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Supplementary Information for

Immune evasion in HPV-negative head and neck precancer-cancer transition is driven by an aneuploid switch involving chromosome 9p loss

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This PDF file includes:

Supplementary Information Text

Methods – Extended Description

Prospective Oral Precancer Cohort

SCNA and Multiplex immune profiling. Chromosome gain was determined by fluorescence *in situ* hybridization, using a chromosome-7 centromeric probe, randomly selected marker of tri-/tetra-somy based on similar phenotypes with different chromosomes in this context (1). After specific PCR-DNA amplification, an automatic capillary DNA analyzer was used to separate microsatellite alleles and to quantify the peak height of individual alleles for each marker. Loss of at least one of the markers (using the criteria described in the statistical section) was considered as loss of that specific chromosomal site. We considered overall SCNA level as chr7 gain and loss at 7 chromosome arms, including 3p, 9p, and 17p and the following: 4q, 8p, 11q, and 13q.

As described in a prior methods report (2), we utilized a validated multiplex immunofluorescence (mIF) panel of five antibodies stained on the same tissue section, and labeled using a tyramide-signal amplification-based kit, including: anti-CD3 (Dako, T lymphocyte marker), anti-CD8 (clone C8/144B, Thermo Scientific, present on cytotoxic T cells), anti-CD68 (clone PG-M1, Dako, macrophage lineage marker), anti-cytokeratin (clone AE1/AE3, Dako), and DAPI (nuclear staining). Each antibody was labeled with a specific fluorophore. All antibodies had been optimized for mIF by examination of positive and negative controls and testing of the antibodies by Western blotting. We performed scanning and image capture with a multispectral microscope (Vectra™, PerkinElmer), and analyzed the images with a specialized software (InForm™, PerkinElmer) capable of counting the number of cells with positive staining for each marker in a specified area. For each sample, 1-10 representative areas (median 6) measuring 1 mm^2 each, were randomly selected for marker quantification. CD3+ and CD8+ T-cells and CD68+ macrophages were evaluated and reported as cell density (i.e., cells/mm^2).

Statistical considerations. Wilcoxon rank-sum tests were used to compare the distribution of continuous variables between two groups defined by a binary variable. Fisher's exact tests were used to assess the association between binary markers and categorical factors. Spearman correlation coefficients were used to evaluate pair-wise correlations between two markers in continuous scale. When analyzing biomarkers assessed in a continuous scale, values from multiple areas were transformed into logarithm scale and were fit with linear mixed-effect models to account for within-patient variation (3). OCFS (model1) was defined as the time from protocol registration until development of the protocol-specified primary endpoint of invasive oral cancer, or death, and estimated by the Kaplan-Meier method. Cox proportional hazard model was used to study marker and OCFS associations. Log-rank test was performed to test the difference in OCFS between groups. All analyses were performed using SAS software (version 9.4; SAS Institute, Cary, NC) and R.

$$Cox\ Model \sim 9p21.3\ Loss\ +\ 3p14\ Loss\ +\ 17p13.1\ Loss\ +\ Histology\ (model1)$$

Throughout the paper, in the univariate (model2) and multivariable (model3) analyses performed to predict the level of a specific parameter (e.g., immune-cell level) based copy-number event, two different cutoffs were used (35 %-65 %, and confirmed with a 50 %). For example, in multivariable logistic regression of precancer cases, we divided the patients into the top and bottom 35 % in terms of percent of immune cells and used loss at 3p14, 9p21.3, or/and

17p13.1, and SCNA level, to determine the contribution of each parameter to the immune-cell landscape. The same cutoffs were used for the analysis of TCGA cases, including IS. The chromosome loss in precancer is defined as the ratio of the peak heights of the two alleles in lesion (L1/L2) DNA and in the corresponding normal lymphocytes (N1/N2) DNA >1.43 or <0.7, consistent with the same cutoffs utilized in the landmark clinical study that prospectively correlated precancer-specific SCNAs with prognosis (4).

The SCNA level was calculated based on the available information on the SCNA level at different genomic loci. More specifically, information was available on the presence of losses at the following loci: 3p21-14, 4q26-28, 4q31.1, 8p22-p23, 9p21.3, 11q13-q22, 13q21, 17p13.1 --SCNA level was calculated based on any SCNA (loss at all microsatellite loci in 3p21-14, 4q26-28, 4q31.1, 8p22, 8p23, 9p21.3, 11q13, 11q22, 13q21, or 17p13.1 and/or chromosome 7 gain):

$$SCNA.\,level^{*} = \begin{pmatrix} no\ SCNA & 0\ (none) \\ any\ Loss\ \mathrm{OR}\ chr7\ gain & 1\ (low) \\ any\ Loss\ \mathrm{AND}\ chr7\ gain & 2\ (high) \end{pmatrix}$$

$$Immune_{infiltrate} \sim 3p14\ Loss\ or\ 9p21.3\ Loss\ or\ 17p13.1\ Loss \times \beta + \varepsilon(random\ effect)\ (model2)$$

$$Immune_{infiltrate} \sim 3p14\ Loss + 9p21.3\ Loss + 17p13.1\ Loss + SCNA.\,level\ (model3)$$

HPV-Negative HNSC in The Cancer Genome Atlas (TCGA)

Statistical considerations. Logistic regression was used to determine the variables most predictive of different parameters representing immune infiltrate (model4-5) and IS levels. All the findings were confirmed using two purity methods (pathology-based and ABSOLUTE, see main manuscript Methods) and reported in the supplemental tables. After purity adjustment, we consider a log2-transformed copy number ratio >0.3 as a gain and <(-0.3) as a loss. Gene expression, mutation and clinical data were downloaded from GDAC Firehose. Patients with nonsense, splice site, frame shift, and missense mutations with Polyphen2-HVAR score > 0.2 (5) were considered as *TP53* mutation-positive patients. HPV-status was determined using a cutoff of RPM >1 (viral reads per million) in tumors of oropharyngeal origin was used as a stringent definition of HPV-positive HNSC, for a limited subset analysis. We used the log2 transformed RSEM values to estimate differences in the immune cell content (different types of immune cells) using CIBERSORT (using the LM22 gene signature) (6). In order to recapitulate in HNSC what was done in oral precancers, RNA expression levels of specific immune markers were applied as a proxy of the level of the corresponding immune cells in the tumor. Previous studies have shown that RNA expression levels (e.g., CD8+) of immune-cell markers highly correlate with cell estimates based on immunofluorescence (7, 8) (see Results). We defined the tumors as having low or high gene expression level using the 35th and 65th percentiles; results were confirmed using a cutoff of 50%. We used the GISTIC2 algorithm to distinguish between the two major types of events--arm-level and focal-level events. When specified, logistic regression was performed after first selecting patients with a certain tumor stage or containing or not *TP53* mutations. In addition, 5-fold cross-validation and variable-importance (size-effect) evaluation (package caret) were also performed to evaluate the accuracy of multivariable logistic regression models, and the size effect of each covariate, respectively.

$$SCNA\ level = \sum arm\ gains + \sum arm\ losses$$

$$Immune_{infiltrate} \sim 3p14\ Loss + 9p21.3\ Loss + 17p13.1\ Loss + Chr\ 7\ Gain + SCNA\ level\ (normalized)\ (model4)$$

$$Immune_{infiltrate} \sim 9p21.3\ Loss(arm) + 9p21.3\ Loss(focal) + 9p21.3\ Loss(arm + focal) + 3p14\ Loss + SCNA\ level\ (normalized)\ (model5)$$

For the least absolute shrinkage and selection operator (*Lasso*) (9) classification, to determine the parameters most predictive of immune-infiltrate level, we defined tumors as having low or high IS levels using the 35th and 65th percentiles, as described previously (10), and used a binomial model. We also applied *Lasso* using 10-fold cross validation. As variables, we included the presence of loss or gain in all possible whole chromosome or chromosome arms across the genome and the overall arm/chromosome SCNA level.

For GSEA (Gene Set Enrichment Analysis) comparing tumor samples with or without the indicated SCNA, we first used DEseq2 package (11) to calculate the log2 fold change and adjusted p-value of differentially expressed genes. Then we calculated the differential-expression score [Exp. Score] based on the formula below. Exp. Score was then used to perform GSEA pathway analysis (pre-ranked model) (12).

$$Exp.Score = sign\ (log_2 FoldChange) \times\ -log_{10}\ (adjusted\ p\_value)$$

HPV-negative HNSC Cell Lines

Statistical considerations. We used GSEA to investigate mechanisms of 9p21.3 or 3p14 (selected based on statistical significance in TCGA analyses) effects on gene- and pathway-change. To have similar numbers of cells in each group we split the cell lines into those having a copy-number level lower or higher than the median value (for example, as a threshold we used the median based on log2 copy-number ratio of -0.45 for 9p21.3 and -0.5 for 3p14 region). We used DEseq2 (11) to estimate the differential expression between the two groups of cell lines. We then used the formula above to calculate a score as input in GSEA (12). For GSEA, we used the comprehensive list of pathway and gene sets from BIOCARTA, KEGG and REACTOME databases. We performed logistic regression (model6) to determine the parameters most predictive of the expression of the SASP signature pathway (see below). We distinguished cell lines as having low or high SASP-signature scores using the 35th/65th, or 50th percentile cutoff (binary) or continuous variable of the distribution (all the continuous variables were normalized before being used in the multivariable models). We applied a logistic model on the dataset using as variables, 3p14 loss or 9p21.3 loss. To determine the contribution of chromosome loss encompassing whole 9p, 3p, and 17p arms as compared to focal losses, we used GISTIC2. Applying GISTIC2 algorithm to segment data derived from the cell lines, we determined the type of loss at 9p21.3 and 3p14: arm-level event versus focal-only event. As in TCGA analyses, a threshold of 70% of arm length (given in units of the fraction of chromosome arm) was used in GISTIC2 to distinguish between cell-line focal- and arm-level events.

$$SASP\ enrichment \sim 9p21.3\ Loss(arm) + 9p21.3\ Loss(focal)\ (model6)$$

SASP and *IFNα* gene set. To derive an aneuploidy-associated SASP signature, we first considered the genes upregulated in SASP as previously reported (13). Then we crossed this gene list with the genes upregulated (log2FC of at least 1.5) in aneuploid cells versus control cells (reversine treated versus control) from (14). The derived list of 20 genes represents the SASP signature and is shown in Table S15. The *IFNα* gene set contains the list of *IFNα* genes that are located on chr 9p21.3 and shown in Table S15. To calculate the SASP gene-expression signature and *IFNα* gene expression we used the single-sample GSEA (ssGSEA package) (12).

Survival analysis of 9p loss in ICB treated HPV-negative HNSC

Statistical, profiling considerations for real-world evidence (RWE) cohort. We employed a novel "virtual karyotyping" platform that allowed interrogation of the associations between loss of genes/chromosomal regions in 9p or 3p and outcomes using linked biomarker-EMR-insurance claim-survival record data. The Caris Life Sciences CODEai database which contains over 215,000 molecular profiles combined with clinical outcomes was leveraged for this study. 2,761 HNSC cases were available of which 1,604 had results from the Caris 592-gene assay. These cases were then segregated by whether therapy was administered prior to the collection of the sample that was profiled. 479 cases were found to have therapy administration only after the collection date of the tumor profiled. The 479 cases were further subdivided into groups based on whether immunotherapy (nivolumab or pembrolizumab) was part of their treatment. An overall survival minimum of 30 days was selected to remove patients with incomplete outcomes records (filtered down to 455). 196 of the 455 cases were HPV negative assessed by p16 IHC status. 122 patients were treated with immunotherapy across various lines of treatments with and without chemotherapy. 74 patients were found to have no immunotherapy treatment (Consort diagram, Fig. S12). TMB in our 592-gene panel was found to be equivalent to the FDA-approved 324-gene companion diagnostic test related to the agnostic use of pembrolizumab for tumors with ≥10 mutations/megabase (15). The 592-gene MI Tumor Seek panel was used to validate anti-PD-1 therapy efficacy in relation to MSI status (16).

Microdissection was performed on all cases and only those that achieved a minimum of 20% of tumor content in the area selected for microdissection were sequenced. We derived the SCNA level by comparing the depth of sequencing of genomic loci to a diploid control as well as the known performance of these genomic loci from a CLIA-validated commercially available assay (MI Tumor Seek 592-gene panel; Caris Life Sciences), as recently described (17). The 592-gene panel arm loss algorithm was CAP/CLIA validated in a study comparing 436 patients with both 592-gene panel arm-loss predictions and FISH results for 1p/19q co-deletion, a pattern shown to be therapeutically relevant in glial-brain tumors, e.g., low-grade gliomas (18). There were 29 samples positive by FISH and 407 samples negative by FISH for 1p/19q co-deletion and the arm-loss algorithm predictions had a sensitivity of 96.6 % (95 % CI: 82.2-99.9) and specificity of 99.5 % (95 % CI: 98.2-99.9). The 592-gene panel arm loss algorithm was further validated against the Caris Life Sciences Whole Exome Sequencing (WES) assay on 369 cases with both 592-gene panel arm-loss predictions and WES arm-loss predictions. WES used a conservative copy-number estimate across entire chromosomes, excluding centromeres and telomeres. This estimate included ~50,000 intronic and intergenic SNPs which were present at minimum every 160,000 base intervals (6.25/megabase) along with depth data from every gene. The calculation used CNVKit (python 3.7, version 0.9.6) and provided confidence in deletion status by examining tens of thousands of data points and returning a call based on consecutive measurements of presence or absence of DNA. The Pearson's correlation between the two assays was 0.828 across 9p loss and 0.773 for 9p21.3 loss. *PD-L1*, *PD-L2*, and *JAK2* were evaluated for copy-number loss using 1.6 copies or less to determine if the gene is deleted as described previously (19). The 592-gene panel arm-loss algorithm evaluated large-scale gene deletions across both arms of all chromosomes where a gene was profiled. The mean copy number across all genes profiled on a region or arm was compared to the mean of all copies for genes profiled on the opposite arm. The resulting ratios for each chromosome must be ≤0.8 and the opposite arm cannot have an average copy number greater than 2.5 for the region or arm under consideration to be evaluated as lost. Larger cohorts using whole-exome or whole-genome sequencing data will be important to extend these findings, including to address the contribution of *TP53* mutations to ICB resistance, an analysis currently limited by statistical power due to the high *TP53* mutation-9p loss co-occurrence rates.

Contributions

SML and TD conceived, planned and provided biologic and clinical (prevention, interception and immune therapy) intellectual input and insight into all aspects of this project, including all patient-cohort and cell-line studies and results—study design, statistical analyses and led the data interpretation, potential application and implications to HNSC, other cancers and aneuploid diseases—copy-number, aneuploid, -immune concept, balance and model development, and writing; WNW and SML planned, assembled and conducted the prospective precancer cohort; HYL and JJL contributed to the design and analysis of the precancer cohort; XZ performed most of the statistical analyses for precancer and TCGA datasets; JJB provided essential contribution to the analyses and their interpretation. JPA, DBS, and SML provided the analysis, data interpretation and insight of the RWE cohort. WC provided essential insight into the development and conduct of the project, including the conception of the model concept. SML, TD, WNW and XZ wrote the manuscript. All the authors contributed to editing the manuscript.

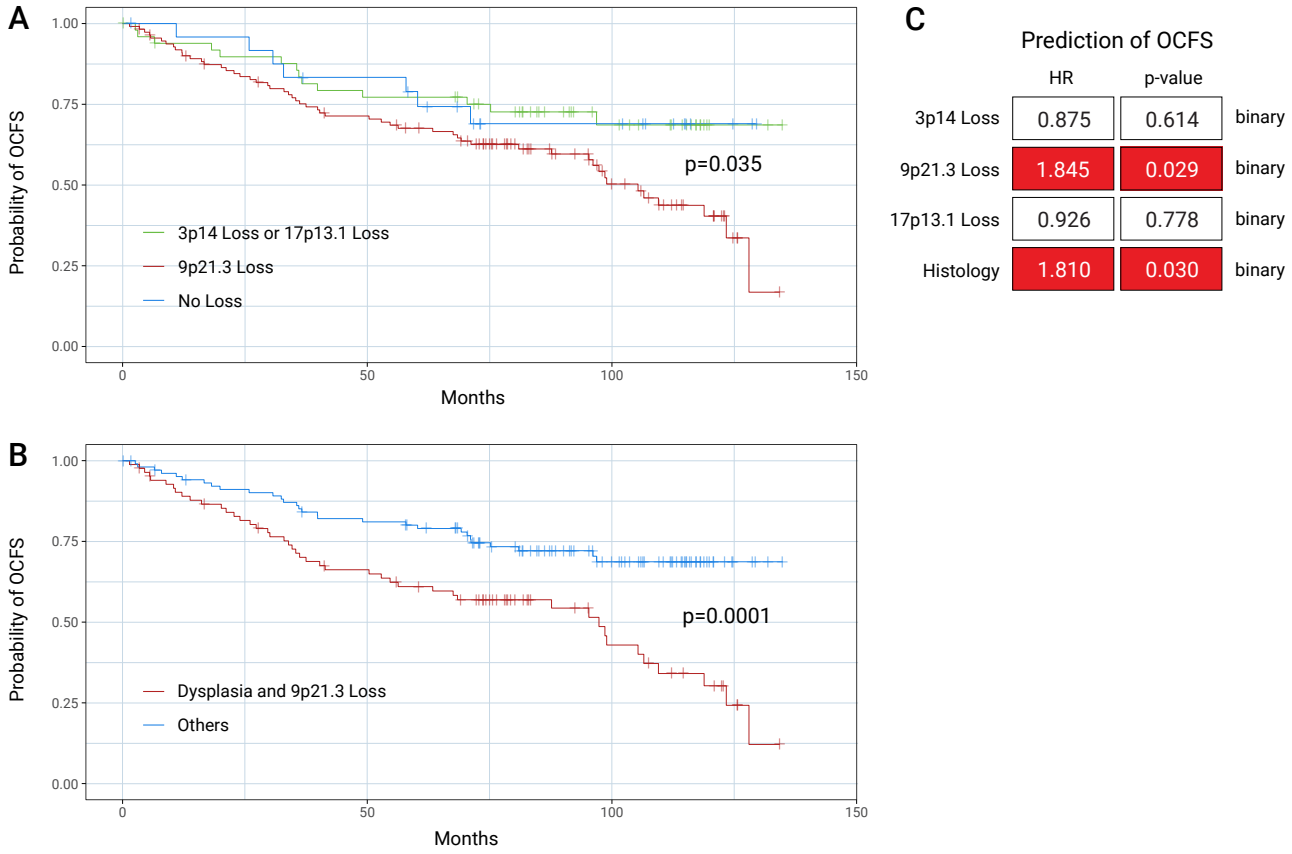

Fig. S1. Predictors of cancer risk in prospective oral precancer cohort

A) Kaplan-Meier curves of oral cancer-free survival (OCFS) by SCNAs (9p21.3, 3p14 or 17p13.1 loss, no chromosomal loss).

B) Kaplan-Meier curves of OCFS by combination of SCNA with histology status (dysplasia and 9p21.3 loss versus others).

C) Multivariable Cox-proportional hazard model for prediction of survival (OCFS).

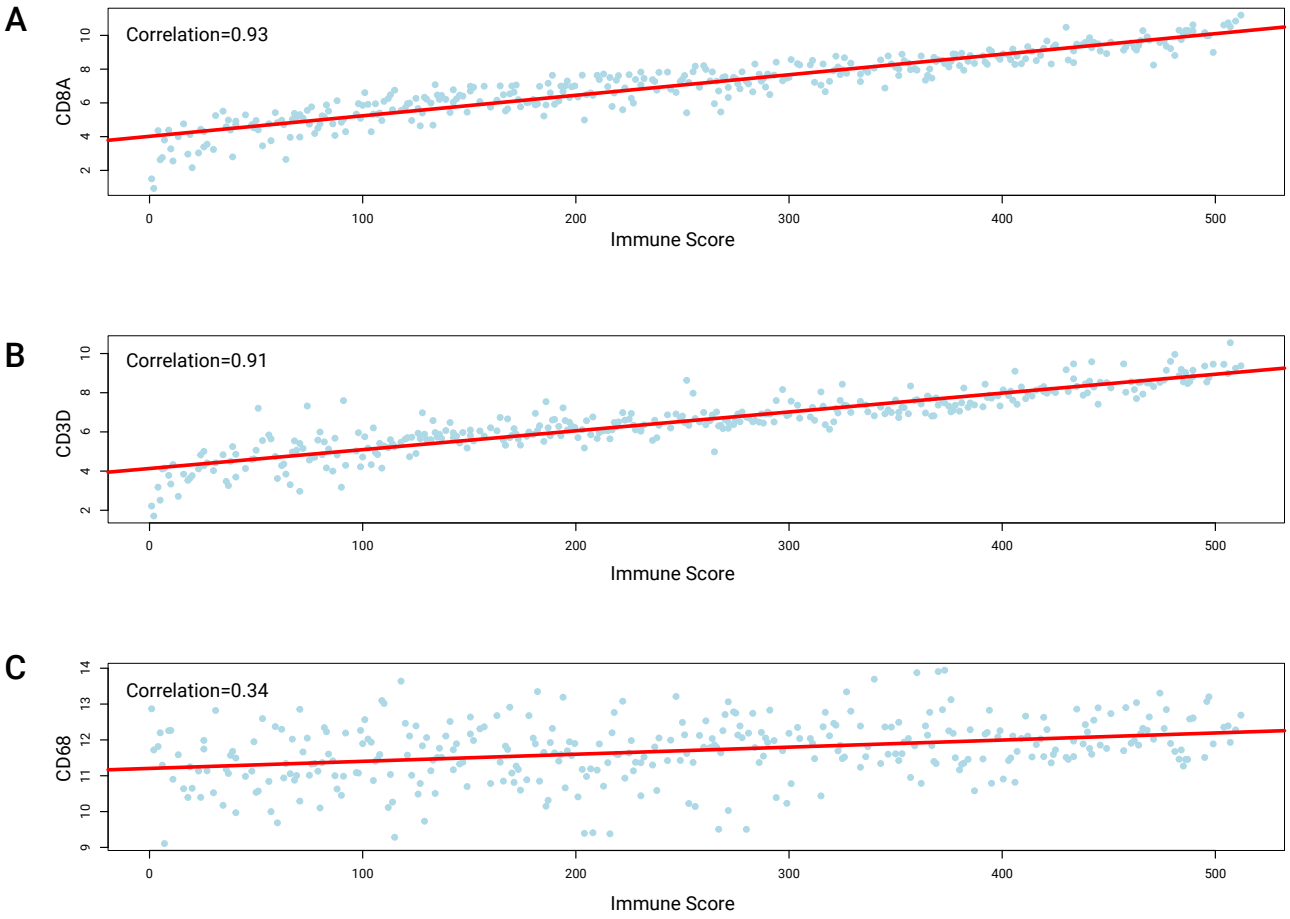

Fig. S2. CD3+ (CD3D), CD8+ (CD8A) or CD68 expression and IS in HNSC

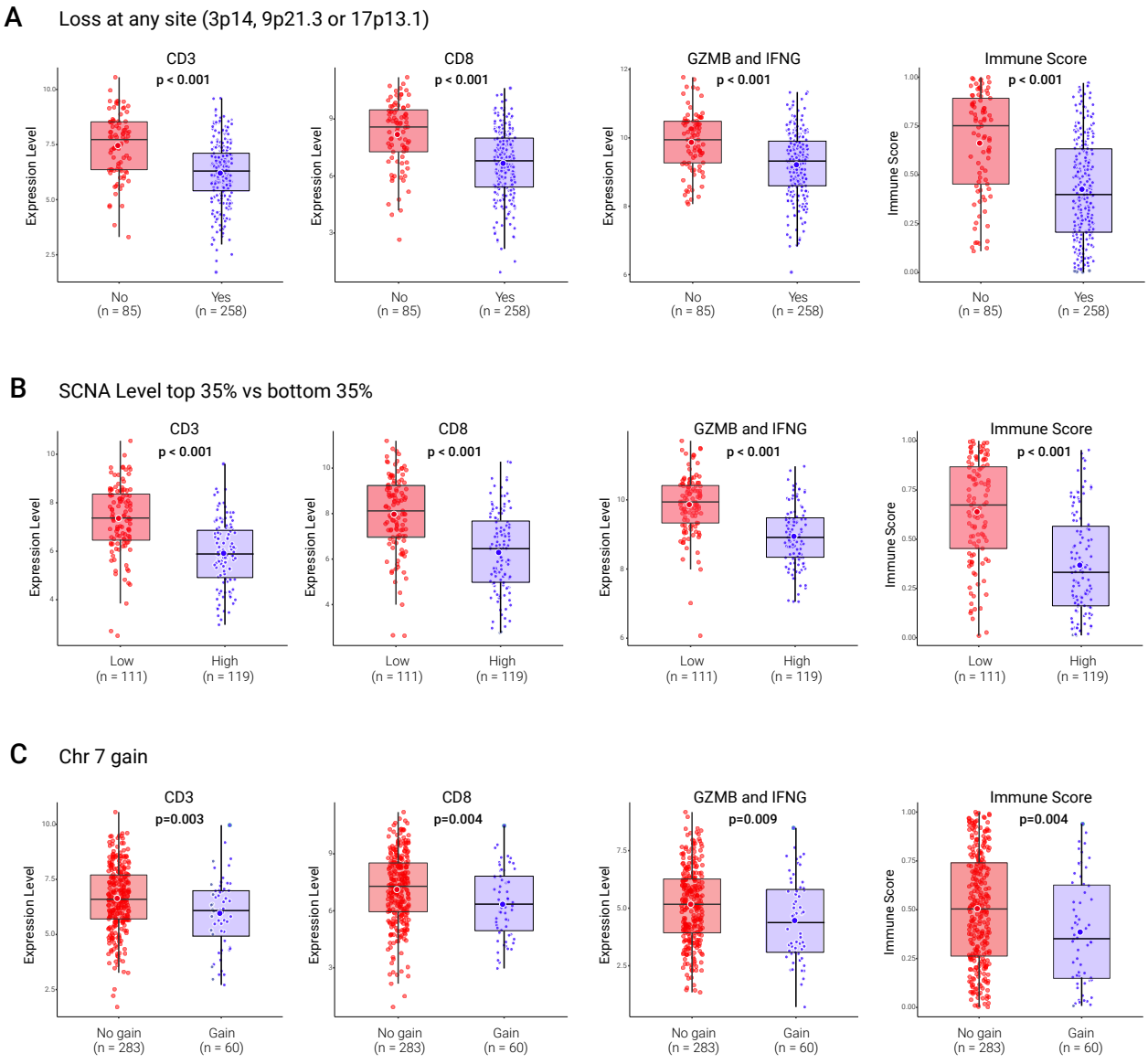

Fig. S3. SCNA associations with CD3+, CD8+, GZMB/IFNg or IS in HNSC

CD3+, CD8+ and GZMB/IFNg (average expression of the two genes) or IS associations with the presence of any loss (arm or focal) at 9p21.3, 3p14, or 17p13 (A), SCNA level (B), or chr7 gain (C).

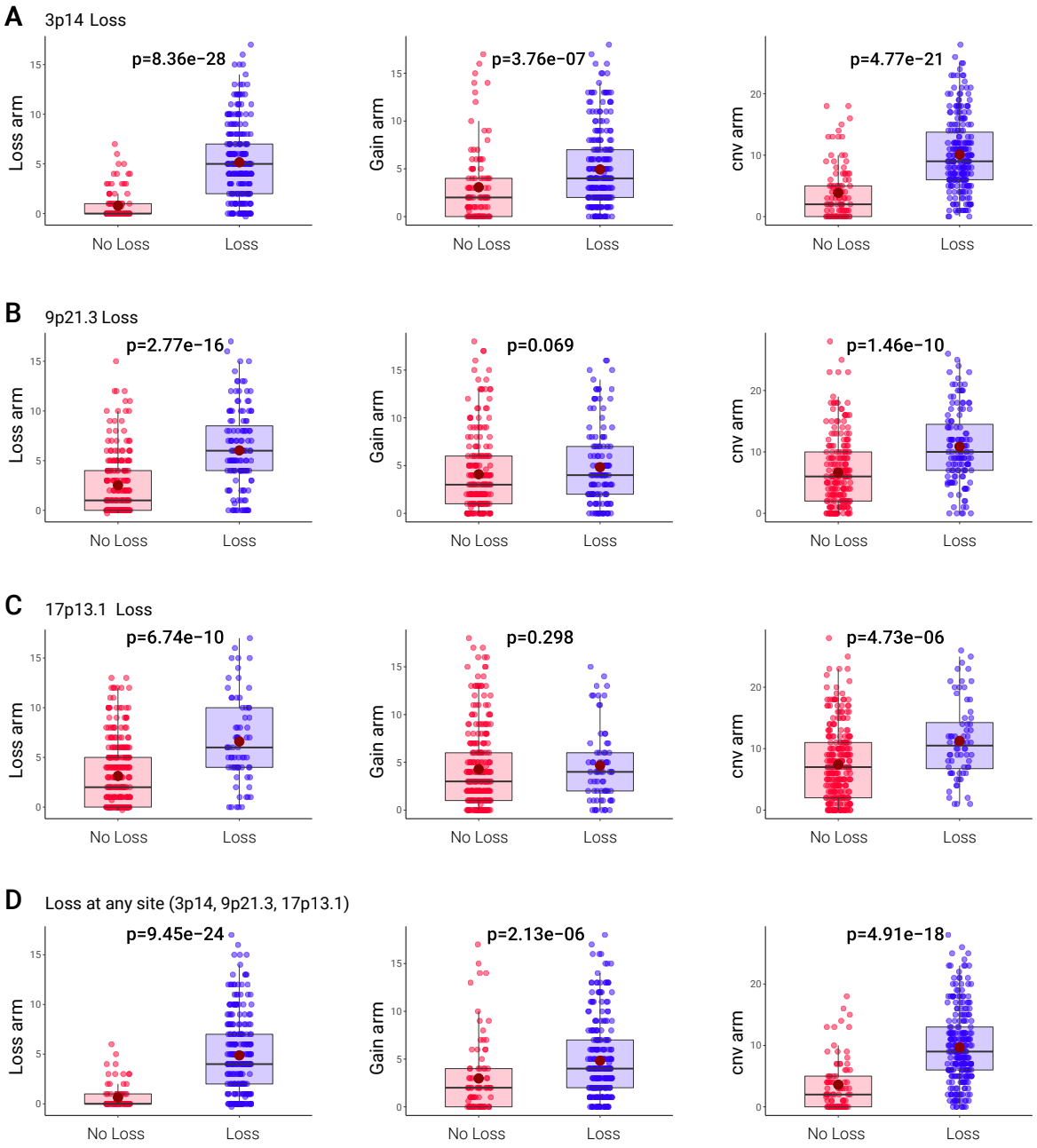

Fig. S4. 3p14, 9p21.3 or 17p.13.1 loss (arm or focal) associated with SCNA level in HNSC

A) Relationship between the number of arm loss (loss_arm), gain (gain_arm) and SCNA level (loss_arm + gain_arm, cnv_Arm) between samples with and without 3p14 loss (arm or focal).

B) Arm loss, gain and SCNA level associations with and without 9p21.3 loss.

C) Arm loss, gain and SCNA level associations with or without 17p13.1 loss.

D) Arm loss, gain and SCNA level associations with or without loss (arm or focal) at any of the three sites (3p14, 9p21.3 or 17p13.1) (p-value is from Wilcoxon test).

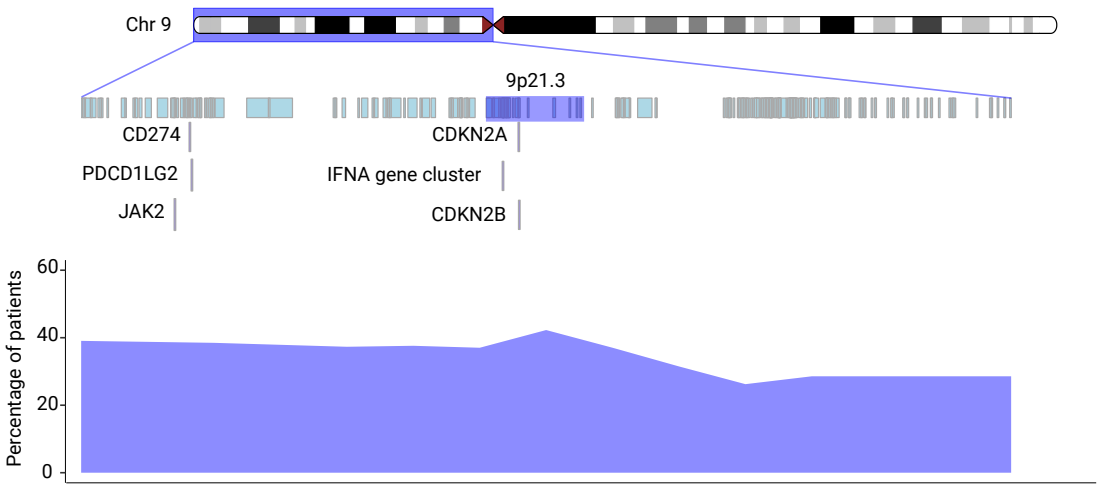

Fig. S5. Percentage of loss on arm 9p in HNSC (based on cytoband regions)

Representative genes indicated.

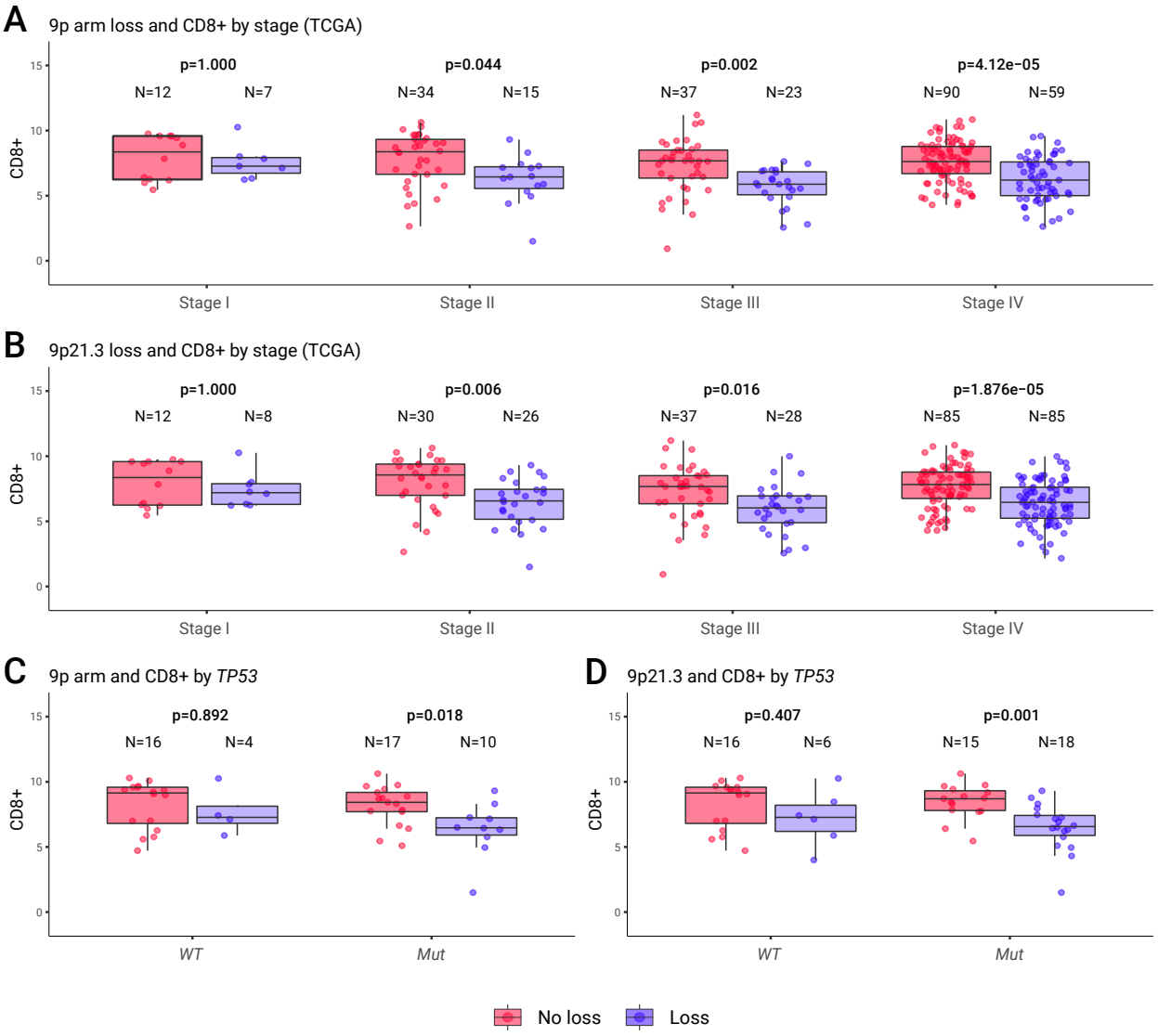

Fig. S6. Chromosome-9p loss and CD8+ T-cell associations with HNSC stage and *TP53* status

Association between CD8+ T-cell levels and 9p loss (A) and 9p21.3 loss (B), in relationship with tumor stage and *TP53* mutation status (C and D) in HPV-negative stage I or II HNSC tissue samples.

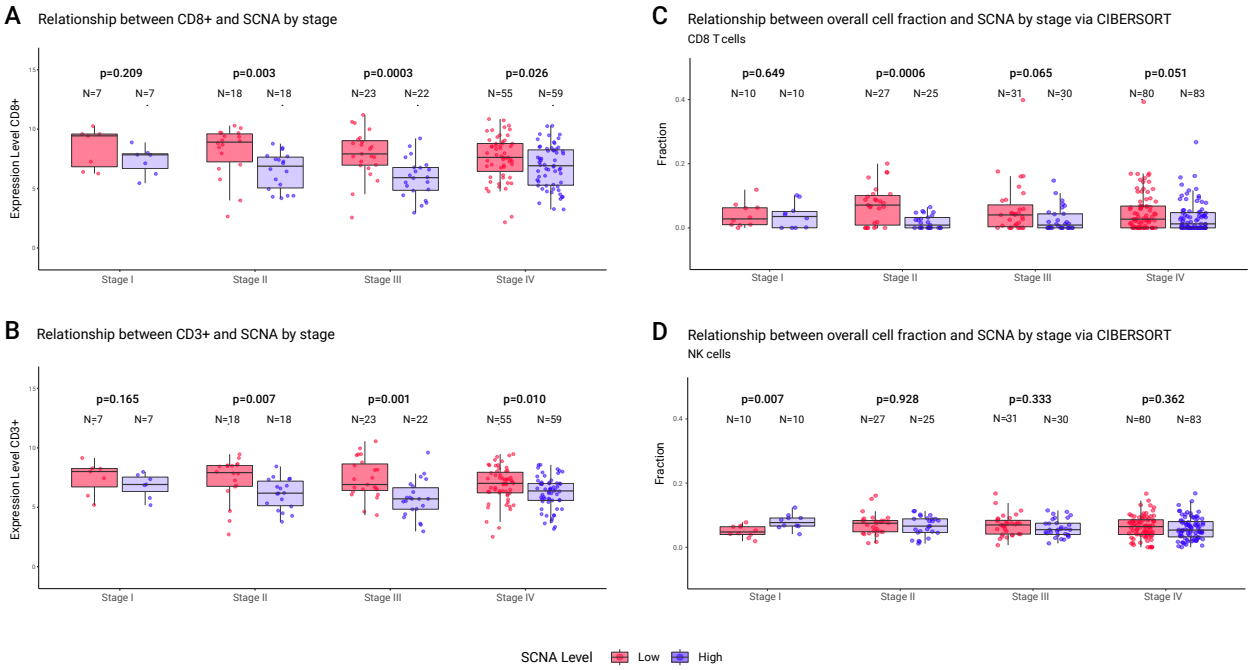

Fig. S7. SCNA level to different HNSC tumor stage

A) SCNA level and CD8+ T cells in relation to tumor stage.
B) SCNA level and CD3+ T cells in relation to tumor stage.
C) SCNA level and CD8 T cells (via CIBERSORT) in relation to tumor stage.
D) SCNA level and NK cells (via CIBERSORT) in relation to tumor stage.

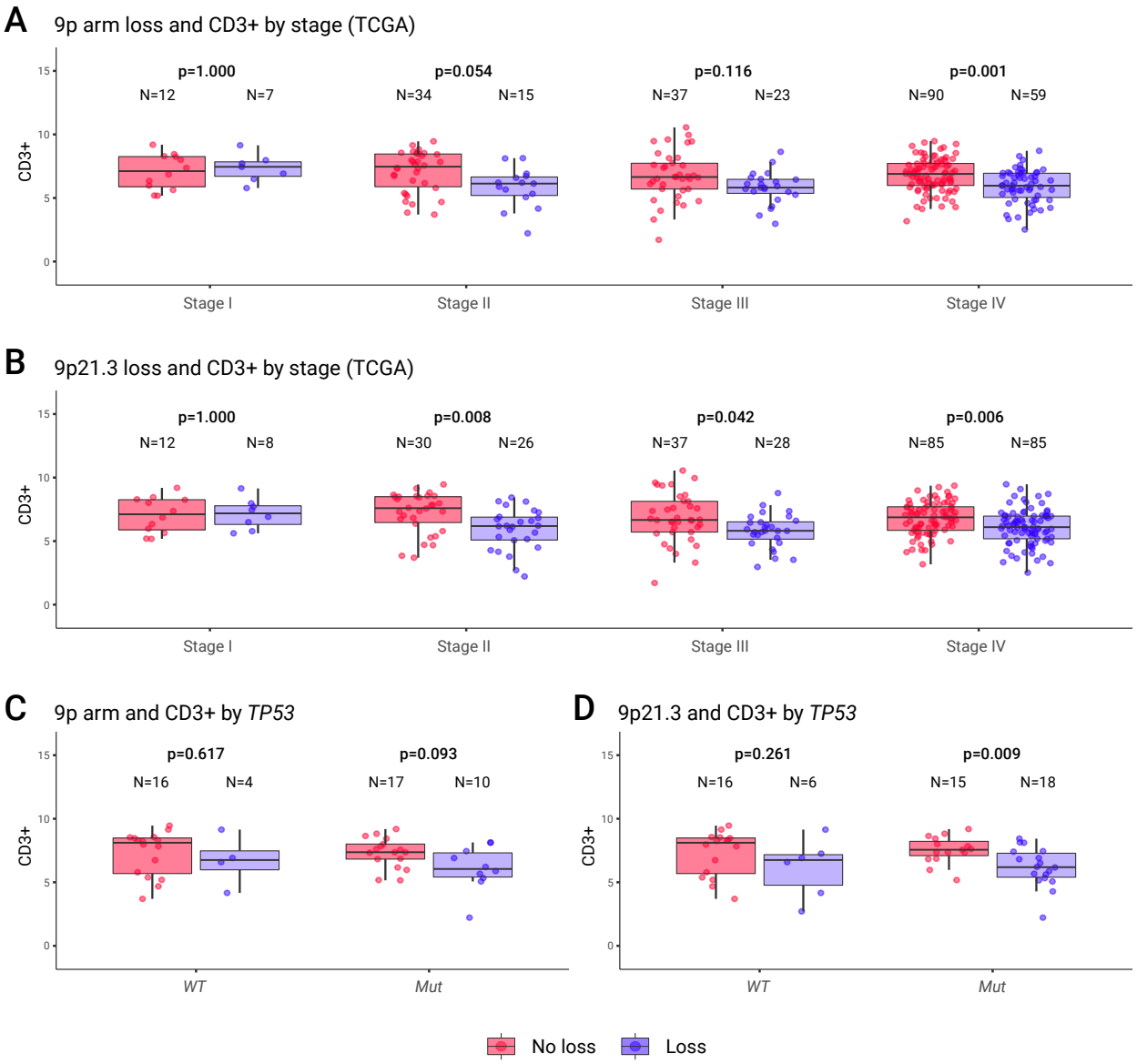

Fig. S8. Chromosome 9p loss and CD3+ T-cell associations with HNSC stage and *TP53*

Association between CD3+ T-cell levels and 9p loss (A) and 9p21.3 loss (B), in relationship with tumor stage and *TP53* mutation status (C and D) in HPV-negative HNSC tissue samples, the latter focused on stage-I and -II samples.

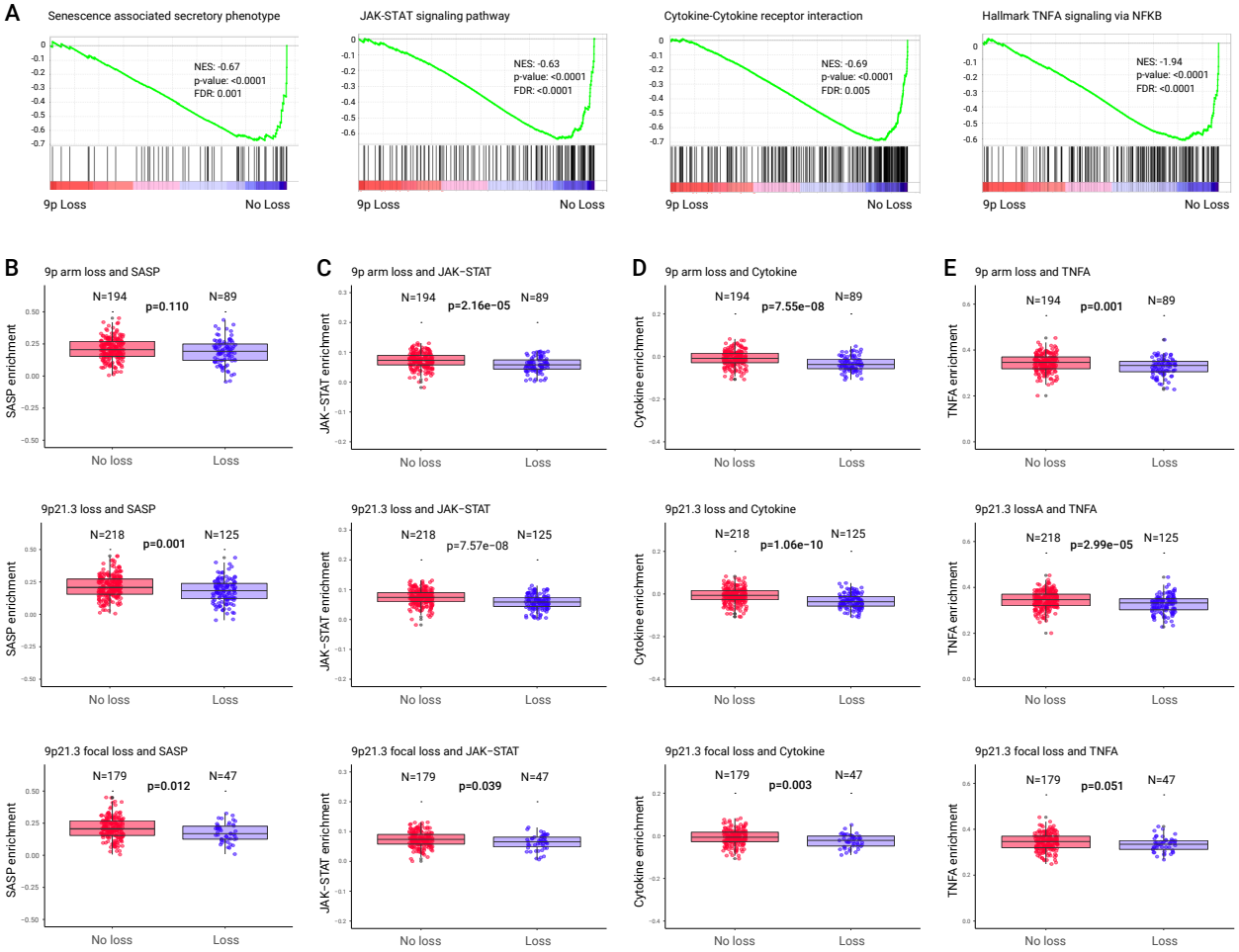

Fig. S9. SASP, JAK/STAT and Cytokine receptor and TNFA Signaling via NFkB Pathways in relationship with 9p or 9p21.3 loss in HPV-negative HNSC tumors

A) Pathway depletion from GSEA analysis of HPV-negative HNSC tumors comparing samples with and without 9p loss. GSEA plots, NES (normalized enrichment score), p-value and FDR.

