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Date: November 12, 2013

To: Dr. M. Barton, S. Jiang, K. Thakkar

HISTOPATHOLOGY REPORT AND DIAGNOS

Group		Summary	TRIM24-2													Summary
	Animal ID		2528	2521	2522	2525	2526	2527	2529	2530	2536	2537	2540	2541	2542	
	Specie		Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse	
	Genotype/Strain		C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	C57/129	
	Sex															
	Age															
	Tumor weight (grams) or size (mm)															
bservations																
Bloc k No.	Organ Morphologic Diagnosis	Incidence or Average Score of lesions	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Lesion Grade	Incidence or Average Score of lesions
	Xenograft tissue sample on the slide	12		P	P	P	P	P	P	P	P	P	P	P	P	12
	Dx: Fibrous tissue															0
	Dx: Epithelial cells intermixed with fibrous tissue	12		P	P	P	P	P	P	P	P	P	P	P	P	12
	Epithelial cells (percent of epithelial cells from the total tumor mass)	24.8		50	40	35	20	35	1	35	20	25	35	60	25	31.8
	Fibrous tissue (percent fibrous tissue and collagen deposition from the total tumor mass)	75.2		50	60	65	80	65	99	65	80	75	65	40	75	68.3
	Cellular atypia of neoplastic epithelial cells (grade 0-4)	2.3		4	4	4	2	4	1	4	2	3	4	4	3	3.3
	Anysokaryosis (grade 0-4)	2.2		3	3	3	3	3	1	4	2	3	4	4	3	3.0
	Mitotic rate (total number of mitotic epithelial cells within the xenograft tumor)	0.8		0	2	2	1	0	0	0	0	2	0	0	0	0.6
	Vascularization (grade 1-4)	1.8		2	2	2	1	2	1	2	1	1	2	2	2	1.7
	Grade of malignancy (grade 0-3)	**1.8**		**3**	**3**	**3**	**1**	**3**	**0**	**3**	**1**	**2**	**3**	**3**	**2**	**2.3**
	Inflammation	12		P	P	P	P	P	P	P	P	P	P	P	P	12
	Infiltration of Neutrophilis and/or Macrophages	3		2	2	1	1	2	1	2	1	3	3	3	2	2
	Infiltration of Lymphocytes	1		3	2	2	1	0	0	0	0	1	3	0	2	1
	Additional Observations		There is no xenograft tumor in this slide, but only normal fibroadipose mouse tissue			there is minimal focal infiltration of tumor cells into surrounding tissue	There is ectasia/dilation of the medullary sinuses and moderate plasmacytosis of the lymph node		I am not sure whether this case is a sampling error or not				There is evidence of invasion	There is evidence of invasion		

LEGEND
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2 = mild atypia (mild nuclear hyperchromasia and pleomorph
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marked atypia (marked nuclear hyperchromasia and pleomo

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4 = 4- or more folds variation in the size of nuclei

Grade of Malignancy
0 = no evidence of neoplasia or malignancy
lls with mild cellular atypia, mild nuclear hyperchromatism a
'e moderate cellular atypia, moderate nuclear hyperchromatis
have marked cellular atypia, marked nuclear hyperchromati

GRADING/SCORING OF OTHER HISTOLOGICAL LESIC
Grade 0 = no histologic lesion
esion is **minimal**, rare, occasional (or affects **less than 10**
ion is **mild**, slight, infrequent, random, sporadic (or affects
esion is **moderate**, frequent, typical, common (or affects **2(**
sion is **marked**, extensive, numerous, severe (or affects **4(**