B-E) Relationship between the gene expression of the SASP (B), JAK/STAT (C), Cytokine-cytokine receptor pathway (D) and TNFA Signaling via NFkB (E), and 9p arm loss, 9p21.3 loss, or 9p21.3 “focal” loss in HNSC tumors. p-value is from Wilcoxon test.

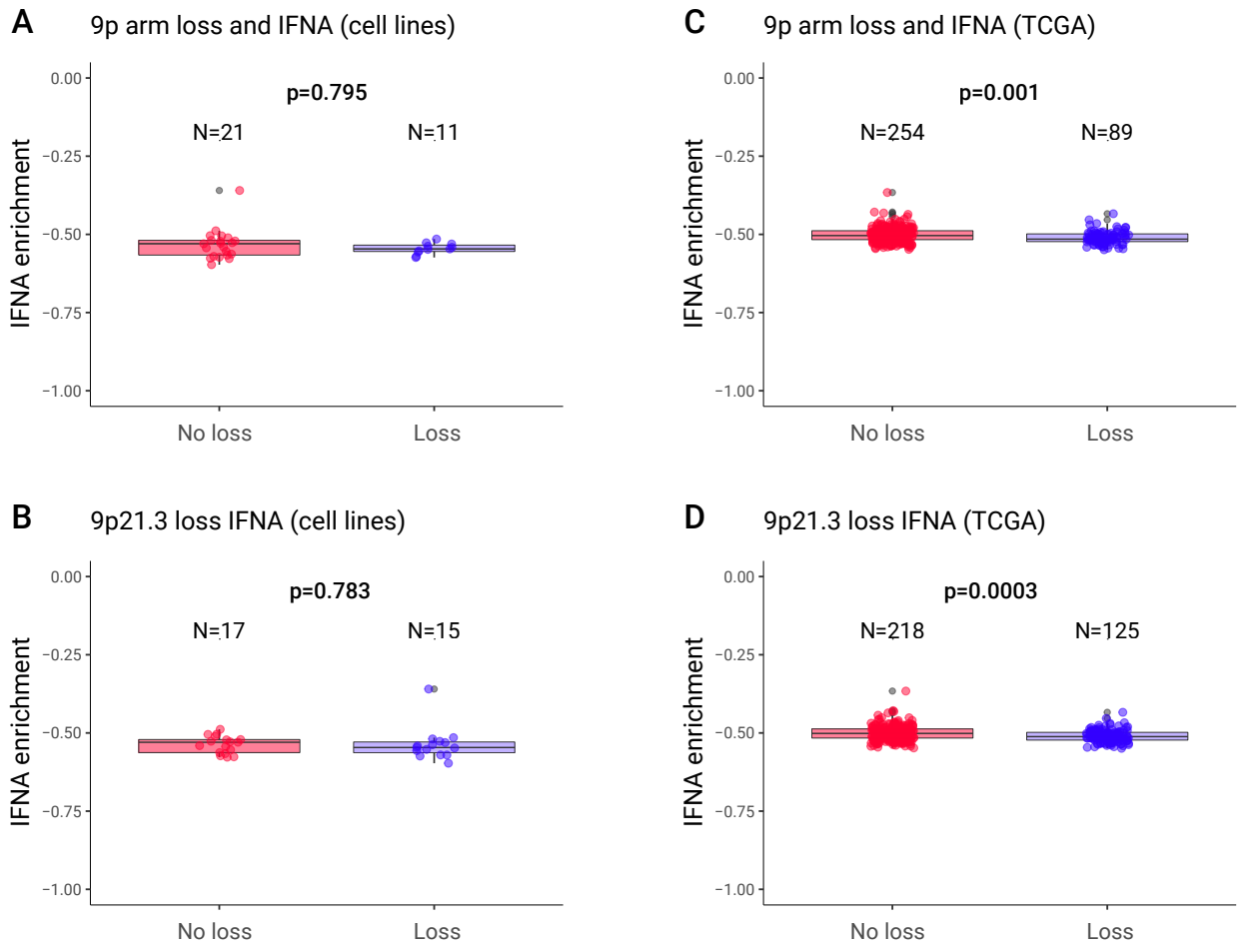

Fig. S10. IFNA gene set enrichment in HPV-negative cell lines or tumors with or without 9p or 9p21.3 loss

A-D) Relationship between *IFNα* gene set enrichment (through ssGSEA, see also Table S15 for gene set) and 9p arm or 9p21.3 loss in HPV-negative cell lines (A, B) or tumors (C, D). p-value is from Wilcoxon test.

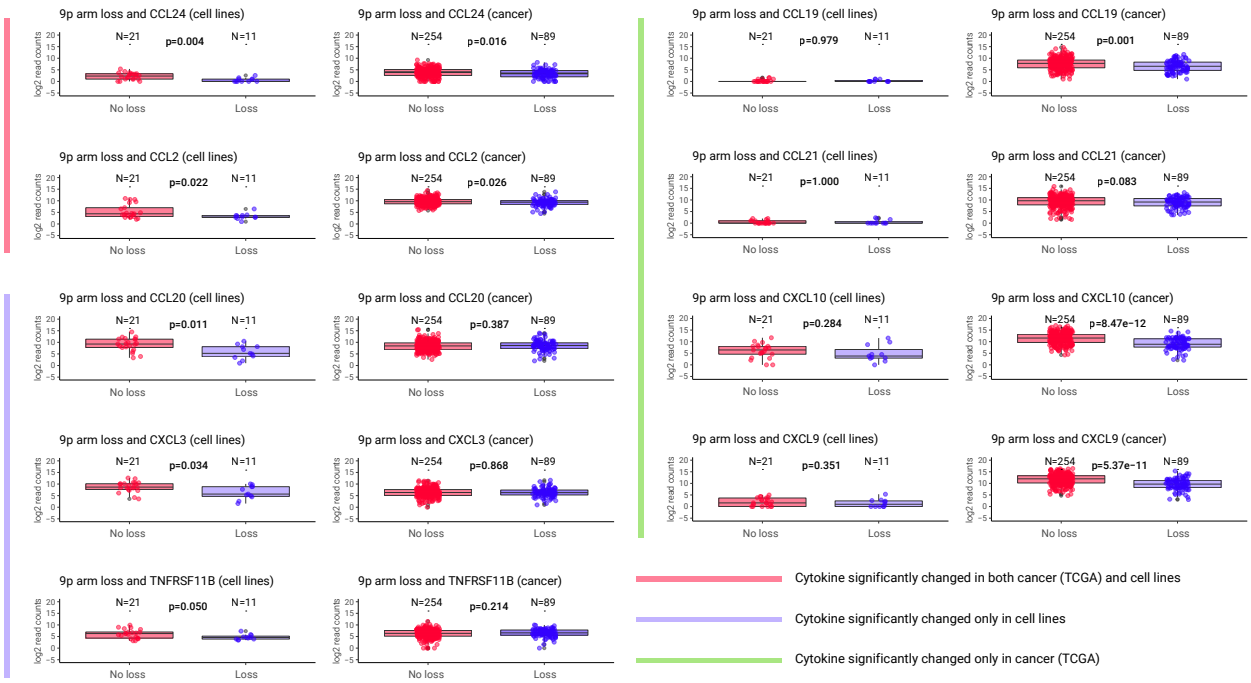

Fig. S11. Representative genes differentially expressed in tumors or cell lines with or without 9p loss

Relationship between the expression level of the indicated genes comparing HPV-negative cell lines or tumors with or without 9p arm-level. p-value is from Wilcoxon test.

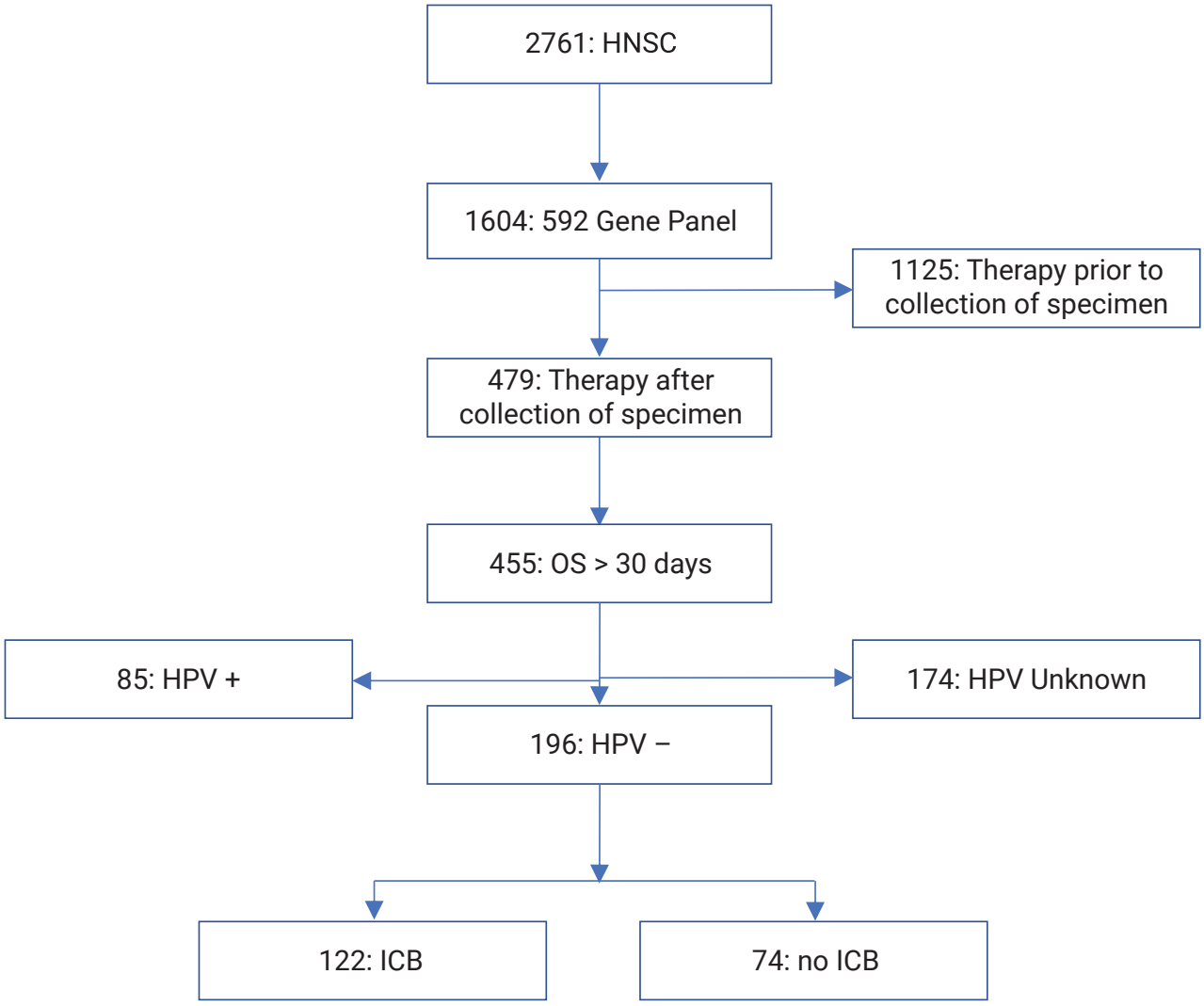

Fig. S12. Consort diagram of Real-World Evidence (RWE) cohort

Cohort of HPV-negative HNSC patients treated with nivolumab or pembrolizumab (or chemotherapy) whose tumors had been profiled using a next generation sequencing platform, as recently described (19).

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Table S1

S1A

Selected patient characteristics and markers for oral precancer cohort.*

	N=188
Prior oral cancers, N (%)	
No	69 (37%)
Yes	119 (63%)
Histology, N (%)	
Hyperplasia	68 (36%)
Mild/moderate dysplasia	107 (57%)
Severe dysplasia	13 (7%)
3p14 Loss, N (%)	
No Loss	105 (56%)
Loss	82 (43%)
9p21.3 Loss, N (%)	
No Loss	76 (40%)
Loss	112 (60%)
17p13.1 Loss, N (%)	
No Loss	62 (33%)
Loss	126 (67%)
Chromosome 7 Gain, N (%)**	
No	114 (61%)
Yes	72 (38%)
Smoking, N (%)	
Current	23(12%)
Former	71 (38%)
Alcohol, N (%)	
Light drinker	81 (43%)
Moderate, Heavy drinkers	23 (12%)
Gender, N (%)	
Male	94(50%)
Female	94(50%)

* See Results section for details

**Missing values (N=2).

S1B

Co-occurrence analysis of SCNAs in oral precancer

Event 1	Event 2	p-Value Mutual Exclusivity	p-Value Co-occurrence
3p14 Loss	9p21.3 Loss	1	1.29302E-07
3p14 Loss	17p13.1 Loss	0.9999976	1.15549E-05
9p21.3 Loss	17p13.1 Loss	0.9939178	0.01424003
3p14 Loss	Chr 7 Gain	0.9999877	4.64218E-05
9p21.3 Loss	Chr 7 Gain	0.9999911	3.62777E-05
17p13.1 Loss	Chr 7 Gain	0.9974528	0.006866455
Major risk loci	Minor risk loci	0.9991201	0.003799281

Table S2
Association between immune parameters and copy number alterations or clinical parameters in oral pre-cancer.

S2A
Distributions of CD3+, CD8+ and CD68+ by different parameters, and p-values for comparing between the two groups for each covariate using the linear mixed effect models on log-transformed data.

		Immune cell infiltrate		
Covariate	**Level**	CD3+	CD8+	CD68+
Age	No	845.53	96.25	68.64
	Yes	812.67	147.83	67.68
Gender	F	1003.17	141.89	72.06
	M	610.87	126.42	66.34
Smoking	Never	894.39	150.69	83.64
	Current+Former	958.12	134.52	56.69
Alcohol	No	1113.59	196.03	218.08
	Yes	871.02	134.52	64.61
Prior OC	No	710.11	94.98	35.59
	Yes	870.13	144.28	92.43
Histology	Hyperplasia	560.52	101.59	59.21
	Dysplasia	1004.47	144.87	80.25
Loss status	No Loss	463.75	58.54	62.07
	3p, 9p or 17p Loss	958.97	148.61	71.53
9p21.3 Loss	No	554.40	89.64	62.07
	Yes	997.63	146.26	78.70
3p14 Loss	No	639.42	92.45	66.16
	Yes	1004.47	167.77	79.98
17p13.1 Loss	No	592.04	88.30	65.19
	Yes	976.56	166.50	74.11
Chr 7 Gain	No	562.00	96.25	57.63
	Yes	1103.79	167.77	89.49

P Value
0.05-0.1
0.01-0.05
0.001-0.01
< 0.001

		N	%	p-value
Dysplasia	Both Gain and Loss	32	28.07017544	
	Either Gain or Loss	41	35.96491228	
	No gain and No Loss	41	35.96491228	4.13E-09
Others	Both Gain and Loss	3	4.615384615	
	Either Gain or Loss	13	20	
	No gain and No Loss	49	75.38461538	

	Dysplasia(N,%)	Others (N,%)	p-value
3p14 Loss	54 (45.76%)	28 (41.18%)	0.5458
3p14 No Loss	64 (54.23%)	40 (58.82%)	
9p21.3 Loss	83 (69.75%)	29 (42.65%)	0.0003
9p21.3 No Loss	36 (30.25%)	39 (57.35%)	
17p13.1 Loss	82 (68.91%)	44 (64.71%)	0.562
17p13.1 No Loss	37 (31.09%)	24 (35.29%)	

Logistic regression analysis for the prediction of dysplasia in precancer.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss	-0.9746484	-2.2547455	0.02414931	0.032199	0.377325	binary
9p21.3 Loss	1.0215396	2.6221582	0.008737487	0.017475	2.777468	binary
17p13.1 Loss	-0.2051308	-0.5260074	0.598883	0.598883	0.814541	binary
SCNA level*	1.4418026	4.6139105	3.95163E-06	1.58E-05	4.228311	continuous

*See Methods section for details

S2B
Logistic regression analysis for the prediction of the indicated parameters (CD3+, CD8+ and CD68+) in precancer data.

Top and bottom 35% of the distributions were considered.

CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	0.1511828	0.3969401	0.691412	0.691412	1.163209	binary
9p21.3 Loss	0.4679057	1.3035477	0.192388	0.384776	1.596647	binary
17p13.1 Loss	0.2853064	0.7977782	0.424999	0.566666	1.33017	binary
SCNA level*	0.5814925	2.2799512	0.022611	0.090442	1.788706	continuous

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	0.44290453	1.18237061	0.237059	0.652752	1.557224	binary
9p21.3 Loss	0.21099797	0.58984611	0.5552294	0.715384	1.23491	binary
17p13.1 Loss	0.3472222	0.98143988	0.326376	0.652752	1.415131	binary
SCNA level*	0.08726638	0.36463539	0.715384	0.715384	1.091187	continuous

CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.15710925	-0.42221049	0.672871	0.967911	0.854611	binary
9p21.3 Loss	-0.01459791	-0.04022858	0.967911	0.967911	0.985508	binary
17p13.1 Loss	-0.1139516	-0.31335467	0.754011	0.967911	0.892301	binary
SCNA level*	0.25857407	1.09017544	0.275636	0.967911	1.295082	continuous

Top and bottom 50% of the distributions were considered.

CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	0.1362396	0.3750311	0.7076373 59	0.707637	1.145956	binary
9p21.3 Loss	0.2148403	0.6039356	0.545886429	0.707637	1.239664	binary
17p13.1 Loss	0.7014885	1.9596562	0.050035987	0.137095	2.016752	binary
SCNA level*	0.4176728	1.8213907	0.068547493	0.137095	1.518424	continuous

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	0.65771287	1.8155497	0.069438475	0.138879	1.930372	binary
9p21.3 Loss	-0.24082004	-0.6659641	0.505434056	0.673912	0.785983	binary
17p13.1 Loss	0.87839163	2.4374008	0.014793273	0.059173	2.407025	binary
SCNA level*	0.08197094	0.3586816	0.719833311	0.719833	1.085424	continuous

CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.1683765	-0.4703277	0.6381209	0.638121	0.845036	binary
9p21.3 Loss	0.2233191	0.6431479	0.5201282	0.638121	1.250219	binary
17p13.1 Loss	0.2315546	0.6661556	0.5053117	0.638121	1.260558	binary
SCNA level*	0.3386527	1.5071471	0.1317729	0.527092	1.403056	continuous

Top and bottom 35% of the distributions were considered.

CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
Losses	0.142116	0.563633	0.573004	0.573004	1.15271	binary
Gains	1.10172	2.648089	0.008095	0.01619	3.009336	binary

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
Losses	-0.22933	-0.79759	0.425106	0.425106	0.795063	binary
Gains	0.767494	1.894502	0.058158	0.116317	2.15436	binary

CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
Losses	-0.17182	-0.71921	0.472014	0.472014	0.842133	binary
Gains	0.778117	1.955462	0.050529	0.101057	2.177367	binary

Top and bottom 35% of the distributions were considered.
For each copy number event, we used copy number values after standardization.

CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
D3S1234 scale	0.21953328	0.7487978	0.453979	0.605305	1.245495	continuous
D9S1748 scale	0.2712074	1.1603948	0.245888	0.491776	1.311547	continuous
D17S786 scale	-0.0248421	-0.1343925	0.893092	0.893092	0.975462	continuous
SCNA level*	0.67961724	2.6749746	0.007473	0.029894	1.973122	continuous

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
D3S1234 scale	0.005479822	0.03282545	0.973814	0.973814	1.005495	continuous
D9S1748 scale	0.04026781	0.2733655	0.973814	0.973814	1.065158	continuous
D17S786 scale	0.109223694	0.59958109	0.548786	0.973814	1.115412	continuous
SCNA level*	0.264728659	1.09420051	0.273867	0.973814	1.303077	continuous

CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
D3S1234 scale	-0.24599124	-1.3336219	0.182328	0.625797	0.781929	continuous
D9S1748 scale	0.03476175	0.2191023	0.82657	0.82657	1.035373	continuous
D17S786 scale	0.13413592	0.6920717	0.488892	0.651856	1.143548	continuous
SCNA level*	0.2406606	1.0091589	0.312898	0.625797	1.277699	continuous

Top and bottom 50% of the distributions were considered.
For each copy number event, we used copy number values after standardization.

CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
D3S1234 scale	0.16733381	0.9802777	0.326949052	0.435932	1.182149	continuous
D9S1748 scale	0.24163555	1.3845474	0.166190904	0.332382	1.27333	continuous
D17S786 scale	0.01808769	0.1167756	0.907037854	0.907038	1.018252	continuous
SCNA level*	0.56200267	2.7551111	0.005867221	0.023469	1.754182	continuous

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
D3S1234 scale	-0.05051387	-0.3242189	0.74577229	0.745772	0.950741	continuous
D9S1748 scale	0.26718611	1.4690315	0.141824225	0.283649	1.306284	continuous
D17S786 scale	0.16133591	0.9995581	0.31752439	0.423366	1.17508	continuous
SCNA level*	0.3447323	1.7258091	0.08438176	0.283649	1.411612	continuous

CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
D3S1234 scale	-0.15343402	-0.9788812	0.32763867	0.644373	0.857757	continuous
D9S1748 scale	0.07084866	0.4615937	0.64437271	0.644373	1.073419	continuous
D17S786 scale	0.0973158	0.6050776	0.54512742	0.644373	1.102208	continuous
SCNA level*	0.35188509	1.7731445	0.07620476	0.304819	1.421745	continuous

*See Methods section for details

S2C
Univariate analysis for prediction of the indicated parameters (CD3+, CD8+ and CD68+) in precancer data.

Top and bottom 35% of the distributions were considered.

Marker	**Covariate**	**p-Value from mixed effect models**	**FDR**	
CD3+	3p14 Loss	0.052027	0.0562	binary
CD3+	9p21.3 Loss	0.03378699	0.0562	binary
CD3+	17p13.1 Loss	0.05622852	0.0562	binary
CD3+	Chr 7 Gain	0.000350	0.0014	binary
CD3+	SCNA level*	0.0232512	0.056229	binary

Marker	**Covariate**	**p-Value from mixed effect models**	**FDR**	
CD8+	3p14 Loss	0.1910317	0.453	binary
CD8+	9p21.3 Loss	0.4851166	0.485	binary
CD8+	17p13.1 Loss	0.3018145	0.453	binary
CD8+	Chr 7 Gain	0.015307	0.0612	binary
CD8+	SCNA level*	0.3324104	0.415513	binary

Marker	**Covariate**	**p-Value from mixed effect models**	**FDR**	
CD68+	3p14 Loss	0.8406007	0.882834	binary
CD68+	9p21.3 Loss	0.882834153	0.882834	binary
CD68+	17p13.1 Loss	0.447982428	0.882834	binary
CD68+	Chr 7 Gain	0.039384	0.1576	binary
CD68+	SCNA level*	0.3536907	0.746637	binary

Top and bottom 50% of the distributions were considered.

Marker	**Covariate**	**p-Value from mixed effect models**	**FDR**	
CD3+	3p14 Loss	0.0722	0.0903	binary
CD3+	9p21.3 Loss	0.0375	0.0903	binary
CD3+	17p13.1 Loss	0.0903	0.0903	binary
CD3+	Chr 7 Gain	0.000415	0.00166	binary
CD3+	SCNA level*	0.01322266	0.03305665	binary

Marker	**Covariate**	**p-Value from mixed effect models**	**FDR**	
CD8+	3p14 Loss	0.2728	0.4554	binary
CD8+	9p21.3 Loss	0.3983	0.4554	binary
CD8+	17p13.1 Loss	0.4554	0.4554	binary
CD8+	Chr 7 Gain	0.024483	0.098	binary
CD8+	SCNA level*	0.1409981	0.3524952	binary

Marker	**Covariate**	**p-Value from mixed effect models**	**FDR**	
CD68+	3p14 Loss	0.719425	0.742	binary
CD68+	9p21.3 Loss	0.741700	0.742	binary
CD68+	17p13.1 Loss	0.290443	0.742	binary
CD68+	Chr 7 Gain	0.046019	0.184076	binary
CD68+	SCNA level*	0.3514733	0.5857888	binary

*See Methods section for details

S2D
Univariate analysis for oral cancer-free survival according to clinical/demographic/biomarker characteristics

Variable		**β coefficient**	**HR**	**95% CI**	**p-Value**	**p-Value for overall effect**
Age	Per year increase	-0.006018072	0.994	0.975-1.014	0.57	
Sex	Male vs Female	-0.051293294	0.95	0.602-1.500	0.83	
Smoking status	Current vs Never	-0.509160344	0.601	0.264-1.367	0.22	0.1706
	Former vs Never	-0.460449416	0.631	0.374-1.064	0.084	
Alcohol use	Yes vs No	-0.578034373	0.561	0.263-1.196	0.13	
Prior oral cancers	Yes vs No	0.208638865	1.232	0.747-2.032	0.41	
Histology	dysplasia vs hyperkeratosis and hyperplasia	0.693347161	2.0004	1.18-3.37	0.00935	
3p14 Loss	3p14 vs no loss	0.058268908	1.06	0.67-1.67	0.795	
9p21.3 Loss	9p21.3 vs no loss	0.658555736	1.932	1.16-3.20	0.0109	
17p13.1 Loss	17p13.1 vs no loss	0.009950331	1.01	0.62-1.65	0.96	
Chr 7 Gain	Increased vs Normal	0.601031892	1.824	1.151-2.889	0.01	
Minor risk loci	loss vs normal	0.4000827	1.491948	0.903-2.464	0.118144	
Major risk loci	loss vs normal	0.2939622	1.341733	0.722-2.491	0.351965	
SCNA level*	(see methods)	0.3721099	1.451	1.092-1.927	0.01	
CD3+ in total	Per 1% increase	0.148420005	1.16	0.920-1.470	0.2013	
CD8+ in total	Per 1% increase	0.009950331	1.01	0.919-1.111	0.825	
CD68+ in total	Per 1% increase	0.029558802	1.03	0.935-1.149	0.491	

Abbreviations: CI (confidence interval), HR (hazard ratio)
*See Methods section for details

S2E
Cox proportional hazards model for OCFS of the indicated parameters in precancer data.

	β coefficient	**HR**	**z value**	**Pr(>|z|)**	**lower .95**	**upper .95**
3p14 Loss	-0.133617111	0.874925	-0.50379	0.614406	0.520252	1.47139
9p21.3 Loss	0.612634713	1.8452868	2.188865	0.028607	1.066163	3.193773
17p13.1 Loss	-0.076356696	0.9264866	-0.28207	0.777889	0.545032	1.574911
Histology	0.593524174	1.8103572	2.170629	0.029959	1.059294	3.09394

	β coefficient	**HR**	**z value**	**Pr(>|z|)**	**lower .95**	**upper .95**
9p21.3 Loss	0.535616436	1.7085011	2.025726	0.042793	1.01754	2.86866
Histology	0.587779998	1.799988	2.13093	0.033095	1.048288	3.090714
Age	-0.004620357	0.9953903	-0.45948	0.645889	0.975965	1.015203
Gender	-0.095096263	0.9092854	-0.40216	0.687563	0.572037	1.445361

	β coefficient	**HR**	**z value**	**Pr(>|z|)**	**lower .95**	**upper .95**
9p21.3 Loss	0.760045587	2.1383737	1.904995	0.056781	0.978308	4.674034
Histology	0.80643399	2.2396062	2.284667	0.022332	1.121439	4.473877
Age	-0.000516333	0.9994838	-0.04384	0.965032	0.976677	1.022823
Gender	-0.125961488	0.8816488	-0.45322	0.650392	0.511357	1.520083
Alcohol	-0.759284846	0.468001	-1.92953	0.053665	0.216417	1.012049

	β coefficient	**HR**	**z value**	**Pr(>|z|)**	**lower .95**	**upper .95**
9p21.3 Loss	0.569002962	1.7665049	1.853857	0.06376	0.967957	3.22384
Histology	0.527060305	1.6939453	1.773169	0.076201	0.94599	3.033278
Age	-0.000406483	0.9995936	-0.03671	0.97072	0.978132	1.021526
Gender	-0.030780029	0.9696886	-0.12235	0.902621	0.592234	1.58771
Smoke	-0.372756708	0.6888328	-1.44804	0.147606	0.415907	1.140858

	β coefficient	**HR**	**z value**	**Pr(>|z|)**	**lower .95**	**upper .95**
3p14 Loss	-0.197395642	0.8208658	-0.73546	0.462062	0.485077	1.389101
9p21.3 Loss	0.569002962	1.7665049	1.853857	0.06376	0.967957	3.22384
17p13.1 Loss	-0.160927256	0.8511354	-0.58271	0.560088	0.495489	1.462806
Chr 7 gain	0.324129448	1.3828263	1.193495	0.232675	0.812079	2.354707
Histology	0.465208275	1.5923458	1.591627	0.111469	0.897934	2.823778

	β coefficient	**HR**	**z value**	**Pr(>|z|)**	**lower .95**	**upper .95**
3p14 Loss	-0.134513818	0.8741408	-0.50698	0.612167	0.519683	1.470363
9p21.3 Loss	0.615113474	1.8498665	2.194705	0.028185	1.068004	3.204114
17p13.1 Loss	-0.081397058	0.9218276	-0.29873	0.765146	0.540402	1.572469
Histology	0.588498634	1.801282	2.139566	0.03239	1.050641	3.088226
CD8+	0.008417722	1.0084472	0.169032	0.865772	0.914732	1.111764

	β coefficient	**HR**	**z value**	**Pr(>|z|)**	**lower .95**	**upper .95**
3p14 Loss	-0.147881233	0.8625508	-0.5581	0.576775	0.513181	1.449769
9p21.3 Loss	0.614590976	1.8489002	2.201147	0.027726	1.069661	3.195809
17p13.1 Loss	-0.16371807	0.8901442	-0.42468	0.67107	0.52025	1.523031
Histology	0.553713029	1.7397006	2.002449	0.045236	1.011817	2.991211
CD3+	0.11063891	1.1169915	0.89819	0.369084	0.877403	1.422004

	β coefficient	**HR**	**z value**	**Pr(>|z|)**	**lower .95**	**upper .95**
3p14 Loss	-0.2622711	0.7693024	-0.93855	0.347961	0.444872	1.330328
9p21.3 Loss	0.5688787	1.7662855	1.975559	0.048205	1.004501	3.105786
17p13.1 Loss	-0.1814841	0.8340315	-0.64639	0.518025	0.481056	1.446004
Histology	0.416548	1.5167168	1.380263	0.167506	0.839501	2.740235
SCNA level*	0.2206448	1.2468804	1.17913	0.238346	0.86406	1.79931

*See Methods section for details

Table S3
Association between immune parameters and copy number alterations in HPV-negative HNSC tumor samples from TCGA.
Unless otherwise specified, '9p21.3 loss', '3p14 loss' or '17p13.1 loss' refer to the presence of a loss at this region irrespective of the length of the deletion (whether the loss encompasses the entire arm or is a focal event).

S3A
Logistic Regression for the prediction of immune infiltrate parameters in HNSC tumor samples ; binary definition of loss or gain.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
Thersholded values were used to define loss and gain
purity method=Pathology

CD8+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss	-0.3447693	-0.8907451	0.373065938	0.373416	0.708384	binary
9p21.3 Loss	-1.2851364	-3.5119797	0.000444782	0.002224	0.276613	binary
17p13.1 Loss	-0.4864328	-1.0343838	0.30095679	0.373416	0.614816	binary
Chr 7 Gain	-0.4301541	-0.890093	0.373415931	0.373416	0.650409	binary
SCNA level	-0.5920483	-3.0591518	0.002219646	0.005549	0.553193	continuous

CD3+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss	-0.37547131	-0.97566585	0.3292301	0.548333	0.686965	binary
9p21.3 Loss	-1.00509409	-2.76141232	0.005755197	0.0144	0.36601	binary
17p13.1 Loss	-0.23739778	-0.50103496	0.6163465	0.77	0.788678	binary
Chr 7 Gain	-0.03966232	-0.08172355	0.9348666	0.935	0.961114	binary
SCNA level	-0.78972058	-3.96858404	7.2301E-05	0.000362	0.453972	continuous

CD68+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss	-0.2587194	-0.7062077	0.480058994	0.600074	0.77204	binary
9p21.3 Loss	-0.2818632	-0.8235714	0.410183134	0.600074	0.754377	binary
17p13.1 Loss	-1.1657164	-2.9183719	0.003518644	0.017593	0.311699	binary
Chr 7 Gain	0.1711939	0.383299	0.701498109	0.600074	1.186721	binary
SCNA level	-0.2047819	-1.1609377	0.245667231	0.600074	0.814825	continuous

Immune Score	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss	-0.34507538	-0.86645724	0.386239466	0.615915	0.708167	binary
9p21.3 Loss	-1.26049604	-3.42009729	0.000625987	0.003108	0.283514	binary
17p13.1 Loss	-0.307384375	-0.68597065	0.492731614	0.615915	0.735368	binary
Chr 7 Gain	-0.005432981	-0.01108702	0.99115402	0.991154	0.994582	binary
SCNA level	-0.64243653	-3.22878692	0.001243165	0.003108	0.526012	continuous

Top and bottom 50% of the distributions were considered.
Thersholded values were used to define loss and gain
purity method=Pathology

CD8+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss	-0.05608472	-0.17982	8.57E-01	8.57E-01	0.945459	binary
9p21.3 Loss	-1.15141152	-3.91886	8.90E-05	4.45E-04	0.31619	binary
17p13.1 Loss	-0.39575333	-1.09952	2.72E-01	4.38E-01	0.673173	binary
Chr 7 Gain	-0.37579148	-0.93555	3.50E-01	4.38E-01	0.686746	binary
SCNA level	-0.44622672	-2.90614	3.66E-03	9.15E-03	0.640039	continuous

CD3+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss	-0.1474242	-0.48175	0.62998	6.30E-01	0.862928	binary
9p21.3 Loss	-0.522495	-1.80861	0.070512	1.18E-01	0.593039	binary
17p13.1 Loss	-0.6463424	-1.81238	0.069928	1.18E-01	0.523959	binary
Chr 7 Gain	0.306699	0.782197	0.434099	5.43E-01	1.358932	binary
SCNA level	-0.6019127	-3.88873	0.000101	5.04E-04	0.547763	continuous

CD68+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss	-0.22637829	-0.74902	0.453843	5.67E-01	0.797416	binary
9p21.3 Loss	-0.56688121	-2.01169	0.044252	1.11E-01	0.567292	binary
17p13.1 Loss	-0.99408838	-2.82842	0.004678	2.34E-02	0.370061	binary
Chr 7 Gain	-0.56713279	-1.49879	0.133928	2.23E-01	0.567149	binary
SCNA level	0.06560041	0.455649	0.648643	6.49E-01	1.0678	continuous

Immune Score	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss	-0.17286705	-0.55854	5.76E-01	8.20E-01	0.841249	binary
9p21.3 Loss	-0.65912625	-2.26129	2.37E-02	5.93E-02	0.517303	binary
17p13.1 Loss	-0.0951213	-0.27352	7.84E-01	8.20E-01	0.909263	binary
Chr 7 Gain	-0.09062148	-0.22761	8.20E-01	8.20E-01	0.913363	binary
SCNA level	-0.66961008	-4.25007	2.14E-05	1.07E-04	0.511908	continuous

S3B
Logistic Regression for the prediction of immune infiltrate parameters in HNSC tumor samples ; copy number level considered as continuous variables.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
For each copy number event, we used copy number values after standardization.
purity method=Pathology

CD8+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 scale	0.58265057	2.6801579	0.007358744	0.0184	1.790779	continuous
9p21.3 scale	0.99222856	4.215259	2.49492E-05	0.000125	2.697239	continuous
17p13.1 scale	-0.10943738	-0.6095428	0.5421647	0.542	0.896338	continuous
Chr 7 scale	-0.46139138	-1.8757769	0.06068592	0.075875	0.630406	continuous
SCNA level	-0.49253233	-2.432903	0.01497831	0.025	0.611077	continuous

CD3+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 scale	0.585404427	2.990331973	0.002786744	0.006975	1.795717	continuous
9p21.3 scale	0.346477146	2.281882434	0.022496282	0.0375	1.414077	continuous
17p13.1 scale	-0.139017476	-0.833503906	0.404560596	0.405	0.870213	continuous
Chr 7 scale	-0.201879339	-0.960880649	0.336612182	0.405	0.817194	continuous
SCNA level	-0.718065287	-3.67174189	0.000240903	0.001205	0.487695	continuous

CD68+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 scale	0.13575464	0.7480921	0.45440464	0.757341	1.145401	continuous
9p21.3 scale	-0.02238652	-0.1615302	0.8716758	0.871676	0.977862	continuous
17p13.1 scale	0.459502115	3.277742	0.00104641	0.005232	1.583286	continuous
Chr 7 scale	-0.03220522	-0.2212268	0.82491586	0.871676	0.968308	continuous
SCNA level	-0.31144482	-1.7993223	0.07196772	0.179919	0.732388	continuous

Immune Score	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 scale	0.60127481	2.81955688	0.004809001	0.012023	1.824443	continuous
9p21.3 scale	0.83016497	3.69845567	0.000216915	0.001085	2.293697	continuous
17p13.1 scale	-0.17180798	-0.9493715	0.342431699	0.342432	0.842141	continuous
Chr 7 scale	-0.24660172	-1.11772355	0.263685081	0.329606	0.781452	continuous
SCNA level	-0.52226561	-2.63805838	0.008338223	0.013897	0.593175	continuous

Top and bottom 50% of the distributions were considered.
For each copy number event, we used copy number values after standardization.
purity method=Pathology

CD8+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 scale	0.34985631	2.134044	3.28E-02	5.47E-02	1.418864	continuous
9p21.3 scale	0.82481657	4.535597	5.74E-06	2.87E-05	2.281462	continuous
17p13.1 scale	-0.10815721	-0.79084	4.29E-01	4.29E-01	0.897486	continuous
Chr 7 scale	-0.37823797	-1.94636	5.16E-02	6.45E-02	0.685067	continuous
SCNA level	-0.35961597	-2.27404	2.30E-02	5.47E-02	0.697944	continuous

CD3+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 scale	0.204676166	1.395206	1.63E-01	2.72E-01	1.227128	continuous
9p21.3 scale	0.262482699	2.032184	4.21E-02	1.05E-01	1.300154	continuous
17p13.1 scale	0.122569144	1.001695	3.16E-01	3.95E-01	1.130397	continuous
Chr 7 scale	-0.05113056	-0.3558	7.22E-01	7.22E-01	0.950155	continuous
SCNA level	-0.58831966	-3.92505	8.67E-05	4.34E-04	0.55526	continuous

CD68+	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 scale	0.03913966	0.278346	0.780747	9.76E-01	1.039916	continuous
9p21.3 scale	0.002536395	0.021191	0.983093	9.83E-01	1.00254	continuous
17p13.1 scale	0.416810801	3.331234	0.000865	4.32E-03	1.517115	continuous
Chr 7 scale	-0.12939531	-0.85796	0.390916	6.52E-01	0.878627	continuous
SCNA level	-0.17825375	-1.28769	0.197854	4.95E-01	0.83673	continuous

Immune Score	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 scale	0.288776167	1.891945	5.85E-02	9.75E-02	1.334793	continuous
9p21.3 scale	0.298725705	2.253876	2.42E-02	6.05E-02	1.34814	continuous
17p13.1 scale	-0.04697644	-0.36688	7.14E-01	7.14E-01	0.95411	continuous
Chr 7 scale	-0.14672459	-0.87476	3.82E-01	4.78E-01	0.863532	continuous
SCNA level	-0.62923678	-4.05633	4.98E-05	2.49E-04	0.532998	continuous

S3C
Logistic Regression for the prediction of CD8+ in HNSC tumor samples - after separating arm-level and focal-level loss at 9p21.3
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
Distinction between tumors showing arm-only, focal-only events and a combination of both.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 Loss: ARM (N=80)	-1.7946255	-3.7209207	0.000198498	0.000992	0.16619	binary
9p21.3 Loss: FOCAL (N=40)	-0.8307357	-1.878884	0.060533996	0.10089	0.435729	binary
9p21.3 Loss: ARM+FOCAL (N=15)	-0.9678614	-1.0792076	0.280495173	0.350619	0.379895	binary
3p14 Loss	-0.2638996	-0.7115412	0.476748908	0.476749	0.768051	binary
SCNA level	-0.6360161	-3.5184969	0.000433999	0.001085	0.529397	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 Loss: ARM (N=71)	-1.6544644	-4.62302	3.78E-06	1.89E-05	0.191194	binary
9p21.3 Loss: FOCAL (N=28)	-0.8571293	-1.95051	5.11E-02	8.52E-02	0.424379	binary
9p21.3 Loss: ARM+FOCAL (N=5)	-0.6608185	-0.68471	4.94E-01	4.94E-01	0.516428	binary
3p14 Loss	-0.3029896	-0.73238	4.64E-01	4.94E-01	0.738607	binary
SCNA level	-0.5148751	-2.91332	3.58E-03	8.95E-03	0.597575	continuous

arm-level CNV at 9p<(-0.3) and focal-level CNV at 9p21.3>(-0.1)
arm-level CNV at 9p>(-0.1) and focal-level CNV at 9p21.3<(-0.3)
arm-level CNV at 9p<(-0.1) and focal-level CNV at 9p21.3>(-0.1)

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at 9p21.3.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 copy number ARM Level	1.06059759	4.0606799	4.893E-05	1.96E-04	2.888096	continuous
9p21.3 copy number FOCAL Level	0.3359024	1.6449093	0.09998852	1.00E-01	1.399202	continuous
3p14 copy number	0.42675867	2.0600627	0.03939255	5.25E-02	1.532278	continuous
SCNA level	-0.63128513	-3.4210336	0.000623836	1.25E-03	0.531908	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 copy number ARM Level	1.16020207	5.265397	1.40E-07	5.60E-07	3.190578	continuous
9p21.3 copy number FOCAL Level	0.42461898	2.407098	1.61E-02	2.15E-02	1.529008	continuous
3p14 copy number	-0.15108156	-0.82381	4.10E-01	4.10E-01	0.859778	continuous
SCNA level	-0.70403169	-4.14026	3.47E-05	6.94E-05	0.494587	continuous

S3D
Logistic Regression for the prediction of CD8+ in HNSC tumor samples - after separating arm-level and focal-level loss at 3p14.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
Distinction between tumors showing arm-only, focal-only events and a combination of both.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss: ARM Level	-0.561452	-1.3802814	0.167500007	2.23E-01	0.57038	binary
3p14 Loss: FOCAL Level	-0.6243176	-1.3481234	0.177618706	2.23E-01	0.535627	binary
3p14 Loss: ARM+FOCAL	-0.446429	-0.6587714	0.510042546	5.10E-01	0.639909	binary
9p21.3 Loss	-1.2971362	-3.6471872	0.000265127	1.33E-03	0.273313	binary
SCNA level	-0.6120982	-3.3376742	0.000844827	2.11E-03	0.542212	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss: ARM Level	-0.1881759	-0.60015	5.48E-01	8.65E-01	0.828469	binary
3p14 Loss: FOCAL Level	-0.1335462	-0.189	8.50E-01	8.50E-01	0.874987	binary
3p14 Loss: ARM+FOCAL	NA	NA	NA	NA	NA	binary
9p21.3 Loss	-1.4579229	-4.94413	7.65E-07	1.91E-06	0.232719	binary
SCNA level	-0.5927001	-3.69653	2.19E-04	3.65E-04	0.552833	continuous

arm-level CNV at 3p<(-0.3) and focal-level CNV at 3p14.2>(-0.1)
arm-level CNV at 3p>(-0.1) and focal-level CNV at 3p14.2<(-0.3)
arm-level CNV at 3p<(-0.1) and focal-level CNV at 3p14.2<(-0.1)

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at 3p14.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 copy number ARM Level	0.54393974	1.6887236	0.09127241	1.22E-01	1.722781	continuous
3p14 copy number FOCAL Level	0.51069669	1.437103	0.1506887	1.51E-01	1.666452	continuous
9p21.3 copy number	0.97727587	4.4153264	1.00858E-05	4.04E-05	2.657208	continuous
SCNA level	-0.70832969	-3.6447575	0.000267644	5.36E-04	0.492466	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 copy number ARM Level	0.07978435	0.547406	5.84E-01	7.19E-01	1.083053	continuous
3p14 copy number FOCAL Level	-0.06358822	-0.36017	7.19E-01	7.19E-01	0.938391	continuous
9p21.3 copy number	0.83252625	4.635329	3.56E-06	9.74E-06	2.29912	continuous
SCNA level	-0.72005762	-4.57039	4.87E-06	9.74E-06	0.486724	continuous

S3E
Logistic Regression for the prediction of CD8+ in HNSC tumor samples - after separating arm-level and focal-level loss at 17p13.1.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
Distinction between tumors showing arm-only, focal-only events and a combination of both.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
17p13.1 Loss: ARM Level	-0.22241012	-0.42151548	0.6733787	8.41E-01	0.800587	binary
17p13.1 Loss: FOCAL Level	0.02086566	0.0278969	0.9778139	9.78E-01	1.021085	binary
17p13.1 Loss: ARM+FOCAL	-0.83787004	-0.66037869	0.5090108	8.41E-01	0.432631	binary
9p21.3 Loss	-1.39556102	-4.08686441	4.37243E-05	1.09E-04	0.247694	binary
SCNA level	-0.72793639	-4.33573242	1.45276E-05	7.25E-05	0.482904	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
17p13.1 Loss: ARM Level	-0.1216593	-0.29825	7.66E-01	9.58E-01	0.88545	binary
17p13.1 Loss: FOCAL Level	-1.9233857	-1.61964	1.05E-01	1.75E-01	0.146111	binary
17p13.1 Loss: ARM+FOCAL	-12.4653969	-0.01412	9.89E-01	9.89E-01	3.86E-06	binary
9p21.3 Loss	-1.4376688	-4.80011	1.59E-06	7.95E-06	0.237481	binary
SCNA level	-0.6169403	-3.86454	1.11E-04	2.78E-04	0.539593	continuous

arm-level CNV at 17p<(-0.3) and focal-level CNV at 17p13.1>(-0.1)
arm-level CNV at 17p>(-0.1) and focal-level CNV at 17p13.1<(-0.3)
arm-level CNV at 17p<(-0.1) and focal-level CNV at 17p13.1<(-0.1)

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at 17p13.1.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
17p13.1 copy number ARM Level	-0.0960243	-0.5611162	0.5747183	7.67E-01	0.908442	continuous
17p13.1 copy number FOCAL Level	0.04654893	0.2821725	0.7778112	7.78E-01	1.047649	continuous
9p21.3 copy number	1.13851095	5.0338412	4.80748E-07	9.62E-07	3.122116	continuous
SCNA level	-0.86372657	-5.1930733	2.06851E-07	8.28E-07	0.421588	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
17p13.1 copy number ARM Level	-0.00029952	-0.00197	9.98E-01	9.98E-01	0.999701	continuous
17p13.1 copy number FOCAL Level	0.173890482	1.075749	2.82E-01	3.76E-01	1.189925	continuous
9p21.3 copy number	0.84933324	4.619385	3.85E-06	1.12E-05	2.338087	continuous
SCNA level	-0.71518525	-4.5409	5.60E-06	1.12E-05	0.489101	continuous

S3F
Co-occurrence analysis of immune infiltrate parameters in HPV-neg HNSC tumor samples .

Event 1	Event 2	p-Value Mutual Exclusivity	p-Value Co-occurrence	FDR
3p14 Loss	17p13.1 Loss	1	3.56E-11	7.12E-11
3p14 Loss	9p21.3 Loss	1	1.73E-26	1.04E-25
17p13.1 Loss	9p21.3 Loss	1	3.39E-08	5.09E-08
9p Arm Loss	3p Arm Loss	1	3.23E-11	7.12E-11
9p Arm Loss	17p Arm Loss	0.9999978	1.10E-05	1.32E-05
9p Arm Loss	17p Arm Loss	0.9993966	1.86E-03	0.00186
3p14 Loss	Chr 7 Gain	0.7080193	4.13E-01	4.13E-01
17p13.1 Loss	Chr 7 Gain	0.971026	6.72E-02	2.02E-01
9p21.3 Loss	Chr 7 Gain	0.8313875	2.66E-01	3.99E-01

S3G
Logistic Regression for the prediction of CD3+ in HNSC tumor samples - after separating arm-level and focal-level loss at 9p21.3.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
Distinction between tumors showing arm-only, focal-only events and a combination of both.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 Loss: ARM (N=80)	-1.5677906	-3.3393469	0.000839756	2.10E-03	0.208505	binary
9p21.3 Loss: FOCAL (N=40)	-0.7797718	-1.7197486	0.08547816	1.43E-01	0.458511	binary
9p21.3 Loss: ARM+FOCAL (N=15)	0.3383003	0.4147073	0.6783562	6.78E-01	1.402562	binary
3p14 Loss	-0.2852583	-0.7569833	0.4490599	5.61E-01	0.75182	binary
SCNA level	-0.797484	-4.2748091	1.91301E-05	9.55E-05	0.450461	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 Loss: ARM (N=71)	-1.5528201	-4.27569	1.91E-05	9.55E-05	0.21165	binary
9p21.3 Loss: FOCAL (N=28)	-0.76408	-1.66962	9.50E-02	1.58E-01	0.465762	binary
9p21.3 Loss: ARM+FOCAL (N=5)	0.2669457	0.315535	7.52E-01	7.52E-01	1.30597	binary
3p14 Loss	-0.1651058	-0.39862	6.90E-01	7.52E-01	0.847804	binary
SCNA level	-0.7100009	-3.9213	8.81E-05	2.20E-04	0.491644	continuous

arm-level CNV at 9p<(-0.3) and focal-level CNV at 9p21.3>(-0.1)
arm-level CNV at 9p>(-0.1) and focal-level CNV at 9p21.3<(-0.3)
arm-level CNV at 9p<(-0.1) and focal-level CNV at 9p21.3>(-0.1)

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at 9p21.3.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 copy number ARM Level	0.71820283	3.0858467	0.002029734	4.06E-03	2.050744	continuous
9p21.3 copy number FOCAL Level	-0.04737708	-0.3019286	0.7627065	7.63E-01	0.953728	continuous
3p14 copy number	0.40273039	2.0267695	0.04268599	5.69E-02	1.495904	continuous
SCNA level	-0.77815811	-4.1645373	3.11985E-05	1.25E-04	0.459251	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 copy number ARM Level	0.959183	4.6677	3.05E-06	6.10E-06	2.609564	continuous
9p21.3 copy number FOCAL Level	0.12915329	0.902566	3.67E-01	3.71E-01	1.137865	continuous
3p14 copy number	-0.15975622	-0.8943	3.71E-01	3.71E-01	0.852352	continuous
SCNA level	-0.82807159	-4.89393	9.88E-07	3.95E-06	0.436891	continuous

S3H
Logistic Regression for the prediction of CD3+ in HNSC tumor samples - after separating arm-level and focal-level loss at 3p14.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
Distinction between tumors showing arm-only, focal-only events and a combination of both.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss: ARM Level	-0.3981015	-0.9607047	0.336700663	0.42272	0.671594	binary
3p14 Loss: FOCAL Level	-0.2849575	-0.6095738	0.542144176	0.542144	0.752046	binary
3p14 Loss: ARM+FOCAL	-0.6836007	-0.9577758	0.338175841	0.42272	0.504796	binary
9p21.3 Loss	-1.0442005	-2.952754	0.003149528	0.007874	0.351973	binary
SCNA level	-0.8093191	-4.3246247	1.52792E-05	7.64E-05	0.445161	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss: ARM Level	-0.12487	-0.399	0.6896	0.862	0.882612	binary
3p14 Loss: FOCAL Level	0.07095	0.095	0.9244	0.9244	1.073528	binary
3p14 Loss: ARM+FOCAL	NA	NA	NA	NA	NA	binary
9p21.3 Loss	-1.28411	-4.344	0.000014	2.33E-05	0.276897	binary
SCNA level	-0.7449	-4.531	5.86E-06	1.47E-05	0.474782	continuous

arm-level CNV at 3p<(-0.3) and focal-level CNV at 3p14.2>(-0.1)
arm-level CNV at 3p>(-0.1) and focal-level CNV at 3p14.2<(-0.3)
arm-level CNV at 3p<(-0.1) and focal-level CNV at 3p14.2<(-0.1)

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at 3p14.
purity method=Pathology

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 copy number ARM Level	0.6263493	2.16924798	0.030063863	0.040085	1.870768	continuous
3p14 copy number FOCAL Level	0.5458438	1.76076504	0.07827818	0.078278	1.726064	continuous
9p21.3 copy number	0.3494518	2.36183869	0.018184553	0.036369	1.41829	continuous

purity method=ABSOLUTE

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 copy number ARM Level	0.08262258	0.56091	0.574859	0.574859	1.086132	continuous
3p14 copy number FOCAL Level	-0.12590309	-0.61193	0.540586	0.574859	0.8817	continuous
9p21.3 copy number	0.47391418	3.265069	0.0011094	0.002189	1.606269	continuous

SCNA level	-0.8460887	-4.45969086	8.2078E-06	3.28E-05	0.42909	continuous	SCNA level	-0.83695332	-5.31712	1.05E-07	4.22E-07	0.433028	continuous		

S3I

Logistic Regression for the prediction of CD3+ in HNSC tumor samples - after separating arm-level and focal-level loss at 17p13.1.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
Distinction between tumors showing arm-only, focal-only events and a combination of both.

purity method=Pathology							**purity method=ABSOLUTE**							
	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**			**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**		
17p13.1 Loss: ARM Level	-0.09798037	-0.1865234	0.852034337	0.852034	0.906667	binary	17p13.1 Loss: ARM Level	-0.1595094	-0.37602	0.7069	0.883626	0.852562	binary	arm-level CNV at 17p<(-0.3) and focal-level CNV at 17p13.1>(-0.1)
17p13.1 Loss: FOCAL Level	0.48513895	0.6317367	0.527558961	0.659449	1.624401	binary	17p13.1 Loss: FOCAL Level	-1.3259309	-1.10586	0.268785	0.447976	0.265556	binary	arm-level CNV at 17p>(-0.1) and focal-level CNV at 17p13.1<(-0.3)
17p13.1 Loss: ARM+FOCAL	-0.89676157	-0.7040811	0.481382247	0.659449	0.407888	binary	17p13.1 Loss: ARM+FOCAL	-12.2703263	-0.0139	0.98891	0.98891	4.69E-06	binary	arm-level CNV at 17p<(-0.1) and focal-level CNV at 17p13.1<(-0.1)
9p21.3 Loss	-1.16468486	-3.4488245	0.000563032	0.001408	0.312021	binary	9p21.3 Loss	-1.2395867	-4.12858	3.65E-05	9.13E-05	0.289504	binary	
SCNA level	-0.89146921	-5.1170008	3.10432E-07	1.55E-06	0.410053	continuous	SCNA level	-0.7441085	-4.57391	4.79E-06	2.39E-05	0.475158	continuous	

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at 17p13.1.

purity method=Pathology							**purity method=ABSOLUTE**						
	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**			**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
17p13.1 copy number ARM Level	-0.05727179	-0.3582032	0.720191218	0.720191	0.944337	continuous	17p13.1 copy number ARM Level	-0.02483379	-0.16073	0.872307	0.872307	0.975472	continuous
17p13.1 copy number FOCAL Level	-0.05792048	-0.3840557	0.700937135	0.720191	0.943725	continuous	17p13.1 copy number FOCAL Level	0.053706	0.356074	0.721785	0.872307	1.055174	continuous
9p21.3 copy number	0.4759906	3.062351	0.002196058	0.004392	1.609511	continuous	9p21.3 copy number	0.48754616	3.277743	0.001046	0.002093	1.628316	continuous
SCNA level	-1.03103735	-6.1175928	9.49995E-10	3.80E-09	0.356637	continuous	SCNA level	-0.8348067	-5.303	1.14E-07	4.56E-07	0.433958	continuous

S3J

Logistic Regression for the prediction of immune infiltrate parameters in HNSC tumor samples with additional clinical parameters binary definition of loss or gain.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
purity method=Pathology

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.33144901	-0.838926	0.40151084	0.533252	0.717883	binary
9p21.3 Loss	-1.29587687	-3.5009815	0.000463548	0.003708	0.273658	binary
17p13.1 Loss	-0.45484819	-0.9479051	0.343177767	0.533252	0.634544	binary
Chr 7 Gain	-0.37512998	-0.7783894	0.436339505	0.533252	0.6872	binary
SCNA level	-0.57075049	-2.9430029	0.003250453	0.013002	0.565101	continuous
AGE	0.02606945	2.0365171	0.041698459	0.111196	1.026412	continuous
Gender	-0.25809749	-0.7280298	0.46659535	0.533252	0.77252	binary
Clinical stage	0.0335191	0.2782435	0.780825466	0.780826	1.034087	category

CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.36617866	-0.93166067	0.351511918	0.562419	0.693379	binary
9p21.3 Loss	-1.00344783	-2.72811095	0.006369818	0.025479	0.366613	binary
17p13.1 Loss	-0.2396997	-0.4987703	0.617941212	0.823922	0.786864	binary
Chr 7 Gain	-0.06999595	-0.14320649	0.886127108	0.886127	0.932398	binary
SCNA level	-0.75188504	-3.75355113	0.000174347	0.001395	0.471477	continuous
AGE	0.01600412	1.26227123	0.206851207	0.536613	1.016133	continuous
Gender	-0.06097764	-0.17219624	0.863283257	0.886127	0.940844	binary
Clinical stage	-0.13334063	-1.10697146	0.268306266	0.536613	0.875167	category

CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.24179217	-0.6543686	0.512874342	0.786676	0.785219	binary
9p21.3 Loss	-0.28685952	-0.8337119	0.404443354	0.786676	0.750617	binary
17p13.1 Loss	-1.17395047	-2.919595	0.003504866	0.028039	0.309143	binary
Chr 7 Gain	0.1807684	0.4011071	0.688341305	0.786676	1.198138	binary
SCNA level	-0.20111753	-1.1357922	0.256043535	0.786676	0.817816	continuous
AGE	-0.00240078	-0.2118004	0.832262791	0.832263	0.997602	continuous
Gender	-0.17325587	-0.5395681	0.589494906	0.786676	0.840922	binary
Clinical stage	0.04163584	0.401676	0.687922468	0.786676	1.042515	category

9p21.3(arm/focal) analysis	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
9p21.3 Loss: ARM (N=80)	-1.741439	-3.5700877	0.000356862	0.002632	0.175268	binary
9p21.3 Loss: FOCAL (N=40)	-0.87064347	-1.9313234	0.05344307	0.118765	0.418682	binary
9p21.3 Loss: ARM+FOCAL (N=15)	-1.02994913	-1.1473106	0.251253258	0.402005	0.357025	binary
3p14 Loss	-0.26166417	-0.6892848	0.490644073	0.560736	0.769769	binary
SCNA level	-0.61670529	-3.4064643	0.000658102	0.002632	0.53972	continuous
AGE	0.02413191	1.8853491	0.059382717	0.118765	1.024425	continuous
Gender	-0.26105556	-0.7388609	0.459991496	0.560736	0.770238	binary
Clinical stage	0.04964305	0.4075561	0.683599598	0.6836	1.050896	category

S3K

5-fold cross validation of Logistic Regression for the prediction of immune infiltrate parameters in HNSC tumor samples with extra clinical information; binary definition of loss or gain.
Top and bottom 35% of the distributions were considered.
purity method=Pathology

CD8+(Accuracy=0.7)	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.3448	-0.891	0.373066	0.373416	0.708362	binary
9p21.3 Loss	-1.2851	-3.512	0.000445	0.002225	0.276823	binary
17p13.1 Loss	-0.4864	-1.034	0.300957	0.373416	0.614836	binary
Chr 7 Gain	-0.4302	-0.89	0.373416	0.373416	0.650379	binary
SCNA level	-0.592	-3.059	0.00222	0.00555	0.55322	continuous

CD3+(Accuracy=0.7)	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.37547	-0.976	0.32923	0.548717	0.686966	binary
9p21.3 Loss	-1.00509	-2.761	0.00576	0.0144	0.366012	binary
17p13.1 Loss	-0.2374	-0.501	0.61635	0.770438	0.788676	binary
Chr 7 Gain	-0.03966	-0.082	0.93487	0.93487	0.961116	binary
SCNA level	-0.78972	-3.969	7.23E-05	0.000362	0.453972	continuous

CD68+(Accuracy=0.61)	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.2587	-0.706	0.48006	0.600075	0.772055	binary
9p21.3 Loss	-0.2819	-0.824	0.41018	0.600075	0.754349	binary
17p13.1 Loss	-1.1657	-2.918	0.00352	0.0176	0.311704	binary
Chr 7 Gain	0.1712	0.383	0.7015	0.7015	1.186728	binary
SCNA level	-0.2048	-1.161	0.24567	0.600075	0.81481	continuous

9p21.3(arm/focal) analysis(Accuracy=0.69)	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**		
9p21.3 Loss: ARM (N=80)	1.7946	3.721	0.000198	0.00099	6.017067	binary	arm-level CNV at 9p<(-0.3) and focal-level CNV at 9p21.3>(-0.1)
9p21.3 Loss: FOCAL (N=40)	0.8307	1.877	0.060534	0.10089	2.294925	binary	arm-level CNV at 9p>(-0.1) and focal-level CNV at 9p21.3<(-0.3)
9p21.3 Loss: ARM+FOCAL (N=15)	0.9679	1.079	0.280495	0.350619	2.632411	binary	arm-level CNV at 9p<(-0.1) and focal-level CNV at 9p21.3<(-0.1)
3p14 Loss	0.2639	0.712	0.476749	0.476749	1.301998	binary	
SCNA level	0.636	3.518	0.000434	0.001085	1.88891	continuous	

S3L

Logistic Regression for the prediction of CD8+ in HNSC tumor samples, binary definition of loss or gain.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
purity method=Pathology

CDKN2A	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**		
CDKN2A Loss: ARM (N=63)	-1.756594188	-3.285028075	0.001019722	0.002549	0.172632	binary	arm-level CNV at 9p<(-0.3) and focal-level CNV at CDKN2A>(-0.1)
CDKN2A Loss: FOCAL (N=92)	-0.396768835	-1.132543224	0.257406123	0.257406	0.672489	binary	arm-level CNV at 9p>(-0.1) and focal-level CNV at CDKN2A<(-0.3)
CDKN2A Loss: ARM+FOCAL (N=38)	-1.427605934	-2.652004462	0.008001548	0.013336	0.239883	binary	arm-level CNV at 9p<(-0.1) and focal-level CNV at CDKN2A<(-0.1)
3p14 Loss	-0.412195349	-1.147432661	0.251202849	0.257406	0.662195	binary	
SCNA level	-0.658335994	-3.59589876	0.000323274	0.001616	0.517712	continuous	

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at CDKN2A.

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
CDKN2A copy number ARM Level	1.140295125	4.247551683	2.16E-05	8.64E-05	3.127691	continuous
CDKN2A copy number FOCAL Level	0.339589154	1.670320658	0.094855938	0.094856	1.40437	continuous
3p14 copy number	0.37892446	1.823578262	0.068215855	0.090954	1.460713	continuous
SCNA level	-0.683612306	-3.621103705	0.000293349	0.000587	0.50479	continuous

IFNA	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
IFNA Loss: ARM (N=83)	-1.691730054	-3.558143309	0.000373486	0.000934	0.184201	binary	arm-level CNV at 9p<(-0.3) and focal-level CNV at IFNA>(-0.1)
IFNA Loss: FOCAL (N=33)	-0.684879942	-1.45913904	0.144526843	0.240878	0.504151	binary	arm-level CNV at 9p>(-0.1) and focal-level CNV at IFNA<(-0.3)
IFNA Loss: ARM+FOCAL (N=10)	-0.758621701	-0.826193991	0.408694056	0.408694	0.468311	binary	arm-level CNV at 9p<(-0.1) and focal-level CNV at IFNA<(-0.1)
3p14 Loss	-0.315036903	-0.858084936	0.390845565	0.408694	0.729762	binary	
SCNA level	-0.662129346	-3.669267915	0.000243246	0.000934	0.515752	continuous	

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at IFNA.

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
IFNA copy number ARM Level	1.100016841	4.41511935	1.01E-05	4.04E-05	3.004217	continuous
IFNA copy number FOCAL Level	0.552584578	2.280004547	0.022607419	0.030143	1.737739	continuous
3p14 copy number	0.396618959	1.900186215	0.057408687	0.057409	1.486789	continuous
SCNA level	-0.664071281	-3.544020328	0.000394075	0.000788	0.514751	continuous

CD274	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
CD274 Loss: ARM (N=85)	-1.756831505	-3.747830094	0.000178371	0.000745	0.172591	binary	arm-level CNV at 9p<(-0.3) and focal-level CNV at CD274>(-0.1)
CD274 Loss: FOCAL (N=12)	-0.760846778	-1.02735452	0.304253559	0.507089	0.467364	binary	arm-level CNV at 9p>(-0.1) and focal-level CNV at CD274<(-0.3)
CD274 Loss: ARM+FOCAL (N=6)	-0.63491014	-0.457723156	0.647151349	0.647151	0.529983	binary	arm-level CNV at 9p<(-0.1) and focal-level CNV at CD274<(-0.1)
3p14 Loss	-0.28123272	-0.764622258	0.444496511	0.555621	0.754849	binary	
SCNA level	-0.655822217	-3.617201126	0.000297806	0.000745	0.519015	continuous	

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at CD274.

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
CD274 copy number ARM Level	1.124493484	4.202921778	2.63E-05	0.000105	3.078657	continuous
CD274 copy number FOCAL Level	0.55635372	3.28521673	0.00101804	0.001359	1.744301	continuous
3p14 copy number	0.435013283	2.051879366	0.040181388	0.040181	1.544984	continuous
SCNA level	-0.697384953	-3.625273017	0.000288656	0.000577	0.497886	continuous

JAK2	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
JAK2 Loss: ARM (N=87)	-1.750822646	-3.728186035	0.000192863	0.000604	0.173631	binary	arm-level CNV at 9p<(-0.3) and focal-level CNV at JAK2>(-0.1)
JAK2 Loss: FOCAL (N=12)	-0.536898038	-0.701011527	0.483295822	0.60412	0.584559	binary	arm-level CNV at 9p>(-0.1) and focal-level CNV at JAK2<(-0.3)
JAK2 Loss: ARM+FOCAL (N=4)	-0.04996171	-0.030249423	0.975868133	0.975868	0.951266	binary	arm-level CNV at 9p<(-0.1) and focal-level CNV at JAK2<(-0.1)
3p14 Loss	-0.276041545	-0.746394919	0.455428888	0.60412	0.758781	binary	
SCNA level	-0.663419537	-3.670943839	0.000241656	0.000604	0.515087	continuous	

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at JAK2.

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
JAK2 copy number ARM Level	1.122035775	4.19918159	2.67881E-05	0.000107	3.0711	continuous
JAK2 copy number FOCAL Level	0.554456965	3.239525555	0.001197287	0.001596	1.740995	continuous
3p14 copy number	0.432241484	2.040923726	0.041258409	0.041258	1.540707	continuous
SCNA level	-0.699929683	-3.63945043	0.000273211	0.000546	0.49662	continuous

JAK2 Loss and CD274 Loss	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
JAK2 Loss and CD274 Loss: ARM (N=85)	-1.7150599	-3.65775075	0.000254438	0.000636	0.179953	binary	arm-level CNV at 9p<(-0.3) and focal-level CNV at JAK2 Loss and CD274 Loss>(-0.1)
JAK2 Loss and CD274 Loss: FOCAL (N=11)	-0.5123101	-0.66930774	0.503299189	0.629124	0.59911	binary	arm-level CNV at 9p>(-0.1) and focal-level CNV at JAK2 Loss and CD274 Loss<(-0.3)
JAK2 Loss and CD274 Loss: ARM+FOCAL (N=4)	-0.0325746	-0.01961703	0.984348879	0.984349	0.96795	binary	arm-level CNV at 9p<(-0.1) and focal-level CNV at JAK2 Loss and CD274 Loss<(-0.1)
3p14 Loss	-0.2913409	-0.78882441	0.430214643	0.629124	0.747261	binary	
SCNA level	-0.6730063	-3.72905528	0.000192199	0.000636	0.510173	continuous	

Standardized copy number values were used to define copy number levels of the different regions and to differentiate arm-level versus focal-level event at JAK2 and CD274.

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
JAK2 and CD274 copy number ARM Level	1.12354536	4.2013797	2.65293E-05	0.000106	3.075739	continuous
JAK2 and CD274 copy number FOCAL Level	0.55437845	3.2635902	0.001100101	0.001467	1.740859	continuous
3p14 copy number	0.433667	2.046411	0.04071595	0.040716	1.542905	continuous
SCNA level	-0.69871154	-3.6324476	0.000280746	0.000561	0.497226	continuous

Table S4

Association between immune parameters and copy number alterations in HPV-negative oral tumor samples from TCGA.

Unless otherwise specified, '9p21.3 loss', '3p14 loss' or '17p13.1 loss' refer to the presence of a loss at this region irrespective of the length of the deletion (whether the loss encompasses the entire arm or is a focal event).'

S4A

Logistic Regression for the prediction of immune infiltrate parameters in oral tumor samples

Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.

Binary definition of loss or gain.

purity method=Pathology

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.0927768	-0.181646	8.56E-01	8.56E-01	0.911397	binary
9p21.3 Loss	-2.0425244	-3.970332	7.18E-05	3.59E-04	0.129701	binary
17p13.1 Loss	-0.9482032	-1.15309	2.49E-01	4.03E-01	0.387437	binary
Chr 7 Gain	0.7283416	0.990505	3.22E-01	4.03E-01	2.071642	binary
SCNA level	-0.9097892	-3.296963	9.77E-04	2.44E-03	0.402609	continuous

CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.4973584	-1.013056	0.311033	0.311033	0.608135	binary
9p21.3 Loss	-1.6183061	-3.2009	0.00137	0.003425	0.198234	binary
17p13.1 Loss	-1.4036496	-1.516095	0.129495	0.215825	0.245699	binary
Chr 7 Gain	0.7122948	1.015339	0.309944	0.311033	2.038664	binary
SCNA level	-0.9353222	-3.304707	0.000951	0.003425	0.392459	continuous

CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	0.4460938	0.940225	0.347102	0.433878	1.562198	binary
9p21.3 Loss	-0.6193774	-1.442211	0.149243	0.248738	0.538279	binary
17p13.1 Loss	-0.9026873	-1.815994	0.069371	0.248738	0.405479	binary
Chr 7 Gain	0.2935597	0.443107	0.657689	0.657689	1.341193	binary
SCNA level	-0.3435666	-1.463083	0.143445	0.248738	0.709236	continuous

Immune Score	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss	-0.07727523	-0.147538	0.882707	0.882707	0.925635	binary
9p21.3 Loss	-1.84832056	-3.607866	0.000309	0.001544	0.157501	binary
17p13.1 Loss	-1.12998716	-1.552851	0.120459	0.200765	0.323037	binary
Chr 7 Gain	0.94756411	1.30175	0.193002	0.241252	2.579419	binary
SCNA level	-0.96903058	-3.392153	0.000693	0.001734	0.379451	continuous

For each copy number event, we used copy number values after standardization.

purity method=Pathology

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 scale	0.6456285	2.152065	3.14E-02	5.23E-02	1.907185	continuous
9p21.3 scale	1.5603175	4.257302	2.07E-05	1.04E-04	4.760332	continuous
17p13.1 scale	-0.3221382	-1.117982	2.64E-01	3.30E-01	0.724598	continuous
Chr 7 scale	-0.2573763	-0.709606	4.78E-01	4.78E-01	0.773077	continuous
SCNA level	-0.6239998	-2.166146	3.03E-02	5.23E-02	0.535797	continuous

CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 scale	0.94246865	3.422997	0.000619	0.003097	2.566309	continuous
9p21.3 scale	0.45085749	2.285872	0.022262	0.037103	1.569658	continuous
17p13.1 scale	0.03674168	0.147436	0.882788	0.882788	1.037425	continuous
Chr 7 scale	-0.1710354	-0.551452	0.581324	0.726655	0.842792	continuous
SCNA level	-0.64705579	-2.364806	0.01804	0.037103	0.523585	continuous

CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 scale	-0.19870062	-0.854913	0.392599	0.490749	0.819795	continuous
9p21.3 scale	-0.09582344	-0.545602	0.58534	0.58534	0.908624	continuous
17p13.1 scale	0.63795188	2.999854	0.002701	0.013505	1.892601	continuous
Chr 7 scale	0.38044836	1.306076	0.191527	0.319212	1.46294	continuous
SCNA level	-0.48139622	-2.005555	0.044904	0.112259	0.61792	continuous

Immune Score	**β coefficient**	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 scale	0.71445954	2.36427	0.018066	0.045164	2.043082	continuous
9p21.3 scale	1.390649	4.036392	5.43E-05	0.000271	4.017457	continuous
17p13.1 scale	-0.07017032	-0.254492	0.799115	0.799115	0.932235	continuous
Chr 7 scale	-0.09509775	-0.273664	0.784343	0.799115	0.909284	continuous
SCNA level	-0.63000651	-2.192166	0.028368	0.047279	0.532588	continuous

S4B

Logistic Regression for the prediction of CD8+ in oral tumor samples - after separating arm-level and focal-level loss at 9p21.3

Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.

Distinction between tumors showing arm-only, focal-only events and a combination of both.

Binary definition of loss or gain.

purity method=Pathology

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
9p21.3 Loss: ARM (N=80)	-3.7291933	-3.45977	0.000541	0.002703	0.024012	binary
9p21.3 Loss: FOCAL (N=40)	-0.9835497	-1.801873	0.071565	0.119276	0.373981	binary
9p21.3 Loss: ARM+FOCAL (N=15)	-16.6563876	-0.012475	0.990046	0.990047	5.84E-08	binary
3p14 Loss	-0.1119033	-0.229746	0.818289	0.990047	0.894131	binary
SCNA level	-0.7339896	-2.826584	0.004705	0.011762	0.47999	continuous

For each copy number event, we used copy number values after standardization.

purity method=Pathology

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
9p21.3 copy number ARM Level	2.3099844	4.450053	8.58E-06	3.43E-05	10.07427	continuous
9p21.3 copy number FOCAL Level	0.412355	1.451957	1.47E-01	1.96E-01	1.510371	continuous
3p14 copy number	0.3604761	1.216953	2.24E-01	2.24E-01	1.434012	continuous
SCNA level	-0.7464163	-2.484486	1.30E-02	2.60E-02	0.474062	continuous

S4C

Logistic Regression for the prediction of CD8+ in oral tumor samples - after separating arm-level and focal-level loss at 3p14.

Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.

Distinction between tumors showing arm-only, focal-only events and a combination of both.

Binary definition of loss or gain.

purity method=Pathology

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 Loss: ARM Level	-0.5338593	-1.030897	3.03E-01	3.03E-01	0.586338	binary
3p14 Loss: FOCAL Level	-0.5939564	-1.031031	3.03E-01	3.03E-01	0.552138	binary
3p14 Loss: ARM+FOCAL	-1.4998566	-1.217132	2.24E-01	3.03E-01	0.223162	binary
9p21.3 Loss	-2.0023121	-3.988118	6.66E-05	3.33E-04	0.135023	binary
SCNA level	-0.766696	-3.062019	2.20E-03	5.50E-03	0.464545	continuous

For each copy number event, we used copy number values after standardization.

purity method=Pathology

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
3p14 copy number ARM Level	0.8072066	1.728135	8.40E-02	1.12E-01	2.241637	continuous
3p14 copy number FOCAL Level	0.4955731	1.083639	2.79E-01	2.79E-01	1.641439	continuous
9p21.3 copy number	1.4691859	4.356877	1.32E-05	5.28E-05	4.345696	continuous
SCNA level	-0.7858527	-2.75483	5.87E-03	1.17E-02	0.455731	continuous

S4D

Logistic Regression for the prediction of CD8+ in oral tumor samples - after separating arm-level and focal-level loss at 17p13.1.

Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.

Distinction between tumors showing arm-only, focal-only events and a combination of both.

Binary definition of loss or gain.

purity method=Pathology

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
17p13.1 Loss: ARM Level	-0.6573481	-0.716571	4.74E-01	6.91E-01	0.518224	binary
17p13.1 Loss: FOCAL Level	0.6678774	0.593938	5.53E-01	6.91E-01	1.950094	binary
17p13.1 Loss: ARM+FOCAL	-16.085137	-0.016596	9.87E-01	9.87E-01	1.03E-07	binary
9p21.3 Loss	-2.1347942	-4.270594	1.95E-05	9.75E-05	0.118269	binary
SCNA level	-0.9148237	-3.919697	8.87E-05	2.22E-04	0.400587	continuous

For each copy number event, we used copy number values after standardization.

purity method=Pathology

	β coefficient	**z value**	**Pr(>|z|)**	**FDR**	**OR**	
17p13.1 copy number ARM Level	-0.2824384	-1.091784	2.75E-01	3.67E-01	0.753943	continuous
17p13.1 copy number FOCAL Level	0.1523539	0.478366	6.32E-01	6.32E-01	1.164572	continuous
9p21.3 copy number	1.7523208	4.896996	9.73E-07	3.89E-06	5.767973	continuous
SCNA level	-1.0356635	-4.436121	9.16E-06	1.83E-05	0.354991	continuous

Table S5
***Lasso*-based prediction model of Immune Score in HNSC tumor samples (TCGA). Variable Selection.**

Parameters	β coefficient	Pvalue
Chr 1	0	NA
Chr 2	0	NA
Chr 3	0	NA
Chr 4	0	NA
Chr 5	0	NA
Chr 6	0	NA
Chr 7	0	NA
Chr 8	0	NA
Chr 9	-0.72(0.18,1.26)	0.0078
Chr 10	-0.22(-1,1.44)	0.7209
Chr 11	0	NA
Chr 12	0	NA
Chr 13	0	NA
Chr 14	0	NA
Chr 15	0	NA
Chr 16	0	NA
Chr 17	0	NA
Chr 18	0	NA
Chr 19	0	NA
Chr 20	0	NA
Chr 21	0	NA
Chr 22	0.24(-0.78,0.3)	0.3764
1p Arm	0	NA
2p Arm	0	NA
3p Arm	0	NA
4p Arm	0	NA
5p Arm	0	NA
6p Arm	-0.43(-0.27,1.13)	0.2108
7p Arm	0	NA
8p Arm	0	NA
9p Arm	-1.13(0.47,1.79)	7.00E-04
10p Arm	0	NA
11p Arm	0	NA
12p Arm	0	NA
16p Arm	0	NA
17p Arm	0	NA
18p Arm	0	NA
19p Arm	0	NA
20p Arm	0	NA
1q Arm	0	NA
2q Arm	0	NA
3q Arm	0	NA
4q Arm	0	NA
5q Arm	0	NA
6q Arm	0	NA
7q Arm	-0.83(-3.57,1.91)	0.5445
8q Arm	0	NA
9q Arm	0	NA
10q Arm	0	NA
11q Arm	0	NA
12q Arm	0	NA
16q Arm	0	NA
17q Arm	0	NA
18q Arm	0	NA
19q Arm	0	NA
20q Arm	0	NA
SCNA level	-1.12(-1.6,-0.64)	0

Table S6

Association between immune parameters and copy number alterations and other parameters in HPV-negative HNSC tumor samples from TCGA. Unless otherwise specified, '9p21.3 loss', '3p14 loss' or '17p13.1 loss' refer to the presence of a loss at this region irrespective of the length of the deletion (whether the loss encompasses the entire arm or is a focal event).

S6A

Logistic Regression for the prediction of CD8+ in HNSC tumor samples after considering the tumor stage.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
purity method=ABSOLUTE
stage I or II (N=76)

	β coefficient	z value	Pr(>|z|)	OR	
3p14 Loss (samples with loss=49)	0.1751775	0.2176969	0.827665	1.191458	binary
9p21.3 Loss (samples with loss=33)	-1.6968636	-2.3427388	0.019143	0.183257	binary
17p13.1 Loss (samples with loss=20)	-1.214868	-1.3559012	0.175131	0.296749	binary
SCNA level	-0.5542126	-1.2550551	0.209459	0.574524	continuous

stage III (N=65)

	β coefficient	z value	Pr(>|z|)	OR	
3p14 Loss (samples with loss=50)	-1.538657	-1.0086105	0.313161	0.214669	binary
9p21.3 Loss (samples with loss=25)	-2.064968	-1.9344592	0.053057	0.126822	binary
17p13.1 Loss (samples with loss=16)	2.017373	1.8246672	0.068051	7.518548	binary
SCNA level	-1.353899	-1.8978269	0.057719	0.258231	continuous

stage IV (N=163)

	β coefficient	z value	Pr(>|z|)	OR	
3p14 Loss (samples with loss=137)	-0.48979533	-0.7251495	0.46836	0.612752	binary
9p21.3 Loss (samples with loss=77)	-1.77733416	-3.8753118	0.000106	0.169088	binary
17p13.1 Loss (samples with loss=32)	-0.00592329	-0.0106613	0.991494	0.994094	binary
SCNA level	-0.29755493	-1.1531567	0.248846	0.742632	continuous

S6B

Logistic Regression for the prediction of CD8+ in HNSC tumor samples after considering the TP53 status.
Top and bottom 35% of the distributions were considered to divide the tumors into those with high or low levels of immune markers.
purity method=ABSOLUTE
TP53 WT (N=22) (stage I or II)

	β coefficient	z value	Pr(>|z|)	OR	
3p14 Loss	-16.021672	-0.004619	0.996315	1.1E-07	binary
9p21.3 Loss	-0.70451	-0.4432798	0.657563	0.494351	binary
SCNA level	-2.565948	-1.3362557	0.181466	0.076846	continuous

TP53 Mut (N=33) (stage I or II)

	β coefficient	z value	Pr(>|z|)	OR	
3p14 Loss	-1.0983191	-0.7301274	0.465312	0.333431	binary
9p21.3 Loss	-2.5883793	-2.4649196	0.013704	0.075142	binary
SCNA level	-0.2980467	-0.5378871	0.590655	0.742267	continuous

S6C

Pearson's correlation analysis between CD8+/CD3+ and 9p arm loss in HNSC tumor samples after considering the TP53 status.
purity method=ABSOLUTE
TP53 WT (N=22) (stage I or II)

	cor	p-value	FDR	
CD8+ ~9p Arm Loss	0.41	0.06	0.12	continuous
CD3+~9p Arm Loss	0.32	0.15	0.3	continuous

TP53 Mut (N=33) (stage I or II)

	cor	p-value	FDR	
CD8+ ~9p Arm Loss	0.51	0.002	0.004	continuous
CD3+~9p Arm Loss	0.36	0.03	0.06	continuous

S6D

Wilcoxon signed rank test between CD8+/CD3+ and 9p arm loss/9p21.3 loss in HNSC tumor samples after considering the TP53 status.
purity method=ABSOLUTE
TP53 WT (N=70) (stage I ~ IV)

	p-value	FDR
CD8+ ~9p Arm Loss	0.00446	0.01784
CD8+ ~9p21.3 focal Loss	0.127	0.1693333
CD3+~9p Arm Loss	0.0563	0.1126
CD3+~9p21.3 focal Loss	0.309	0.309

TP53 Mut (N=146) (stage I ~ IV)

	p-value	FDR
CD8+ ~9p Arm Loss	0.00286	0.01144
CD8+ ~9p21.3 focal Loss	0.864	0.864
CD3+~9p Arm Loss	0.0194	0.0388
CD3+~9p21.3 focal Loss	0.755	0.864

Table S7

Relationship between Immune Markers and SCNA Events in HPV-positive HNSC (N=36)

Unless otherwise specified, '9p21.3 loss', '3p14 loss' or '17p13.1 loss' refer to the presence of a loss at this region irrespective of the length of the deletion (whether the loss encompasses the entire arm or is a focal event).

S7A

Comparison of the frequencies of different copy number events in HPV positive and negative HNSC

Events	Frequency in HPV positive HNSC (oropharynx, N=36)	Frequency in HPV negative HNSC (all, N=343)	Frequency in HPV negative HNSC (oral pharynx,N=232)
17p13.1 Loss	0.167	0.167	0.138
3p14 Loss	0.306	0.558	0.621
9p21.3 Loss	0.056	0.367	0.388
17p13.1 Focal Loss	0.028	0.027	0.031
3p14 Focal Loss	0.139	0.039	0.022
9p21.3 Focal Loss	0	0.116	0.094
3p Arm Loss	0.139	0.388	0.406
9p Arm Loss	0.056	0.26	0.281
9p Arm Gain	0.121	0.125	0.137
17p Arm Loss	0.167	0.122	0.138
Chr 7 Gain	0	0.125	0.08
Average number of arm-level Gain	4.69	5.05	4.46
Average number of arm-level Loss	3.18	4.74	4.12

S7B

Logistic Regression for the prediction of immune infiltrate parameters in HPV-positive HNSC tumor samples; binary definition of loss or gain

Thresholded values were used to define Loss and Gain in HPV-positive samples

HPV positie HNSC (oropharynx)

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**OR**		
3p14 Loss		0.5177	0.537	0.592	1.6781634	binary
9p21.3 Loss		-35.4044	-0.007	0.994	4.208E-16	binary
17p13.1 Loss		18.0518	0.005	0.996	69150787	binary
Chr 7 Gain	NA	NA	NA	NA	NA	binary
SCNA level		0.2352	0.443	0.658	1.2651618	continuous
CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**OR**		
3p14 Loss		-0.02513	-0.025	0.98	0.9751831	binary
9p21.3 Loss		-17.62253	-0.006	0.995	2.221E-08	binary
17p13.1 Loss		-0.31789	-0.204	0.838	0.7276828	binary
Chr 7 Gain	NA	NA	NA	NA	NA	binary
SCNA level		-0.31853	-0.568	0.57	0.7272173	continuous
CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**OR**		
3p14 Loss		-0.34485	-0.371	0.711	0.7083266	binary
9p21.3 Loss		-16.25612	-0.007	0.995	8.711E-08	binary
17p13.1 Loss		-0.48031	-0.405	0.685	0.6185916	binary
Chr 7 Gain	NA	NA	NA	NA	NA	binary
SCNA level		-0.92103	-1.474	0.141	0.3981088	continuous

S7C

Logistic Regression for the prediction of immune infiltrate parameters in HPV-positive HNSC tumor samples; copy number level considered as continuous data.

For each copy number event (HPV-positive), we used copy number values after standardization.

HPV positie HNSC (oropharynx)

CD8+	**β coefficient**	**z value**	**Pr(>|z|)**	**OR**		
3p14 scale	0.009591503	0.022416157	0.982116	1.0096376	continuous	
9p21.3 scale	1.261262916	1.339749544	0.1803268	3.5298766	continuous	
17p13.1 scale	-0.182965451	-0.303090653	0.7618208	0.8327969	continuous	
Chr 7 scale	-3.988996857	-0.006119591	0.9951173	0.0185183	continuous	
SCNA level	-0.183671061	-0.34096679	0.7331286	0.8322095	continuous	
CD3+	**β coefficient**	**z value**	**Pr(>|z|)**	**OR**		
3p14 scale	0.2581585	0.49707339	0.6191373	1.294544	continuous	
9p21.3 scale	0.2347384	0.498746708	0.6179578	1.2645779	continuous	
17p13.1 scale	1.0354722	1.081391702	0.2795229	2.8164358	continuous	
Chr 7 scale	-4.7208476	-0.00677584	0.9945937	0.0089076	continuous	
SCNA level	-0.6893639	-0.985145189	0.3245528	0.5018952	continuous	
CD68+	**β coefficient**	**z value**	**Pr(>|z|)**	**OR**		
3p14 scale	0.1582568	0.342368875	0.73207331	1.171467	continuous	
9p21.3 scale	1.1535477	0.976983156	0.32857749	3.1694171	continuous	
17p13.1 scale	0.2566075	0.490022554	0.62411794	1.2925377	continuous	
Chr 7 scale	-4.2568355	-0.006530487	0.99478946	0.0141671	continuous	
SCNA level	-1.2051899	-1.656786082	0.09756273	0.2996351	continuous	

Table S8

HPV-negative HNSC cell lines and corresponding CNV for different genomic regions

CCLE name	3p Arm cnv	9p Arm cnv	17p Arm cnv	17p13.1 cnv	3p14 cnv	9p21.3 cnv	TP53 mutation	SASP_enrichment
SCC9_UPPER_AERODIGESTIVE_TRACT	0	-0.614	0	0.559	-0.645	-0.693	0	0.138674957
SCC25_UPPER_AERODIGESTIVE_TRACT	-0.504	-0.841	-0.009	0.24	-0.82	-0.859	1	0.311574821
DETROIT562_UPPER_AERODIGESTIVE_TRACT	-0.638	-0.586	0.059	0.687	-0.648	-0.628	1	0.229371271
BICR31_UPPER_AERODIGESTIVE_TRACT	-0.888	-0.438	-0.264	-0.264	-0.888	-0.59	1	0.299130188
SCC4_UPPER_AERODIGESTIVE_TRACT	-0.748	-0.437	-0.356	-0.356	-0.748	-0.437	1	0.24427235
SCC15_UPPER_AERODIGESTIVE_TRACT	0.083	-0.409	0.929	0.955	-0.46	-0.443	1	0.403180505
BICR6_UPPER_AERODIGESTIVE_TRACT	-0.586	-0.606	0	-0.049	-0.673	-0.606	1	0.154112043
HSC2_UPPER_AERODIGESTIVE_TRACT	-0.276	0.105	0.91	0.91	-0.276	0.105	1	0.269425399
SNU46_UPPER_AERODIGESTIVE_TRACT	-0.523	0	0.624	0.689	-0.523	-0.018	1	0.024359176
BICR16_UPPER_AERODIGESTIVE_TRACT	-0.596	0.178	-0.223	0.371	-0.596	-0.53	1	0.162163423
CAL33_UPPER_AERODIGESTIVE_TRACT	0.005	0	0	-0.017	-0.997	0.015	1	0.2549407
HSC4_UPPER_AERODIGESTIVE_TRACT	0.402	0.464	0.498	0.498	-0.113	1.095	1	0.158259287
BHY_UPPER_AERODIGESTIVE_TRACT	-0.274	0.635	-0.25	-0.392	-0.274	0.528	1	0.285596712
SNU1076_UPPER_AERODIGESTIVE_TRACT	-0.576	0.071	-0.326	-0.326	-0.576	-0.951	1	0.20324502
PECAPJ34CLONEC12_UPPER_AERODIGESTIVE_TRACT	0.011	0	0.879	-0.094	-0.978	-0.027	1	0.223535876
SNU1041_UPPER_AERODIGESTIVE_TRACT	0	0	0	-0.071	-0.902	-0.133	1	0.166218258
PECAPJ15_UPPER_AERODIGESTIVE_TRACT	-0.531	-0.744	0.239	0.239	-0.819	-0.744	1	0.098837199
YD8_UPPER_AERODIGESTIVE_TRACT	0	0.509	1.045	1.045	-0.633	0.478	1	0.093072471
SNU1066_UPPER_AERODIGESTIVE_TRACT	-0.82	0.123	0.135	0.112	-0.82	-0.797	1	0.236743808
SNU899_UPPER_AERODIGESTIVE_TRACT	-0.531	0	0	-0.018	-0.531	-0.036	1	0.278886299
SNU1214_UPPER_AERODIGESTIVE_TRACT	-0.979	-0.964	0	-0.007	-0.979	-0.967	1	0.11958324
YD10B_UPPER_AERODIGESTIVE_TRACT	-0.676	-0.218	0.152	0.152	-0.676	0.898	1	0.186047685
PECAPJ41CLONED2_UPPER_AERODIGESTIVE_TRACT	-0.956	-0.978	0	-0.002	-0.963	-0.978	1	0.280160386
PECAPJ49_UPPER_AERODIGESTIVE_TRACT	-0.954	0	0	0.003	-0.98	0.004	1	0.33584896
A253_SALIVARY_GLAND	-0.626	-0.541	0	0.487	-0.462	-0.541	1	0.004138976
YD38_UPPER_AERODIGESTIVE_TRACT	-0.639	0	0.214	0.214	-0.639	-0.003	1	0.310609016
BICR56_UPPER_AERODIGESTIVE_TRACT	-0.978	0	0	0.011	-0.978	-0.001	1	0.263762592
HSC3_UPPER_AERODIGESTIVE_TRACT	-0.582	0.448	0.149	0.392	-0.582	0.448	1	0.336701744
CAL27_UPPER_AERODIGESTIVE_TRACT	-0.953	0	0	-0.035	-0.964	0.07	1	0.31333995
YD15_SALIVARY_GLAND	-0.615	-0.637	0.502	0.658	-0.65	-0.675	1	0.118655673
FADU_UPPER_AERODIGESTIVE_TRACT	0	-0.65	0	0.045	-0.64	-0.65	1	0.04112478
BICR18_UPPER_AERODIGESTIVE_TRACT	-0.573	-0.543	0	0.087	-0.573	-0.575	1	-0.039028669

Table S9

GSEA Analysis on HNSC cancer cell lines comparing cell lines with or without 9p21.3 loss (arm or focal), Pathways Enriched