T7

Cloning Primers

TRIM24-F1	ATTTTACACGTGATGGAGGTGGCGGTGGAGAA
TRIM24-R1	CGGGGCTCTAGATTATTTAAGCAACTGGCGTT

qRT-PCR primers

Gene	Species	Forward primer	Reverse primer
TRIM24	Human	GTGGATCAGCAAGCAGGAG	TTTGTCAAGAAAGGGTGTAACG
β-ACTIN	Human	GGACTTCGAGCAAGAGATGG	AGCACTGTGTTGGCGTACAG
TP53	Human	AAAGAAGAAACCACTGGATG	ATTCAGCTCTCGGAACAT
GLUT1	Human	CCA GCT GCC ATT GCC GTT	GAC GTA GGG ACC ACA CAG TTGC
GLUT4	Human	GTCGGGCTTCCAACAGATAG	ACCCCAATGTTGTACCCAAA
HK2	Human	ATG AGG GGC GGA TGT GTA TCA	GGT TCA GTG AGC CCA TGT CAA
ENO1	Human	AAA GCT GGT GCC GTT GAG AAG	AGC ATG AGA ACC GCC ATT GAT
ALDO-A	Human	GGG TGT CAT CCT CTT CCA TGA	GAC CAC GCC CTT GTC TAC CTT
PGM1	Human	ACC CAC TCC CTT CAT ACA ATC	CTC CTC ACT GGT CAT GGC TTA
PDK1	Human	CCG CTC TCC ATG AAG CAG TT	TTG CCG CAG AAA CAT AAA TGA G
GPI	Human	GGT ACA CAG GCA AGA CCA TC	GTT TTG GCA ATG TGA GTT CC
PKM1	Human	CGAGCCTCAAGTCACTCCAC	GTGAGCAGACCTGCCAGACT
PKM2	Human	ATTATTTGAGGAACTCCGCCGCCT	ATTCCGGGTCACAGCAATGATGG
LDHC	Human	CCTCTTGGGCTATTGGACTG30	GCCTCCTCCTCAGAATTCAA30
ACO1	Human	TTGGAGGATTCAAGATATGG	ACTCATCACAATTCCGAAT
DLAT	Human	GTTCCTACAGGTGTCTTC	AAGGTAATAATGAGGTATGGT
IDH1	Human	GAGATAACCTACACACCAAGT	AACACCACCACCTTCTTC
IDH2	Human	GATGGATGGTGATGAGAT	AAATACTTTAGCTGGATGTC
MDH2	Human	TGTGATGTGGTAGTTATTCC	ATTGGTGTTGAACAGGTC
OGDH	Human	AATGTCATCAGGAAGGAG	GGTGGTACTTCACATCTC
PDHA1	Human	ATGTATGCCAAGAACTTC	ATTATACTTACAGGCTAGAG
PDHB	Human	AGGAGTTGAATGTGAGGTGATAA	ATGACACTGGCTTCTATGGT
SDHA	Human	ATGCCATCCACTACATGA	ATAAATCTTCCCATCTTCAGTT
SDHB	Human	GACACCAACCTCAATAAG	GATTCATCCTTCTTCTTCAA
SDHD	Human	ACCGACCTATCCCAGAATG	CAGCCTTGGAGCCAGAAT
FH	Human	TTAAGATTGGAGGTGTGA	CATAATCCTGGTTTACTTCA

T8			
Antibody details (Catalog)	**Species**	**Company**	**Application**
TRIM24 (NB100-2597)	Rabbit	Novus Biologicals	Western
TRIM24 (14208-1-AP)	Rabbit	Protein tech	IHC
p53(DO1)-HRP (sc-126)	Mouse	Santa Cruz	Western
β-Actin- HRP (5125)	Rabbit	Cell Signaling	Western
Hexokinase II (2687)	Rabbit	Cell Signaling	Western
Aldolase (3188)	Rabbit	Cell Signaling	Western
Enolase -1 (3810)	Rabbit	Cell Signaling	Western
PDHK1 (3820)	Rabbit	Cell Signaling	Western
LDHA/ LDHC (3538)	Rabbit	Cell Signaling	Western
PGM1 (ab55616)	Mouse	Abcam	Western