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX	LEADING EDGE
BIOCARTA_EDG1_PATHWAY	26	0.770171	1.732077	0.005163511	1	0.923	3988	tags=50%, list=16%, signal=59%
REACTOME_STRIATED_MUSCLE_CONTRACTION	23	0.747589	1.675122	0.005067567	1	0.989	2947	tags=17%, list=12%, signal=20%
KEGG_TASTE_TRANSDUCTION	33	0.716086	1.662948	0.013675214	1	0.993	516	tags=12%, list=2%, signal=12%
BIOCARTA_BARRESTIN_SRC_PATHWAY	15	0.778297	1.621138	0.028725315	1	0.999	3223	tags=27%, list=13%, signal=31%
REACTOME_METAL_ION_SLC_TRANSPORTERS	21	0.722715	1.573749	0.037478704	1	1	769	tags=19%, list=3%, signal=20%
REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS	25	0.689001	1.570837	0.027350428	1	1	17	tags=4%, list=0%, signal=4%
REACTOME_TIGHT_JUNCTION_INTERACTIONS	28	0.686324	1.569755	0.021885522	1	1	99	tags=7%, list=0%, signal=7%
KEGG_CELL_ADHESION_MOLECULES_CAMS	102	0.564584	1.564531	0.020057306	1	1	508	tags=9%, list=2%, signal=9%
KEGG_STEROID_HORMONE_BIOSYNTHESIS	40	0.645129	1.56117	0.028428094	1	1	2719	tags=30%, list=11%, signal=34%
REACTOME_GAP_JUNCTION_TRAFFICKING	23	0.722779	1.558618	0.036206897	1	1	2479	tags=35%, list=10%, signal=38%
REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	49	0.624921	1.557937	0.02728732	1	1	247	tags=8%, list=1%, signal=8%
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	22	0.700953	1.528772	0.051194537	1	1	5667	tags=50%, list=22%, signal=64%
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	20	0.709791	1.51637	0.05263158	1	1	2719	tags=30%, list=11%, signal=34%
KEGG_PARKINSONS_DISEASE	93	0.55174	1.489339	0.033282906	1	1	5910	tags=30%, list=23%, signal=39%
REACTOME_CELL_JUNCTION_ORGANIZATION	70	0.550621	1.462215	0.037936267	1	1	247	tags=6%, list=1%, signal=6%
KEGG_ARACHIDONIC_ACID_METABOLISM	45	0.593656	1.450863	0.039808918	1	1	2830	tags=27%, list=11%, signal=30%
REACTOME_REGULATORY_RNA_PATHWAYS	21	0.670205	1.448237	0.078397214	1	1	5076	tags=57%, list=20%, signal=71%
REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT	19	0.669201	1.441679	0.08148148	1	1	3876	tags=42%, list=15%, signal=50%
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	63	0.556189	1.429341	0.046104927	1	1	7464	tags=49%, list=29%, signal=69%
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	40	0.595014	1.426465	0.07017544	1	1	2719	tags=28%, list=11%, signal=31%
KEGG_TYPE_II_DIABETES_MELLITUS	41	0.580894	1.418746	0.068515494	1	1	1927	tags=17%, list=8%, signal=18%
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	38	0.592241	1.416961	0.07692308	1	1	4083	tags=37%, list=16%, signal=44%
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	34	0.596848	1.409571	0.07826087	1	1	324	tags=9%, list=1%, signal=9%
BIOCARTA_RHO_PATHWAY	32	0.604687	1.405141	0.07272727	1	1	1084	tags=13%, list=4%, signal=13%
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	91	0.521835	1.403979	0.055072464	1	1	4013	tags=22%, list=16%, signal=26%
REACTOME_MICRORNA_MIRNA_BIOGENESIS	18	0.672858	1.400063	0.10124334	1	1	5810	tags=61%, list=23%, signal=79%
BIOCARTA_BAD_PATHWAY	24	0.628961	1.399039	0.087628864	1	1	4674	tags=38%, list=18%, signal=46%
REACTOME_M_G1_TRANSITION	78	0.526321	1.395061	0.07969925	1	1	6059	tags=35%, list=24%, signal=45%
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	54	0.554225	1.390763	0.07042254	1	1	7464	tags=50%, list=29%, signal=71%
REACTOME_RNA_POL_I_PROMOTER_OPENING	55	0.556454	1.386685	0.07605178	1	1	6397	tags=38%, list=25%, signal=51%
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	18	0.657341	1.379645	0.11599297	1	1	2481	tags=22%, list=10%, signal=25%
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	54	0.540148	1.374899	0.07988165	1	1	6059	tags=39%, list=24%, signal=51%
REACTOME_RECYCLING_PATHWAY_OF_L1	26	0.611553	1.373821	0.114617944	1	1	2286	tags=23%, list=9%, signal=25%
REACTOME_PACKAGING_OF_TELOMERE_ENDS	42	0.555223	1.373576	0.07820299	1	1	6397	tags=40%, list=25%, signal=54%
REACTOME_FANCONI_ANEMIA_PATHWAY	20	0.622841	1.366789	0.104166664	1	1	4032	tags=30%, list=16%, signal=36%
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	50	0.551495	1.365638	0.08796296	1	1	7428	tags=50%, list=29%, signal=70%
REACTOME_OXYGEN_DEPENDENT_PROLINE_HYDROXYLATION_OF_HYPOXIA_INDUCIBLE_FACTOR_ALPHA	15	0.658078	1.361504	0.11900533	1	1	2363	tags=27%, list=9%, signal=29%
REACTOME_NCAM1_INTERACTIONS	36	0.576865	1.35965	0.10305958	1	1	1496	tags=17%, list=6%, signal=18%
KEGG_STARCH_AND_SUCROSE_METABOLISM	37	0.563694	1.354787	0.097087376	1	1	2719	tags=19%, list=11%, signal=21%
REACTOME_PHASE_II_CONJUGATION	56	0.534087	1.35351	0.0913242	1	1	2719	tags=20%, list=11%, signal=22%
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	65	0.526172	1.353487	0.0892587	1	1	7464	tags=48%, list=29%, signal=67%
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	56	0.532197	1.351076	0.10108865	1	1	8555	tags=54%, list=34%, signal=80%
REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	22	0.608178	1.335548	0.14086956	1	1	2871	tags=45%, list=11%, signal=51%
BIOCARTA_VEGF_PATHWAY	29	0.579152	1.335398	0.13866232	1	1	1927	tags=21%, list=8%, signal=22%
BIOCARTA_GSK3_PATHWAY	25	0.603801	1.333843	0.122689076	1	1	2309	tags=16%, list=9%, signal=18%
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	46	0.543932	1.331843	0.111821085	1	1	7925	tags=54%, list=31%, signal=79%
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	63	0.51879	1.331077	0.09968847	1	1	6059	tags=37%, list=24%, signal=48%
BIOCARTA_GCR_PATHWAY	19	0.624814	1.32915	0.1465798	1	1	1927	tags=21%, list=8%, signal=23%
REACTOME_G1_S_TRANSITION	108	0.471804	1.32304	0.08640227	1	1	7925	tags=44%, list=31%, signal=63%
REACTOME_APOPTOTIC_EXECUTION_PHASE	51	0.520198	1.320914	0.09693053	1	1	3278	tags=18%, list=13%, signal=20%
REACTOME_INFLAMMASOMES	16	0.626617	1.320492	0.16187051	1	1	2021	tags=19%, list=8%, signal=20%
CANCER-TESTIS-ANTIGEN	94	0.480333	1.320344	0.081871346	1	1	2265	tags=18%, list=9%, signal=20%
REACTOME_STEROID_HORMONES	20	0.608023	1.316482	0.15412845	1	1	1767	tags=10%, list=7%, signal=11%
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	47	0.53453	1.315992	0.12480499	1	1	6059	tags=36%, list=24%, signal=47%
KEGG_SMALL_CELL_LUNG_CANCER	84	0.491926	1.315584	0.10644678	1	1	3948	tags=26%, list=15%, signal=31%
REACTOME_PLATELET_HOMEOSTASIS	71	0.505701	1.315359	0.1036036	1	1	3010	tags=24%, list=12%, signal=27%
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	48	0.532281	1.314497	0.11568938	0.9915861	1	7428	tags=46%, list=29%, signal=65%
REACTOME_MEIOTIC_RECOMBINATION	75	0.494345	1.309656	0.11179173	0.9995672	1	6099	tags=35%, list=24%, signal=45%
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	34	0.553904	1.306764	0.14214046	0.9971052	1	2719	tags=21%, list=11%, signal=23%
REACTOME_NEPHRIN_INTERACTIONS	19	0.610365	1.303367	0.14160839	0.99678326	1	2927	tags=21%, list=11%, signal=24%
BIOCARTA_HCMV_PATHWAY	17	0.634228	1.299367	0.1598023	1	1	3223	tags=29%, list=13%, signal=34%
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	20	0.603066	1.295536	0.17750439	1	1	5080	tags=45%, list=20%, signal=56%
REACTOME_IL_3_5_AND_GM_CSF_SIGNALING	39	0.545913	1.295336	0.1356784	0.98893344	1	2481	tags=18%, list=10%, signal=20%
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	23	0.583281	1.295098	0.15939598	0.9745598	1	4103	tags=22%, list=16%, signal=26%
BIOCARTA_AKT_PATHWAY	20	0.595165	1.293943	0.17875211	0.96540487	1	1927	tags=15%, list=8%, signal=16%
BIOCARTA_MCM_PATHWAY	18	0.599264	1.287011	0.17572464	0.9850114	1	7581	tags=61%, list=30%, signal=87%
REACTOME_SIGNALING_BY_ERBB2	95	0.478423	1.285279	0.10237389	0.9792291	1	726	tags=5%, list=3%, signal=5%
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	73	0.482904	1.28432	0.12708019	0.96953064	1	2517	tags=12%, list=10%, signal=14%
REACTOME_MITOTIC_M_M_G1_PHASES	160	0.441203	1.281349	0.0945758	0.9704232	1	7832	tags=41%, list=31%, signal=59%
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	21	0.590084	1.278812	0.17190082	0.968655	1	1534	tags=14%, list=6%, signal=15%
BIOCARTA_BCELLSURVIVAL_PATHWAY	16	0.608918	1.275065	0.18053098	0.9731757	1	1927	tags=25%, list=8%, signal=27%
REACTOME_CGMP_EFFECTS	18	0.606413	1.273005	0.18412162	0.9688615	1	2871	tags=50%, list=11%, signal=56%
BIOCARTA_IL2RB_PATHWAY	37	0.542148	1.26937	0.16221035	0.97210085	1	1927	tags=14%, list=8%, signal=15%
BIOCARTA_IL7_PATHWAY	17	0.615094	1.263601	0.20344828	0.98673224	1	3068	tags=29%, list=12%, signal=33%
REACTOME_SEMAPHORIN_INTERACTIONS	64	0.489497	1.262914	0.14198473	0.9766299	1	1993	tags=9%, list=8%, signal=10%
REACTOME_S_PHASE	106	0.456783	1.260745	0.12957746	0.97360575	1	6059	tags=34%, list=24%, signal=44%
BIOCARTA_ACH_PATHWAY	15	0.610333	1.258094	0.19604316	0.9735438	1	4191	tags=33%, list=16%, signal=40%
BIOCARTA_RAS_PATHWAY	23	0.566833	1.25686	0.19765495	0.96747756	1	3223	tags=17%, list=13%, signal=20%
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	29	0.548324	1.25185	0.19410746	0.9778379	1	819	tags=14%, list=3%, signal=14%
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	29	0.547522	1.25035	0.19966997	0.9721544	1	1927	tags=17%, list=8%, signal=19%
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	66	0.485244	1.245534	0.14678898	0.98283905	1	7428	tags=39%, list=29%, signal=55%
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	46	0.505773	1.242985	0.16666667	0.9822829	1	7428	tags=46%, list=29%, signal=64%
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	52	0.496983	1.24226	0.1827957	0.9738304	1	6059	tags=35%, list=24%, signal=45%
REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_D	22	0.567338	1.238708	0.208981	0.97848606	1	1767	tags=9%, list=7%, signal=10%
REACTOME_POTASSIUM_CHANNELS	81	0.46349	1.234446	0.16228747	0.98609084	1	3010	tags=20%, list=12%, signal=22%
KEGG_PROTEASOME	40	0.515849	1.233867	0.19936204	0.97699887	1	8930	tags=63%, list=35%, signal=96%
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	26	0.554316	1.233243	0.19400352	0.96881586	1	4894	tags=38%, list=19%, signal=48%
REACTOME_SYNTHESIS_OF_DNA	90	0.455107	1.232121	0.15889212	0.9633374	1	7726	tags=46%, list=30%, signal=65%
BIOCARTA_ARF_PATHWAY	17	0.592508	1.230947	0.22459893	0.9579939	1	2456	tags=24%, list=10%, signal=26%
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	111	0.441511	1.23074	0.13439307	0.94826597	1	1697	tags=10%, list=7%, signal=11%
REACTOME_MRNA_SPLICING	104	0.440185	1.229712	0.13960114	0.9422683	1	4609	tags=24%, list=18%, signal=29%
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	23	0.549386	1.224801	0.20950705	0.9532556	1	4894	tags=35%, list=19%, signal=43%
REACTOME_AMYLOIDS	67	0.471208	1.22172	0.18045112	0.9564032	1	6460	tags=36%, list=25%, signal=48%
KEGG_ECM_RECEPTOR_INTERACTION	80	0.461412	1.220652	0.17557251	0.95048606	1	4121	tags=26%, list=16%, signal=31%
REACTOME_PYRUVATE_METABOLISM	18	0.573971	1.218216	0.24551971	0.95061475	1	214	tags=17%, list=1%, signal=17%
REACTOME_CELL_CELL_COMMUNICATION	109	0.439852	1.216262	0.16550764	0.94906795	1	2482	tags=10%, list=10%, signal=11%
BIOCARTA_CXCR4_PATHWAY	24	0.533307	1.214863	0.24377224	0.94516504	1	3948	tags=29%, list=15%, signal=34%
BIOCARTA_HDAC_PATHWAY	26	0.545908	1.214384	0.21631205	0.93753886	1	3171	tags=27%, list=12%, signal=31%
REACTOME_MEIOSIS	102	0.4471	1.210212	0.17914832	0.94591445	1	6397	tags=35%, list=25%, signal=47%
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	45	0.501203	1.209037	0.21753247	0.9411948	1	8930	tags=58%, list=35%, signal=89%
KEGG_RETINOL_METABOLISM	47	0.488926	1.20459	0.20414673	0.951021	1	6361	tags=43%, list=25%, signal=57%
REACTOME_FORMATION_OF_THE_HIV1_EARLY_ELONGATION_COMPLEX	29	0.527094	1.202129	0.2359736	0.9519279	1	3876	tags=28%, list=15%, signal=32%
REACTOME_DNA_REPLICATION	180	0.415707	1.200826	0.14171124	0.9478919	1	7832	tags=41%, list=31%, signal=59%
REACTOME_MITOTIC_G1_G1_S_PHASES	133	0.423975	1.198573	0.17574932	0.9486519	1	6059	tags=32%, list=24%, signal=41%
BIOCARTA_UCALPAIN_PATHWAY	18	0.571252	1.197948	0.260177	0.94228095	1	3948	tags=22%, list=15%, signal=26%
REACTOME_PI_METABOLISM	45	0.486646	1.194814	0.2194745	0.9468292	1	819	tags=9%, list=3%, signal=9%
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	37	0.50351	1.19473	0.22778675	0.9382639	1	3278	tags=16%, list=13%, signal=19%
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	64	0.465597	1.193102	0.21092564	0.9363979	1	8524	tags=50%, list=33%, signal=75%
BIOCARTA_ERK5_PATHWAY	17	0.584524	1.192736	0.24725275	0.9293335	1	3223	tags=29%, list=13%, signal=34%
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	61	0.462385	1.192286	0.21165644	0.92257553	1	1496	tags=11%, list=6%, signal=12%
REACTOME_OLFACTORY_SIGNALING_PATHWAY	22	0.541508	1.191279	0.24664429	0.9184289	1	1844	tags=23%, list=7%, signal=24%
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	45	0.490087	1.189302	0.22570533	0.9183065	1	6483	tags=33%, list=25%, signal=45%

REACTOME_ER_PHAGOSOME_PATHWAY	53	0.479617	1.183286	0.21677215	0.93497497	1	7428	tags=42%, list=29%, signal=58%
REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	47	0.479964	1.178353	0.23557693	0.94732136	1	1296	tags=17%, list=5%, signal=18%
REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	15	0.567257	1.176389	0.2621528	0.94686437	1	826	tags=20%, list=3%, signal=21%
REACTOME_HIV_INFECTION	183	0.398153	1.175642	0.16425756	0.9417862	1	6059	tags=27%, list=24%, signal=35%
REACTOME_COMPLEMENT_CASCADE	19	0.553815	1.175389	0.25215888	0.93473417	1	3193	tags=16%, list=13%, signal=18%
REACTOME_NEURONAL_SYSTEM	237	0.388085	1.172839	0.16216215	0.9371651	1	3010	tags=16%, list=12%, signal=18%
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	116	0.420565	1.172216	0.20735294	0.931804	1	6059	tags=28%, list=24%, signal=36%
BIOCARTA_MEF2D_PATHWAY	18	0.556291	1.171223	0.28347826	0.92817926	1	3657	tags=17%, list=14%, signal=19%
REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	17	0.561425	1.1702	0.29491526	0.9245167	1	1065	tags=18%, list=4%, signal=18%
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	47	0.47508	1.169553	0.24052718	0.9195563	1	8524	tags=53%, list=33%, signal=80%
REACTOME_G0_AND_EARLY_G1	24	0.529691	1.168521	0.26206896	0.9161775	1	1794	tags=13%, list=7%, signal=13%
REACTOME_MRNA_CAPPING	29	0.506602	1.167014	0.2487725	0.914512	1	3876	tags=24%, list=15%, signal=28%
REACTOME_MUSCLE_CONTRACTION	42	0.476894	1.165613	0.2540453	0.9128417	1	272	tags=5%, list=1%, signal=5%
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	57	0.459249	1.163865	0.2643857	0.912247	1	8524	tags=49%, list=33%, signal=74%
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	53	0.463973	1.157116	0.240625	0.9311158	1	2719	tags=23%, list=11%, signal=25%
BIOCARTA_PTEN_PATHWAY	17	0.543969	1.156465	0.2967626	0.92647946	1	4756	tags=41%, list=19%, signal=51%
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	65	0.4395	1.153899	0.2435484	0.92903095	1	8524	tags=49%, list=33%, signal=74%
BIOCARTA_GLEEVEC_PATHWAY	23	0.526525	1.15111	0.28500825	0.93255705	1	4756	tags=26%, list=19%, signal=32%
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	77	0.438799	1.143079	0.24707602	0.95709497	1	3193	tags=21%, list=13%, signal=24%
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	40	0.469304	1.142999	0.285956	0.9502089	1	3876	tags=20%, list=15%, signal=24%
REACTOME_ELONGATION_ARREST_AND_RECOVERY	24	0.516869	1.140171	0.30633804	0.9542445	1	4298	tags=38%, list=17%, signal=45%
BIOCARTA_CDC42RAC_PATHWAY	16	0.542043	1.14007	0.28849557	0.9474684	1	1927	tags=19%, list=8%, signal=20%
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	41	0.474302	1.139583	0.267101	0.94232595	1	1847	tags=12%, list=7%, signal=13%
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	40	0.47257	1.138542	0.28805238	0.93947893	1	4517	tags=28%, list=18%, signal=33%
REACTOME_MEIOTIC_SYNAPSIS	64	0.445869	1.137998	0.24423963	0.93476504	1	6397	tags=38%, list=25%, signal=50%
REACTOME_HEMOSTASIS	408	0.35995	1.13715	0.15441176	0.9311093	1	3223	tags=15%, list=13%, signal=17%
BIOCARTA_PPARA_PATHWAY	53	0.455039	1.136978	0.28526148	0.92507076	1	2410	tags=17%, list=9%, signal=19%
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	34	0.47616	1.13461	0.2821369	0.92699677	1	8198	tags=44%, list=32%, signal=65%
REACTOME_TIE2_SIGNALING	17	0.538143	1.134483	0.29965752	0.9211186	1	4756	tags=41%, list=19%, signal=51%
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	23	0.522251	1.133356	0.30981067	0.91860086	1	3317	tags=17%, list=13%, signal=20%
BIOCARTA_GH_PATHWAY	26	0.509876	1.131194	0.30819672	0.91998446	1	4756	tags=35%, list=19%, signal=43%
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	20	0.513814	1.12831	0.31088084	0.9238655	1	4488	tags=40%, list=18%, signal=48%
REACTOME_IRON_UPTAKE_AND_TRANSPORT	35	0.484411	1.127345	0.29307568	0.92074007	1	6543	tags=34%, list=26%, signal=46%
REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING	31	0.477726	1.121135	0.30882353	0.93722785	1	1943	tags=16%, list=8%, signal=17%
REACTOME_ACYL_CHAIN_REMODELLING_OF_PE	17	0.530067	1.117459	0.32841328	0.9444429	1	3133	tags=29%, list=12%, signal=34%
BIOCARTA_SPPA_PATHWAY	21	0.513941	1.113905	0.3429054	0.9511328	1	3948	tags=24%, list=15%, signal=28%
REACTOME_BASIGIN_INTERACTIONS	24	0.50102	1.11295	0.3275563	0.9480991	1	2642	tags=21%, list=10%, signal=23%
REACTOME_REGULATION_OF_APOPTOSIS	56	0.448525	1.111617	0.31104198	0.946798	1	7428	tags=43%, list=29%, signal=60%
BIOCARTA_CTCF_PATHWAY	23	0.5002	1.107803	0.316609	0.9540625	1	1927	tags=13%, list=8%, signal=14%
REACTOME_PYRIMIDINE_METABOLISM	19	0.51103	1.10762	0.33854166	0.948499	1	2530	tags=21%, list=10%, signal=23%
BIOCARTA_ALK_PATHWAY	34	0.465284	1.107515	0.31764707	0.94270605	1	3367	tags=18%, list=13%, signal=20%
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	104	0.397397	1.100761	0.29555237	0.9611441	1	6618	tags=39%, list=26%, signal=53%
BIOCARTA_MTA3_PATHWAY	18	0.516858	1.100322	0.33862433	0.9565695	1	5750	tags=50%, list=23%, signal=64%
REACTOME_CA_DEPENDENT_EVENTS	26	0.488411	1.096338	0.3416252	0.96457756	1	4010	tags=15%, list=16%, signal=18%
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	67	0.422136	1.092489	0.31455398	0.9719719	1	7617	tags=49%, list=30%, signal=70%
KEGG_PROTEIN_EXPORT	23	0.494251	1.089206	0.3529412	0.97816294	1	1337	tags=13%, list=5%, signal=14%
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	65	0.417983	1.08915	0.32668713	0.9721706	1	7617	tags=49%, list=30%, signal=70%
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	75	0.409058	1.089129	0.3023952	0.96613574	1	2564	tags=13%, list=10%, signal=15%
REACTOME_SIGNAL_TRANSDUCTION_BY_L1	34	0.460313	1.088953	0.33663365	0.96076256	1	3223	tags=24%, list=13%, signal=27%
REACTOME_REGULATION_OF_HYPOXIA_INDUCIBLE_FACTOR_HIF_BY_OXYGEN	22	0.485985	1.086738	0.35643566	0.9625683	1	2363	tags=18%, list=9%, signal=20%
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	53	0.425152	1.085944	0.3146965	0.95960766	1	2719	tags=21%, list=11%, signal=23%
REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE	44	0.444373	1.08424	0.3418124	0.959853	1	136	tags=7%, list=1%, signal=7%
REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	24	0.483548	1.083424	0.35049835	0.9570774	1	1296	tags=17%, list=5%, signal=18%
BIOCARTA_TOLL_PATHWAY	35	0.454853	1.083222	0.32495812	0.95202965	1	3837	tags=17%, list=15%, signal=20%
REACTOME_AXON_GUIDANCE	229	0.363818	1.082009	0.2859025	0.9508083	1	2286	tags=10%, list=9%, signal=11%
KEGG_CALCIUM_SIGNALING_PATHWAY	155	0.374026	1.081834	0.30769232	0.94576424	1	2602	tags=15%, list=10%, signal=17%
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	41	0.440825	1.077368	0.33774835	0.9557531	1	798	tags=10%, list=3%, signal=10%
REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS	64	0.416151	1.075247	0.35407406	0.9576428	1	3570	tags=19%, list=14%, signal=22%
REACTOME_RNA_POL_I_TRANSCRIPTION	79	0.405248	1.074662	0.35103244	0.9543587	1	6099	tags=30%, list=24%, signal=40%
BIOCARTA_INSULIN_PATHWAY	21	0.497225	1.074358	0.37122557	0.9497413	1	4756	tags=33%, list=19%, signal=41%
BIOCARTA_CCR3_PATHWAY	22	0.487966	1.072629	0.383821	0.95029545	1	3948	tags=23%, list=15%, signal=27%
BIOCARTA_PROTEASOME_PATHWAY	28	0.47399	1.072008	0.37221268	0.94695824	1	9190	tags=61%, list=36%, signal=95%
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	81	0.397911	1.071451	0.33576643	0.9433855	1	7731	tags=37%, list=30%, signal=53%
KEGG_CITRATE_CYCLE_TCA_CYCLE	29	0.463083	1.070106	0.36963695	0.94279945	1	5080	tags=31%, list=20%, signal=39%
REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	28	0.474424	1.06765	0.37024793	0.94543433	1	1296	tags=14%, list=5%, signal=15%
KEGG_OLFACTORY_TRANSDUCTION	49	0.436154	1.065596	0.34923077	0.946852	1	3840	tags=22%, list=15%, signal=26%
REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_AND_AMINE_COMPOUNDS	70	0.408192	1.064668	0.35603714	0.9445531	1	3704	tags=21%, list=15%, signal=25%
REACTOME_BIOLOGICAL_OXIDATIONS	108	0.383011	1.062848	0.34705883	0.9453967	1	2830	tags=17%, list=11%, signal=19%
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	30	0.464579	1.06164	0.38758388	0.9441915	1	5860	tags=30%, list=23%, signal=39%
BIOCARTA_HER2_PATHWAY	22	0.4875	1.061318	0.39826086	0.94015795	1	3223	tags=27%, list=13%, signal=31%
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	162	0.363005	1.058879	0.33065596	0.94288766	1	2038	tags=12%, list=8%, signal=13%
REACTOME_CELL_CYCLE_CHECKPOINTS	110	0.374502	1.056504	0.36947218	0.9454774	1	7774	tags=38%, list=30%, signal=55%
KEGG_RNA_POLYMERASE	29	0.460851	1.052341	0.38039866	0.95361567	1	5810	tags=45%, list=23%, signal=58%
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	132	0.369415	1.051145	0.34051725	0.9525287	1	7887	tags=39%, list=31%, signal=56%
REACTOME_RNA_POL_II_TRANSCRIPTION	94	0.387534	1.046157	0.37896255	0.96397644	1	5865	tags=27%, list=23%, signal=34%
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_IN_EMT_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	15	0.50879	1.043892	0.42105263	0.96637994	1	410	tags=7%, list=2%, signal=7%
REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT	27	0.463726	1.042353	0.42708334	0.96646893	1	4032	tags=22%, list=16%, signal=26%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	97	0.379157	1.04131	0.36363637	0.9646104	1	6397	tags=30%, list=25%, signal=40%
REACTOME_SIGNALING_BY_WNT	62	0.399967	1.038993	0.3934681	0.9673461	1	7428	tags=45%, list=29%, signal=64%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	50	0.419264	1.038868	0.39556962	0.96267295	1	708	tags=6%, list=3%, signal=6%
REACTOME_CHROMOSOME_MAINTENANCE	110	0.368148	1.038594	0.38152012	0.95862854	1	6799	tags=33%, list=27%, signal=44%
REACTOME_SYNTHESIS_OF_PC	17	0.497442	1.037893	0.4224599	0.9560122	1	4582	tags=41%, list=18%, signal=50%
REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	17	0.49187	1.03777	0.41696113	0.95153594	1	5216	tags=35%, list=20%, signal=44%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	24	0.476274	1.035872	0.43674177	0.9528378	1	1879	tags=21%, list=7%, signal=22%
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	49	0.422384	1.03521	0.3984	0.9501987	1	6059	tags=37%, list=24%, signal=48%
REACTOME_TRANSCRIPTION	189	0.34948	1.030321	0.40684932	0.96073335	1	6099	tags=30%, list=24%, signal=39%
REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	20	0.483378	1.028077	0.43463498	0.96298033	1	2030	tags=25%, list=8%, signal=27%
BIOCARTA_NGF_PATHWAY	18	0.481127	1.025717	0.45360824	0.96555406	1	4756	tags=33%, list=19%, signal=41%
REACTOME_SYNTHESIS_OF_PA	21	0.470951	1.024683	0.4214047	0.9640587	1	2145	tags=14%, list=8%, signal=16%
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	33	0.435586	1.0239	0.41373533	0.9617074	1	5390	tags=30%, list=21%, signal=38%
REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION	16	0.497575	1.02388	0.44181818	0.9570173	1	136	tags=13%, list=1%, signal=13%
KEGG_FOCAL_ADHESION	193	0.347182	1.022012	0.41888297	0.9584095	1	4571	tags=22%, list=18%, signal=27%
REACTOME_INSULIN_RECEPTOR_RECYCLING	21	0.466664	1.021347	0.43816254	0.9560218	1	8247	tags=52%, list=32%, signal=77%
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	54	0.407431	1.018268	0.41259843	0.96095806	1	1084	tags=6%, list=4%, signal=6%
REACTOME_OPIOID_SIGNALLING	70	0.382542	1.017559	0.41768292	0.95853245	1	5120	tags=24%, list=20%, signal=30%
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	52	0.404349	1.01641	0.43393394	0.9575536	1	5810	tags=27%, list=23%, signal=35%
REACTOME_SHC_MEDIATED_CASCADE	22	0.458125	1.014745	0.46192053	0.9581807	1	136	tags=9%, list=1%, signal=9%
REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	50	0.407264	1.013426	0.43670887	0.95767987	1	6181	tags=30%, list=24%, signal=40%
BIOCARTA_IGF1_PATHWAY	21	0.469602	1.012779	0.44821733	0.9550803	1	4756	tags=33%, list=19%, signal=41%
REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	24	0.468986	1.011766	0.45502645	0.95375943	1	6412	tags=33%, list=25%, signal=44%
REACTOME_CELL_CYCLE	385	0.323822	1.008796	0.4337051	0.9586682	1	6799	tags=31%, list=27%, signal=42%
KEGG_VEGF_SIGNALING_PATHWAY	68	0.379911	1.008744	0.42442748	0.9543868	1	4163	tags=25%, list=16%, signal=30%
REACTOME_CELL_CYCLE_MITOTIC	302	0.327504	1.008232	0.42469135	0.9516067	1	7464	tags=36%, list=29%, signal=50%
REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	17	0.484867	1.008199	0.470483	0.9473097	1	1344	tags=12%, list=5%, signal=12%
REACTOME_TELOMERE_MAINTENANCE	69	0.388492	1.005466	0.43252033	0.95116633	1	8555	tags=46%, list=34%, signal=70%
BIOCARTA_RAC1_PATHWAY	23	0.44841	1.00505	0.46101695	0.94813395	1	1927	tags=13%, list=8%, signal=14%
KEGG_INOSITOL_PHOSPHATE_METABOLISM	53	0.394178	1.004955	0.4442623	0.94413143	1	2564	tags=13%, list=10%, signal=15%
KEGG_TGF_BETA_SIGNALING_PATHWAY	82	0.376383	1.003587	0.43438914	0.94403297	1	3350	tags=18%, list=13%, signal=21%
BIOCARTA_TFF_PATHWAY	20	0.452208	1.002917	0.45518455	0.9418561	1	4756	tags=35%, list=19%, signal=43%
KEGG_SPLICEOSOME	123	0.357774	1.002658	0.43841642	0.9384592	1	7070	tags=28%, list=28%, signal=38%
KEGG_O_GLYCAN_BIOSYNTHESIS	23	0.456993	1.002246	0.4696707	0.93549734	1	1151	tags=13%, list=5%, signal=14%
REACTOME_DEADENYLATION_OF_MRNA	17	0.479905	1.001634	0.46306306	0.9330687	1	5892	tags=35%, list=23%, signal=46%
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	18	0.474937	1.000125	0.45794392	0.93366075	1	7601	tags=50%, list=30%, signal=71%
REACTOME_MEMBRANE_TRAFFICKING	121	0.354617	1.000026	0.4522472	0.92981356	1	5316	tags=25%, list=21%, signal=31%
BIOCARTA_MAL_PATHWAY	19	0.470994	0.998681	0.455516	0.9297485	1	3367	tags=16%, list=13%, signal=18%
KEGG_ACUTE_MYELOID_LEUKEMIA	56	0.391498	0.997766	0.4573269	0.9283932	1	933	tags=11%, list=4%, signal=11%
REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	78	0.376593	0.997357	0.4775194	0.9255577	1	625	tags=5%, list=2%, signal=5%

KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	196	0.333043	0.997316	0.4654498	0.9216861	1	1985	tags=9%, list=8%, signal=9%
KEGG_OXIDATIVE_PHOSPHORYLATION	93	0.364322	0.992618	0.46439168	0.9314307	1	7617	tags=44%, list=30%, signal=63%
BIOCARTA_EIF4_PATHWAY	24	0.454314	0.992603	0.4645799	0.92744845	1	4401	tags=29%, list=17%, signal=35%
BIOCARTA_RACCYCD_PATHWAY	26	0.453136	0.991761	0.47058824	0.92596346	1	3918	tags=19%, list=15%, signal=23%
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	17	0.46121	0.990672	0.4642857	0.92506176	1	3001	tags=18%, list=12%, signal=20%
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	44	0.40635	0.98968	0.4752	0.9236713	1	2125	tags=16%, list=8%, signal=17%
BIOCARTA_TPO_PATHWAY	24	0.445407	0.987427	0.47586206	0.9262785	1	4756	tags=33%, list=19%, signal=41%
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	36	0.415403	0.98679	0.46042004	0.92431706	1	4298	tags=25%, list=17%, signal=30%
REACTOME_PI_3K_CASCADE	48	0.401157	0.981814	0.4648986	0.93463576	1	1943	tags=13%, list=8%, signal=14%
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA	19	0.464643	0.979319	0.48776224	0.9378079	1	4894	tags=37%, list=19%, signal=46%
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	77	0.36916	0.977297	0.4673748	0.9396402	1	7428	tags=42%, list=29%, signal=58%
BIOCARTA_PAR1_PATHWAY	35	0.424061	0.976889	0.5024793	0.9369703	1	2564	tags=14%, list=10%, signal=16%
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	27	0.42986	0.974219	0.4788494	0.9408243	1	3972	tags=19%, list=16%, signal=22%
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	20	0.449045	0.970033	0.516696	0.94870734	1	4887	tags=40%, list=19%, signal=49%
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	38	0.409589	0.969931	0.49447078	0.9451058	1	1515	tags=5%, list=6%, signal=6%
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	181	0.328012	0.969148	0.49395972	0.9435023	1	2405	tags=13%, list=9%, signal=15%
KEGG_HUNTINGTONS_DISEASE	151	0.340599	0.967813	0.52136755	0.94318163	1	5910	tags=29%, list=23%, signal=38%
BIOCARTA_ECM_PATHWAY	24	0.44006	0.965659	0.49834436	0.9452904	1	4488	tags=25%, list=18%, signal=30%
KEGG_ENDOCYTOSIS	166	0.32825	0.96221	0.52387846	0.95091015	1	2194	tags=10%, list=9%, signal=10%
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	102	0.352034	0.962175	0.5138282	0.9472084	1	1296	tags=9%, list=5%, signal=9%
BIOCARTA_TID_PATHWAY	18	0.454762	0.961406	0.5103448	0.9455111	1	1146	tags=11%, list=4%, signal=12%
REACTOME_KINESINS	23	0.435081	0.960266	0.5	0.94502604	1	1697	tags=13%, list=7%, signal=14%
REACTOME_APOPTOSIS	141	0.337335	0.958305	0.53781515	0.94667584	1	5068	tags=20%, list=20%, signal=25%
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	323	0.310894	0.95458	0.5613609	0.953517	1	5127	tags=22%, list=20%, signal=28%
KEGG_GALACTOSE_METABOLISM	22	0.444307	0.952272	0.48861647	0.955984	1	3026	tags=18%, list=12%, signal=21%
REACTOME_DNA_REPAIR	103	0.348417	0.951385	0.5553997	0.9546865	1	6105	tags=24%, list=24%, signal=32%
BIOCARTA_MET_PATHWAY	37	0.402348	0.950428	0.5190972	0.9534686	1	4943	tags=27%, list=19%, signal=33%
REACTOME_MRNA_3_END_PROCESSING	33	0.407936	0.94884	0.5281457	0.954141	1	6491	tags=30%, list=25%, signal=41%
REACTOME_GABA_B_RECEPTOR_ACTIVATION	35	0.406812	0.94576	0.5472637	0.95902675	1	458	tags=9%, list=2%, signal=9%
REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	57	0.368225	0.944629	0.53051645	0.95847267	1	6181	tags=30%, list=24%, signal=39%
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	61	0.367968	0.943634	0.55007946	0.95736504	1	6059	tags=33%, list=24%, signal=43%
REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	48	0.386106	0.943418	0.5378549	0.9542804	1	3308	tags=17%, list=13%, signal=19%
REACTOME_GLUCOSE_METABOLISM	61	0.366172	0.942956	0.5504732	0.95180583	1	5231	tags=26%, list=21%, signal=33%
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	111	0.338788	0.941688	0.52949643	0.9517764	1	1927	tags=8%, list=8%, signal=9%
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	20	0.437831	0.94157	0.5253378	0.9484884	1	5216	tags=40%, list=20%, signal=50%
REACTOME_SIGNALING_BY_FGFR	100	0.344609	0.93548	0.5433186	0.9614403	1	1943	tags=8%, list=8%, signal=9%
REACTOME_FRS2_MEDIATED_CASCADE	30	0.405349	0.931791	0.5519591	0.96775407	1	1943	tags=13%, list=8%, signal=14%
REACTOME_DEVELOPMENTAL_BIOLOGY	351	0.299815	0.931634	0.6528436	0.9645708	1	2286	tags=10%, list=9%, signal=10%
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	23	0.411626	0.928894	0.5457627	0.9683162	1	3814	tags=26%, list=15%, signal=31%
REACTOME_FORMATION_OF_TRANSCRIPTION_COUPLED_NER_TC_NER_REPAIR_COMPLEX	29	0.404948	0.928306	0.56435645	0.9662625	1	3876	tags=24%, list=15%, signal=28%
REACTOME_TRANSLATION	170	0.318631	0.927793	0.5813953	0.964087	1	2012	tags=9%, list=8%, signal=10%
KEGG_NON_SMALL_CELL_LUNG_CANCER	54	0.362061	0.927255	0.5629984	0.9619992	1	1993	tags=15%, list=8%, signal=16%
KEGG_HEMATOPOIETIC_CELL_LINEAGE	65	0.353527	0.926227	0.5602504	0.9611508	1	3317	tags=23%, list=13%, signal=26%
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	120	0.327145	0.92525	0.5872781	0.9601035	1	4894	tags=27%, list=19%, signal=33%
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	124	0.324293	0.924517	0.5905849	0.95858544	1	4167	tags=19%, list=16%, signal=22%
REACTOME_PLC_BETA_MEDIATED_EVENTS	38	0.383426	0.923014	0.57284766	0.958949	1	2913	tags=13%, list=11%, signal=15%
BIOCARTA_FMLP_PATHWAY	36	0.390879	0.922345	0.54545456	0.95721847	1	3756	tags=22%, list=15%, signal=26%
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	24	0.422422	0.921434	0.55126053	0.9560874	1	4894	tags=25%, list=19%, signal=31%
REACTOME_COLLAGEN_FORMATION	53	0.365426	0.917878	0.5771605	0.96197516	1	2999	tags=19%, list=12%, signal=21%
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	204	0.308082	0.917777	0.6464516	0.9588161	1	3130	tags=14%, list=12%, signal=16%
REACTOME_MITOTIC_PROMETAPHASE	78	0.346136	0.917552	0.58651024	0.9558988	1	7832	tags=38%, list=31%, signal=55%
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI	17	0.432253	0.915649	0.5621806	0.9576169	1	560	tags=12%, list=2%, signal=12%
REACTOME_ACYL_CHAIN_REMODELLING_OF_PC	18	0.427161	0.914478	0.57699114	0.9571742	1	3133	tags=22%, list=12%, signal=25%
REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	114	0.324995	0.91253	0.62608695	0.9589143	1	4345	tags=17%, list=17%, signal=20%
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	29	0.39865	0.908796	0.58132046	0.9649857	1	3010	tags=17%, list=12%, signal=20%
REACTOME_METABOLISM_OF_CARBOHYDRATES	215	0.300602	0.903468	0.6744186	0.97487676	1	5758	tags=24%, list=23%, signal=30%
REACTOME_EGFR_DOWNREGULATION	25	0.407542	0.901761	0.5721562	0.97594285	1	4032	tags=28%, list=16%, signal=33%
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	42	0.369531	0.898961	0.59587955	0.97953606	1	5067	tags=24%, list=20%, signal=30%
BIOCARTA_NKCELLS_PATHWAY	18	0.422056	0.898936	0.6016667	0.9762099	1	3223	tags=17%, list=13%, signal=19%
BIOCARTA_CREB_PATHWAY	26	0.400396	0.897263	0.58949095	0.97718066	1	4756	tags=27%, list=19%, signal=33%
BIOCARTA_MCALPAIN_PATHWAY	23	0.405298	0.89686	0.6044143	0.9747981	1	129	tags=4%, list=1%, signal=4%
BIOCARTA_AMI_PATHWAY	17	0.427062	0.892331	0.57829183	0.98305625	1	6876	tags=53%, list=27%, signal=72%
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	15	0.442303	0.891693	0.603321	0.9812917	1	3001	tags=20%, list=12%, signal=23%
KEGG_MELANOMA	64	0.347552	0.890275	0.6053812	0.9814557	1	1943	tags=13%, list=8%, signal=13%
REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR	88	0.330166	0.889066	0.63274336	0.98108006	1	1943	tags=8%, list=8%, signal=9%
KEGG_PATHWAYS_IN_CANCER	304	0.289375	0.888547	0.72073174	0.97910595	1	2481	tags=11%, list=10%, signal=12%
REACTOME_HIV_LIFE_CYCLE	107	0.315885	0.887848	0.658858	0.9775375	1	5397	tags=22%, list=21%, signal=28%
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	22	0.406319	0.885495	0.6207483	0.9801927	1	410	tags=5%, list=2%, signal=5%
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	94	0.325089	0.885023	0.66312593	0.9780901	1	5810	tags=24%, list=23%, signal=32%
BIOCARTA_PDGF_PATHWAY	32	0.374941	0.882989	0.61833334	0.979926	1	4756	tags=22%, list=19%, signal=27%
BIOCARTA_IGF1R_PATHWAY	22	0.396924	0.881202	0.6260575	0.98102975	1	4756	tags=27%, list=19%, signal=33%
BIOCARTA_NO1_PATHWAY	28	0.391823	0.879905	0.6258741	0.98099935	1	4571	tags=21%, list=18%, signal=26%
KEGG_PURINE_METABOLISM	142	0.309216	0.879048	0.7053942	0.9797346	1	4169	tags=22%, list=16%, signal=26%
BIOCARTA_FCER1_PATHWAY	36	0.371332	0.877034	0.64786327	0.981215	1	4756	tags=25%, list=19%, signal=31%
REACTOME_GRB2_SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTERGRINS_	15	0.438555	0.876101	0.6360544	0.9802957	1	6876	tags=60%, list=27%, signal=82%
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	82	0.329827	0.873133	0.6519757	0.9842461	1	1769	tags=11%, list=7%, signal=12%
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	77	0.32529	0.871913	0.675841	0.98400563	1	5346	tags=27%, list=21%, signal=34%
REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	18	0.411237	0.871188	0.61565834	0.98245525	1	4894	tags=28%, list=19%, signal=34%
REACTOME_MRNA_PROCESSING	151	0.300296	0.869799	0.7253521	0.9825897	1	7887	tags=35%, list=31%, signal=51%
REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	15	0.433531	0.869013	0.63738316	0.98127246	1	3948	tags=33%, list=15%, signal=39%
KEGG_PROSTATE_CANCER	84	0.324747	0.868399	0.6743827	0.97958845	1	1993	tags=13%, list=8%, signal=14%
REACTOME_GPCR_DOWNSTREAM_SIGNALING	357	0.281552	0.86709	0.796319	0.97947335	1	2405	tags=10%, list=9%, signal=11%
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	32	0.36967	0.862071	0.6247934	0.9881526	1	3972	tags=19%, list=16%, signal=22%
KEGG_RENAL_CELL_CARCINOMA	66	0.329005	0.861862	0.67771083	0.9854452	1	3223	tags=14%, list=13%, signal=16%
REACTOME_HS_GAG_DEGRADATION	19	0.403421	0.858129	0.65180105	0.9911212	1	1034	tags=11%, list=4%, signal=11%
REACTOME_SIGNALLING_BY_NGF	206	0.288705	0.857243	0.7720685	0.99005795	1	4260	tags=15%, list=17%, signal=18%
BIOCARTA_CASPASE_PATHWAY	23	0.387227	0.855904	0.67657346	0.9902075	1	3730	tags=17%, list=15%, signal=20%
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	20	0.394777	0.855312	0.6403509	0.9885222	1	410	tags=5%, list=2%, signal=5%
REACTOME_G_PROTEIN_ACTIVATION	23	0.390369	0.85446	0.65656567	0.9873108	1	4937	tags=26%, list=19%, signal=32%
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	80	0.316155	0.851483	0.6972477	0.99134755	1	6326	tags=30%, list=25%, signal=40%
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	29	0.36805	0.849027	0.6491525	0.9939637	1	1857	tags=14%, list=7%, signal=15%
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	131	0.293028	0.845885	0.74110955	0.99817467	1	1959	tags=9%, list=8%, signal=10%
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	20	0.397045	0.844449	0.6579407	0.9983575	1	3193	tags=25%, list=13%, signal=29%
REACTOME_SIGNALING_BY_CONSTITUTIVELY_ACTIVE_EGFR	18	0.399531	0.843605	0.65591395	0.99716955	1	1927	tags=17%, list=8%, signal=18%
KEGG_PENTOSE_PHOSPHATE_PATHWAY	23	0.381611	0.842917	0.6627517	0.99577045	1	7082	tags=39%, list=28%, signal=54%
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	23	0.380348	0.842746	0.66435987	0.99304473	1	458	tags=9%, list=2%, signal=9%
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	111	0.307818	0.842743	0.7573099	0.9899986	1	6099	tags=31%, list=24%, signal=40%
REACTOME_DAG_AND_IP3_SIGNALING	28	0.364748	0.842039	0.6730769	0.98853767	1	125	tags=4%, list=0%, signal=4%
KEGG_ETHER_LIPID_METABOLISM	23	0.384826	0.84185	0.6730769	0.98599505	1	3608	tags=22%, list=14%, signal=25%
REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	19	0.392729	0.8412	0.67911714	0.98438364	1	4894	tags=26%, list=19%, signal=33%
REACTOME_L1CAM_INTERACTIONS	81	0.3127	0.840488	0.73417723	0.98308355	1	3595	tags=16%, list=14%, signal=19%
BIOCARTA_NFKB_PATHWAY	23	0.386471	0.840144	0.68456376	0.98090637	1	67	tags=4%, list=0%, signal=4%
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	42	0.349118	0.839235	0.696875	0.9799033	1	4401	tags=17%, list=17%, signal=20%
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	26	0.375507	0.839232	0.6464471	0.97697777	1	5216	tags=31%, list=20%, signal=39%
BIOCARTA_TCR_PATHWAY	43	0.336042	0.837426	0.6970684	0.9781385	1	4756	tags=23%, list=19%, signal=29%
REACTOME_IL_RECEPTOR_SHC_SIGNALING	23	0.382502	0.837248	0.68576103	0.9756342	1	2431	tags=22%, list=10%, signal=24%
REACTOME_METABOLISM_OF_MRNA	230	0.274984	0.836629	0.8348745	0.97407556	1	7295	tags=29%, list=29%, signal=40%
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	64	0.326126	0.835972	0.71791047	0.9726612	1	4086	tags=20%, list=16%, signal=24%
REACTOME_LIPOPROTEIN_METABOLISM	24	0.377266	0.83416	0.6828859	0.97379166	1	216	tags=4%, list=1%, signal=4%
REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLP1	15	0.418548	0.834134	0.67581475	0.9709644	1	3010	tags=20%, list=12%, signal=23%
REACTOME_HS_GAG_BIOSYNTHESIS	28	0.368518	0.831278	0.68770766	0.974246	1	2126	tags=11%, list=8%, signal=12%
KEGG_BUTANOATE_METABOLISM	29	0.361931	0.827536	0.6751269	0.9792064	1	5451	tags=21%, list=21%, signal=26%
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	77	0.313184	0.825642	0.75808936	0.9804241	1	4756	tags=26%, list=19%, signal=32%
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_2_PROMOTER	23	0.372369	0.823207	0.6650165	0.9826569	1	6060	tags=43%, list=24%, signal=57%
KEGG_AXON_GUIDANCE	123	0.290004	0.818192	0.8081805	0.99040127	1	4541	tags=17%, list=18%, signal=21%
BIOCARTA_P53_PATHWAY	16	0.389123	0.817812	0.69624573	0.98831415	1	7100	tags=44%, list=28%, signal=61%
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	19	0.384522	0.815483	0.6985816	0.9903469	1	1034	tags=11%, list=4%, signal=11%

REACTOME_GLYCOLYSIS	25	0.371162	0.814231	0.7111486	0.98997134	1	4678	tags=28%, list=18%, signal=34%
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	30	0.346175	0.813167	0.7419355	0.98930585	1	4649	tags=23%, list=18%, signal=28%
KEGG_DILATED_CARDIOMYOPATHY	78	0.306368	0.806922	0.7848485	0.99923086	1	3317	tags=15%, list=13%, signal=18%
REACTOME_METABOLISM_OF_PROTEINS	430	0.253995	0.805984	0.93787336	0.9982001	1	2244	tags=8%, list=9%, signal=9%
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	74	0.304273	0.805763	0.7807808	0.9958392	1	3317	tags=15%, list=13%, signal=17%
REACTOME_PHOSPHOLIPID_METABOLISM	176	0.275192	0.8049	0.8630319	0.9948158	1	3906	tags=16%, list=15%, signal=19%
REACTOME_INFLUENZA_LIFE_CYCLE	157	0.279685	0.803935	0.86052996	0.9938954	1	4167	tags=16%, list=16%, signal=19%
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	66	0.308368	0.803192	0.7776097	0.992433	1	4756	tags=26%, list=19%, signal=32%
BIOCARTA_RARRXR_PATHWAY	15	0.389477	0.802852	0.68705034	0.9903209	1	2579	tags=13%, list=10%, signal=15%
BIOCARTA_CK1_PATHWAY	16	0.391346	0.801747	0.7101695	0.9896448	1	6447	tags=44%, list=25%, signal=59%
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	129	0.279422	0.797922	0.86609685	0.9946702	1	4416	tags=16%, list=17%, signal=20%
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	350	0.256757	0.796416	0.9357231	0.9946787	1	4894	tags=20%, list=19%, signal=24%
REACTOME_GLUCONEOGENESIS	30	0.346007	0.796333	0.7629382	0.99209505	1	4629	tags=30%, list=18%, signal=37%
REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	26	0.349594	0.795941	0.7385965	0.9900732	1	4032	tags=23%, list=16%, signal=27%
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	24	0.360591	0.794235	0.74176776	0.9904164	1	5467	tags=29%, list=21%, signal=37%
REACTOME_NRIF_SIGNALS_CELL_DEATH_FROM_THE_NUCLEUS	15	0.391797	0.793951	0.7241379	0.98826975	1	410	tags=7%, list=2%, signal=7%
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	25	0.353815	0.791745	0.72183096	0.9897952	1	4602	tags=24%, list=18%, signal=29%
REACTOME_INNATE_IMMUNE_SYSTEM	199	0.262118	0.79169	0.90247077	0.9871895	1	4406	tags=14%, list=17%, signal=16%
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	183	0.27065	0.790907	0.8738502	0.9860624	1	4756	tags=20%, list=19%, signal=24%
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_DIFFERENTIATION	68	0.305295	0.786203	0.82182986	0.99220073	1	6228	tags=32%, list=24%, signal=43%
KEGG_CARDIAC_MUSCLE_CONTRACTION	59	0.305706	0.780503	0.82115084	0.99987906	1	6845	tags=31%, list=27%, signal=42%
REACTOME_METABOLISM_OF_RNA	274	0.256283	0.778546	0.94382024	1	1	7295	tags=29%, list=29%, signal=40%
KEGG_CHEMOKINE_SIGNALING_PATHWAY	155	0.26771	0.772236	0.8931909	1	1	3031	tags=12%, list=12%, signal=13%
REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS	74	0.296212	0.7718	0.83557546	1	1	4837	tags=22%, list=19%, signal=27%
KEGG_TIGHT_JUNCTION	117	0.274345	0.769347	0.8861314	1	1	1677	tags=5%, list=7%, signal=5%
REACTOME_SIGNALING_BY_FGFR1_FUSION_MUTANTS	18	0.367146	0.768394	0.76842105	1	1	7003	tags=44%, list=27%, signal=61%
REACTOME_CD28_CO_STIMULATION	30	0.337009	0.768171	0.7723577	1	1	4756	tags=30%, list=19%, signal=37%
REACTOME_PEPTIDE_CHAIN_ELONGATION	108	0.276174	0.767283	0.9101449	1	1	1959	tags=9%, list=8%, signal=10%
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	85	0.284372	0.766152	0.8539493	1	1	1927	tags=9%, list=8%, signal=10%
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	36	0.319211	0.76369	0.7971474	1	1	3972	tags=19%, list=16%, signal=23%
BIOCARTA_ACTINY_PATHWAY	20	0.354388	0.75125	0.79136693	1	1	1985	tags=10%, list=8%, signal=11%
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	41	0.306725	0.746935	0.8398744	1	1	6131	tags=29%, list=24%, signal=38%
REACTOME_G1_PHASE	36	0.316415	0.746304	0.8424437	1	1	1444	tags=11%, list=6%, signal=12%
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	35	0.312086	0.744976	0.8338558	1	1	7671	tags=37%, list=30%, signal=53%
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	20	0.345718	0.741844	0.8115702	1	1	2554	tags=20%, list=10%, signal=22%
REACTOME_DNA_STRAND_ELONGATION	30	0.321354	0.741428	0.8159204	1	1	4536	tags=27%, list=18%, signal=32%
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	31	0.321179	0.738558	0.8374793	1	1	4032	tags=16%, list=16%, signal=19%
REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	98	0.270821	0.736611	0.92539454	1	1	4726	tags=20%, list=19%, signal=25%
REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	17	0.352533	0.736191	0.8077634	1	1	4996	tags=24%, list=20%, signal=29%
REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMATE_BINDING_AND_ACTIVATION	15	0.366194	0.732353	0.81395346	1	1	3396	tags=27%, list=13%, signal=31%
REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	104	0.263309	0.727346	0.9388972	1	1	3156	tags=13%, list=12%, signal=14%
REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	81	0.274715	0.727344	0.89522344	1	1	4312	tags=15%, list=17%, signal=18%
KEGG_LONG_TERM_POTENTIATION	65	0.281273	0.723506	0.8773006	1	1	3811	tags=18%, list=15%, signal=22%
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	29	0.313815	0.722691	0.8241206	1	1	5544	tags=24%, list=22%, signal=31%
BIOCARTA_MPR_PATHWAY	33	0.305272	0.720274	0.8474026	1	1	4010	tags=15%, list=16%, signal=18%
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	129	0.258674	0.720192	0.94017094	1	1	4416	tags=16%, list=17%, signal=19%
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	44	0.294971	0.717555	0.8758278	1	1	4361	tags=18%, list=17%, signal=22%
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	18	0.339436	0.716812	0.8344827	1	1	3014	tags=11%, list=12%, signal=13%
KEGG_GAP_JUNCTION	82	0.266389	0.715417	0.93777776	1	1	5216	tags=24%, list=20%, signal=31%
REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	17	0.343497	0.714292	0.8298611	1	1	7076	tags=47%, list=28%, signal=65%
KEGG_DNA_REPLICATION	36	0.300549	0.712964	0.87081337	1	1	5721	tags=25%, list=22%, signal=32%
REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	43	0.295014	0.712322	0.8923328	1	1	5544	tags=23%, list=22%, signal=30%
REACTOME_G2_M_CHECKPOINTS	41	0.295785	0.711594	0.8901099	1	1	5860	tags=27%, list=23%, signal=35%
BIOCARTA_INTRINSIC_PATHWAY	18	0.33992	0.709666	0.8612521	1	1	3193	tags=28%, list=13%, signal=32%
BIOCARTA_INTEGRIN_PATHWAY	38	0.294555	0.709244	0.89621085	1	1	4943	tags=24%, list=19%, signal=29%
REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE	24	0.317919	0.709056	0.8545781	1	1	5120	tags=25%, list=20%, signal=31%
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS	44	0.285039	0.703516	0.9018692	1	1	3837	tags=16%, list=15%, signal=19%
KEGG_FATTY_ACID_METABOLISM	37	0.29585	0.703329	0.8659794	1	1	3976	tags=16%, list=16%, signal=19%
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	60	0.272976	0.703197	0.9178515	1	1	1682	tags=7%, list=7%, signal=7%
BIOCARTA_NOS1_PATHWAY	20	0.320737	0.702329	0.8583916	1	1	4010	tags=20%, list=16%, signal=24%
REACTOME_RNA_POL_III_CHAIN_ELONGATION	17	0.325353	0.697044	0.85561496	1	1	5620	tags=41%, list=22%, signal=53%
REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	71	0.268627	0.696846	0.9411765	1	1	4312	tags=15%, list=17%, signal=19%
REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS	15	0.333374	0.696731	0.8531952	1	1	4602	tags=33%, list=18%, signal=41%
KEGG_CELL_CYCLE	123	0.248222	0.696488	0.97179127	1	1	6377	tags=28%, list=25%, signal=38%
REACTOME_G_ALPHA1213_SIGNALLING_EVENTS	72	0.262559	0.696485	0.9425626	1	1	3239	tags=14%, list=13%, signal=16%
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	26	0.307167	0.692975	0.87261146	1	1	4696	tags=31%, list=18%, signal=38%
REACTOME_BASE_EXCISION_REPAIR	19	0.322773	0.692511	0.85464096	1	1	590	tags=5%, list=2%, signal=5%
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS	29	0.300828	0.691318	0.88566554	1	1	4014	tags=21%, list=16%, signal=25%
REACTOME_REGULATION_OF_INSULIN_SECRETION	79	0.25598	0.689401	0.9482014	1	1	3031	tags=11%, list=12%, signal=13%
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	22	0.31396	0.688438	0.8836425	1	1	4894	tags=27%, list=19%, signal=34%
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	49	0.277517	0.684542	0.9220986	1	1	4361	tags=16%, list=17%, signal=20%
KEGG_PROPANOATE_METABOLISM	32	0.300051	0.682703	0.9086116	1	1	3497	tags=19%, list=14%, signal=22%
REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY	17	0.331592	0.682479	0.86013985	1	1	590	tags=6%, list=2%, signal=6%
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	45	0.281861	0.680661	0.9241706	1	1	5082	tags=22%, list=20%, signal=28%
REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	30	0.291909	0.679698	0.9070946	1	1	4894	tags=23%, list=19%, signal=29%
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	35	0.282035	0.676328	0.9159802	1	1	216	tags=3%, list=1%, signal=3%
KEGG_LONG_TERM_DEPRESSION	59	0.268245	0.675805	0.9555921	1	1	3659	tags=19%, list=14%, signal=22%
REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE	129	0.238969	0.674494	0.9869754	1	1	4260	tags=16%, list=17%, signal=19%
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	56	0.266325	0.671147	0.9344512	1	1	7430	tags=39%, list=29%, signal=55%
BIOCARTA_FAS_PATHWAY	29	0.287691	0.663761	0.9095652	1	1	586	tags=3%, list=2%, signal=4%
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	97	0.241399	0.662976	0.9851852	1	1	3811	tags=16%, list=15%, signal=19%
REACTOME_PROTEIN_FOLDING	50	0.26514	0.662704	0.95961225	1	1	5216	tags=26%, list=20%, signal=33%
KEGG_BASE_EXCISION_REPAIR	34	0.282527	0.662322	0.9325658	0.99992186	1	5611	tags=26%, list=22%, signal=34%
REACTOME_MITOTIC_G2_G2_M_PHASES	78	0.244171	0.658318	0.98121387	1	1	6544	tags=31%, list=26%, signal=41%
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	63	0.248583	0.648792	0.9727273	1	1	7430	tags=38%, list=29%, signal=54%
KEGG_ONE_CARBON_POOL_BY_FOLATE	17	0.312031	0.647882	0.899115	1	1	3780	tags=18%, list=15%, signal=21%
BIOCARTA_TNFR2_PATHWAY	17	0.300952	0.64111	0.9029982	1	1	2488	tags=12%, list=10%, signal=13%
REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	15	0.314239	0.638467	0.90017515	1	1	6447	tags=33%, list=25%, signal=45%
KEGG_BETA_ALANINE_METABOLISM	20	0.295497	0.637264	0.9255499	1	1	4089	tags=20%, list=16%, signal=24%
REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS	38	0.264926	0.637239	0.93771046	1	1	5544	tags=24%, list=22%, signal=30%
BIOCARTA_GPCR_PATHWAY	33	0.276447	0.636476	0.93791944	1	1	4010	tags=18%, list=16%, signal=22%
REACTOME_MYOGENESIS	22	0.289066	0.631216	0.92691624	1	1	5380	tags=23%, list=21%, signal=29%
REACTOME_SIGNALING_BY_NOTCH1	68	0.237348	0.621752	0.9782271	1	1	4334	tags=18%, list=17%, signal=21%
REACTOME_CTLA4_INHIBITORY_SIGNALING	19	0.291152	0.620857	0.9201331	1	1	6447	tags=32%, list=25%, signal=42%
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	92	0.230357	0.619251	0.9884058	1	1	6059	tags=26%, list=24%, signal=34%
KEGG_TYROSINE_METABOLISM	37	0.259039	0.613437	0.9736842	1	1	4850	tags=30%, list=19%, signal=37%
REACTOME_SIGNAL_AMPLIFICATION	29	0.26354	0.607643	0.9378151	1	1	5467	tags=24%, list=21%, signal=31%
BIOCARTA_P53HYPOXIA_PATHWAY	22	0.274569	0.598838	0.94954956	1	1	4465	tags=23%, list=17%, signal=28%
BIOCARTA_IL2_PATHWAY	21	0.266801	0.572123	0.9502573	1	1	4756	tags=19%, list=19%, signal=23%
REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLLAPSE	25	0.255286	0.566477	0.96940416	1	1	1993	tags=8%, list=8%, signal=9%
REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	15	0.276371	0.562698	0.9422383	1	1	5695	tags=33%, list=22%, signal=43%
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	51	0.218359	0.546356	0.9953344	1	1	7857	tags=33%, list=31%, signal=48%
REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDATION_IN_MUSCLE	18	0.253547	0.534824	0.9770723	1	1	892	tags=6%, list=3%, signal=6%
REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	51	0.213589	0.53472	0.9921875	1	1	3830	tags=12%, list=15%, signal=14%
KEGG_BASAL_TRANSCRIPTION_FACTORS	33	0.230495	0.531035	0.992	1	1	5792	tags=18%, list=23%, signal=23%
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_SYNTHESIS	25	0.238686	0.524326	0.99319726	1	1	6709	tags=36%, list=26%, signal=49%
KEGG_LYSOSOME	118	0.183579	0.511115	1	1	1	6416	tags=25%, list=25%, signal=34%
REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB	15	0.25	0.506549	0.98761064	1	1	5544	tags=27%, list=22%, signal=34%
BIOCARTA_P38MAPK_PATHWAY	39	0.210427	0.501706	1	1	1	4756	tags=13%, list=19%, signal=16%
BIOCARTA_MITOCHONDRIA_PATHWAY	21	0.234342	0.501085	0.9829642	1	1	3730	tags=14%, list=15%, signal=17%
KEGG_HOMOLOGOUS_RECOMBINATION	26	0.22136	0.496869	0.98694944	1	1	975	tags=4%, list=4%, signal=4%
BIOCARTA_CHREBP2_PATHWAY	39	0.204844	0.494083	0.99517685	1	1	2292	tags=8%, list=9%, signal=8%
REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	30	0.212383	0.490236	0.99169433	0.998529	1	1993	tags=7%, list=8%, signal=7%
KEGG_RNA_DEGRADATION	53	0.190189	0.484336	0.99841267	0.9969448	1	3943	tags=11%, list=15%, signal=13%
REACTOME_SIGNALING_BY_BMP	21	0.211124	0.45915	0.98967296	0.99678284	1	5637	tags=24%, list=22%, signal=31%

Table S10
GSEA Analysis on HNSC cancer cell lines comparing cell lines with or without 9p21.3 loss (arm or focal), Pathways Depleted

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX
SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE	51	-0.78458	-2.17592	0	0	0	2818
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	192	-0.5017	-1.72496	0	0.64153993	0.697	3133
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	23	-0.71864	-1.68964	0.00952381	0.6409758	0.837	565
REACTOME_SIGNALING_BY_HIPPO	20	-0.71361	-1.66068	0.01946472	0.6629962	0.924	1698
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	35	-0.64063	-1.64026	0.007692308	0.6528666	0.96	1387
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	-0.74765	-1.63676	0.027542373	0.5652866	0.963	2650
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	26	-0.66388	-1.62693	0.018518519	0.53538847	0.973	3465
BIOCARTA_NTHI_PATHWAY	23	-0.68215	-1.6259	0.02173913	0.4731624	0.974	374
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	15	-0.73479	-1.5942	0.027713627	0.5736192	0.999	2248
BIOCARTA_IL1R_PATHWAY	33	-0.62444	-1.58528	0.013850415	0.5587936	0.999	3128
BIOCARTA_IL10_PATHWAY	16	-0.69405	-1.56933	0.03640777	0.5820398	1	2803
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	54	-0.5555	-1.5417	0.022160664	0.66784996	1	3213
REACTOME_UNFOLDED_PROTEIN_RESPONSE	76	-0.52139	-1.5358	0.002906977	0.64771	1	3682
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	24	-0.65094	-1.52842	0.039443154	0.6385009	1	1843
REACTOME_IL1_SIGNALING	38	-0.57482	-1.51709	0.026455026	0.652598	1	3213
REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_TTP	17	-0.69289	-1.51668	0.04090909	0.6142278	1	1843
REACTOME_DIABETES_PATHWAYS	121	-0.47113	-1.50756	0.003401361	0.61802757	1	3682
BIOCARTA_INFLAM_PATHWAY	19	-0.663	-1.50589	0.05263158	0.5900839	1	4562
REACTOME_GLYCOSPHINGOLIPID_METABOLISM	32	-0.57711	-1.49357	0.025943397	0.6133317	1	4028
REACTOME_PERK_REGULATED_GENE_EXPRESSION	27	-0.59888	-1.49041	0.04292929	0.5957531	1	1843
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	18	-0.67034	-1.48716	0.05936073	0.5812557	1	3066
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	-0.60789	-1.46884	0.047281325	0.63391376	1	5586
BIOCARTA_CARDIACEGF_PATHWAY	17	-0.66098	-1.46853	0.064665124	0.6077781	1	2049
KEGG_JAK_STAT_SIGNALING_PATHWAY	119	-0.45683	-1.46711	0.006644518	0.5883832	1	2986
BIOCARTA_CCR5_PATHWAY	16	-0.67326	-1.46374	0.08411215	0.5778716	1	3622
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	20	-0.62341	-1.459	0.08056872	0.5746095	1	3843
REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	22	-0.62243	-1.45494	0.05140187	0.56986964	1	809
KEGG_STEROID_BIOSYNTHESIS	16	-0.65482	-1.43354	0.07042254	0.63690263	1	2164
REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	20	-0.60637	-1.42405	0.09046455	0.6541453	1	1545
REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	16	-0.61962	-1.41864	0.09134615	0.654754	1	3561
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	42	-0.51974	-1.41837	0.038674034	0.63479376	1	383
REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC	15	-0.6509	-1.41791	0.06823529	0.61653024	1	4863
REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1	17	-0.63866	-1.4121	0.107913665	0.621837	1	1843
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	16	-0.63288	-1.40151	0.07981221	0.64661723	1	565
REACTOME_SPHINGOLIPID_METABOLISM	58	-0.4828	-1.35851	0.07012987	0.81679744	1	4028
REACTOME_RAP1_SIGNALLING	15	-0.61959	-1.35347	0.11111111	0.817296	1	1669
KEGG_BLADDER_CANCER	40	-0.49848	-1.35323	0.089058526	0.7965306	1	3640
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	39	-0.51584	-1.34685	0.08478803	0.8051114	1	1078
BIOCARTA_TOB1_PATHWAY	15	-0.61235	-1.34295	0.11648352	0.8027014	1	6134
REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI	16	-0.60241	-1.3421	0.11111111	0.78618205	1	1457
REACTOME_BOTULINUM_NEUROTOXICITY	18	-0.58246	-1.3413	0.14186047	0.77120435	1	3392
REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	15	-0.61863	-1.34109	0.12107623	0.7537293	1	3546
REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	33	-0.52025	-1.33942	0.11764706	0.74291164	1	3100
BIOCARTA_G1_PATHWAY	28	-0.53841	-1.33444	0.10930233	0.7475818	1	3640
REACTOME_SIGNALING_BY_NODAL	15	-0.60018	-1.33109	0.13777778	0.7434885	1	3396
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	44	-0.4947	-1.31581	0.10962567	0.79034215	1	3585
REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS	16	-0.60328	-1.31301	0.1485849	0.7859284	1	3392
REACTOME_TRNA_AMINOACYLATION	42	-0.47725	-1.30805	0.08746356	0.78982204	1	7329
BIOCARTA_IGF1MTOR_PATHWAY	20	-0.55706	-1.30408	0.14868106	0.79016745	1	1084
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	20	-0.57063	-1.30304	0.12177986	0.7789526	1	101
BIOCARTA_BIOPEPTIDES_PATHWAY	39	-0.48886	-1.29675	0.11851852	0.789896	1	2779
REACTOME_ION_CHANNEL_TRANSPORT	40	-0.48697	-1.29588	0.11358025	0.778584	1	1519
KEGG_ADHERENS_JUNCTION	66	-0.44603	-1.28371	0.07058824	0.8153611	1	2422
BIOCARTA_IL22BP_PATHWAY	15	-0.58041	-1.28025	0.1670429	0.81481624	1	2474
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	38	-0.48961	-1.27998	0.12958436	0.8010514	1	4941
BIOCARTA_MTOR_PATHWAY	23	-0.54278	-1.27733	0.15254237	0.7975162	1	10
KEGG_ABC_TRANSPORTERS	41	-0.4855	-1.27342	0.12953368	0.7986073	1	3184
REACTOME_PKB_MEDIATED_EVENTS	28	-0.50921	-1.27294	0.16504854	0.78696555	1	10
BIOCARTA_EIF_PATHWAY	16	-0.58704	-1.27179	0.19310345	0.778332	1	3149
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	18	-0.56213	-1.27159	0.1879518	0.7662122	1	5385
REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	18	-0.54682	-1.26079	0.18203309	0.7974001	1	2181
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	64	-0.42532	-1.25212	0.11171662	0.8188745	1	2779
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	29	-0.50293	-1.24816	0.17091836	0.82217526	1	4395
KEGG_VIRAL_MYOCARDITIS	41	-0.45657	-1.2462	0.15206185	0.8175235	1	4395
REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	26	-0.50453	-1.24021	0.17848411	0.827238	1	996
REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	15	-0.57283	-1.23644	0.18485524	0.83017355	1	996
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	21	-0.52866	-1.23625	0.20179372	0.81872016	1	6499
BIOCARTA_AGR_PATHWAY	34	-0.47956	-1.23398	0.19900498	0.81527966	1	1127
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	55	-0.43186	-1.22046	0.15789473	0.85688514	1	4953
REACTOME_SHC_MEDIATED_SIGNALLING	15	-0.55442	-1.21907	0.2260274	0.85035044	1	3546
BIOCARTA_TEL_PATHWAY	18	-0.54131	-1.21745	0.22931442	0.8444314	1	4376
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	128	-0.37685	-1.21283	0.12014134	0.85079575	1	4109
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK	155	-0.36736	-1.20691	0.08802817	0.8638452	1	3777
REACTOME_GLUTATHIONE_CONJUGATION	19	-0.53192	-1.20373	0.27051	0.8637716	1	485
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	51	-0.43897	-1.20298	0.21276596	0.8550459	1	4688
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	51	-0.424	-1.19436	0.17816092	0.8777522	1	752
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATION_OF_SECOND_MESSENGERS	29	-0.47411	-1.19196	0.200489	0.87619543	1	2049
REACTOME_CHOLESTEROL_BIOSYNTHESIS	20	-0.51398	-1.19057	0.25526932	0.87011504	1	5482
BIOCARTA_STATHMIN_PATHWAY	16	-0.54363	-1.18571	0.2665148	0.87849724	1	5405
REACTOME_SMOOTH_MUSCLE_CONTRACTION	23	-0.50655	-1.18159	0.23376623	0.8843391	1	2084
REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFATASE_ACTIVATION	21	-0.50317	-1.18044	0.2451923	0.8779067	1	2204
KEGG_ALZHEIMERS_DISEASE	137	-0.3657	-1.17194	0.15309446	0.90151817	1	1282
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	106	-0.36919	-1.15502	0.17610063	0.9593367	1	1554
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	179	-0.34355	-1.15388	0.14457831	0.9528445	1	1949
REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKS_COMPLEX	23	-0.47444	-1.1487	0.27525252	0.9622248	1	4870
REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	27	-0.45835	-1.14853	0.2725061	0.9516227	1	5461
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS	26	-0.4723	-1.14803	0.27272728	0.94270134	1	2960
REACTOME_SIGNALING_BY_ERBB4	83	-0.37438	-1.14219	0.19402985	0.9550951	1	4870
KEGG_TYPE_I_DIABETES_MELLITUS	17	-0.50106	-1.14111	0.2867647	0.9489478	1	374
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.43631	-1.14099	0.25593668	0.9389376	1	5911
REACTOME_PEROXISOMAL_LIPID_METABOLISM	20	-0.49636	-1.13889	0.30904523	0.9375294	1	3090
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	79	-0.38014	-1.13332	0.23964497	0.94997895	1	4901
KEGG_RIBOSOME	86	-0.37229	-1.13237	0.23493975	0.94339454	1	2730
BIOCARTA_PML_PATHWAY	16	-0.50987	-1.13196	0.30935252	0.935073	1	5039

REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	27	-0.45141	-1.12964	0.31026253	0.93379277	1	3468
KEGG_APOPTOSIS	82	-0.3707	-1.12718	0.24362606	0.93340075	1	4870
BIOCARTA_ARAP_PATHWAY	17	-0.50256	-1.12588	0.31381732	0.928381	1	2320
REACTOME_TRAF6_MEDIATED_NFKB_ACTIVATION	21	-0.48862	-1.12468	0.3101737	0.92327595	1	5414
REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING	36	-0.42433	-1.12244	0.2543641	0.92342484	1	5034
KEGG_PEROXISOME	75	-0.3751	-1.11664	0.24852072	0.93679214	1	3793
REACTOME_SIGNALING_BY_GPCR	446	-0.30338	-1.11042	0.14569536	0.9510424	1	1949
KEGG_GNRH_SIGNALING_PATHWAY	90	-0.36524	-1.10516	0.26666668	0.9623404	1	3622
KEGG_ERBB_SIGNALING_PATHWAY	85	-0.36778	-1.10411	0.24293785	0.95717233	1	3318
BIOCARTA_RELA_PATHWAY	16	-0.50789	-1.10305	0.31506848	0.9518538	1	4870
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN	28	-0.44149	-1.10142	0.31042653	0.9490436	1	5280
REACTOME_SIGNALLING_TO_RAS	27	-0.4637	-1.10075	0.33793104	0.94278616	1	4676
REACTOME_PURINE_METABOLISM	31	-0.43708	-1.09468	0.31782946	0.95706284	1	1953
BIOCARTA_CELLCYCLE_PATHWAY	23	-0.46085	-1.09169	0.33568075	0.9597506	1	4006
REACTOME_GLOBAL_GENOMIC_NER_GG_NER	33	-0.42752	-1.08948	0.32843137	0.95921445	1	6499
REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	42	-0.41481	-1.08707	0.31578946	0.9594663	1	809
KEGG_PPAR_SIGNALING_PATHWAY	59	-0.37115	-1.08186	0.31989247	0.9700675	1	835
BIOCARTA_SPRY_PATHWAY	18	-0.46819	-1.07968	0.3476298	0.9698046	1	4042
KEGG_LYSINE_DEGRADATION	39	-0.40624	-1.07847	0.32048193	0.96604973	1	1590
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	28	-0.43346	-1.07693	0.3478261	0.9636791	1	2998
KEGG_WNT_SIGNALING_PATHWAY	139	-0.3304	-1.07518	0.27972028	0.9614057	1	1669
KEGG_GLIOMA	65	-0.36599	-1.07291	0.32777777	0.96178913	1	4376
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	21	-0.46299	-1.06601	0.3770115	0.97892004	1	1437
KEGG_PRION_DISEASES	28	-0.42456	-1.06286	0.39141414	0.9831543	1	4289
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	79	-0.36069	-1.05906	0.32173914	0.9891139	1	4547
KEGG_PYRIMIDINE_METABOLISM	91	-0.3448	-1.05738	0.32218844	0.9876187	1	1648
KEGG_MAPK_SIGNALING_PATHWAY	243	-0.30641	-1.05419	0.2764977	0.9915983	1	4212
REACTOME_SIGNALING_BY_ILS	101	-0.3385	-1.05342	0.33116883	0.9860404	1	3213
KEGG_MELANOGENESIS	94	-0.33279	-1.04841	0.36212623	0.9966328	1	1669
REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_DAI	18	-0.45895	-1.04743	0.39240506	0.9923055	1	647
REACTOME_SHC_RELATED_EVENTS	16	-0.47886	-1.04598	0.39485982	0.9897641	1	3546
BIOCARTA_TGFB_PATHWAY	19	-0.45855	-1.04554	0.430622	0.9835973	1	162
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	16	-0.48511	-1.04209	0.4097222	0.98877114	1	12
REACTOME_SIGNALING_BY_FGFR_MUTANTS	37	-0.39738	-1.04067	0.39083558	0.986348	1	233
BIOCARTA_PGC1A_PATHWAY	22	-0.44047	-1.04046	0.4241706	0.97935855	1	5405
REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	15	-0.4686	-1.03808	0.41025642	0.9803864	1	5450
REACTOME_GABA_RECEPTOR_ACTIVATION	42	-0.38625	-1.03646	0.36507937	0.97875273	1	808
KEGG_SPHINGOLIPID_METABOLISM	33	-0.40901	-1.03282	0.416	0.9846134	1	3988
REACTOME_TCR_SIGNALING	41	-0.38532	-1.03259	0.38659793	0.97808063	1	5385
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	26	-0.41685	-1.02823	0.40048543	0.98703104	1	2949
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	181	-0.30475	-1.02579	0.39694658	0.9886298	1	3281
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	95	-0.33036	-1.02325	0.38291138	0.9908038	1	3833
REACTOME_RNA_POL_III_TRANSCRIPTION_TERMINATION	19	-0.44031	-1.02299	0.43601894	0.9845582	1	518
BIOCARTA_AT1R_PATHWAY	31	-0.39812	-1.02215	0.40759495	0.98054165	1	5394
REACTOME_NETRIN1_SIGNALING	34	-0.39174	-1.02079	0.42964825	0.97848386	1	2377
BIOCARTA_IL6_PATHWAY	22	-0.42996	-1.01575	0.41411763	0.9892666	1	6108
BIOCARTA_IL12_PATHWAY	16	-0.46013	-1.01412	0.45971563	0.98792946	1	5394
REACTOME_NOD1_2_SIGNALING_PATHWAY	29	-0.41275	-1.01405	0.44533333	0.9811635	1	4870
REACTOME_SIGNALING_BY_SCF_KIT	74	-0.34595	-1.01383	0.4034091	0.97501534	1	5034
BIOCARTA_EPO_PATHWAY	19	-0.44963	-1.01359	0.44923857	0.9689287	1	5394
REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	134	-0.31789	-1.01334	0.41744548	0.9630945	1	3777
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	24	-0.4216	-1.01321	0.4390244	0.95691824	1	2960
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	21	-0.43413	-1.01264	0.44868734	0.9525308	1	2480
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	24	-0.42255	-1.01215	0.44604316	0.94787043	1	4288
KEGG_THYROID_CANCER	29	-0.40631	-1.00895	0.45	0.9526414	1	2923
REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING	27	-0.40506	-1.00667	0.42892158	0.9538928	1	1545
REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	36	-0.38336	-1.00466	0.4781491	0.9546423	1	4806
REACTOME_GPCR_LIGAND_BINDING	252	-0.2878	-1.0005	0.42156863	0.96210396	1	1949
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES	80	-0.33639	-1.00046	0.44508672	0.9559652	1	1078
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	168	-0.29941	-0.99947	0.39922482	0.9528854	1	3077
KEGG_BASAL_CELL_CARCINOMA	51	-0.35938	-0.99389	0.46835443	0.9659308	1	1926
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	21	-0.40885	-0.99311	0.4608076	0.9623119	1	2703
REACTOME_SIGNALING_BY_FGFR1_MUTANTS	25	-0.40768	-0.99069	0.44963145	0.96421856	1	2979
KEGG_LEISHMANIA_INFECTION	51	-0.35281	-0.99047	0.44031832	0.95892656	1	374
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	26	-0.39971	-0.9877	0.46601942	0.96208173	1	4175
REACTOME_DARPP_32_EVENTS	23	-0.41147	-0.98363	0.47016707	0.9696435	1	1669
REACTOME_PI3K_CASCADE	61	-0.34048	-0.9751	0.52	0.9922334	1	233
REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	49	-0.35355	-0.9724	0.4847561	0.99528515	1	5394
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	37	-0.37037	-0.97216	0.51005024	0.99006045	1	2949
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	230	-0.28018	-0.97213	0.52100843	0.9841234	1	3843
REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	26	-0.3982	-0.9718	0.48586118	0.9792237	1	4762
REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS	53	-0.34488	-0.96964	0.4903581	0.981036	1	2946
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	-0.40909	-0.96922	0.49427918	0.976411	1	3911
BIOCARTA_SHH_PATHWAY	15	-0.4326	-0.96512	0.49311927	0.98433006	1	1926
BIOCARTA_CSK_PATHWAY	18	-0.41884	-0.96411	0.48994976	0.9817641	1	5811
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION	15	-0.44176	-0.95794	0.51746726	0.99680334	1	3026
KEGG_REGULATION_OF_AUTOPHAGY	20	-0.40775	-0.95616	0.5122549	0.9969625	1	3537
REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	38	-0.36273	-0.95565	0.51344085	0.9929596	1	5562
KEGG_INSULIN_SIGNALING_PATHWAY	128	-0.29887	-0.95377	0.5628931	0.99384964	1	4134
BIOCARTA_ATM_PATHWAY	19	-0.41873	-0.95225	0.49408984	0.9931128	1	6299
BIOCARTA_NFAT_PATHWAY	48	-0.34847	-0.95101	0.55376345	0.9914395	1	1669
REACTOME_SIGNALING_BY_RHO_GTPASES	108	-0.30396	-0.9492	0.5765472	0.9914564	1	4100
KEGG_DORSO_VENTRAL_AXIS_FORMATION	23	-0.40375	-0.94809	0.52102804	0.98946506	1	1245
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	67	-0.33024	-0.94805	0.55588233	0.9839927	1	935
BIOCARTA_BCR_PATHWAY	34	-0.36103	-0.94191	0.53333336	0.99838036	1	2779
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	422	-0.25658	-0.936	0.75	1	1	3445
KEGG_ENDOMETRIAL_CANCER	50	-0.3373	-0.93584	0.5380435	1	1	1408
REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	32	-0.36013	-0.93392	0.5364706	1	1	378
REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	73	-0.30993	-0.93138	0.5770492	1	1	5034
BIOCARTA_WNT_PATHWAY	24	-0.3795	-0.91785	0.55504584	1	1	190
BIOCARTA_PYK2_PATHWAY	28	-0.36563	-0.91643	0.58780485	1	1	5957
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	-0.38021	-0.91589	0.56222224	1	1	5034
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	33	-0.35948	-0.91459	0.57462686	1	1	1277
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	95	-0.29628	-0.91452	0.64576805	1	1	3425
REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	77	-0.30828	-0.9131	0.6126126	1	1	723
REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	43	-0.33946	-0.91232	0.58679706	1	1	5920
REACTOME_METABOLISM_OF_NUCLEOTIDES	64	-0.31793	-0.91204	0.59375	1	1	1953
REACTOME_SIGNALING_BY_ROBO_RECEPTOR	27	-0.37038	-0.90807	0.58542717	1	1	5110
BIOCARTA_VIP_PATHWAY	25	-0.37879	-0.90586	0.614486	1	1	4953
REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS	26	-0.36696	-0.90556	0.6167076	1	1	1095

REACTOME_SIGNALLING_TO_ERKS	35	-0.34729	-0.90439	0.6	1	1	3823
REACTOME_ARMS_MEDIATED_ACTIVATION	17	-0.39948	-0.89962	0.5970516	1	1	3823
BIOCARTA_ERK_PATHWAY	28	-0.36533	-0.89914	0.615942	1	1	4376
KEGG_COLORECTAL_CANCER	62	-0.30849	-0.89908	0.65591395	1	1	1408
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TAK1	16	-0.40099	-0.89869	0.57798165	1	1	3318
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	39	-0.33575	-0.89788	0.6393443	1	1	2946
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRANE	16	-0.4099	-0.89657	0.6	1	1	5749
REACTOME_GAB1_SIGNALOSOME	36	-0.33854	-0.89513	0.6315789	1	1	5461
BIOCARTA_NDKDYNAMIN_PATHWAY	18	-0.39241	-0.89184	0.5788235	1	1	812
KEGG_PANCREATIC_CANCER	69	-0.30684	-0.89136	0.6571429	1	1	4870
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	458	-0.24302	-0.88942	0.9440559	1	1	5075
REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	31	-0.35065	-0.88891	0.62857145	1	1	5450
BIOCARTA_CDMAC_PATHWAY	16	-0.40406	-0.88695	0.60807604	1	1	374
REACTOME_ERK_MAPK_TARGETS	21	-0.38032	-0.88567	0.6518847	1	1	4676
KEGG_GLUTATHIONE_METABOLISM	43	-0.32352	-0.88413	0.6666667	1	1	485
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	128	-0.27591	-0.88106	0.75767916	1	1	1949
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	-0.34566	-0.88103	0.6627635	1	1	5394
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	58	-0.31524	-0.88041	0.67639256	1	1	1084
BIOCARTA_EGF_PATHWAY	31	-0.3464	-0.87992	0.64871794	1	1	2813
BIOCARTA_CARM_ER_PATHWAY	34	-0.34286	-0.87976	0.66190475	1	1	2156
REACTOME_RNA_POL_III_TRANSCRIPTION	33	-0.34797	-0.87559	0.6967419	1	1	938
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	46	-0.3221	-0.87521	0.6717949	1	1	9073
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	61	-0.30603	-0.87468	0.6857143	1	1	4432
REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	30	-0.34774	-0.87274	0.6244019	1	1	2670
KEGG_MTOR_SIGNALING_PATHWAY	49	-0.31416	-0.87266	0.6666667	1	1	4543
REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	97	-0.27702	-0.87216	0.77627116	0.99968946	1	723
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	66	-0.29703	-0.8635	0.7318436	1	1	10
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	33	-0.34183	-0.86321	0.6466165	1	1	1545
REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR7_8_OR_9_ACTIVATION	73	-0.2921	-0.86192	0.71387285	1	1	5105
REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	20	-0.37615	-0.85429	0.64568764	1	1	1910
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	47	-0.31503	-0.851	0.69529086	1	1	3911
BIOCARTA_NKT_PATHWAY	21	-0.35455	-0.84152	0.702765	1	1	7183
REACTOME_SIGNALING_BY_NOTCH	96	-0.27373	-0.84135	0.8262195	1	1	2860
REACTOME_ACTIVATED_TLR4_SIGNALLING	91	-0.28211	-0.84056	0.82729805	1	1	5034
REACTOME_SULFUR_AMINO_ACID_METABOLISM	23	-0.35543	-0.83682	0.692494	1	1	1527
REACTOME_TOLL_RECEPTOR_CASCADES	108	-0.26752	-0.83583	0.85119045	1	1	5105
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	-0.28447	-0.83284	0.78571427	1	1	4198
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	42	-0.30621	-0.83002	0.7350649	1	1	3769
KEGG_OOCYTE_MEIOSIS	102	-0.26411	-0.82904	0.85755813	1	1	2174
REACTOME_PLATELET_SENSITIZATION_BY_LDL	16	-0.36631	-0.82527	0.70159453	1	1	2129
KEGG_ARGININE_AND_PROLINE_METABOLISM	48	-0.29806	-0.82358	0.78370786	1	1	3519
REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	19	-0.35666	-0.82318	0.74125874	1	1	4710
KEGG_LINOLEIC_ACID_METABOLISM	20	-0.3465	-0.82202	0.6944444	1	1	520
KEGG_RIBOFLAVIN_METABOLISM	15	-0.37095	-0.82124	0.6723716	1	1	7594
REACTOME_SIGNALING_BY_PDGF	114	-0.25992	-0.82092	0.89320385	1	1	5034
REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	19	-0.35006	-0.81445	0.71566266	1	1	3823
BIOCARTA_MAPK_PATHWAY	86	-0.26426	-0.81277	0.8628049	1	1	5034
KEGG_OTHER_GLYCAN_DEGRADATION	15	-0.37517	-0.8127	0.7024608	1	1	5304
REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRCADIAN_EXPRESSION	32	-0.32016	-0.81153	0.79	1	1	4297
KEGG_VIBRIO_CHOLERAE_INFECTION	51	-0.29173	-0.81041	0.8161209	1	1	2080
REACTOME_REGULATION_OF_KIT_SIGNALING	16	-0.36385	-0.80992	0.7334852	1	1	1104
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	220	-0.23357	-0.80947	0.9823009	1	1	4109
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	88	-0.26681	-0.8031	0.87261146	1	1	5034
KEGG_TRYPTOPHAN_METABOLISM	37	-0.30639	-0.80124	0.786385	1	1	5006
REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	15	-0.35583	-0.80059	0.7414188	1	1	3467
KEGG_GLYCEROLIPID_METABOLISM	37	-0.30099	-0.79991	0.8025641	1	1	3714
REACTOME_IL_2_SIGNALING	37	-0.30467	-0.79455	0.80548626	1	1	3622
REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	21	-0.33956	-0.79434	0.7651163	1	1	7329
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	103	-0.25296	-0.79148	0.9297125	1	1	5034
REACTOME_DOWNSTREAM_TCR_SIGNALING	25	-0.32258	-0.78891	0.7570755	1	1	5385
REACTOME_PI3K_AKT_ACTIVATION	36	-0.30825	-0.78808	0.80100757	1	1	5461
KEGG_PYRUVATE_METABOLISM	36	-0.30706	-0.78766	0.8230769	1	1	5006
BIOCARTA_KERATINOCYTE_PATHWAY	45	-0.29103	-0.78757	0.83715016	1	1	5961
REACTOME_INTERFERON_SIGNALING	129	-0.24288	-0.7861	0.94055945	1	1	5451
REACTOME_INTERFERON_GAMMA_SIGNALING	46	-0.28457	-0.78583	0.8314917	1	1	6107
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	26	-0.32581	-0.78332	0.76960784	1	1	4626
REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	18	-0.34914	-0.78163	0.74647886	1	1	4806
KEGG_PRIMARY_IMMUNODEFICIENCY	29	-0.30775	-0.77593	0.80100757	1	1	6756
REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION_INDEPENDENT_DOUBLE_STRAND_BREAKS	15	-0.35425	-0.77278	0.7529412	1	1	6774
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	75	-0.25835	-0.76891	0.91354465	1	1	5343
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	31	-0.30054	-0.76809	0.8230769	1	1	6114
REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY	20	-0.3326	-0.76527	0.7975	1	1	2484
BIOCARTA_DEATH_PATHWAY	33	-0.29956	-0.76417	0.80987656	1	1	677
REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION	23	-0.31524	-0.76246	0.7943925	1	1	5562
BIOCARTA_CALCINEURIN_PATHWAY	18	-0.34525	-0.76199	0.7708831	1	1	3715
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	121	-0.23761	-0.76117	0.97077924	1	1	5461
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	124	-0.23524	-0.75659	0.9685315	1	1	5405
REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	58	-0.2644	-0.7564	0.9017341	1	1	3823
BIOCARTA_ETS_PATHWAY	18	-0.33422	-0.7498	0.82678986	1	1	5964
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	-0.33041	-0.74948	0.79586565	1	1	3936
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM	17	-0.33051	-0.74918	0.8252427	1	1	1481
REACTOME_GLUCOSE_TRANSPORT	33	-0.28789	-0.74814	0.89637303	1	1	4175
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	189	-0.21976	-0.74806	0.9920949	1	1	2977
REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULES	29	-0.30017	-0.74654	0.8440594	1	1	2295
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	21	-0.3276	-0.74494	0.7849224	1	1	6774
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	-0.27268	-0.74458	0.8680739	1	1	6499
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	19	-0.32744	-0.73987	0.795045	1	1	8696
BIOCARTA_CHEMICAL_PATHWAY	22	-0.32053	-0.73927	0.8202765	1	1	4395
REACTOME_CIRCADIAN_CLOCK	49	-0.26779	-0.73866	0.8981723	1	1	4428
BIOCARTA_G2_PATHWAY	24	-0.30449	-0.7303	0.8633257	1	1	6980
REACTOME_EXTENSION_OF_TELOMERES	27	-0.29517	-0.73003	0.84782606	1	1	3467
BIOCARTA_HIF_PATHWAY	15	-0.32845	-0.72503	0.8315098	1	1	6303
REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM	160	-0.21672	-0.72134	0.99622643	1	1	3845
BIOCARTA_MYOSIN_PATHWAY	30	-0.28501	-0.72128	0.8912037	1	1	1126
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	51	-0.2585	-0.71529	0.92268044	1	1	4676
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	22	-0.30523	-0.71408	0.875	1	1	4621
BIOCARTA_PTDINS_PATHWAY	23	-0.29339	-0.71269	0.89638555	1	1	2049

REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI	17	-0.31683	-0.7114	0.8538283	1	1	7712
REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	17	-0.31788	-0.71009	0.8294931	1	1	4676
KEGG_NITROGEN_METABOLISM	18	-0.3065	-0.70693	0.8413793	1	1	1646
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	26	-0.28525	-0.70485	0.8829517	1	1	4175
KEGG_HISTIDINE_METABOLISM	26	-0.28976	-0.70409	0.9253012	1	1	5006
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	22	-0.30076	-0.69762	0.8628429	1	1	162
REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_LIKE_PEPTIDE1	37	-0.26501	-0.69403	0.91161615	1	1	2514
REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BETA_PATHWAYS	61	-0.23847	-0.69007	0.9833795	1	1	5414
KEGG_P53_SIGNALING_PATHWAY	65	-0.23988	-0.68973	0.9769452	1	1	4571
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	16	-0.30359	-0.68733	0.8591224	1	1	3936
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	25	-0.2883	-0.6871	0.8973747	0.99728656	1	162
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	52	-0.24121	-0.67471	0.97493035	1	1	2173
KEGG_SELENOAMINO_ACID_METABOLISM	25	-0.27707	-0.67118	0.9123223	1	1	4971
BIOCARTA_ATRBRCA_PATHWAY	20	-0.2893	-0.67043	0.8905908	1	1	4320
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	41	-0.24886	-0.66913	0.9678284	0.99861455	1	4739
KEGG_NOTCH_SIGNALING_PATHWAY	45	-0.24723	-0.66434	0.9680851	0.998819	1	4782
BIOCARTA_STRESS_PATHWAY	25	-0.27321	-0.66347	0.94089836	0.9962066	1	5394
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	65	-0.22592	-0.66099	0.982906	0.9947969	1	4626
KEGG_PHENYLALANINE_METABOLISM	17	-0.28562	-0.64004	0.9022727	1	1	6019
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	18	-0.28349	-0.63916	0.9375	1	1	5568
REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	17	-0.27737	-0.63632	0.9236111	1	1	4676
REACTOME_LAGGING_STRAND_SYNTHESIS	19	-0.2727	-0.63083	0.91484183	0.9997657	1	3467
BIOCARTA_HIVNEF_PATHWAY	57	-0.21901	-0.61826	0.9945355	1	1	4953
REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSION_BY_REV_ERBA	22	-0.261	-0.61313	0.9291139	1	1	4428
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION	20	-0.24995	-0.59132	0.95486933	1	1	6499
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	31	-0.23107	-0.58688	0.98288506	1	1	4175
REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION	23	-0.24234	-0.57592	0.97932816	1	1	3778
REACTOME_RNA_POL_I_TRANSCRIPTION_INITIATION	24	-0.23945	-0.56971	0.9683377	1	1	7540
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	44	-0.20788	-0.55669	0.9839142	1	1	5318
KEGG_N_GLYCAN_BIOSYNTHESIS	46	-0.19773	-0.54484	0.9948052	1	1	7592
BIOCARTA_TNFR1_PATHWAY	29	-0.21167	-0.54224	0.9832134	1	1	5394
KEGG_MISMATCH_REPAIR	23	-0.21676	-0.51991	0.99012345	1	1	5634
BIOCARTA_CERAMIDE_PATHWAY	22	-0.19858	-0.47425	0.99766356	1	1	4953
REACTOME_ENOS_ACTIVATION_AND_REGULATION	20	-0.20465	-0.4731	0.9928058	0.9995718	1	5892
REACTOME_METABOLISM_OF_NON_CODING_RNA	47	-0.15849	-0.43849	1	0.9984103	1	4801

Table S11
GSEA Analysis on HNSC cancer cell lines comparing cell lines with or without 3p14 loss (arm or focal), Pathways Enriched

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	46	0.686839	2.017796	0	0.03808225	0.029	2295
BIOCARTA_IL10_PATHWAY	16	0.850333	1.998172	0	0.027396193	0.042	2368
BIOCARTA_EGF_PATHWAY	31	0.725028	1.976686	0.002074689	0.027658742	0.062	2923
BIOCARTA_UCALPAIN_PATHWAY	18	0.812485	1.950201	0	0.03271272	0.095	3556
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	56	0.620288	1.917387	0	0.045216814	0.158	4950
BIOCARTA_CARDIACEGF_PATHWAY	17	0.78272	1.882528	0	0.06111385	0.246	4107
BIOCARTA_BIOPEPTIDES_PATHWAY	40	0.660166	1.864919	0	0.06725534	0.303	4131
BIOCARTA_INTEGRIN_PATHWAY	38	0.648654	1.844852	0	0.07714481	0.381	4107
REACTOME_INNATE_IMMUNE_SYSTEM	203	0.500823	1.837069	0	0.07531488	0.411	4743
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	55	0.606927	1.828466	0	0.077763855	0.452	4743
BIOCARTA_IL22BP_PATHWAY	15	0.773198	1.812113	0	0.08729269	0.524	2368
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	202	0.493666	1.80793	0	0.08436844	0.544	3869
KEGG_ENDOCYTOSIS	167	0.501309	1.79826	0	0.0887444	0.587	6468
BIOCARTA_MCALPAIN_PATHWAY	24	0.6872	1.77433	0.006122449	0.10921511	0.689	3873
REACTOME_BIOLOGICAL_OXIDATIONS	114	0.521996	1.772599	0	0.103937484	0.697	4670
REACTOME_INFLAMMASOMES	16	0.750388	1.743263	0.004024145	0.13809709	0.811	4365
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	41	0.604673	1.730804	0.002074689	0.15005088	0.857	4670
REACTOME_PHASE_II_CONJUGATION	57	0.573539	1.73072	0.002070393	0.14208245	0.857	4670
KEGG_STEROID_HORMONE_BIOSYNTHESIS	42	0.580274	1.724634	0.001956947	0.142546	0.87	5638
REACTOME_GLUTATHIONE_CONJUGATION	19	0.701097	1.721556	0.012195122	0.13977915	0.88	3308
REACTOME_GAP_JUNCTION_TRAFFICKING	23	0.671241	1.721516	0.007984032	0.13318181	0.88	6226
KEGG_LEISHMANIA_INFECTION	53	0.573002	1.7215	0	0.12718904	0.88	4371
BIOCARTA_PYK2_PATHWAY	28	0.640576	1.711879	0.012048192	0.13585825	0.91	4107
BIOCARTA_IL2_PATHWAY	21	0.68202	1.703661	0.004040404	0.14224027	0.929	4107
BIOCARTA_SPPA_PATHWAY	22	0.663488	1.702261	0.015810277	0.1382186	0.933	4131
BIOCARTA_P38MAPK_PATHWAY	39	0.591586	1.69169	0.006	0.14730193	0.947	4187
BIOCARTA_BCR_PATHWAY	34	0.61743	1.688239	0.008	0.1474686	0.952	4107
KEGG_LYSOSOME	118	0.488175	1.682691	0	0.15050945	0.96	5764
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	54	0.554913	1.680984	0.008281574	0.14826089	0.962	4950
REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	33	0.610973	1.675757	0.002012072	0.15028886	0.967	1170
BIOCARTA_CDMAC_PATHWAY	16	0.698265	1.668873	0.013806706	0.15471157	0.972	4107
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	87	0.503621	1.667431	0	0.15197039	0.976	4159
REACTOME_NEPHRIN_INTERACTIONS	19	0.675558	1.664187	0.016877636	0.15250166	0.982	1761
BIOCARTA_MAPK_PATHWAY	86	0.522284	1.656636	0.002040816	0.15821443	0.987	4187
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS	44	0.558994	1.655168	0.012269938	0.15587047	0.987	4743
BIOCARTA_PDGF_PATHWAY	32	0.609752	1.646635	0.010309278	0.16247787	0.99	2923
BIOCARTA_AT1R_PATHWAY	31	0.61128	1.644561	0.01968504	0.16081741	0.99	4107
KEGG_RETINOL_METABOLISM	49	0.552517	1.64234	0.006085193	0.15911849	0.99	1829
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	231	0.445832	1.639144	0.002150538	0.15888587	0.991	5175
BIOCARTA_ERK_PATHWAY	28	0.607521	1.636463	0.02258727	0.15866181	0.991	3870
REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	17	0.683276	1.63231	0.008163265	0.15974177	0.992	1357
REACTOME_COMPLEMENT_CASCADE	20	0.660162	1.628864	0.020746889	0.16039301	0.993	4429
REACTOME_SIGNALING_BY_ERBB4	83	0.495766	1.62869	0.006185567	0.15678217	0.993	3843
BIOCARTA_FMLP_PATHWAY	36	0.571627	1.615349	0.01178782	0.1702875	0.996	2962
REACTOME_INTERFERON_SIGNALING	130	0.459915	1.606669	0	0.17892316	0.999	5133
REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	71	0.502907	1.606152	0.006224067	0.17599392	0.999	4405
KEGG_STARCH_AND_SUCROSE_METABOLISM	37	0.573212	1.600472	0.015904572	0.18019453	0.999	4670
REACTOME_INTERFERON_GAMMA_SIGNALING	47	0.549689	1.598932	0.016985139	0.17843114	0.999	5133
REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	30	0.592487	1.584375	0.027253669	0.19672939	1	3895
REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	49	0.524949	1.583902	0.006147541	0.19347088	1	4743
BIOCARTA_MEF2D_PATHWAY	18	0.646194	1.576296	0.034615386	0.2013734	1	3873
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	0.602246	1.557688	0.033333335	0.22818737	1	2180
KEGG_JAK_STAT_SIGNALING_PATHWAY	121	0.446985	1.55324	0	0.23109154	1	3820
BIOCARTA_KERATINOCYTE_PATHWAY	45	0.529442	1.55276	0.021611001	0.22762153	1	4107
REACTOME_SYNTHESIS_OF_PC	17	0.649543	1.549802	0.029880479	0.22819215	1	2782
KEGG_BLADDER_CANCER	40	0.533328	1.547848	0.034552846	0.22708426	1	2203
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	24	0.605597	1.545681	0.028513238	0.22645083	1	5699
REACTOME_SMOOTH_MUSCLE_CONTRACTION	23	0.610022	1.541739	0.041753653	0.22911346	1	2981
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	0.57742	1.541562	0.019313306	0.22562908	1	4405
REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	73	0.484397	1.541423	0.027139874	0.22217019	1	4405
REACTOME_SIGNALLING_TO_RAS	27	0.58692	1.527182	0.044989776	0.24288434	1	3843
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	98	0.460646	1.524654	0.012072435	0.24327937	1	4099
BIOCARTA_HER2_PATHWAY	22	0.593121	1.520559	0.045081966	0.24649934	1	2356
REACTOME_IL1_SIGNALING	38	0.541258	1.519893	0.02357564	0.24372031	1	4743
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	65	0.487304	1.519455	0.019067796	0.24078202	1	5521
REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	21	0.597952	1.505653	0.07429719	0.26065952	1	1336
BIOCARTA_NKT_PATHWAY	23	0.597288	1.505178	0.046184737	0.25764087	1	148
BIOCARTA_MTA3_PATHWAY	18	0.622337	1.504501	0.04842105	0.2552773	1	2104
REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS	58	0.485799	1.503185	0.014285714	0.25401804	1	4514
KEGG_ERBB_SIGNALING_PATHWAY	85	0.457561	1.502749	0.012605042	0.2511481	1	4588
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	56	0.501523	1.496063	0.026584867	0.259553	1	3347
KEGG_PEROXISOME	75	0.477935	1.495746	0.01898734	0.25643414	1	1691
REACTOME_TOLL_RECEPTOR_CASCADES	110	0.433939	1.494847	0.012631579	0.2543982	1	6167
BIOCARTA_PPARA_PATHWAY	55	0.491539	1.491638	0.028248588	0.2566261	1	4481
REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	15	0.642482	1.491517	0.06720977	0.25339377	1	2356
REACTOME_CELL_CELL_COMMUNICATION	110	0.447882	1.488167	0.006329114	0.2556282	1	3625
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	67	0.477458	1.486575	0.01875	0.25545558	1	5521
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	38	0.517957	1.477337	0.045454547	0.26962426	1	3391
KEGG_MAPK_SIGNALING_PATHWAY	245	0.392033	1.473653	0.002008032	0.27309734	1	4623
BIOCARTA_IL1R_PATHWAY	33	0.533966	1.471739	0.045553144	0.27296752	1	4599
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	56	0.491582	1.471419	0.038535647	0.2700622	1	4010
BIOCARTA_MYOSIN_PATHWAY	31	0.537814	1.469719	0.055214725	0.2695166	1	4168
BIOCARTA_PGC1A_PATHWAY	22	0.577249	1.469277	0.0708502	0.2668614	1	3286
BIOCARTA_GLEEVEC_PATHWAY	23	0.566666	1.468876	0.05263158	0.26437607	1	1057
BIOCARTA_IL7_PATHWAY	17	0.621543	1.46527	0.06477733	0.26783362	1	1578
REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLLAPSE	25	0.559042	1.458801	0.06504065	0.2768721	1	3895
KEGG_MELANOGENESIS	95	0.44115	1.457579	0.022403259	0.27592278	1	4054
REACTOME_SIGNALING_BY_CONSTITUTIVELY_ACTIVE_EGFR	18	0.608721	1.45408	0.061833687	0.27900308	1	17
REACTOME_SIGNALING_BY_FGFR1_MUTANTS	26	0.566184	1.454039	0.047817048	0.27595574	1	1354
REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR7_8_OR_9_ACTIVATION	74	0.455245	1.452074	0.031055901	0.2765132	1	4405
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TAK1	16	0.619287	1.448858	0.08064516	0.27953622	1	4743
BIOCARTA_CCR3_PATHWAY	22	0.576794	1.447708	0.054655872	0.2786366	1	3843
REACTOME_SIGNALING_BY_FGFR1_FUSION_MUTANTS	18	0.598699	1.444444	0.072164945	0.28085178	1	1354
KEGG_HEMATOPOIETIC_CELL_LINEAGE	69	0.455463	1.441602	0.035714287	0.28309318	1	4599
REACTOME_SIGNALLING_BY_NGF	208	0.390279	1.439782	0.008298756	0.28307655	1	4728
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	76	0.452711	1.438965	0.028571429	0.28148225	1	4224
BIOCARTA_GSK3_PATHWAY	26	0.55	1.437662	0.06776181	0.28081816	1	4705

BIOCARTA_TPO_PATHWAY	24	0.570404	1.434288	0.07172996	0.28356126	1	4107
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	79	0.441417	1.43162	0.03368421	0.28536975	1	3556
KEGG_PATHWAYS_IN_CANCER	308	0.373698	1.43034	0.00610998	0.28479326	1	4705
KEGG_ACUTE_MYELOID_LEUKEMIA	57	0.471051	1.43023	0.046092186	0.28211516	1	3036
REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	22	0.571816	1.428543	0.07628866	0.28245556	1	2336
REACTOME_OLFACTORY_SIGNALING_PATHWAY	33	0.517458	1.425672	0.06517312	0.28492475	1	4186
REACTOME_SIGNALING_BY_ILS	101	0.430565	1.421835	0.032388665	0.28863552	1	4009
REACTOME_ACYL_CHAIN_REMODELLING_OF_PE	17	0.599179	1.41935	0.09978768	0.29005456	1	4603
KEGG_CELL_ADHESION_MOLECULES_CAMS	103	0.418087	1.419211	0.024539877	0.28751364	1	2081
REACTOME_ACYL_CHAIN_REMODELLING_OF_PC	18	0.585065	1.41704	0.10602911	0.2884082	1	4603
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	20	0.571171	1.415431	0.08097166	0.28837374	1	1549
REACTOME_ACTIVATED_TLR4_SIGNALLING	91	0.431472	1.412648	0.036960986	0.29044873	1	6167
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	38	0.505393	1.410987	0.05882353	0.29039705	1	5095
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	201	0.385787	1.409857	0.008230452	0.28979754	1	4563
REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BETA_PATHWAYS	61	0.455131	1.409713	0.05042017	0.28741753	1	4010
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	41	0.487386	1.408514	0.06126482	0.286941	1	4080
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	188	0.387191	1.404992	0.014141414	0.29108855	1	4224
REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT	19	0.563275	1.404347	0.09939148	0.28963813	1	1737
KEGG_PRION_DISEASES	28	0.522523	1.399641	0.070281126	0.2953265	1	2097
BIOCARTA_TCR_PATHWAY	44	0.474657	1.399626	0.05905512	0.2928132	1	4107
BIOCARTA_IL2RB_PATHWAY	37	0.499138	1.39853	0.058232933	0.29218844	1	3843
KEGG_CHEMOKINE_SIGNALING_PATHWAY	159	0.392609	1.396169	0.014344262	0.29409236	1	4054
KEGG_LINOLEIC_ACID_METABOLISM	21	0.562401	1.395564	0.085192695	0.29255933	1	1045
BIOCARTA_RAC1_PATHWAY	23	0.552032	1.394549	0.09012876	0.29170436	1	194
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	198	0.3825	1.393388	0.02536998	0.29118428	1	3584
REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	26	0.530352	1.391071	0.08811475	0.29295298	1	2518
KEGG_VEGF_SIGNALING_PATHWAY	68	0.445586	1.385973	0.054054055	0.2989034	1	4350
REACTOME_SIGNALING_BY_ROBO_RECEPTOR	27	0.537687	1.38571	0.1097561	0.29692537	1	1528
REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	81	0.430846	1.38565	0.046558704	0.29467133	1	4743
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	34	0.509359	1.384504	0.08041237	0.29414976	1	4670
KEGG_NITROGEN_METABOLISM	20	0.552161	1.379972	0.11717172	0.29981008	1	4332
BIOCARTA_PML_PATHWAY	16	0.587829	1.379181	0.11354582	0.29865587	1	1662
BIOCARTA_ARAP_PATHWAY	17	0.574025	1.37866	0.108050846	0.29738218	1	5821
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	42	0.47312	1.37837	0.06507592	0.29575202	1	3601
REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	15	0.579891	1.37305	0.11776062	0.302951	1	1825
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES	81	0.427848	1.373038	0.05068226	0.3007027	1	2130
BIOCARTA_EDG1_PATHWAY	26	0.517052	1.369356	0.076612905	0.30469263	1	3843
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	31	0.500487	1.365875	0.08450704	0.30862522	1	6881
BIOCARTA_INTRINSIC_PATHWAY	19	0.555001	1.362914	0.114173226	0.3118995	1	4596
BIOCARTA_FCER1_PATHWAY	37	0.482008	1.358812	0.07755102	0.31688565	1	4107
KEGG_OLFACTORY_TRANSDUCTION	60	0.447303	1.357869	0.08163265	0.31622046	1	4186
KEGG_ETHER_LIPID_METABOLISM	23	0.52509	1.356354	0.103869654	0.3169825	1	3605
KEGG_HEDGEHOG_SIGNALING_PATHWAY	51	0.453226	1.356004	0.07024793	0.3152928	1	5955
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	41	0.467113	1.353601	0.09919028	0.31722793	1	2417
BIOCARTA_IL12_PATHWAY	18	0.560519	1.352765	0.11788618	0.31656227	1	2368
REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	79	0.422239	1.347337	0.051124744	0.3246332	1	4446
REACTOME_OXYGEN_DEPENDENT_PROLINE_HYDROXYLATION_OF_HYPOXIA_INDUCIBLE_FACTOR_ALPHA	15	0.593079	1.344557	0.13087934	0.32742846	1	2175
REACTOME_SIGNALING_BY_PDGF	114	0.393822	1.343997	0.049484536	0.32615593	1	4054
BIOCARTA_TGFB_PATHWAY	19	0.555736	1.337474	0.12291667	0.3361205	1	5608
BIOCARTA_ACTINY_PATHWAY	20	0.546928	1.336909	0.124197	0.3348173	1	6982
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	115	0.398826	1.336797	0.055888224	0.33270356	1	3584
BIOCARTA_GH_PATHWAY	26	0.513988	1.333755	0.12301587	0.33614743	1	2923
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	112	0.39149	1.331873	0.058	0.33733767	1	3625
REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKS_COMPLEX	23	0.537752	1.32988	0.1329114	0.33876273	1	4743
REACTOME_SIGNALING_BY_SCF_KIT	74	0.416019	1.329136	0.06431536	0.33787316	1	3843
KEGG_ARACHIDONIC_ACID_METABOLISM	47	0.451012	1.328561	0.09580839	0.3367789	1	6576
REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS	25	0.511845	1.322287	0.12809917	0.34602213	1	1528
BIOCARTA_TOLL_PATHWAY	36	0.463723	1.321844	0.11515152	0.34470934	1	4159
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	100	0.393826	1.321523	0.06048387	0.3430518	1	3588
REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	49	0.44218	1.320998	0.09320388	0.34179294	1	5457
KEGG_ALZHEIMERS_DISEASE	138	0.376151	1.320978	0.047131147	0.339662	1	5552
BIOCARTA_PTDINS_PATHWAY	23	0.516853	1.320859	0.11627907	0.33776337	1	7655
REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING	27	0.498027	1.320575	0.12623274	0.33618498	1	3347
BIOCARTA_CCR5_PATHWAY	16	0.564716	1.320441	0.15655577	0.3343861	1	4107
REACTOME_GPCR_LIGAND_BINDING	276	0.348734	1.320232	0.024291499	0.3326331	1	4035
KEGG_O_GLYCAN_BIOSYNTHESIS	24	0.516249	1.319924	0.14105263	0.3311942	1	5369
KEGG_GNRH_SIGNALING_PATHWAY	91	0.410636	1.318673	0.07024793	0.3315366	1	4107
BIOCARTA_CARM_ER_PATHWAY	34	0.484459	1.318428	0.11422846	0.32999364	1	1727
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	78	0.40469	1.315552	0.07676349	0.33296704	1	3556
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	21	0.526357	1.315488	0.15384616	0.33113676	1	3156
REACTOME_STEROID_HORMONES	23	0.514005	1.314093	0.14225942	0.3317409	1	2146
KEGG_PANCREATIC_CANCER	69	0.412628	1.313399	0.08811475	0.3308312	1	1662
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	45	0.445024	1.312837	0.10191083	0.3297512	1	5068
KEGG_NOTCH_SIGNALING_PATHWAY	45	0.455172	1.311687	0.12156863	0.32974795	1	6558
REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	142	0.370894	1.306704	0.029227557	0.3367531	1	4867
REACTOME_MEMBRANE_TRAFFICKING	121	0.379689	1.305599	0.07645875	0.33679035	1	6009
BIOCARTA_VIP_PATHWAY	25	0.498673	1.301555	0.14653465	0.34250623	1	2962
REACTOME_NRIF_SIGNALS_CELL_DEATH_FROM_THE_NUCLEUS	15	0.564086	1.300255	0.17456897	0.34285665	1	4446
REACTOME_SIGNALLING_TO_ERKS	35	0.465373	1.296475	0.13127413	0.34732372	1	3843
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	42	0.458196	1.293842	0.13346614	0.35044035	1	2767
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATION_OF_SECOND_MESSENGERS	29	0.485547	1.292529	0.15132925	0.35116798	1	2356
REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_D	25	0.491701	1.292212	0.13882864	0.34983176	1	2146
REACTOME_EGFR_DOWNREGULATION	25	0.4953	1.291624	0.1602434	0.34896016	1	17
REACTOME_SIGNALING_BY_FGFR_MUTANTS	39	0.456624	1.290423	0.13305613	0.3493316	1	1354
REACTOME_HEMOSTASIS	415	0.327151	1.289346	0.012269938	0.3492194	1	4224
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	62	0.418688	1.286207	0.09920635	0.35312486	1	3536
KEGG_BASAL_CELL_CARCINOMA	51	0.425745	1.283308	0.12248996	0.35597086	1	5483
KEGG_PPAR_SIGNALING_PATHWAY	62	0.412198	1.282167	0.103238866	0.356265	1	5402
KEGG_FOCAL_ADHESION	195	0.352511	1.282057	0.045081966	0.3545071	1	4245
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	22	0.495978	1.27998	0.14738806	0.35627687	1	209
REACTOME_SIGNALING_BY_GPCR	481	0.323153	1.27991	0.012875536	0.3544713	1	4416
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	88	0.397497	1.278796	0.088	0.35469085	1	4054
REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	42	0.43801	1.276418	0.14508928	0.35707375	1	3655
BIOCARTA_AGR_PATHWAY	34	0.467814	1.276378	0.14285715	0.35528478	1	5629
REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	28	0.472232	1.274278	0.15151516	0.35729614	1	1971
REACTOME_GPCR_DOWNSTREAM_SIGNALING	391	0.322918	1.27032	0.028629856	0.36300594	1	4416
REACTOME_IL_2_SIGNALING	37	0.447002	1.266489	0.15221988	0.36803728	1	2356
BIOCARTA_CALCINEURIN_PATHWAY	18	0.528856	1.265694	0.19126819	0.3678026	1	2477
BIOCARTA_PAR1_PATHWAY	37	0.456827	1.264843	0.13968958	0.36744836	1	4168
REACTOME_GAB1_SIGNALOSOME	36	0.452478	1.264253	0.15082644	0.36672872	1	3655
REACTOME_REGULATION_OF_HYPOXIA_INDUCIBLE_FACTOR_HIF_BY_OXYGEN	22	0.514253	1.2613	0.16969697	0.37040636	1	2752
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK	163	0.356398	1.261095	0.072463766	0.36889768	1	4867
REACTOME_LIPOPROTEIN_METABOLISM	25	0.476906	1.259153	0.1961207	0.37064096	1	5095

REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	19	0.509267	1.259081	0.19838056	0.36889997	1	2194
BIOCARTA_ALK_PATHWAY	34	0.467943	1.257415	0.15767635	0.3704068	1	6122
BIOCARTA_MAL_PATHWAY	19	0.506313	1.255478	0.17826086	0.37208974	1	3843
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	73	0.393153	1.25505	0.12076271	0.37108478	1	4527
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	24	0.496168	1.2524	0.16194332	0.3741039	1	3347
BIOCARTA_WNT_PATHWAY	25	0.482863	1.247631	0.18647541	0.38145277	1	4705
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	35	0.450347	1.242201	0.17901234	0.39060065	1	3347
REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_ACTIVITY_BY_INSULIN_LIKE_GROWTH_FACTOR_BINDING_PROTEINS_IGFBPS	15	0.54872	1.241691	0.20472442	0.3896407	1	4131
REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	99	0.374027	1.241601	0.0995935	0.38797426	1	4481
REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE	130	0.360496	1.241262	0.08033827	0.38683754	1	6732
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	44	0.427903	1.24024	0.15306123	0.3866831	1	5874
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	55	0.406652	1.235723	0.13496932	0.39347294	1	6079
BIOCARTA_DC_PATHWAY	15	0.53378	1.231054	0.2172043	0.40063146	1	2261
BIOCARTA_NKCELLS_PATHWAY	19	0.512766	1.224286	0.206	0.41234764	1	3843
REACTOME_TIGHT_JUNCTION_INTERACTIONS	28	0.461733	1.222532	0.18619247	0.41418982	1	1861
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	20	0.495056	1.218697	0.22410148	0.4195732	1	4670
REACTOME_BASIGIN_INTERACTIONS	24	0.470993	1.217275	0.21205822	0.42027628	1	3556
REACTOME_REGULATION_OF_KIT_SIGNALING	16	0.514845	1.215621	0.23620309	0.42172283	1	1403
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	462	0.306797	1.214245	0.039832287	0.42276227	1	4080
KEGG_HISTIDINE_METABOLISM	27	0.459501	1.213798	0.208	0.4217377	1	2604
KEGG_HUNTINGTONS_DISEASE	154	0.341111	1.210829	0.11811024	0.42562252	1	4618
BIOCARTA_RAS_PATHWAY	23	0.482659	1.207732	0.23251028	0.430203	1	2077
BIOCARTA_EPO_PATHWAY	19	0.495957	1.207715	0.23966943	0.42829096	1	4107
REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	57	0.394612	1.204863	0.18525897	0.43230233	1	3229
REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	50	0.404826	1.19833	0.19721116	0.44310215	1	3229
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	37	0.428109	1.197841	0.22008547	0.44214228	1	5634
BIOCARTA_GPCR_PATHWAY	33	0.436003	1.197505	0.21129707	0.44095778	1	4107
REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_TTP	17	0.494123	1.196913	0.24409449	0.4401633	1	160
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	429	0.3014	1.196813	0.051391862	0.43845877	1	5412
REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	24	0.46404	1.194868	0.22334003	0.44040427	1	1219
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI	18	0.496263	1.191676	0.24448898	0.44532186	1	3460
REACTOME_ELONGATION_ARREST_AND_RECOVERY	24	0.464974	1.189258	0.22978723	0.44829568	1	4417
KEGG_PHENYLALANINE_METABOLISM	17	0.492236	1.185419	0.2422998	0.4547256	1	5333
REACTOME_METAL_ION_SLC_TRANSPORTERS	21	0.462977	1.185378	0.24421053	0.45286423	1	5696
BIOCARTA_ETS_PATHWAY	18	0.483509	1.183301	0.24117647	0.4549805	1	4107
BIOCARTA_IGF1_PATHWAY	21	0.467449	1.182781	0.25316456	0.45416072	1	4107
KEGG_GLUTATHIONE_METABOLISM	43	0.417158	1.182663	0.22131148	0.4524913	1	3604
REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_DAI	18	0.490313	1.182155	0.24444444	0.45153937	1	3782
BIOCARTA_SPRY_PATHWAY	18	0.490414	1.178603	0.25979382	0.45670417	1	2992
KEGG_OXIDATIVE_PHOSPHORYLATION	94	0.355385	1.177385	0.17515275	0.45730326	1	5764
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	77	0.365818	1.176781	0.18012422	0.45670626	1	4728
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	26	0.451803	1.174597	0.23830736	0.45959693	1	5634
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	104	0.349787	1.168847	0.18181819	0.46974835	1	2539
REACTOME_CTLA4_INHIBITORY_SIGNALING	19	0.476401	1.168016	0.25894737	0.4695443	1	7332
REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	18	0.485249	1.166492	0.2545825	0.47096044	1	7148
REACTOME_IL_3_5_AND_GM_CSF_SIGNALING	39	0.410276	1.165269	0.25298804	0.4717496	1	2356
REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY	20	0.461846	1.160487	0.28169015	0.47962078	1	2175
BIOCARTA_CREB_PATHWAY	26	0.450671	1.158899	0.2772074	0.48084098	1	2354
REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	44	0.402305	1.157379	0.25786164	0.48218805	1	4831
REACTOME_ERK_MAPK_TARGETS	21	0.461564	1.156723	0.2889813	0.48163536	1	6682
KEGG_ARGININE_AND_PROLINE_METABOLISM	48	0.385527	1.153088	0.2371134	0.48735654	1	4566
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	98	0.34821	1.152896	0.18023255	0.48588794	1	3944
REACTOME_PLATELET_SENSITIZATION_BY_LDL	16	0.497832	1.152547	0.27405858	0.48469013	1	1825
BIOCARTA_PTEN_PATHWAY	17	0.47462	1.148476	0.26415095	0.4915718	1	3843
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_DIFFERENTIATION	69	0.366639	1.148418	0.24058577	0.48973486	1	4512
REACTOME_MUSCLE_CONTRACTION	41	0.393264	1.14762	0.25604838	0.4895796	1	3248
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS	29	0.426785	1.144712	0.2808081	0.4942867	1	7392
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	67	0.367614	1.14023	0.2514507	0.5015522	1	7781
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	64	0.365609	1.13163	0.23413567	0.5182	1	3827
REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM	161	0.314594	1.123023	0.20773931	0.5349893	1	4481
REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	17	0.457896	1.122318	0.32539684	0.5344078	1	10077
REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI	16	0.468138	1.116071	0.29958677	0.546532	1	5552
BIOCARTA_IL6_PATHWAY	22	0.418725	1.113934	0.31288344	0.5492611	1	4107
BIOCARTA_TALL1_PATHWAY	15	0.4689	1.113539	0.32298136	0.54811025	1	5745
BIOCARTA_CXCR4_PATHWAY	24	0.434532	1.112624	0.32271764	0.5479441	1	3843
REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS	68	0.352224	1.110662	0.26499033	0.55040234	1	5345
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	92	0.335989	1.104241	0.25	0.56315273	1	3843
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	121	0.320049	1.098583	0.27217743	0.57448584	1	7213
REACTOME_SEMAPHORIN_INTERACTIONS	64	0.350745	1.098473	0.28721175	0.57257324	1	4630
REACTOME_SIGNALING_BY_NOTCH1	68	0.350247	1.096808	0.3043478	0.57441235	1	6558
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	40	0.38681	1.095602	0.3448276	0.57507384	1	3529
REACTOME_CELL_JUNCTION_ORGANIZATION	71	0.345653	1.094786	0.28633407	0.57469815	1	3625
REACTOME_DEVELOPMENTAL_BIOLOGY	357	0.281625	1.089769	0.2219917	0.584061	1	4728
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	0.342474	1.088731	0.2845361	0.58418757	1	3869
KEGG_THYROID_CANCER	29	0.416922	1.088423	0.3346856	0.58270526	1	4185
KEGG_ECM_RECEPTOR_INTERACTION	83	0.335351	1.086966	0.29484537	0.58417237	1	4133
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	173	0.300866	1.084879	0.2808081	0.5868445	1	5154
BIOCARTA_INSULIN_PATHWAY	21	0.428896	1.081914	0.35728544	0.59157115	1	4921
KEGG_ADHERENS_JUNCTION	67	0.352542	1.080375	0.3295238	0.593293	1	5819
KEGG_TIGHT_JUNCTION	118	0.317307	1.076925	0.28455284	0.5993459	1	3825
REACTOME_AXON_GUIDANCE	231	0.287672	1.071722	0.2805139	0.60933495	1	4728
REACTOME_UNFOLDED_PROTEIN_RESPONSE	76	0.328072	1.070112	0.33887735	0.6110774	1	5117
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	19	0.430432	1.068103	0.35222673	0.61376923	1	4010
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	30	0.394058	1.068045	0.36174637	0.61173123	1	3508
BIOCARTA_AMI_PATHWAY	19	0.43316	1.065483	0.36907217	0.61558604	1	4596
REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	33	0.384241	1.062403	0.36863545	0.62065166	1	5154
BIOCARTA_BAD_PATHWAY	24	0.407758	1.062169	0.3787575	0.61905223	1	34
REACTOME_SIGNALING_BY_NOTCH	96	0.318802	1.060736	0.31041667	0.62020826	1	6558
KEGG_OTHER_GLYCAN_DEGRADATION	15	0.450108	1.05938	0.4019231	0.62129676	1	5284
REACTOME_GABA_B_RECEPTOR_ACTIVATION	36	0.373314	1.050592	0.37367302	0.6401229	1	4825
BIOCARTA_CHEMICAL_PATHWAY	22	0.421392	1.04862	0.3983051	0.6429787	1	3338
BIOCARTA_TNFR2_PATHWAY	17	0.438535	1.047081	0.42398286	0.64445245	1	4010
REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION	23	0.408748	1.04329	0.3895349	0.6518204	1	1578
BIOCARTA_EIF4_PATHWAY	24	0.396458	1.039522	0.39791667	0.6588789	1	6499
BIOCARTA_DEATH_PATHWAY	33	0.375158	1.039288	0.37704918	0.6571987	1	2962
REACTOME_NOD1_2_SIGNALING_PATHWAY	29	0.389489	1.038974	0.37917486	0.65578395	1	4743
REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	58	0.344455	1.038875	0.4122449	0.653798	1	4446
KEGG_WNT_SIGNALING_PATHWAY	140	0.301067	1.03761	0.3426295	0.65470433	1	2354
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	43	0.355757	1.036148	0.38274336	0.6560538	1	3912
KEGG_REGULATION_OF_AUTOPHAGY	20	0.412965	1.032816	0.3943662	0.6621374	1	6804
KEGG_TGF_BETA_SIGNALING_PATHWAY	83	0.316958	1.031549	0.38762885	0.66322255	1	5955
KEGG_SELENOAMINO_ACID_METABOLISM	25	0.406354	1.03137	0.39872068	0.6614733	1	2949
REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_AND_AMINE_COMPOUNDS	73	0.322752	1.030749	0.36746988	0.66076404	1	3289
KEGG_PARKINSONS_DISEASE	94	0.313255	1.030454	0.38607594	0.6592878	1	5521

BIOCARTA_NTHI_PATHWAY	23	0.406069	1.02891	0.4271047	0.66086507	1	4009
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	208	0.280046	1.028287	0.35805085	0.66022366	1	2467
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	0.404479	1.027523	0.3979798	0.6599365	1	6545
BIOCARTA_MPR_PATHWAY	33	0.374404	1.026822	0.41093117	0.65946287	1	6045
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	19	0.427523	1.026676	0.43253967	0.65772766	1	1528
REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRCADIAN_EXPRESSION	33	0.3715	1.026251	0.40591967	0.6565331	1	1578
KEGG_LONG_TERM_DEPRESSION	59	0.331436	1.020447	0.42379957	0.66894436	1	4099
REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	26	0.391325	1.020376	0.4032258	0.6670069	1	6782
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	38	0.354928	1.019553	0.4120083	0.6668714	1	5391
KEGG_CARDIAC_MUSCLE_CONTRACTION	60	0.334393	1.018655	0.41629955	0.6668934	1	5413
REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSION_BY_REV_ERBA	22	0.401838	1.016667	0.41700405	0.6695113	1	1578
BIOCARTA_ECM_PATHWAY	24	0.40223	1.016568	0.4331984	0.66759646	1	6595
REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	116	0.296989	1.012066	0.42094862	0.67665154	1	4054
BIOCARTA_FAS_PATHWAY	29	0.372579	1.011036	0.40820736	0.6769007	1	4107
KEGG_GAP_JUNCTION	84	0.307149	1.009075	0.41975307	0.67965895	1	4054
BIOCARTA_BARRESTIN_SRC_PATHWAY	15	0.433343	1.009054	0.44032922	0.67756295	1	3843
REACTOME_CD28_CO_STIMULATION	30	0.374456	1.00584	0.451417	0.68324	1	3271
KEGG_ENDOMETRIAL_CANCER	51	0.341984	1.005268	0.4486373	0.6825004	1	3843
REACTOME_L1CAM_INTERACTIONS	82	0.308033	1.002077	0.4168421	0.688113	1	2591
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	124	0.289418	0.996798	0.41787943	0.6988381	1	4527
REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS	74	0.309925	0.996757	0.43333334	0.6968117	1	3827
KEGG_TYROSINE_METABOLISM	37	0.357921	0.99635	0.44618395	0.6956425	1	5333
REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1	17	0.411565	0.994897	0.4561753	0.696925	1	29
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	21	0.404034	0.991667	0.4607438	0.70275486	1	4230
BIOCARTA_NGF_PATHWAY	18	0.411063	0.986566	0.45148516	0.71299165	1	4107
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	103	0.28905	0.983053	0.48007968	0.7194328	1	4115
BIOCARTA_ERK5_PATHWAY	17	0.415648	0.980571	0.4928717	0.7233695	1	6499
CANCER-TESTIS-ANTIGEN	105	0.28456	0.976817	0.49056605	0.73094356	1	2047
REACTOME_PROTEIN_FOLDING	50	0.332508	0.976414	0.48846152	0.72971237	1	4413
REACTOME_SIGNALING_BY_WNT	62	0.31448	0.975813	0.4751491	0.7290211	1	7114
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	67	0.311427	0.975038	0.49382716	0.7288615	1	1664
REACTOME_TRAF6_MEDIATED_NFKB_ACTIVATION	21	0.392958	0.974779	0.47974414	0.7273263	1	3367
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	139	0.280455	0.973865	0.50851065	0.7274508	1	4054
KEGG_NON_SMALL_CELL_LUNG_CANCER	54	0.323966	0.971885	0.481409	0.7302097	1	3843
REACTOME_COLLAGEN_FORMATION	53	0.323753	0.971598	0.49795082	0.72870314	1	4816
REACTOME_REGULATION_OF_APOPTOSIS	56	0.32081	0.971275	0.48653847	0.727356	1	7114
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	79	0.300918	0.966577	0.51687765	0.736662	1	4816
REACTOME_SPHINGOLIPID_METABOLISM	58	0.310862	0.961824	0.5079681	0.7465455	1	6365
KEGG_RENAL_CELL_CARCINOMA	66	0.307634	0.960963	0.5020243	0.74638903	1	1578
REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	17	0.40706	0.959682	0.5245203	0.7472979	1	3428
BIOCARTA_CDC42RAC_PATHWAY	16	0.411964	0.956695	0.51452285	0.75239867	1	6330
BIOCARTA_RELA_PATHWAY	16	0.403155	0.956493	0.51731163	0.7507109	1	2962
KEGG_TRYPTOPHAN_METABOLISM	37	0.33798	0.953389	0.5302714	0.75629616	1	4477
REACTOME_SIGNAL_TRANSDUCTION_BY_L1	34	0.342408	0.952269	0.5220126	0.7568668	1	3843
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	92	0.290524	0.951145	0.51898736	0.75726175	1	7114
REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	15	0.407783	0.950053	0.52609605	0.7577039	1	3347
BIOCARTA_GCR_PATHWAY	19	0.392113	0.946527	0.5365344	0.7643431	1	2134
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	65	0.303785	0.943096	0.54375	0.77067333	1	3070
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	221	0.252386	0.936624	0.6147705	0.7841329	1	3998
REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFATASE_ACTIVATION	23	0.368844	0.934807	0.560241	0.7865787	1	953
REACTOME_DIABETES_PATHWAYS	123	0.273845	0.931513	0.58811474	0.79258996	1	5117
REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	43	0.327424	0.930616	0.55463916	0.79253274	1	4354
KEGG_AXON_GUIDANCE	123	0.266724	0.930353	0.6286837	0.7909612	1	5870
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	68	0.292503	0.928027	0.56916994	0.79440653	1	3660
KEGG_GALACTOSE_METABOLISM	22	0.365317	0.926948	0.5636008	0.7948523	1	4442
REACTOME_CIRCADIAN_CLOCK	50	0.31747	0.926503	0.5711382	0.79374146	1	6324
REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC	15	0.390222	0.924141	0.55353534	0.7973043	1	5154
KEGG_PROTEASOME	40	0.322606	0.922665	0.5690722	0.7986509	1	7440
REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	24	0.360552	0.921533	0.543021	0.7994798	1	7676
REACTOME_SIGNALING_BY_ERBB2	95	0.278745	0.91979	0.60206187	0.8014449	1	4054
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	104	0.275687	0.917674	0.6273292	0.8042741	1	5521
KEGG_GLIOMA	65	0.30009	0.917618	0.6034858	0.80222833	1	3870
REACTOME_TCR_SIGNALING	42	0.315418	0.916969	0.594	0.8016283	1	4336
REACTOME_SHC_MEDIATED_SIGNALLING	15	0.384189	0.91591	0.5667351	0.8020575	1	3843
REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	17	0.386299	0.909292	0.6019802	0.8157512	1	1401
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	61	0.29366	0.906983	0.62288135	0.8191055	1	5634
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	81	0.282438	0.906856	0.6260504	0.8171557	1	2646
BIOCARTA_NFAT_PATHWAY	49	0.300439	0.905315	0.61473686	0.8187881	1	4527
REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS	26	0.342815	0.903066	0.59583336	0.8220762	1	399
BIOCARTA_ARF_PATHWAY	17	0.371673	0.901239	0.5785124	0.824407	1	1662
BIOCARTA_PROTEASOME_PATHWAY	28	0.343327	0.900794	0.61044174	0.8233053	1	7440
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	358	0.234831	0.900624	0.77951	0.82156163	1	4054
BIOCARTA_CTCF_PATHWAY	23	0.35508	0.900468	0.6051081	0.8197913	1	1662
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	96	0.273984	0.899352	0.6645702	0.8202801	1	4107
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN	28	0.338245	0.898438	0.60618556	0.8202253	1	87
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	25	0.338541	0.896813	0.5842217	0.8218918	1	1439
BIOCARTA_AKT_PATHWAY	20	0.366557	0.896047	0.62236285	0.8215082	1	3655
REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS	38	0.314782	0.895281	0.6080508	0.8212475	1	4831
BIOCARTA_TOB1_PATHWAY	16	0.387647	0.895147	0.59961313	0.81939137	1	3869
BIOCARTA_RHO_PATHWAY	32	0.329561	0.894637	0.59491193	0.8184516	1	6971
KEGG_CALCIUM_SIGNALING_PATHWAY	161	0.253323	0.894559	0.70711297	0.8164467	1	4054
REACTOME_NETRIN1_SIGNALING	35	0.321405	0.892804	0.6501976	0.8185304	1	5870
REACTOME_GLYCOSPHINGOLIPID_METABOLISM	32	0.327599	0.886696	0.6376518	0.8309685	1	4134
REACTOME_ER_PHAGOSOME_PATHWAY	53	0.288342	0.885205	0.65591395	0.8322753	1	7440
BIOCARTA_HDAC_PATHWAY	26	0.339741	0.884987	0.62753034	0.8307217	1	6499
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	75	0.278274	0.883049	0.68442625	0.83297235	1	3869
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	20	0.357562	0.876904	0.64908254	0.8451968	1	6564
KEGG_DORSO_VENTRAL_AXIS_FORMATION	23	0.341999	0.876383	0.66597074	0.8442421	1	4532
BIOCARTA_INFLAM_PATHWAY	19	0.353648	0.87359	0.65863454	0.8483327	1	3869
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	24	0.34214	0.87335	0.64241165	0.8468012	1	1146
REACTOME_SIGNALING_BY_BMP	21	0.351554	0.872173	0.641129	0.84748596	1	2521
REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	20	0.350314	0.870905	0.64285713	0.8483228	1	4588
REACTOME_GRB2_SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTERGRINS_	15	0.385179	0.86924	0.662	0.84997284	1	3347
BIOCARTA_IGF1R_PATHWAY	22	0.345324	0.867393	0.65208334	0.852019	1	3870
REACTOME_METABOLISM_OF_CARBOHYDRATES	218	0.234895	0.862938	0.8127572	0.859675	1	2539
REACTOME_SHC_RELATED_EVENTS	16	0.372984	0.862489	0.6407186	0.8584594	1	4921
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	24	0.329542	0.858864	0.6491935	0.8641819	1	4825
REACTOME_PEROXISOMAL_LIPID_METABOLISM	20	0.345757	0.858336	0.62473345	0.8631553	1	1691
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	25	0.329326	0.854663	0.65789473	0.86902946	1	1492
REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	33	0.310071	0.853775	0.68329716	0.8687406	1	2950
REACTOME_SHC_MEDIATED_CASCADE	24	0.337701	0.853733	0.6793587	0.8666814	1	3345
REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR	90	0.26122	0.851902	0.7387755	0.86840713	1	4054
REACTOME_SIGNALING_BY_NODAL	15	0.368126	0.851644	0.67167383	0.86685866	1	5608

REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	89	0.261256	0.848165	0.753507	0.8719027	1	4831
KEGG_COLORECTAL_CANCER	62	0.278068	0.847499	0.751503	0.8712353	1	4553
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	18	0.340515	0.844276	0.6735537	0.8758328	1	3363
REACTOME_INSULIN_RECEPTOR_RECYCLING	21	0.338426	0.842944	0.6884211	0.8765195	1	7190
BIOCARTA_HCMV_PATHWAY	17	0.348669	0.83972	0.6680851	0.8810412	1	1643
REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION	18	0.34853	0.838898	0.68623483	0.8806103	1	806
KEGG_DILATED_CARDIOMYOPATHY	80	0.263503	0.838018	0.7714286	0.8802133	1	4054
REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE	46	0.286061	0.834007	0.74734604	0.88652396	1	1982
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	42	0.290104	0.827776	0.7240664	0.89677906	1	2417
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	24	0.326466	0.824864	0.7057654	0.90030897	1	5441
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	23	0.321104	0.824767	0.6995885	0.8983178	1	5505
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	61	0.267551	0.82454	0.7858586	0.89657974	1	7114
REACTOME_FORMATION_OF_THE_HIV1_EARLY_ELONGATION_COMPLEX	29	0.306693	0.821526	0.7386831	0.90010124	1	1737
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	51	0.274087	0.821497	0.78361344	0.89802873	1	2228
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	26	0.31499	0.821415	0.72	0.8961249	1	4831
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	65	0.259868	0.818717	0.800813	0.8991504	1	4911
REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	21	0.333626	0.817928	0.7171315	0.8985675	1	2081
REACTOME_AMYLOIDS	68	0.262532	0.81773	0.8033126	0.89682895	1	5759
REACTOME_SIGNALING_BY_HIPPO	20	0.332242	0.81433	0.70235544	0.90089077	1	3894
BIOCARTA_BCELLSURVIVAL_PATHWAY	16	0.343535	0.80787	0.70485437	0.9106744	1	6499
REACTOME_PI_3K_CASCADE	50	0.271242	0.805931	0.7730924	0.9120843	1	3655
REACTOME_FRS2_MEDIATED_CASCADE	32	0.293351	0.803326	0.7656566	0.91480887	1	1057
BIOCARTA_RACCYCD_PATHWAY	26	0.311326	0.801326	0.72147	0.9162816	1	3923
REACTOME_SIGNAL_AMPLIFICATION	30	0.295366	0.799947	0.7719665	0.9167713	1	5441
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	22	0.319291	0.799393	0.756	0.91562486	1	5152
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	50	0.270945	0.797085	0.8080169	0.91760635	1	7440
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	52	0.261792	0.794185	0.8424242	0.9204928	1	3271
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	38	0.278337	0.787512	0.7956778	0.9296676	1	3843
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	30	0.291375	0.787385	0.7887324	0.927777	1	3821
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	30	0.294814	0.785724	0.7878788	0.92845005	1	4831
REACTOME_SIGNALING_BY_RHO_GTPASES	108	0.236216	0.785341	0.9070707	0.92698705	1	6392
REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	99	0.233786	0.784861	0.8953975	0.9256529	1	6732
REACTOME_APOPTOSIS	141	0.224121	0.784678	0.922	0.9238522	1	4797
REACTOME_PI3K_AKT_ACTIVATION	36	0.279163	0.784041	0.8231827	0.92288065	1	6732
KEGG_SPHINGOLIPID_METABOLISM	33	0.28652	0.780629	0.7871486	0.9262007	1	6782
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	61	0.250403	0.779214	0.8787276	0.92643726	1	3964
REACTOME_G_ALPHA1213_SIGNALLING_EVENTS	72	0.250002	0.777356	0.8486141	0.92720693	1	4831
BIOCARTA_TID_PATHWAY	18	0.323834	0.776418	0.7525355	0.92651445	1	6507
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	189	0.213322	0.772266	0.962963	0.930882	1	3998
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	25	0.297237	0.77147	0.79123175	0.9299467	1	5608
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	47	0.263672	0.770166	0.8286853	0.9297703	1	7440
KEGG_STEROID_BIOSYNTHESIS	16	0.322578	0.761293	0.76987445	0.94052535	1	4703
REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING	36	0.274097	0.760895	0.8269231	0.9390314	1	6732
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	42	0.266138	0.757629	0.8362919	0.9415617	1	4867
REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	27	0.287589	0.754652	0.8472222	0.943593	1	3655
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	46	0.261712	0.75245	0.8533605	0.94480103	1	7440
BIOCARTA_RARRXR_PATHWAY	15	0.320085	0.745784	0.8125	0.9516764	1	5537
KEGG_INOSITOL_PHOSPHATE_METABOLISM	53	0.247913	0.744625	0.8935698	0.95112914	1	6330
REACTOME_MICRORNA_MIRNA_BIOGENESIS	18	0.311454	0.743339	0.79710144	0.9508355	1	558
KEGG_VIBRIO_CHOLERAE_INFECTION	51	0.24664	0.741956	0.8925781	0.95045155	1	8110
REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	38	0.2585	0.741441	0.8613861	0.94903135	1	6130
BIOCARTA_CERAMIDE_PATHWAY	22	0.292305	0.738991	0.84458077	0.94986856	1	3843
BIOCARTA_NFKB_PATHWAY	23	0.291631	0.737837	0.81670064	0.94925135	1	4599
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	37	0.259829	0.734837	0.87216496	0.9509681	1	4651
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	33	0.265061	0.731663	0.86758894	0.9525964	1	4236
BIOCARTA_MITOCHONDRIA_PATHWAY	21	0.295432	0.731104	0.84504133	0.95125604	1	2739
REACTOME_PLATELET_HOMEOSTASIS	71	0.233266	0.730352	0.9445585	0.9501847	1	5984
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	29	0.267044	0.726674	0.86270493	0.9523865	1	4238
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	128	0.20891	0.726664	0.9800399	0.95035136	1	5392
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	16	0.307258	0.726642	0.83366334	0.94834423	1	3601
REACTOME_PLC_BETA_MEDIATED_EVENTS	38	0.254572	0.72497	0.89959013	0.94827175	1	1982
BIOCARTA_NDKDYNAMIN_PATHWAY	18	0.298751	0.724794	0.8280922	0.94643676	1	7295
REACTOME_SIGNALING_BY_FGFR	102	0.214972	0.72425	0.9718875	0.94503284	1	4054
REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDATION_IN_MUSCLE	18	0.302037	0.723724	0.8136646	0.9436106	1	2331
REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	79	0.224857	0.72331	0.952	0.9420398	1	6732
BIOCARTA_HIVNEF_PATHWAY	57	0.237355	0.720467	0.9072165	0.94325614	1	3338
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	49	0.24262	0.712819	0.91493773	0.94949543	1	7440
KEGG_VIRAL_MYOCARDITIS	40	0.249811	0.710649	0.907173	0.94966793	1	6018
REACTOME_DAG_AND_IP3_SIGNALING	28	0.269531	0.707446	0.9068323	0.9509038	1	1982
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	80	0.224134	0.704955	0.9657258	0.95123607	1	942
KEGG_GLYCEROLIPID_METABOLISM	37	0.249283	0.701447	0.9238477	0.9524025	1	5286
BIOCARTA_TEL_PATHWAY	18	0.286668	0.691086	0.8784648	0.9599762	1	1662
REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	27	0.259913	0.690172	0.9054054	0.9587776	1	6867
REACTOME_DOWNSTREAM_TCR_SIGNALING	26	0.26152	0.684557	0.9113402	0.96142703	1	4009
BIOCARTA_MET_PATHWAY	37	0.245862	0.679189	0.93621397	0.9638144	1	6476
REACTOME_RAP1_SIGNALLING	15	0.296628	0.675964	0.8772636	0.96436995	1	703
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	47	0.231825	0.673265	0.9526627	0.96454066	1	7440
REACTOME_CA_DEPENDENT_EVENTS	26	0.255721	0.668972	0.9275654	0.96577233	1	1067
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	15	0.283503	0.665795	0.8956693	0.9660553	1	1524
REACTOME_CHOLESTEROL_BIOSYNTHESIS	20	0.261531	0.658986	0.918	0.9687153	1	4917
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	46	0.225493	0.657731	0.94409937	0.9675507	1	7440
BIOCARTA_HIF_PATHWAY	15	0.28126	0.644042	0.8964803	0.973704	1	5489
BIOCARTA_NO1_PATHWAY	28	0.240736	0.643134	0.9444444	0.97222584	1	7317
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	54	0.208157	0.634355	0.98802394	0.97503847	1	7440
REACTOME_PKB_MEDIATED_EVENTS	28	0.239507	0.629376	0.94368935	0.9756334	1	8955
REACTOME_PI3K_CASCADE	63	0.201559	0.618031	0.9877551	0.97895384	1	6732
BIOCARTA_VEGF_PATHWAY	29	0.223343	0.60182	0.96875	0.98336315	1	5489
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	18	0.233869	0.561483	0.9758065	0.9930799	1	7213
BIOCARTA_TFF_PATHWAY	20	0.228964	0.558293	0.97885835	0.99176514	1	3843
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	20	0.223082	0.554742	0.9640592	0.99054354	1	3271
REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	16	0.19094	0.453163	0.99346405	1	1	4080
REACTOME_TIE2_SIGNALING	17	0.177128	0.421895	0.989899	0.9991627	1	6330

Table S12
GSEA Analysis on HNSC cancer cell lines comparing cell lines with or without 3p14 loss (arm or focal), Pathways Depleted

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION	15	-0.78569	-1.81899	0	1	0.776	3915
REACTOME_G2_M_CHECKPOINTS	41	-0.62153	-1.80462	0.002053388	0.5901293	0.805	5783
KEGG_DNA_REPLICATION	36	-0.62724	-1.7728	0.003853565	0.5264487	0.893	6658
KEGG_RNA_DEGRADATION	53	-0.57231	-1.7264	0	0.58631593	0.966	5882
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	21	-0.67796	-1.70202	0.014732965	0.5632023	0.985	5415
REACTOME_CELL_CYCLE	387	-0.43893	-1.68771	0	0.5245929	0.993	6667
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	34	-0.60032	-1.67467	0.011881189	0.49464625	0.996	6632
KEGG_HOMOLOGOUS_RECOMBINATION	26	-0.65458	-1.67194	0.007604563	0.44189286	0.996	6108
REACTOME_CHROMOSOME_MAINTENANCE	112	-0.4951	-1.66934	0	0.4007066	0.996	6658
REACTOME_MITOTIC_G2_G2_M_PHASES	78	-0.52309	-1.66598	0.002020202	0.36893672	0.997	2570
REACTOME_MEIOSIS	104	-0.49685	-1.65568	0.004040404	0.36404335	0.999	6204
REACTOME_MITOTIC_PROMETAPHASE	78	-0.51703	-1.63278	0.003929273	0.3938234	1	5202
REACTOME_CELL_CYCLE_MITOTIC	302	-0.43344	-1.632	0.001838235	0.36551595	1	6667
REACTOME_DNA_STRAND_ELONGATION	30	-0.61119	-1.62769	0.026	0.35075778	1	8067
REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION_INDEPENDENT_DOUBLE_STRAND_BREAKS	15	-0.69914	-1.62423	0.019120459	0.33541065	1	4935
REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	15	-0.68035	-1.61212	0.019157087	0.34164026	1	1767
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	35	-0.57947	-1.61147	0.023109244	0.3228539	1	9138
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	51	-0.53723	-1.6049	0.013592233	0.31922644	1	7055
REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMATE_BINDING_AND_ACTIVATION	15	-0.6697	-1.6033	0.036398467	0.30625546	1	1358
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	26	-0.60894	-1.59659	0.03195489	0.3041328	1	7055
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	26	-0.61076	-1.58809	0.03076923	0.30704293	1	7055
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.5444	-1.58756	0.024621213	0.2941715	1	6290
REACTOME_EXTENSION_OF_TELOMERES	27	-0.58735	-1.58381	0.034979425	0.28821093	1	6658
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	-0.60454	-1.58361	0.028571429	0.27647474	1	6215
REACTOME_ION_CHANNEL_TRANSPORT	41	-0.5577	-1.58255	0.023076924	0.2671123	1	3818
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	30	-0.57429	-1.57942	0.03976143	0.26187417	1	6658
REACTOME_DNA_REPLICATION	180	-0.434	-1.5489	0.005870841	0.30797014	1	6667
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	31	-0.55558	-1.53774	0.019762846	0.31994355	1	7055
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	42	-0.53998	-1.53749	0.04411765	0.30933598	1	4165
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	33	-0.55491	-1.53731	0.019569471	0.29934233	1	3913
REACTOME_DNA_REPAIR	103	-0.46254	-1.53668	0.011560693	0.2905247	1	5779
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	63	-0.49984	-1.53229	0.019455252	0.2888139	1	2570
REACTOME_GLUCOSE_TRANSPORT	33	-0.55777	-1.52896	0.037698414	0.28605098	1	7055
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	18	-0.65079	-1.52881	0.039447732	0.27778438	1	6632
BIOCARTA_ATRBRCA_PATHWAY	20	-0.63377	-1.52471	0.06097561	0.27682507	1	4163
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	26	-0.57637	-1.52317	0.033898305	0.27191514	1	7055
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	31	-0.54639	-1.49591	0.043071162	0.31414673	1	7055
REACTOME_GLOBAL_GENOMIC_NER_GG_NER	33	-0.54787	-1.49552	0.05511811	0.3068624	1	6950
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	21	-0.60038	-1.49349	0.06175299	0.302627	1	4236
KEGG_PROPANOATE_METABOLISM	32	-0.54149	-1.49184	0.054108217	0.29832283	1	3886
REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	15	-0.63988	-1.48871	0.05108055	0.29632074	1	6104
REACTOME_FANCONI_ANEMIA_PATHWAY	20	-0.60761	-1.48191	0.06641366	0.30095765	1	4362
REACTOME_MITOTIC_M_M_G1_PHASES	160	-0.42408	-1.48143	0.005639098	0.29491073	1	6075
KEGG_BASE_EXCISION_REPAIR	34	-0.54204	-1.48024	0.049701788	0.29049784	1	8023
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	56	-0.48801	-1.47642	0.0407767	0.2902651	1	2570
REACTOME_MRNA_PROCESSING	151	-0.42055	-1.46874	0.009541985	0.29823396	1	8642
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	36	-0.51906	-1.46522	0.05904059	0.29814547	1	1358
REACTOME_MRNA_3_END_PROCESSING	33	-0.5359	-1.45907	0.0499002	0.3031185	1	4165
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	23	-0.56956	-1.45471	0.09090909	0.30516508	1	4165
REACTOME_TRNA_AMINOACYLATION	42	-0.49506	-1.4447	0.058479533	0.31819943	1	6215
REACTOME_MEIOTIC_RECOMBINATION	76	-0.4546	-1.44156	0.048237476	0.31726608	1	7958
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	42	-0.49734	-1.42708	0.06841046	0.33884966	1	5836
REACTOME_MEIOTIC_SYNAPSIS	66	-0.45918	-1.42118	0.048828125	0.3440926	1	7958
REACTOME_G1_PHASE	36	-0.50961	-1.4189	0.071570575	0.34168512	1	4159
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	28	-0.53001	-1.41705	0.07017544	0.33915693	1	3645
REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS	15	-0.61184	-1.41581	0.08795411	0.33558962	1	1797
KEGG_RIBOSOME	87	-0.44005	-1.41195	0.03976143	0.3379309	1	7871
KEGG_MISMATCH_REPAIR	23	-0.55376	-1.40278	0.07453416	0.35022163	1	8074
REACTOME_PI_METABOLISM	46	-0.48433	-1.40189	0.076620825	0.34582546	1	4009
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	132	-0.41243	-1.40101	0.040152963	0.34163177	1	8642
REACTOME_LAGGING_STRAND_SYNTHESIS	19	-0.56676	-1.39488	0.09056604	0.3485094	1	8067
REACTOME_SULFUR_AMINO_ACID_METABOLISM	23	-0.54133	-1.39437	0.07824428	0.34391168	1	3532
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	18	-0.58376	-1.38989	0.1003937	0.34726012	1	4241
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	131	-0.39986	-1.38347	0.04040404	0.3544835	1	8228
KEGG_CELL_CYCLE	124	-0.40539	-1.38192	0.044715445	0.35230216	1	4163
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	22	-0.54561	-1.36825	0.10037175	0.37392864	1	3638
REACTOME_METABOLISM_OF_NON_CODING_RNA	47	-0.46772	-1.35784	0.07846715	0.38969472	1	7055
REACTOME_CELL_CYCLE_CHECKPOINTS	110	-0.40556	-1.35318	0.03937008	0.39391476	1	5783
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	20	-0.54106	-1.34729	0.13671875	0.39995158	1	2192
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	18	-0.54952	-1.34697	0.13721804	0.39498737	1	5270
REACTOME_INFLUENZA_LIFE_CYCLE	159	-0.37847	-1.33849	0.04191617	0.4071701	1	7497
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	131	-0.39313	-1.33669	0.04868914	0.40561327	1	8228
REACTOME_RNA_POL_II_TRANSCRIPTION	94	-0.40756	-1.32977	0.056640625	0.41525397	1	4411
REACTOME_TELOMERE_MAINTENANCE	70	-0.43482	-1.32698	0.087890625	0.41567427	1	8067
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_SYNTHESIS	25	-0.51131	-1.32526	0.11133603	0.41389996	1	580
REACTOME_MITOTIC_G1_G1_S_PHASES	133	-0.37831	-1.31173	0.045801528	0.43753025	1	6658
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	36	-0.46847	-1.30894	0.12749004	0.4379554	1	4834
REACTOME_RNA_POL_I_TRANSCRIPTION_INITIATION	24	-0.50215	-1.30889	0.11614173	0.4323954	1	7948
REACTOME_PEPTIDE_CHAIN_ELONGATION	110	-0.39084	-1.30861	0.062135924	0.42756757	1	8228
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION	20	-0.51859	-1.29806	0.15991902	0.44569847	1	7948
REACTOME_SYNTHESIS_OF_PA	21	-0.51978	-1.29359	0.13786009	0.45063344	1	951
REACTOME_ENOS_ACTIVATION_AND_REGULATION	20	-0.53661	-1.28928	0.15127702	0.4551319	1	3882
BIOCARTA_CELLCYCLE_PATHWAY	23	-0.50164	-1.28831	0.15895373	0.4519399	1	2311
BIOCARTA_G2_PATHWAY	24	-0.49888	-1.28605	0.1284585	0.45166963	1	5472
REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	15	-0.56612	-1.28006	0.17197452	0.46072608	1	7366
KEGG_PYRUVATE_METABOLISM	37	-0.46289	-1.27801	0.15686275	0.45997265	1	6249
REACTOME_MRNA_SPLICING	104	-0.38122	-1.27522	0.09055118	0.46158388	1	8642
REACTOME_TRANSCRIPTION	189	-0.35483	-1.27439	0.06007752	0.45827904	1	8208
REACTOME_TRANSLATION	172	-0.35293	-1.27265	0.08477842	0.45690095	1	8228
REACTOME_G1_S_TRANSITION	108	-0.3836	-1.27002	0.10114504	0.45782387	1	6658
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	25	-0.48798	-1.26789	0.18585859	0.45763767	1	1797
BIOCARTA_P53HYPOXIA_PATHWAY	22	-0.50693	-1.26047	0.1625709	0.46906495	1	401
KEGG_BETA_ALANINE_METABOLISM	20	-0.51563	-1.26042	0.17142858	0.46413073	1	3886
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	111	-0.37149	-1.25116	0.107942976	0.4805671	1	7958
REACTOME_DEADENYLATION_OF_MRNA	17	-0.51135	-1.24942	0.19959266	0.47930723	1	1387
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_IN_EMT_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	15	-0.52822	-1.24697	0.1770073	0.48000267	1	4449
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM	17	-0.52656	-1.24043	0.21649484	0.49007306	1	6244
KEGG_ONE_CARBON_POOL_BY_FOLATE	17	-0.52701	-1.24034	0.21176471	0.4852833	1	5705
REACTOME_HIV_LIFE_CYCLE	107	-0.3727	-1.2352	0.099236645	0.49215144	1	4899
KEGG_SPLICEOSOME	123	-0.3595	-1.22662	0.11003861	0.50734067	1	7102
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	29	-0.47041	-1.22343	0.1984127	0.50997996	1	4009
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	-0.42337	-1.22311	0.18379447	0.50575304	1	6950
BIOCARTA_MCM_PATHWAY	18	-0.50009	-1.21336	0.2	0.524658	1	9138
REACTOME_NEURONAL_SYSTEM	244	-0.33196	-1.21261	0.09158879	0.5213349	1	4986

REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	67	-0.39425	-1.21253	0.15891473	0.5166455	1	8181
REACTOME_HS_GAG_DEGRADATION	20	-0.49479	-1.20896	0.22111554	0.5200214	1	580
REACTOME_POTASSIUM_CHANNELS	86	-0.37626	-1.207	0.1532567	0.51973367	1	4986
REACTOME_METABOLISM_OF_RNA	276	-0.32336	-1.20587	0.08092485	0.5177228	1	5515
KEGG_MTOR_SIGNALING_PATHWAY	49	-0.41228	-1.20551	0.18661258	0.5136918	1	2729
KEGG_BASAL_TRANSCRIPTION_FACTORS	35	-0.43274	-1.20016	0.20961538	0.5220258	1	591
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	123	-0.34928	-1.18897	0.13663366	0.544851	1	2287
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	41	-0.41787	-1.18863	0.20242915	0.5408341	1	7004
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	126	-0.34879	-1.18752	0.1553398	0.5387365	1	7871
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	27	-0.45117	-1.18746	0.25204918	0.53417426	1	1358
REACTOME_RNA_POL_I_TRANSCRIPTION	79	-0.36668	-1.18624	0.19411765	0.53248334	1	7958
KEGG_LYSINE_DEGRADATION	39	-0.41645	-1.18533	0.19771864	0.5300367	1	4385
KEGG_P53_SIGNALING_PATHWAY	65	-0.38527	-1.18363	0.17228465	0.5293112	1	5466
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	59	-0.39942	-1.18032	0.18687873	0.53293574	1	8002
REACTOME_PYRUVATE_METABOLISM	18	-0.48003	-1.17616	0.257874	0.5382588	1	7004
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	40	-0.40609	-1.17498	0.20446096	0.5366197	1	3020
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	16	-0.48642	-1.17389	0.259887	0.5346488	1	6250
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	24	-0.45472	-1.16714	0.2623574	0.5466117	1	2996
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	20	-0.47072	-1.16587	0.27494907	0.5451125	1	6250
KEGG_TYPE_II_DIABETES_MELLITUS	42	-0.40988	-1.16463	0.24414062	0.54377675	1	6550
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	94	-0.35671	-1.16408	0.187251	0.5406857	1	4899
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	26	-0.45138	-1.16118	0.2851711	0.54308414	1	5187
REACTOME_METABOLISM_OF_MRNA	232	-0.3143	-1.16116	0.14428858	0.53888184	1	5515
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	133	-0.33797	-1.15948	0.17567568	0.53848404	1	7871
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	165	-0.32631	-1.15394	0.16573557	0.5473797	1	4750
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	44	-0.4104	-1.15345	0.22789784	0.5445394	1	6244
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	44	-0.3947	-1.14636	0.23929961	0.5567561	1	6950
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	49	-0.38791	-1.14617	0.23772103	0.5530198	1	6950
REACTOME_SYNTHESIS_OF_DNA	90	-0.35417	-1.14477	0.22222222	0.5522423	1	6667
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	27	-0.43227	-1.14125	0.28265107	0.55585444	1	6280
REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	15	-0.49547	-1.14063	0.3018868	0.5531763	1	5304
REACTOME_G0_AND_EARLY_G1	24	-0.45095	-1.13936	0.27290836	0.5521333	1	6632
KEGG_PYRIMIDINE_METABOLISM	91	-0.34731	-1.13665	0.24521072	0.5544299	1	6658
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	56	-0.37746	-1.13345	0.24493554	0.55813533	1	7958
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	45	-0.39208	-1.13327	0.26666668	0.55462927	1	4806
REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	18	-0.46153	-1.13318	0.31176472	0.55085236	1	4436
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	32	-0.41626	-1.13131	0.2737864	0.5513393	1	2287
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	-0.47243	-1.12045	0.31853282	0.57328767	1	6250
REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	30	-0.41543	-1.12018	0.28346458	0.5698996	1	3818
REACTOME_KINESINS	23	-0.43164	-1.10732	0.30097088	0.5971286	1	6216
REACTOME_S_PHASE	106	-0.33301	-1.10515	0.25651303	0.59829485	1	6667
KEGG_TYPE_I_DIABETES_MELLITUS	17	-0.46621	-1.1041	0.33466935	0.59670913	1	7334
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	23	-0.43637	-1.09884	0.3326923	0.6055318	1	5304
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	22	-0.44879	-1.09861	0.32774675	0.6019861	1	6250
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	18	-0.45375	-1.0969	0.3339806	0.6022092	1	6250
REACTOME_METABOLISM_OF_NUCLEOTIDES	64	-0.35022	-1.09442	0.29783037	0.60381645	1	4109
REACTOME_GABA_RECEPTOR_ACTIVATION	44	-0.3663	-1.08113	0.31360948	0.63203406	1	3787
KEGG_LONG_TERM_POTENTIATION	66	-0.34793	-1.07613	0.32405567	0.6404889	1	3117
REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLP1	16	-0.46189	-1.07275	0.36633664	0.64464706	1	4359
REACTOME_PURINE_METABOLISM	31	-0.39661	-1.07092	0.35458168	0.6452075	1	4109
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	23	-0.41866	-1.06972	0.3472222	0.6440823	1	3082
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	26	-0.40815	-1.06952	0.35757574	0.6404983	1	3082
KEGG_OOCYTE_MEIOSIS	104	-0.31455	-1.05804	0.31262136	0.66568995	1	1177
REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	21	-0.43177	-1.05752	0.3709981	0.6629065	1	7388
BIOCARTA_CK1_PATHWAY	16	-0.4525	-1.05382	0.38610038	0.6685725	1	1268
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	47	-0.35323	-1.04268	0.35573122	0.6929653	1	580
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	20	-0.41782	-1.04051	0.4173077	0.694191	1	4342
KEGG_CITRATE_CYCLE_TCA_CYCLE	29	-0.39489	-1.03837	0.4108818	0.69543713	1	6249
REACTOME_M_G1_TRANSITION	78	-0.32709	-1.03819	0.37428024	0.691607	1	6658
BIOCARTA_G1_PATHWAY	28	-0.38845	-1.03492	0.38314176	0.6959043	1	2311
REACTOME_FORMATION_OF_TRANSCRIPTION_COUPLED_NER_TC_NER_REPAIR_COMPLEX	29	-0.38889	-1.0318	0.3988212	0.6996197	1	4236
BIOCARTA_NOS1_PATHWAY	20	-0.42348	-1.03096	0.4177449	0.69744277	1	4012
REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING	33	-0.3635	-1.01596	0.42940038	0.73164314	1	3000
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS	26	-0.37915	-1.00802	0.4211577	0.74840355	1	4943
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	24	-0.39255	-1.0075	0.4354528	0.74542105	1	4943
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	201	-0.27668	-1.00538	0.4370229	0.7467691	1	3019
KEGG_MELANOMA	66	-0.32559	-1.00378	0.4468504	0.7464347	1	2729
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	53	-0.33022	-0.98639	0.46583852	0.7883721	1	6319
REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	51	-0.33036	-0.98403	0.4766537	0.7901903	1	5220
KEGG_RNA_POLYMERASE	29	-0.37047	-0.9836	0.4642857	0.78699565	1	1889
BIOCARTA_STATHMIN_PATHWAY	17	-0.41421	-0.98329	0.46954814	0.78336376	1	1177
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	183	-0.27575	-0.97999	0.49315068	0.787852	1	5418
REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	50	-0.33033	-0.97525	0.45783132	0.7961709	1	580
BIOCARTA_EIF_PATHWAY	16	-0.40863	-0.97483	0.484375	0.79277503	1	5154
REACTOME_RECYCLING_PATHWAY_OF_L1	26	-0.36333	-0.972	0.48638132	0.79595554	1	57
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	52	-0.32019	-0.96608	0.47713718	0.8081452	1	4411
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	-0.41584	-0.96448	0.49425286	0.8081773	1	1055
REACTOME_REGULATION_OF_INSULIN_SECRETION	80	-0.3024	-0.96097	0.492126	0.8132927	1	4747
KEGG_PURINE_METABOLISM	143	-0.27923	-0.95949	0.50676984	0.81275564	1	5858
BIOCARTA_TNFR1_PATHWAY	29	-0.36064	-0.95844	0.52683896	0.81118387	1	4065
REACTOME_RNA_POL_III_CHAIN_ELONGATION	17	-0.40011	-0.94989	0.5277778	0.8297482	1	1592
REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	20	-0.38585	-0.94794	0.5199203	0.83046514	1	3788
KEGG_FATTY_ACID_METABOLISM	38	-0.33366	-0.94572	0.48665297	0.83194494	1	2588
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	30	-0.34845	-0.94531	0.52371544	0.8284064	1	3082
KEGG_INSULIN_SIGNALING_PATHWAY	129	-0.27511	-0.94096	0.56626505	0.83550745	1	3356
REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	50	-0.31872	-0.9402	0.5425101	0.8331491	1	3638
REACTOME_BASE_EXCISION_REPAIR	19	-0.38429	-0.93814	0.555332	0.8341458	1	7366
BIOCARTA_CASPASE_PATHWAY	23	-0.37278	-0.93498	0.5647059	0.8382201	1	656
KEGG_PRIMARY_IMMUNODEFICIENCY	31	-0.3442	-0.93171	0.5425743	0.84239936	1	3016
REACTOME_HS_GAG_BIOSYNTHESIS	29	-0.34816	-0.93158	0.53474903	0.8383624	1	580
KEGG_ABC_TRANSPORTERS	43	-0.32697	-0.92688	0.5652174	0.84641623	1	2834
BIOCARTA_STRESS_PATHWAY	25	-0.35604	-0.92502	0.5378788	0.8470583	1	1862
KEGG_N_GLYCAN_BIOSYNTHESIS	46	-0.32113	-0.91997	0.5647969	0.8558683	1	8207
REACTOME_DARPP_32_EVENTS	23	-0.35575	-0.91862	0.6054159	0.85483325	1	1268
REACTOME_PYRIMIDINE_METABOLISM	19	-0.36474	-0.90867	0.5839844	0.876513	1	3580
REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_LIKE_PEPTIDE1	37	-0.32009	-0.90457	0.606	0.88306355	1	3117
REACTOME_MRNA_CAPPING	29	-0.33652	-0.8972	0.6146245	0.89792556	1	4236
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	81	-0.27922	-0.89419	0.66346157	0.90112054	1	2729
REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	36	-0.32697	-0.89087	0.61480075	0.9053882	1	951
REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	107	-0.26407	-0.89057	0.6909091	0.90177554	1	4870
REACTOME_RNA_POL_III_TRANSCRIPTION_TERMINATION	19	-0.37011	-0.89003	0.6095764	0.898845	1	7425
BIOCARTA_MTOR_PATHWAY	23	-0.35458	-0.88958	0.620229	0.89565504	1	4449
REACTOME_HIV_INFECTION	183	-0.24856	-0.88793	0.7103321	0.8956749	1	5321
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	15	-0.38389	-0.8866	0.62310606	0.8947809	1	1358
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	77	-0.27535	-0.86607	0.7041985	0.9426873	1	5901
REACTOME_PERK_REGULATED_GENE_EXPRESSION	27	-0.32308	-0.85867	0.6414729	0.95651925	1	2746
BIOCARTA_ACH_PATHWAY	15	-0.36833	-0.85832	0.63825756	0.9528427	1	4890
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	17	-0.35687	-0.85712	0.65995973	0.95111716	1	5305

REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	112	-0.25412	-0.85658	0.7708738	0.94791764	1	5674
KEGG_APOPTOSIS	82	-0.26318	-0.85528	0.7218814	0.9464275	1	5747
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	325	-0.22455	-0.85527	0.8950495	0.9420661	1	6272
REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	17	-0.36086	-0.85347	0.6496063	0.94201744	1	3363
KEGG_TASTE_TRANSDUCTION	35	-0.31112	-0.85327	0.66927594	0.9382261	1	6435
KEGG_RIBOFLAVIN_METABOLISM	15	-0.36268	-0.85295	0.6461825	0.93464226	1	2907
REACTOME_PHOSPHOLIPID_METABOLISM	177	-0.23716	-0.84951	0.8241966	0.93847656	1	4420
REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY	17	-0.35263	-0.84945	0.6420233	0.9343616	1	7366
REACTOME_RNA_POL_III_TRANSCRIPTION	33	-0.3046	-0.84919	0.71009177	0.9306715	1	9379
KEGG_BUTANOATE_METABOLISM	29	-0.3198	-0.84247	0.6673077	0.9416033	1	4810
BIOCARTA_IGF1MTOR_PATHWAY	20	-0.33935	-0.83758	0.68473893	0.94836736	1	4009
REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI	17	-0.35409	-0.83626	0.6952191	0.9470011	1	4943
REACTOME_METABOLISM_OF_PROTEINS	437	-0.21484	-0.83555	0.95229006	0.94445914	1	5540
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	65	-0.26891	-0.83404	0.751503	0.9437442	1	5321
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA	19	-0.34351	-0.82924	0.69719625	0.9499042	1	4359
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	48	-0.27931	-0.82337	0.7713718	0.9582862	1	5321
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	63	-0.2689	-0.82255	0.7943396	0.9558644	1	5783
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	75	-0.26277	-0.82141	0.78557116	0.9540864	1	3294
REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	18	-0.33655	-0.82139	0.71	0.9499842	1	4359
KEGG_SMALL_CELL_LUNG_CANCER	84	-0.25914	-0.82027	0.8004115	0.94816387	1	4009
BIOCARTA_ATM_PATHWAY	19	-0.33641	-0.81114	0.7061144	0.9628532	1	5214
KEGG_PROSTATE_CANCER	86	-0.24925	-0.8058	0.86564296	0.9691689	1	4009
REACTOME_ARMS_MEDIATED_ACTIVATION	17	-0.33721	-0.80424	0.71929824	0.96821976	1	1177
REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	31	-0.29753	-0.80186	0.7740668	0.9687531	1	4643
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	26	-0.29963	-0.79334	0.748538	0.9808601	1	6451
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	20	-0.31823	-0.79329	0.75435203	0.9768265	1	2176
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	26	-0.30759	-0.79301	0.7810651	0.9732097	1	2390
REACTOME_RNA_POL_I_PROMOTER_OPENING	55	-0.26379	-0.79205	0.81431335	0.970916	1	7958
REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	17	-0.33299	-0.791	0.7348178	0.96888906	1	2296
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	40	-0.27535	-0.78904	0.82778865	0.9684718	1	3619
REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS	16	-0.32716	-0.78227	0.76982594	0.97639394	1	2737
REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULES	30	-0.2915	-0.78178	0.77757007	0.97322243	1	5551
REACTOME_PACKAGING_OF_TELOMERE_ENDS	43	-0.27077	-0.77546	0.822736	0.98003745	1	7958
REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	19	-0.3169	-0.77454	0.77238804	0.97762376	1	1177
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	36	-0.27322	-0.75724	0.8246628	1	1	4411
REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	20	-0.30588	-0.75612	0.8062016	0.99857086	1	4359
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	22	-0.29497	-0.74976	0.8233083	1	1	4359
REACTOME_IL_RECEPTOR_SHC_SIGNALING	23	-0.29722	-0.74619	0.825188	1	1	4009
BIOCARTA_P53_PATHWAY	16	-0.32146	-0.74428	0.8187023	1	1	1164
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	65	-0.23918	-0.74381	0.9080675	1	1	5321
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	30	-0.27282	-0.743	0.8446602	0.99746615	1	4750
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRANE	17	-0.31243	-0.74191	0.81409	0.995004	1	5177
REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT	27	-0.28283	-0.74147	0.84063745	0.99172986	1	467
BIOCARTA_CSK_PATHWAY	19	-0.29855	-0.74107	0.78515625	0.98837787	1	7351
REACTOME_BOTULINUM_NEUROTOXICITY	18	-0.30763	-0.73622	0.819802	0.9909563	1	2737
REACTOME_OPIOID_SIGNALLING	71	-0.23454	-0.73211	0.93385214	0.99236876	1	3787
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_2_PROMOTER	23	-0.28766	-0.73164	0.8241107	0.9891374	1	9379
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	22	-0.28594	-0.72511	0.8678862	0.9933764	1	992
REACTOME_IRON_UPTAKE_AND_TRANSPORT	35	-0.26092	-0.72476	0.8790036	0.9899676	1	2834
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	64	-0.23498	-0.72397	0.9201597	0.98724705	1	5321
REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION	23	-0.2834	-0.71637	0.8466135	0.99244124	1	5712
REACTOME_GLUCONEOGENESIS	30	-0.26578	-0.71443	0.85626286	0.9907701	1	8178
REACTOME_G_PROTEIN_ACTIVATION	24	-0.26902	-0.71068	0.8698885	0.99109393	1	4359
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	57	-0.23698	-0.70912	0.92734224	0.9890383	1	5321
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	52	-0.23725	-0.7077	0.9390244	0.9868264	1	5321
REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE	24	-0.27689	-0.69319	0.88323915	0.9976971	1	4359
KEGG_PENTOSE_PHOSPHATE_PATHWAY	24	-0.27207	-0.68799	0.8787276	0.99867594	1	2522
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	116	-0.20425	-0.68796	0.98998	0.99500364	1	5321
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	23	-0.2652	-0.66852	0.89366055	1	1	4118
REACTOME_GLUCOSE_METABOLISM	62	-0.21953	-0.6655	0.9701789	1	1	6249
REACTOME_NCAM1_INTERACTIONS	36	-0.24121	-0.66008	0.9217221	1	1	1121
REACTOME_REGULATORY_RNA_PATHWAYS	21	-0.26054	-0.6534	0.90818363	1	1	6451
REACTOME_STRIATED_MUSCLE_CONTRACTION	22	-0.25804	-0.65254	0.92738587	1	1	3491
REACTOME_APOPTOTIC_EXECUTION_PHASE	51	-0.21899	-0.65222	0.9526749	1	1	3899
REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB	15	-0.28293	-0.649	0.925636	0.9994366	1	2287
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	46	-0.21974	-0.64531	0.96	0.9981019	1	423
REACTOME_GLYCOLYSIS	26	-0.24966	-0.64092	0.9419729	0.9971357	1	5142
REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	15	-0.27471	-0.64038	0.9158513	0.99388343	1	6783
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	63	-0.20425	-0.63596	0.9831461	0.9928616	1	5321
REACTOME_MYOGENESIS	22	-0.25107	-0.6327	0.94497156	0.9910975	1	2785
REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	17	-0.26377	-0.63034	0.9291667	0.98885316	1	4967
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	20	-0.24691	-0.61606	0.93737376	0.99204016	1	3733
REACTOME_CGMP_EFFECTS	18	-0.25093	-0.6092	0.93907565	0.9914725	1	1289
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	54	-0.20706	-0.60814	0.99206346	0.98845905	1	5321
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	45	-0.18741	-0.56148	0.99019605	0.99935603	1	4174
REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	22	-0.21918	-0.54869	0.9881188	0.9986603	1	3882
BIOCARTA_SHH_PATHWAY	15	-0.23905	-0.54429	0.9705882	0.9960576	1	5560
KEGG_PROTEIN_EXPORT	23	-0.20266	-0.51983	0.982659	0.996304	1	3673
BIOCARTA_CHREBP2_PATHWAY	40	-0.17642	-0.50042	0.9980732	0.995005	1	967

Table S13

GSEA Analysis on HNSC cancer cell lines comparing cell lines with or without 9p loss, Pathways Enriched

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	132	0.693861	2.494881	0	0	0	4670
REACTOME_MITOTIC_M_M_G1_PHASES	160	0.67517	2.468867	0	0	0	5458
REACTOME_DNA_REPLICATION	180	0.659862	2.462934	0	0	0	5301
REACTOME_MRNA_PROCESSING	151	0.660543	2.40644	0	0	0	4670
REACTOME_MRNA_SPLICING	104	0.685527	2.337217	0	0	0	4670
REACTOME_MITOTIC_PROMETAPHASE	78	0.692163	2.294766	0	0	0	5409
REACTOME_CELL_CYCLE_MITOTIC	302	0.57337	2.262947	0	1.67E-04	0.001	5409
KEGG_SPLICEOSOME	123	0.649128	2.262351	0	1.46E-04	0.001	4669
REACTOME_S_PHASE	106	0.643946	2.244365	0	2.62E-04	0.002	5285
REACTOME_CELL_CYCLE	386	0.551498	2.21687	0	6.92E-04	0.006	5409
REACTOME_G1_S_TRANSITION	108	0.637051	2.199632	0	6.29E-04	0.006	5745
REACTOME_SYNTHESIS_OF_DNA	90	0.644697	2.197592	0	8.47E-04	0.009	5285
REACTOME_M_G1_TRANSITION	78	0.67081	2.197561	0	7.81E-04	0.009	5301
REACTOME_CELL_CYCLE_CHECKPOINTS	110	0.618006	2.150051	0	0.001454764	0.018	5301
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	63	0.676049	2.136876	0	0.001969277	0.026	5283
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	51	0.695889	2.124182	0	0.00254431	0.036	4666
REACTOME_G2_M_CHECKPOINTS	41	0.706178	2.110665	0	0.00319334	0.047	2797
REACTOME_METABOLISM_OF_NON_CODING_RNA	47	0.682909	2.080815	0.002688172	0.004772937	0.074	4869
REACTOME_RNA_POL_II_TRANSCRIPTION	94	0.609564	2.066283	0	0.006246312	0.1	6106
REACTOME_DNA_STRAND_ELONGATION	30	0.734794	2.056153	0.002531646	0.006552346	0.109	2793
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	77	0.608307	2.043345	0	0.007429553	0.129	5745
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	54	0.654928	2.039111	0	0.007386203	0.135	5745
REACTOME_DNA_REPAIR	103	0.587406	2.034166	0	0.007456618	0.142	2794
REACTOME_TRANSCRIPTION	189	0.537041	2.023867	0	0.007852923	0.153	6106
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	35	0.710276	2.021889	0.004784689	0.007716651	0.155	2793
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	65	0.628001	2.015225	0	0.007841747	0.162	5283
REACTOME_HIV_INFECTION	183	0.531331	2.005839	0	0.00872501	0.186	5913
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	94	0.582473	1.997839	0	0.00933307	0.204	5623
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	40	0.679152	1.990329	0	0.009630313	0.213	4670
KEGG_DNA_REPLICATION	36	0.691858	1.989694	0.005277045	0.009346941	0.214	3551
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	64	0.604835	1.980124	0	0.009891395	0.232	5745
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	48	0.640852	1.979145	0	0.009690324	0.233	5745
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	65	0.605743	1.97256	0.002610966	0.009874193	0.244	5745
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	30	0.714913	1.971498	0.002659574	0.009685312	0.246	5301
REACTOME_REGULATORY_RNA_PATHWAYS	21	0.766536	1.960858	0	0.010483149	0.266	5145
REACTOME_FANCONI_ANEMIA_PATHWAY	20	0.761456	1.960317	0.002409639	0.01025511	0.267	2464
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	26	0.728669	1.958572	0	0.010285798	0.273	4666
REACTOME_G0_AND_EARLY_G1	24	0.732917	1.957807	0	0.010161566	0.277	4446
REACTOME_MITOTIC_G1_G1_S_PHASES	133	0.551113	1.957377	0	0.009958377	0.278	5301
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	34	0.69602	1.954677	0	0.010038723	0.286	5458
REACTOME_CHROMOSOME_MAINTENANCE	111	0.557803	1.951904	0	0.010149768	0.296	5289
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	63	0.603334	1.945988	0.002824859	0.010600726	0.313	5745
REACTOME_MEIOTIC_RECOMBINATION	76	0.591853	1.945159	0	0.010457746	0.315	2676
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	31	0.695927	1.940127	0	0.010620962	0.327	4666
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	116	0.544848	1.939638	0	0.010433005	0.329	5097
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	47	0.635003	1.93825	0.002801121	0.010304521	0.332	5745
REACTOME_HIV_LIFE_CYCLE	107	0.546392	1.923507	0	0.011139016	0.358	4713
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	42	0.639868	1.921616	0	0.011119207	0.363	4468
REACTOME_FORMATION_OF_THE_HIV1_EARLY_ELONGATION_COMPLEX	29	0.678998	1.911858	0.00248139	0.01172088	0.381	5878
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	45	0.631747	1.90933	0.002597403	0.011872244	0.389	4615
REACTOME_MRNA_3_END_PROCESSING	33	0.674667	1.906236	0	0.012079673	0.399	4468
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	50	0.631946	1.90377	0.002604167	0.01212935	0.407	5745
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	46	0.634522	1.898009	0	0.012413337	0.423	5745
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	65	0.588572	1.894864	0	0.012516805	0.435	6796
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	54	0.603436	1.894636	0	0.012309035	0.436	5745
REACTOME_MICRORNA_MIRNA_BIOGENESIS	18	0.762627	1.890009	0.00243309	0.012566478	0.452	5049
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	67	0.56689	1.878338	0	0.014007346	0.502	6796
REACTOME_MRNA_CAPPING	29	0.677608	1.873239	0	0.014372379	0.516	5878
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	31	0.677483	1.871676	0.007444169	0.014377671	0.524	4666
REACTOME_MEIOSIS	103	0.53219	1.864988	0	0.014816841	0.542	5119
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	57	0.594246	1.857762	0	0.015598525	0.56	5745
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	49	0.615328	1.857089	0.005012531	0.015365027	0.561	5745
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	46	0.616753	1.855026	0.005235602	0.015316033	0.564	5745
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	52	0.590475	1.854518	0	0.015129349	0.564	6083
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	26	0.689827	1.851429	0.007692308	0.015207868	0.575	4666
REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION_INDEPENDENT_DOUBLE_STRAND_BREAKS	15	0.757704	1.842309	0.012135922	0.016158408	0.607	2655
REACTOME_ELONGATION_ARREST_AND_RECOVERY	24	0.690468	1.840295	0.007518797	0.016238444	0.613	5230
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	56	0.588036	1.830712	0.010638298	0.01742812	0.636	5289
REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT	19	0.736812	1.823959	0.005037783	0.01797845	0.656	5230
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	36	0.634985	1.821474	0.00982801	0.018060498	0.663	5878
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	40	0.614052	1.818519	0.011396011	0.018344318	0.673	6083
REACTOME_METABOLISM_OF_RNA	275	0.467385	1.813148	0	0.018803325	0.685	5386
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION	20	0.690987	1.811127	0.011337869	0.018733745	0.689	5878
BIOCARTA_PROTEASOME_PATHWAY	28	0.661989	1.803934	0.007444169	0.019455109	0.711	5745
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	46	0.590681	1.801866	0.009876544	0.019454112	0.718	5745
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	26	0.667003	1.795246	0.007263923	0.020146223	0.734	4666
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	21	0.711395	1.790793	0.004962779	0.020566924	0.745	2655
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	81	0.529802	1.789956	0	0.020389978	0.746	5745
BIOCARTA_MCM_PATHWAY	18	0.726469	1.788416	0.007894737	0.020348663	0.749	4756
REACTOME_SIGNALING_BY_WNT	62	0.562125	1.784629	0.002932551	0.020677065	0.757	5745
KEGG_HOMOLOGOUS_RECOMBINATION	26	0.671254	1.782513	0.005167959	0.020669205	0.766	2655
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	52	0.567917	1.782312	0.008595988	0.020459393	0.766	5745
KEGG_PROTEASOME	40	0.610897	1.780509	0.007425743	0.02042878	0.767	5745
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	47	0.584562	1.770564	0.011080332	0.021871218	0.813	5745
KEGG_RNA_POLYMERASE	29	0.638428	1.767836	0.012285012	0.022172447	0.821	5491
KEGG_PYRIMIDINE_METABOLISM	91	0.518731	1.760545	0.002941177	0.02316025	0.833	5728
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	18	0.714788	1.759357	0.007407407	0.02312329	0.833	5458
REACTOME_RNA_POL_I_TRANSCRIPTION_INITIATION	24	0.66541	1.759151	0.011820331	0.022885563	0.833	5878
REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	15	0.742196	1.74569	0.006993007	0.024778638	0.862	2797
REACTOME_MITOTIC_G2_G2_M_PHASES	78	0.529336	1.741783	0.002849003	0.025304528	0.87	5811
REACTOME_ER_PHAGOSOME_PATHWAY	53	0.562854	1.721108	0.014005602	0.029447146	0.904	5745
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	61	0.540692	1.721098	0.002832861	0.029127067	0.904	5745
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	67	0.535732	1.719712	0.005714286	0.029181018	0.908	5745
KEGG_CELL_CYCLE	124	0.483465	1.716641	0	0.029503899	0.914	4305
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	44	0.575785	1.691555	0.010443864	0.03574003	0.951	4723
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	104	0.487611	1.689094	0.00310559	0.036017433	0.954	6393
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	49	0.557271	1.680821	0.013477089	0.037995484	0.961	5878
REACTOME_RNA_POL_I_TRANSCRIPTION	79	0.503842	1.667769	0.002808989	0.0412844	0.972	5949

REACTOME_LAGGING_STRAND_SYNTHESIS	19	0.656333	1.656258	0.01627907	0.044543635	0.978	3551
REACTOME_INFLUENZA_LIFE_CYCLE	158	0.445655	1.647239	0	0.046789758	0.987	5231
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	111	0.476217	1.644688	0.011940299	0.04734022	0.988	5949
REACTOME_APOPTOTIC_EXECUTION_PHASE	51	0.529593	1.639327	0.010810811	0.04867023	0.991	3074
REACTOME_TELOMERE_MAINTENANCE	70	0.504476	1.629595	0.009118541	0.05117969	0.994	5285
REACTOME_EXTENSION_OF_TELOMERES	27	0.595369	1.623164	0.017721519	0.053144533	0.995	5285
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	42	0.543628	1.619165	0.015151516	0.054186232	0.995	5355
KEGG_PARKINSONS_DISEASE	93	0.473435	1.619122	0.002777778	0.053685904	0.995	6640
REACTOME_RECYCLING_PATHWAY_OF_L1	26	0.597583	1.618269	0.0325	0.053517908	0.995	3670
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	63	0.501035	1.618216	0.012987013	0.053032562	0.995	5997
REACTOME_GLUCOSE_TRANSPORT	33	0.57128	1.6175	0.01946472	0.052792754	0.995	4666
KEGG_MISMATCH_REPAIR	23	0.617601	1.614672	0.028503563	0.05315678	0.995	4723
REACTOME_GAP_JUNCTION_TRAFFICKING	23	0.608337	1.603442	0.026385223	0.057159882	0.998	5030
REACTOME_METABOLISM_OF_MRNA	231	0.417397	1.601278	0	0.057531472	0.998	5386
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	56	0.505421	1.598034	0.002710027	0.05808404	0.998	5997
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	0.533398	1.585778	0.027160494	0.0629554	1	5878
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	23	0.606996	1.583899	0.020942409	0.06316972	1	4468
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	20	0.626641	1.579669	0.023622047	0.06454258	1	4974
KEGG_HUNTINGTONS_DISEASE	153	0.437504	1.576277	0.012944984	0.065594174	1	5506
REACTOME_FORMATION_OF_TRANSCRIPTION_COUPLED_NER_TC_NER_REPAIR_COMPLEX	29	0.56973	1.554994	0.027568921	0.075066805	1	5878
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	65	0.485027	1.553657	0.005555556	0.07506675	1	5894
REACTOME_OXYGEN_DEPENDENT_PROLINE_HYDROXYLATION_OF_HYPOXIA_INDUCIBLE_FACTOR_ALPHA	15	0.656963	1.552771	0.04556355	0.07499313	1	4713
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_2_PROMOTER	23	0.589883	1.550648	0.026960785	0.07542176	1	5466
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	20	0.609624	1.546952	0.044843048	0.07673808	1	4713
KEGG_PROTEIN_EXPORT	23	0.580332	1.544652	0.05109489	0.077141754	1	4469
KEGG_OOCYTE_MEIOSIS	103	0.443049	1.534612	0.015015015	0.081912346	1	3544
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	20	0.605812	1.531826	0.029748283	0.08280439	1	2839
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	22	0.599208	1.530311	0.033591732	0.08302209	1	4713
REACTOME_METABOLISM_OF_NUCLEOTIDES	64	0.481049	1.521762	0.03550296	0.08667642	1	5749
REACTOME_REGULATION_OF_APOPTOSIS	56	0.482192	1.516789	0.03448276	0.08870932	1	5745
REACTOME_MEIOTIC_SYNAPSIS	65	0.465027	1.513508	0.011695907	0.089642905	1	5119
KEGG_RNA_DEGRADATION	53	0.489236	1.501424	0.041237112	0.09629622	1	5355
REACTOME_SYNTHESIS_OF_PC	17	0.599899	1.49885	0.05050505	0.09705742	1	3561
BIOCARTA_ATRBRCA_PATHWAY	20	0.595701	1.493362	0.057534248	0.09964886	1	2464
REACTOME_NEPHRIN_INTERACTIONS	19	0.59487	1.479608	0.057603687	0.10765443	1	1074
REACTOME_REGULATION_OF_HYPOXIA_INDUCIBLE_FACTOR_HIF_BY_OXYGEN	22	0.567419	1.477027	0.046798028	0.10863815	1	5020
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	0.608252	1.476273	0.06127451	0.108281255	1	4026
REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	15	0.618751	1.471592	0.06378132	0.11099053	1	3551
REACTOME_PROTEIN_FOLDING	50	0.475581	1.461569	0.058524173	0.11736168	1	2850
REACTOME_RNA_POL_III_CHAIN_ELONGATION	17	0.602255	1.451139	0.089201875	0.12412026	1	1028
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	18	0.591966	1.445471	0.085051544	0.12725726	1	4294
REACTOME_GLUCOSE_METABOLISM	61	0.451829	1.433689	0.033942558	0.13535808	1	4072
REACTOME_RNA_POL_III_TRANSCRIPTION	33	0.504444	1.429555	0.0703125	0.13774107	1	5579
REACTOME_SULFUR_AMINO_ACID_METABOLISM	23	0.55963	1.425851	0.0990099	0.14005461	1	4288
REACTOME_RNA_POL_I_PROMOTER_OPENING	55	0.458376	1.425664	0.032	0.13926677	1	3999
REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS	26	0.524504	1.422653	0.07733333	0.14069	1	2850
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	26	0.524181	1.417273	0.07819905	0.14424989	1	4837
KEGG_OXIDATIVE_PHOSPHORYLATION	94	0.419195	1.415738	0.04225352	0.14467674	1	6796
KEGG_CITRATE_CYCLE_TCA_CYCLE	29	0.49933	1.411044	0.09296482	0.14748429	1	4974
REACTOME_PYRIMIDINE_METABOLISM	19	0.558708	1.404275	0.10294118	0.15243743	1	5728
BIOCARTA_BARRESTIN_SRC_PATHWAY	15	0.577966	1.40427	0.09466019	0.15141436	1	15
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	26	0.520062	1.404026	0.07672634	0.15055618	1	2839
KEGG_PURINE_METABOLISM	142	0.385508	1.394831	0.016286645	0.15744121	1	5780
REACTOME_METAL_ION_SLC_TRANSPORTERS	21	0.540431	1.392376	0.08192771	0.15863596	1	127
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	80	0.42217	1.390723	0.04310345	0.15899508	1	4361
REACTOME_GLYCOLYSIS	25	0.521107	1.386726	0.07611549	0.16143118	1	4072
REACTOME_GLOBAL_GENOMIC_NER_GG_NER	33	0.488243	1.385597	0.0691358	0.16134298	1	5878
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	18	0.554013	1.385321	0.11502347	0.16057059	1	1339
KEGG_BASE_EXCISION_REPAIR	34	0.484743	1.381446	0.06699752	0.16302349	1	4798
REACTOME_DEADENYLATION_OF_MRNA	17	0.561673	1.377799	0.11678832	0.16549319	1	5355
REACTOME_RNA_POL_III_TRANSCRIPTION_TERMINATION	19	0.553017	1.365498	0.09382716	0.17597009	1	1028
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA	19	0.529722	1.361571	0.11583924	0.17860627	1	4837
REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	19	0.537424	1.353931	0.106796116	0.18505976	1	912
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	26	0.500134	1.350643	0.10093897	0.18724103	1	5466
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	23	0.51121	1.342366	0.111979164	0.19465956	1	4837
REACTOME_TRANSLATION	171	0.362985	1.340223	0.027777778	0.19592744	1	5428
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	37	0.466629	1.338461	0.09181141	0.19666287	1	3074
BIOCARTA_ERK5_PATHWAY	17	0.559119	1.334488	0.13138686	0.19962549	1	2701
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	125	0.368881	1.303009	0.052173913	0.23388699	1	5561
REACTOME_GLUCONEOGENESIS	30	0.463334	1.293987	0.13235295	0.24417733	1	4615
REACTOME_APOPTOSIS	141	0.355245	1.276182	0.05818182	0.26506922	1	5097
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	41	0.426765	1.272105	0.12468828	0.26880106	1	6081
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	16	0.538764	1.26642	0.18969555	0.27489835	1	4026
KEGG_BUTANOATE_METABOLISM	29	0.456921	1.264531	0.15458937	0.27596858	1	2710
BIOCARTA_G2_PATHWAY	24	0.46383	1.233491	0.18518518	0.31888148	1	5666
REACTOME_KINESINS	23	0.473328	1.223728	0.1937046	0.33229792	1	4154
BIOCARTA_RARRXR_PATHWAY	15	0.509955	1.21545	0.21444695	0.3438944	1	5010
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	33	0.426928	1.210093	0.18244803	0.35069513	1	4341
REACTOME_PURINE_METABOLISM	31	0.436589	1.203168	0.21393035	0.36011088	1	5749
REACTOME_PACKAGING_OF_TELOMERE_ENDS	43	0.396729	1.199149	0.19060053	0.36476365	1	5119
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	130	0.335514	1.192165	0.10691824	0.37476796	1	5561
REACTOME_OPIOID_SIGNALLING	70	0.363505	1.190381	0.15300547	0.37613162	1	3599
REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	17	0.491167	1.190182	0.23488373	0.37441242	1	2343
REACTOME_SIGNALLING_TO_ERKS	35	0.409188	1.176619	0.21428572	0.39627647	1	1771
KEGG_BASAL_TRANSCRIPTION_FACTORS	33	0.414654	1.171642	0.23098591	0.40313083	1	6083
KEGG_MTOR_SIGNALING_PATHWAY	49	0.378711	1.169046	0.21204188	0.40598425	1	2701
REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	18	0.460142	1.162677	0.28640777	0.41546547	1	4837
REACTOME_ARMS_MEDIATED_ACTIVATION	17	0.471835	1.162621	0.26573426	0.4133661	1	912
REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	20	0.459987	1.157296	0.28648648	0.42108613	1	4837
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	33	0.40947	1.156651	0.24484536	0.4200068	1	6156
BIOCARTA_EIF4_PATHWAY	24	0.434876	1.154335	0.26448363	0.42216873	1	6775
REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	17	0.473492	1.150549	0.29777777	0.42681447	1	5591
REACTOME_CA_DEPENDENT_EVENTS	26	0.413666	1.142601	0.2725	0.43950796	1	53
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	30	0.413367	1.141826	0.24813896	0.43865824	1	6047
KEGG_RENAL_CELL_CARCINOMA	66	0.350443	1.124774	0.22879177	0.4695022	1	3678
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	182	0.297719	1.123479	0.15384616	0.4696613	1	2804
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	130	0.313032	1.122772	0.21316615	0.4685687	1	5561
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	189	0.302703	1.121204	0.18772563	0.4693914	1	5139
REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	17	0.4607	1.104557	0.29908675	0.50175923	1	6332
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	66	0.338011	1.104	0.22849463	0.50047094	1	5561
KEGG_LYSINE_DEGRADATION	39	0.381226	1.101228	0.3090909	0.5037589	1	4917
KEGG_PROPANOATE_METABOLISM	32	0.386307	1.093038	0.3325062	0.51902944	1	2710
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	98	0.318574	1.09226	0.25619835	0.518069	1	4017

BIOCARTA_BCELLSURVIVAL_PATHWAY	16	0.447591	1.09083	0.34920636	0.5184715	1	2701
REACTOME_IL_3_5_AND_GM_CSF_SIGNALING	39	0.36685	1.086045	0.32020998	0.52616584	1	1582
REACTOME_EGFR_DOWNREGULATION	25	0.399228	1.086021	0.31565657	0.5236529	1	1757
REACTOME_STRIATED_MUSCLE_CONTRACTION	23	0.415412	1.085521	0.35162094	0.5220966	1	4627
REACTOME_METABOLISM_OF_PROTEINS	433	0.264715	1.085329	0.15841584	0.5199988	1	5703
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTIO N	111	0.309847	1.082143	0.29595014	0.52463	1	2769
REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	15	0.45156	1.077565	0.37064677	0.53207034	1	3544
REACTOME_G_PROTEIN_ACTIVATION	23	0.417875	1.072341	0.37980768	0.5418186	1	4837
BIOCARTA_P53_PATHWAY	16	0.438375	1.072143	0.34988713	0.5396453	1	6979
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	132	0.292231	1.068727	0.27457628	0.54494554	1	5561
BIOCARTA_VEGF_PATHWAY	29	0.385321	1.052764	0.3696145	0.5791721	1	2701
BIOCARTA_ATM_PATHWAY	19	0.429337	1.051801	0.37203792	0.57854885	1	1681
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	92	0.305694	1.030312	0.37299034	0.62755764	1	5745
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	221	0.270776	1.026946	0.33766234	0.63266605	1	5345
REACTOME_BASE_EXCISION_REPAIR	19	0.402722	1.022504	0.39772728	0.64085984	1	3551
REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	21	0.405153	1.017763	0.4274809	0.6497654	1	6163
REACTOME_ENOS_ACTIVATION_AND_REGULATION	20	0.397055	1.013906	0.41958043	0.65659606	1	5698
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	32	0.359403	1.013374	0.41145834	0.6549083	1	3879
REACTOME_SIGNAL_TRANSDUCTION_BY_L1	34	0.3435	1.00586	0.39583334	0.6705732	1	2440
REACTOME_G1_PHASE	36	0.34253	1.001918	0.43867925	0.67729515	1	2883
REACTOME_PYRUVATE_METABOLISM	18	0.403215	0.991897	0.47727272	0.69979054	1	1587
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	22	0.384804	0.986958	0.45118734	0.70976746	1	4837
BIOCARTA_GSK3_PATHWAY	26	0.371489	0.986942	0.4607595	0.70663273	1	3552
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	27	0.360276	0.986719	0.43658537	0.7040875	1	3879
KEGG_TASTE_TRANSDUCTION	34	0.343346	0.984089	0.46210268	0.70739836	1	1307
REACTOME_PLC_BETA_MEDIATED_EVENTS	38	0.337553	0.983067	0.47044334	0.70683485	1	683
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	206	0.257493	0.979577	0.5	0.7128388	1	2739
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	41	0.328997	0.979367	0.4910486	0.71020675	1	1996
KEGG_LONG_TERM_POTENTIATION	65	0.302706	0.974065	0.48265895	0.7210816	1	1697
REACTOME_MEMBRANE_TRAFFICKING	121	0.275509	0.971574	0.55518395	0.7246011	1	4713
KEGG_ONE_CARBON_POOL_BY_FOLATE	17	0.405478	0.970892	0.5037975	0.72302836	1	2443
REACTOME_AMYLOIDS	69	0.30038	0.969294	0.48710603	0.724319	1	2676
REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	105	0.277173	0.964431	0.5224719	0.7336046	1	4116
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	121	0.269795	0.963522	0.5157593	0.7327583	1	5745
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	23	0.362886	0.960374	0.5184275	0.73795366	1	6718
REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT	27	0.360633	0.958838	0.49363866	0.73897886	1	2456
BIOCARTA_HER2_PATHWAY	22	0.373754	0.956297	0.5201005	0.7421841	1	2701
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	24	0.362486	0.950845	0.52284265	0.7533081	1	4837
REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLP1	15	0.401406	0.945737	0.5407407	0.7635271	1	6332
REACTOME_SIGNALING_BY_FGFR1_FUSION_MUTANTS	18	0.390008	0.944122	0.5683962	0.76453465	1	3927
REACTOME_PEPTIDE_CHAIN_ELONGATION	109	0.267092	0.940354	0.56626505	0.770967	1	5561
REACTOME_SIGNALING_BY_FGFR1_MUTANTS	25	0.348274	0.939981	0.53435117	0.7687826	1	2701
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	124	0.260404	0.939674	0.5925926	0.7664553	1	2885
REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_P ATHWAY	17	0.375048	0.935446	0.52582157	0.7743081	1	3551
REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS	25	0.349509	0.934323	0.5374677	0.77412176	1	2554
BIOCARTA_TFF_PATHWAY	20	0.371392	0.932543	0.5535714	0.7756317	1	2701
REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	22	0.357876	0.932373	0.58064514	0.77295715	1	2371
REACTOME_SIGNALING_BY_CONSTITUTIVELY_ACTIVE_EGFR	18	0.379888	0.931476	0.5212264	0.7722643	1	4713
BIOCARTA_CARM_ER_PATHWAY	34	0.325247	0.930631	0.5614035	0.7713948	1	5155
REACTOME_CGMP_EFFECTS	18	0.383487	0.930215	0.53125	0.76934016	1	2371
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_E VENTS	36	0.320249	0.928428	0.5902062	0.7709861	1	3879
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM	17	0.379304	0.926591	0.53571427	0.7722873	1	3103
REACTOME_PLATELET_HOMEOSTASIS	71	0.283193	0.923721	0.60162604	0.77655655	1	3572
BIOCARTA_CHREBP2_PATHWAY	39	0.311538	0.912941	0.5595855	0.8013145	1	4403
REACTOME_SIGNAL_AMPLIFICATION	30	0.322809	0.909696	0.6074074	0.80642956	1	4837
REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	15	0.374715	0.905199	0.56148493	0.8145164	1	1929
BIOCARTA_GCR_PATHWAY	19	0.357006	0.903584	0.58481014	0.8152801	1	5698
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	58	0.287181	0.901495	0.6504065	0.817553	1	5561
BIOCARTA_EIF_PATHWAY	16	0.359926	0.900489	0.5724299	0.8169117	1	6626
REACTOME_DARPP_32_EVENTS	23	0.344944	0.900437	0.57279235	0.81389076	1	5698
REACTOME_DAG_AND_IP3_SIGNALING	28	0.32878	0.89232	0.61630696	0.8310884	1	53
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	17	0.35959	0.884822	0.590604	0.84629077	1	734
REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE	24	0.326395	0.883928	0.6498801	0.845227	1	4837
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	44	0.295167	0.877646	0.66502464	0.85699683	1	3103
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	20	0.34805	0.877068	0.6159601	0.8552066	1	214
BIOCARTA_BAD_PATHWAY	24	0.325571	0.870876	0.64248705	0.8669945	1	8870
REACTOME_REGULATION_OF_INSULIN_SECRETION	79	0.263035	0.868758	0.71428573	0.86865807	1	3765
BIOCARTA_ACTINY_PATHWAY	20	0.346318	0.868367	0.6708543	0.86642903	1	3071
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRANE	16	0.364002	0.868208	0.6259169	0.86356413	1	3596
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	91	0.252398	0.865906	0.76687115	0.8658738	1	4387
BIOCARTA_MYOSIN_PATHWAY	30	0.308971	0.858998	0.70068026	0.87901294	1	2437
REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	17	0.346983	0.856061	0.68345326	0.8826157	1	5386
KEGG_THYROID_CANCER	29	0.31189	0.851682	0.7064439	0.8892864	1	912
REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	17	0.346396	0.851327	0.6445916	0.88683295	1	2236
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION	15	0.360511	0.847817	0.6938776	0.8916603	1	2129
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	22	0.320539	0.845118	0.6801909	0.894345	1	2117
BIOCARTA_GH_PATHWAY	26	0.312312	0.84422	0.6813725	0.8931359	1	2701
KEGG_COLORECTAL_CANCER	62	0.262846	0.843233	0.78711486	0.89201415	1	3159
BIOCARTA_EDG1_PATHWAY	26	0.315118	0.840648	0.7085427	0.8943307	1	2701
BIOCARTA_ARF_PATHWAY	17	0.340984	0.823667	0.7023256	0.9265229	1	948
BIOCARTA_CASPASE_PATHWAY	23	0.309605	0.81092	0.7692308	0.9479027	1	1298
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	21	0.311038	0.809407	0.7322275	0.94750744	1	734
KEGG_PENTOSE_PHOSPHATE_PATHWAY	23	0.309466	0.808169	0.7392405	0.9464674	1	4058
BIOCARTA_GLEEVEC_PATHWAY	23	0.310958	0.801111	0.7546296	0.9561905	1	2831
KEGG_GALACTOSE_METABOLISM	22	0.304416	0.799084	0.7605985	0.956534	1	765
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	45	0.26685	0.792894	0.795082	0.96393704	1	1171
BIOCARTA_MTOR_PATHWAY	23	0.30587	0.788172	0.7980535	0.968746	1	4415
BIOCARTA_MEF2D_PATHWAY	18	0.313795	0.77924	0.7728337	0.98046196	1	8393
BIOCARTA_ALK_PATHWAY	34	0.272079	0.775407	0.81360203	0.9834346	1	3340
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	21	0.294928	0.770886	0.78960395	0.9868679	1	5878
REACTOME_INFLAMMASOMES	16	0.321801	0.767651	0.77458036	0.9886151	1	2289
BIOCARTA_IGF1MTOR_PATHWAY	20	0.303244	0.762644	0.79350346	0.9929019	1	4483
REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	50	0.248286	0.760917	0.89540815	0.991927	1	5030
KEGG_ALZHEIMERS_DISEASE	138	0.210775	0.756473	0.9662577	0.99523056	1	6011
REACTOME_CHOLESTEROL_BIOSYNTHESIS	20	0.298434	0.756383	0.82051283	0.9920641	1	8452
BIOCARTA_CXCR4_PATHWAY	24	0.284891	0.756087	0.8497537	0.9891243	1	2701
BIOCARTA_MITOCHONDRIA_PATHWAY	21	0.30339	0.755268	0.8161209	0.98684365	1	7068
REACTOME_PLATELET_SENSITIZATION_BY_LDL	16	0.308833	0.748026	0.8	0.99319655	1	3544
BIOCARTA_RHO_PATHWAY	32	0.261214	0.746035	0.8537859	0.99245644	1	3071
BIOCARTA_ETS_PATHWAY	18	0.300689	0.744898	0.799511	0.9905086	1	200
BIOCARTA_PTEN_PATHWAY	17	0.299979	0.741279	0.81560284	0.9917554	1	3552
BIOCARTA_P53HYPOXIA_PATHWAY	22	0.274888	0.726122	0.861244	1	1	5432
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	20	0.285394	0.717201	0.8414918	1	1	4238

REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	57	0.224579	0.717003	0.9476584	1	1	4577
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TAK1	16	0.29738	0.715557	0.8639618	1	1	5033
BIOCARTA_ACH_PATHWAY	15	0.304614	0.71059	0.85560346	1	1	2701
KEGG_BETA_ALANINE_METABOLISM	20	0.275958	0.708319	0.8824885	1	1	3192
KEGG_BASAL_CELL_CARCINOMA	51	0.230112	0.707152	0.9435484	1	1	4296
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	26	0.262805	0.706071	0.89	1	1	4837
REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1	17	0.282723	0.702595	0.8517588	1	1	10039
REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION	23	0.266009	0.701646	0.8915663	1	1	1968
REACTOME_SIGNALLING_TO_RAS	27	0.260808	0.701602	0.91022444	1	1	1771
BIOCARTA_RACCYCD_PATHWAY	26	0.258186	0.696851	0.875	1	1	5033
REACTOME_TIGHT_JUNCTION_INTERACTIONS	28	0.252525	0.694508	0.91022444	1	1	899
BIOCARTA_INTEGRIN_PATHWAY	38	0.232565	0.693842	0.9276486	0.9976979	1	1776
REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	44	0.233614	0.693446	0.9661017	0.99492216	1	5877
REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	79	0.210563	0.692214	0.9844237	0.9928695	1	2885
REACTOME_SIGNALING_BY_BMP	21	0.263774	0.69077	0.87616825	0.9910225	1	4471
REACTOME_CTLA4_INHIBITORY_SIGNALING	19	0.27077	0.685635	0.88941175	0.9921806	1	4017
BIOCARTA_ECM_PATHWAY	24	0.258711	0.684961	0.913486	0.9896728	1	6151
BIOCARTA_AKT_PATHWAY	20	0.26825	0.678527	0.89320385	0.9915761	1	5033
BIOCARTA_IGF1R_PATHWAY	22	0.25784	0.66813	0.90951276	0.9959315	1	8870
REACTOME_CIRCADIAN_CLOCK	49	0.220549	0.667369	0.97680414	0.99338967	1	5796
BIOCARTA_HDAC_PATHWAY	26	0.244853	0.660639	0.92957747	0.9945235	1	7203
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS	30	0.24224	0.660095	0.92561984	0.9918345	1	7127
REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS	67	0.20182	0.657849	0.994429	0.99029386	1	3572
BIOCARTA_TEL_PATHWAY	18	0.268798	0.654044	0.9178744	0.9897232	1	7032
KEGG_FATTY_ACID_METABOLISM	38	0.21791	0.648345	0.9614396	0.9899922	1	2710
REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_LIKE_PEPTIDE1	37	0.221832	0.642486	0.9514563	0.9902519	1	5154
BIOCARTA_FCER1_PATHWAY	36	0.215791	0.637713	0.9748111	0.9897374	1	2831
REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS	38	0.214891	0.624516	0.9691517	0.9930952	1	5877
REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	24	0.230602	0.612281	0.9625293	0.9952525	1	6375
REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	17	0.247289	0.606279	0.94549763	0.9945977	1	4116
REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	18	0.23974	0.605789	0.95591646	0.99180514	1	712
KEGG_RIBOSOME	87	0.174154	0.588277	0.99681526	0.9943779	1	5220
REACTOME_NRIF_SIGNALS_CELL_DEATH_FROM_THE_NUCLEUS	15	0.220933	0.5307	0.96511626	1	1	1046
BIOCARTA_CERAMIDE_PATHWAY	22	0.20748	0.530025	0.990099	1	1	6921
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_IN_EMT_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	15	0.219892	0.522174	0.9744186	0.9987877	1	1046
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	34	0.175859	0.507369	0.9974619	0.9974923	1	2731
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	30	0.168902	0.469727	0.9972826	0.99754775	1	5877

Table S14

GSEA Analysis on HNSC cancer cell lines comparing cell lines with or without 9p loss, Pathways Depleted

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX	LEADING EDGE
SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE	51	-0.772871	-2.250641	0	0	0	3066	tags=47%, list=12%, signal=53%
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	197	-0.573049	-1.976124	0	0.00510559	0.011	3469	tags=29%, list=13%, signal=34%
BIOCARTA_INFLAM_PATHWAY	19	-0.75603	-1.806025	0.00350877	0.1220251	0.329	2915	tags=42%, list=11%, signal=47%
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	55	-0.608631	-1.786258	0.00490998	0.12943506	0.44	3772	tags=38%, list=14%, signal=44%
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	27	-0.688119	-1.754507	0.00336134	0.16310361	0.594	4463	tags=41%, list=17%, signal=49%
KEGG_JAK_STAT_SIGNALING_PATHWAY	119	-0.532904	-1.738127	0	0.16643207	0.666	3746	tags=28%, list=14%, signal=32%
BIOCARTA_NKCELLS_PATHWAY	19	-0.73372	-1.735301	0.00687285	0.14726791	0.678	1699	tags=37%, list=6%, signal=39%
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	23	-0.687442	-1.726055	0.00333333	0.14691405	0.727	3811	tags=39%, list=14%, signal=46%
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	80	-0.547705	-1.699129	0.00153846	0.18008018	0.821	4613	tags=30%, list=18%, signal=36%
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	110	-0.518756	-1.693121	0	0.17264935	0.837	3026	tags=22%, list=11%, signal=25%
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_SYNTHESIS	25	-0.683643	-1.688055	0.00653595	0.16814484	0.854	2555	tags=32%, list=10%, signal=35%
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	24	-0.665577	-1.678705	0.01065719	0.17061862	0.882	3193	tags=29%, list=12%, signal=33%
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	47	-0.587551	-1.678639	0.00776398	0.15771307	0.882	6569	tags=49%, list=25%, signal=65%
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	20	-0.696246	-1.675371	0.0051458	0.15251938	0.893	3559	tags=30%, list=14%, signal=35%
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	36	-0.607684	-1.66585	0.00646204	0.15910569	0.917	2952	tags=28%, list=11%, signal=31%
REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	49	-0.572222	-1.661382	0.00320513	0.15725698	0.921	2948	tags=24%, list=11%, signal=28%
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS	26	-0.642855	-1.653414	0.01360544	0.16082002	0.936	3983	tags=35%, list=15%, signal=41%
REACTOME_INTERFERON_GAMMA_SIGNALING	47	-0.565823	-1.645757	0.0031746	0.16680615	0.954	2005	tags=23%, list=8%, signal=25%
REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS	55	-0.560993	-1.63522	0.00648298	0.17702466	0.967	2435	tags=20%, list=9%, signal=22%
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	16	-0.715375	-1.633036	0.01601424	0.1718686	0.972	3811	tags=44%, list=14%, signal=51%
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	38	-0.591896	-1.62856	0.00993378	0.17144372	0.98	4996	tags=42%, list=19%, signal=52%
REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_ACTIVITY_BY_INSULIN_LIKE_GROWTH_FACTOR_BINDING_PROTEINS_IGFBPS	15	-0.707112	-1.626162	0.01535836	0.16745079	0.981	388	tags=20%, list=1%, signal=20%
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	185	-0.468116	-1.624203	0	0.16389488	0.982	4768	tags=28%, list=18%, signal=33%
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	15	-0.705749	-1.604396	0.01861252	0.19278039	0.993	2207	tags=27%, list=8%, signal=29%
REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING	36	-0.580383	-1.565473	0.02272727	0.27464584	1	4848	tags=33%, list=18%, signal=41%
BIOCARTA_IL1R_PATHWAY	33	-0.577936	-1.562081	0.0275974	0.27318075	1	5205	tags=36%, list=20%, signal=45%
BIOCARTA_CCR5_PATHWAY	16	-0.677979	-1.558808	0.01978417	0.27100047	1	1780	tags=19%, list=7%, signal=20%
REACTOME_HS_GAG_DEGRADATION	20	-0.645047	-1.553039	0.03040541	0.27534795	1	2948	tags=40%, list=11%, signal=45%
REACTOME_DIABETES_PATHWAYS	122	-0.471506	-1.544001	0.00151515	0.28955537	1	3615	tags=18%, list=14%, signal=21%
REACTOME_BIOLOGICAL_OXIDATIONS	111	-0.47193	-1.538454	0.00589102	0.29495624	1	2435	tags=13%, list=9%, signal=14%
REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	42	-0.553834	-1.528722	0.01610306	0.31119573	1	4848	tags=36%, list=18%, signal=44%
REACTOME_GLUTATHIONE_CONJUGATION	19	-0.637538	-1.51263	0.04326123	0.34670132	1	1827	tags=16%, list=7%, signal=17%
REACTOME_NCAM1_INTERACTIONS	36	-0.561919	-1.510919	0.02618658	0.34122378	1	3434	tags=28%, list=13%, signal=32%
REACTOME_PERK_REGULATED_GENE_EXPRESSION	27	-0.578825	-1.510875	0.03764321	0.33137983	1	4181	tags=26%, list=16%, signal=31%
REACTOME_COMPLEMENT_CASCADE	20	-0.632534	-1.508473	0.03786575	0.3288656	1	4720	tags=50%, list=18%, signal=61%
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	40	-0.542188	-1.501004	0.02555366	0.34211212	1	2435	tags=15%, list=9%, signal=17%
KEGG_ECM_RECEPTOR_INTERACTION	83	-0.480408	-1.49918	0.01259843	0.33796713	1	1843	tags=22%, list=7%, signal=23%
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	24	-0.596271	-1.483035	0.0367893	0.37554204	1	1621	tags=13%, list=6%, signal=13%
REACTOME_GPCR_LIGAND_BINDING	261	-0.412133	-1.472638	0.00136426	0.39883953	1	4770	tags=25%, list=18%, signal=30%
REACTOME_UNFOLDED_PROTEIN_RESPONSE	76	-0.478535	-1.465652	0.01708075	0.41085005	1	3406	tags=18%, list=13%, signal=21%
KEGG_SELENOAMINO_ACID_METABOLISM	25	-0.57568	-1.464576	0.04288165	0.4046251	1	2200	tags=12%, list=8%, signal=13%
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	61	-0.494311	-1.452336	0.03606558	0.43327665	1	3505	tags=25%, list=13%, signal=28%
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	21	-0.600691	-1.448632	0.0665529	0.43552688	1	709	tags=19%, list=3%, signal=20%
REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	19	-0.608673	-1.439753	0.0754717	0.45386344	1	5018	tags=42%, list=19%, signal=52%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	-0.638255	-1.436971	0.07248765	0.4539163	1	4948	tags=40%, list=19%, signal=49%
REACTOME_HS_GAG_BIOSYNTHESIS	28	-0.559694	-1.434084	0.03287197	0.45316792	1	2555	tags=21%, list=10%, signal=24%
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	97	-0.452263	-1.431766	0.02308802	0.45096847	1	6862	tags=38%, list=26%, signal=51%
REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	27	-0.562345	-1.429847	0.06060606	0.4481107	1	4848	tags=33%, list=18%, signal=41%
BIOCARTA_NTHI_PATHWAY	23	-0.577453	-1.427871	0.05564648	0.44566813	1	3798	tags=30%, list=14%, signal=36%
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	170	-0.417123	-1.425555	0.010279	0.44413692	1	4991	tags=24%, list=19%, signal=29%
REACTOME_GLYCOSPHINGOLIPID_METABOLISM	32	-0.535799	-1.418723	0.04786325	0.45813754	1	3251	tags=31%, list=12%, signal=36%
REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS	16	-0.613594	-1.413783	0.08362369	0.4659593	1	4917	tags=56%, list=19%, signal=69%
REACTOME_GABA_RECEPTOR_ACTIVATION	43	-0.504891	-1.4112	0.04140128	0.46563563	1	2164	tags=19%, list=8%, signal=20%
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	52	-0.480321	-1.403503	0.0487013	0.48260796	1	5358	tags=35%, list=20%, signal=43%
REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	22	-0.558636	-1.401844	0.08614865	0.47928753	1	3070	tags=27%, list=12%, signal=31%
REACTOME_ION_CHANNEL_TRANSPORT	40	-0.504808	-1.399066	0.06484642	0.47967824	1	3463	tags=25%, list=13%, signal=29%
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	103	-0.435159	-1.398674	0.0259542	0.4723998	1	6569	tags=39%, list=25%, signal=52%
BIOCARTA_IL10_PATHWAY	16	-0.601131	-1.396926	0.0797227	0.47033563	1	5377	tags=44%, list=20%, signal=55%
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK	157	-0.414648	-1.396506	0.01780416	0.46376404	1	3741	tags=18%, list=14%, signal=21%
KEGG_MELANOMA	64	-0.464429	-1.395702	0.05607477	0.45848128	1	3162	tags=25%, list=12%, signal=28%
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	132	-0.418302	-1.393808	0.02456647	0.45649913	1	4768	tags=27%, list=18%, signal=33%
KEGG_HEMATOPOIETIC_CELL_LINEAGE	69	-0.464554	-1.393747	0.04682779	0.44928604	1	3125	tags=28%, list=12%, signal=31%
BIOCARTA_CARDIACEGF_PATHWAY	17	-0.595188	-1.391857	0.09966216	0.4481908	1	6862	tags=47%, list=26%, signal=64%
REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	136	-0.413741	-1.384097	0.02173913	0.46575284	1	4755	tags=22%, list=18%, signal=27%
REACTOME_LIPOPROTEIN_METABOLISM	24	-0.555006	-1.383086	0.07432433	0.46183172	1	3444	tags=21%, list=13%, signal=24%
REACTOME_SIGNALING_BY_SCF_KIT	74	-0.45148	-1.375693	0.03622047	0.47881177	1	5393	tags=30%, list=20%, signal=37%
REACTOME_SPHINGOLIPID_METABOLISM	58	-0.46583	-1.370732	0.06750392	0.48771384	1	5843	tags=38%, list=22%, signal=49%
REACTOME_SIGNALING_BY_HIPPO	20	-0.560901	-1.369572	0.11073254	0.4842657	1	5616	tags=45%, list=21%, signal=57%
REACTOME_SIGNALING_BY_GPCR	459	-0.367277	-1.368403	0.00126582	0.48094478	1	3762	tags=19%, list=14%, signal=21%
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	55	-0.463354	-1.366072	0.06774194	0.48160776	1	3078	tags=20%, list=12%, signal=23%
BIOCARTA_AGR_PATHWAY	34	-0.509611	-1.366066	0.07885906	0.474851	1	1780	tags=21%, list=7%, signal=22%
REACTOME_BOTULINUM_NEUROTOXICITY	18	-0.589099	-1.363935	0.12020906	0.47454688	1	4917	tags=50%, list=19%, signal=61%
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	-0.559326	-1.363925	0.09031199	0.46809655	1	3108	tags=25%, list=12%, signal=28%
REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	20	-0.561264	-1.363011	0.10204082	0.46466482	1	3070	tags=25%, list=12%, signal=28%
KEGG_DORSO_VENTRAL_AXIS_FORMATION	23	-0.537876	-1.355097	0.10576923	0.48277572	1	2884	tags=22%, list=11%, signal=24%
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	46	-0.480732	-1.354615	0.07804878	0.47798976	1	4418	tags=24%, list=17%, signal=29%
KEGG_GLUTATHIONE_METABOLISM	43	-0.476321	-1.352115	0.09119497	0.48000106	1	2993	tags=19%, list=11%, signal=21%
REACTOME_COLLAGEN_FORMATION	53	-0.46549	-1.351205	0.08634223	0.47664803	1	7980	tags=51%, list=30%, signal=73%
REACTOME_GPCR_DOWNSTREAM_SIGNALING	369	-0.367721	-1.350284	0.00645161	0.47352064	1	3742	tags=20%, list=14%, signal=22%
REACTOME_SIGNALING_BY_PDGF	114	-0.414078	-1.349617	0.03143713	0.46957594	1	5547	tags=29%, list=21%, signal=37%
REACTOME_NETRIN1_SIGNALING	34	-0.50639	-1.344257	0.09493671	0.479745	1	3542	tags=24%, list=13%, signal=27%
BIOCARTA_IL22BP_PATHWAY	15	-0.590655	-1.340783	0.1184669	0.48443347	1	6480	tags=47%, list=25%, signal=62%
KEGG_TRYPTOPHAN_METABOLISM	37	-0.491003	-1.328281	0.10210697	0.5193456	1	2728	tags=19%, list=10%, signal=21%
REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI	17	-0.567675	-1.323576	0.13518198	0.5285903	1	6104	tags=41%, list=23%, signal=54%
REACTOME_POTASSIUM_CHANNELS	84	-0.424134	-1.322386	0.06855439	0.52597183	1	3856	tags=29%, list=15%, signal=33%
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	188	-0.380775	-1.321549	0.03212291	0.52250004	1	5497	tags=27%, list=21%, signal=33%
BIOCARTA_NKT_PATHWAY	22	-0.544464	-1.315494	0.11092437	0.5357683	1	2868	tags=23%, list=11%, signal=25%
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	24	-0.516366	-1.312547	0.1239531	0.538913	1	1314	tags=21%, list=5%, signal=22%
REACTOME_INNATE_IMMUNE_SYSTEM	201	-0.374602	-1.305207	0.03561644	0.55729854	1	6253	tags=31%, list=24%, signal=41%
BIOCARTA_INTRINSIC_PATHWAY	20	-0.546224	-1.302573	0.16410257	0.5600622	1	5168	tags=35%, list=20%, signal=44%
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	23	-0.521765	-1.301417	0.1356784	0.5579782	1	4194	tags=35%, list=16%, signal=41%
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	79	-0.417145	-1.299657	0.07064364	0.5578419	1	4991	tags=22%, list=19%, signal=26%
REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	16	-0.579305	-1.296758	0.15719064	0.56109065	1	4675	tags=31%, list=18%, signal=38%
KEGG_TGF_BETA_SIGNALING_PATHWAY	82	-0.411932	-1.296558	0.07902736	0.55571043	1	4322	tags=20%, list=16%, signal=23%
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	78	-0.420131	-1.295577	0.08990537	0.5529653	1	994	tags=13%, list=4%, signal=13%
KEGG_LEISHMANIA_INFECTION	52	-0.448097	-1.291304	0.13190185	0.56122005	1	6480	tags=35%, list=25%, signal=46%
REACTOME_CD28_CO_STIMULATION	30	-0.48834	-1.2882	0.14590164	0.5652618	1	5358	tags=37%, list=20%, signal=46%
KEGG_BLADDER_CANCER	40	-0.461414	-1.288075	0.12727273	0.560012	1	2867	tags=18%, list=11%, signal=20%
REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC	15	-0.577763	-1.286934	0.17290552	0.5582858	1	4165	tags=33%, list=16%, signal=40%
KEGG_GLYCEROLIPID_METABOLISM	37	-0.47427	-1.286915	0.12438625	0.5527583	1	4712	tags=24%, list=18%, signal=30%
KEGG_ABC_TRANSPORTERS	42	-0.460946	-1.284359	0.12676056	0.55478597	1	3527	tags=26%, list=13%, signal=30%
CANCER-TESTIS-ANTIGEN	101	-0.401684	-1.282846	0.06259542	0.55399233	1	1915	tags=21%, list=7%, signal=22%
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	78	-0.414281	-1.281072	0.08641975	0.55407625	1	3434	tags=24%, list=13%, signal=28%
REACTOME_GAB1_SIGNALOSOME	36	-0.477535	-1.280292	0.13474026	0.5509872	1	4848	tags=33%, list=18%, signal=41%
KEGG_AXON_GUIDANCE	123	-0.386842	-1.272633	0.07762557	0.5697742	1	7674	tags=35%, list=29%, signal=49%
REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	20	-0.521956	-1.262838	0.17133443	0.59561354	1	8115	tags=65%, list=31%, signal=94%
BIOCARTA_IL2_PATHWAY	21	-0.51529	-1.260608	0.15859766	0.59729475	1	6418	tags=43%, list=24%, signal=57%
REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	32	-0.480286	-1.259396	0.16503268	0.5957078	1	2405	tags=16%, list=9%, signal=17%
REACTOME_PI3K_AKT_ACTIVATION	36	-0.458279	-1.25417	0.15360501	0.607498	1	5777	tags=33%, list=22%, signal=43%
BIOCARTA_AT1R_PATHWAY	31	-0.477966	-1.246246	0.17470881	0.62794596	1	6566	tags=42%, list=25%, signal=56%
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	20	-0.512686	-1.244444	0.19458544	0.6283403	1	4057	tags=30%, list=15%, signal=35%

KEGG_PPAR_SIGNALING_PATHWAY	60	-0.419786	-1.244032	0.1292407	0.6242687	1	833 tags=12%, list=3%, signal=12%
BIOCARTA_PGC1A_PATHWAY	22	-0.505492	-1.24398	0.2159864	0.6188924	1	6717 tags=45%, list=26%, signal=61%
KEGG_PRIMARY_IMMUNODEFICIENCY	31	-0.460179	-1.242278	0.16773163	0.6193042	1	2005 tags=16%, list=8%, signal=17%
REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION	16	-0.537226	-1.241573	0.20695971	0.6162524	1	727 tags=19%, list=3%, signal=19%
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	42	-0.446709	-1.231657	0.1697479	0.6440631	1	2524 tags=26%, list=10%, signal=29%
BIOCARTA_G1_PATHWAY	28	-0.475912	-1.230642	0.18043844	0.6422045	1	2333 tags=18%, list=9%, signal=20%
REACTOME_PHOSPHOLIPID_METABOLISM	176	-0.357263	-1.227796	0.09219858	0.6467201	1	5843 tags=27%, list=22%, signal=35%
REACTOME_NEURONAL_SYSTEM	241	-0.340649	-1.221381	0.08957219	0.6628042	1	4766 tags=26%, list=18%, signal=31%
BIOCARTA_AMI_PATHWAY	18	-0.511299	-1.217118	0.2125206	0.67252755	1	4194 tags=28%, list=16%, signal=33%
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	86	-0.388508	-1.213814	0.14149444	0.67830366	1	6353 tags=36%, list=24%, signal=47%
KEGG_O_GLYCAN_BIOSYNTHESIS	24	-0.480667	-1.208952	0.20913884	0.6900073	1	5379 tags=33%, list=20%, signal=42%
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	41	-0.430618	-1.201965	0.18302828	0.7083832	1	2354 tags=15%, list=9%, signal=16%
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	22	-0.488378	-1.198163	0.23235801	0.7165214	1	1854 tags=18%, list=7%, signal=20%
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	75	-0.385197	-1.194546	0.16558442	0.7239093	1	3549 tags=20%, list=13%, signal=23%
KEGG_HISTIDINE_METABOLISM	27	-0.462676	-1.192997	0.21238938	0.72394514	1	3190 tags=19%, list=12%, signal=21%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	51	-0.416657	-1.191127	0.19614148	0.72490174	1	8873 tags=47%, list=34%, signal=71%
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	44	-0.419449	-1.188037	0.20483871	0.7301334	1	3199 tags=16%, list=12%, signal=18%
KEGG_MAPK_SIGNALING_PATHWAY	243	-0.330681	-1.184515	0.12638889	0.73738486	1	5274 tags=28%, list=20%, signal=34%
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	21	-0.484401	-1.184255	0.27164686	0.7326346	1	3233 tags=29%, list=12%, signal=33%
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	35	-0.441678	-1.184244	0.22893482	0.7270979	1	4740 tags=37%, list=18%, signal=45%
KEGG_PRION_DISEASES	28	-0.459548	-1.184219	0.24273504	0.7216523	1	3534 tags=32%, list=13%, signal=37%
REACTOME_PI_3K_CASCADE	48	-0.413834	-1.182462	0.22096774	0.7221847	1	5152 tags=29%, list=20%, signal=36%
REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	26	-0.46673	-1.180542	0.22416534	0.7234931	1	2023 tags=15%, list=8%, signal=17%
BIOCARTA_CELLCYCLE_PATHWAY	23	-0.47752	-1.180402	0.24870466	0.71866363	1	2333 tags=22%, list=9%, signal=24%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	-0.48513	-1.179863	0.27115718	0.71537125	1	7142 tags=55%, list=27%, signal=75%
REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	30	-0.450371	-1.178299	0.23026316	0.7156705	1	4434 tags=20%, list=17%, signal=24%
REACTOME_SIGNALING_BY_NODAL	15	-0.53155	-1.176583	0.27468583	0.7167893	1	7082 tags=47%, list=27%, signal=64%
BIOCARTA_TOB1_PATHWAY	16	-0.5113	-1.173188	0.2783688	0.72362113	1	3469 tags=13%, list=13%, signal=14%
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	28	-0.457309	-1.172467	0.22185971	0.72087944	1	2752 tags=21%, list=10%, signal=24%
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	54	-0.401239	-1.169959	0.21166667	0.7244747	1	3390 tags=19%, list=13%, signal=21%
KEGG_VIRAL_MYOCARDITIS	41	-0.419638	-1.169018	0.23642172	0.72246885	1	6353 tags=32%, list=24%, signal=42%
BIOCARTA_KERATINOCYTE_PATHWAY	45	-0.410398	-1.164849	0.22544283	0.73195356	1	5368 tags=33%, list=20%, signal=42%
REACTOME_BASIGIN_INTERACTIONS	24	-0.479381	-1.163539	0.25160256	0.7313094	1	994 tags=17%, list=4%, signal=17%
REACTOME_SIGNALING_BY_ILS	101	-0.35877	-1.163254	0.1808176	0.72725475	1	3105 tags=23%, list=12%, signal=26%
REACTOME_TRNA_AMINOACYLATION	42	-0.417742	-1.162825	0.23296355	0.7238532	1	3108 tags=14%, list=12%, signal=16%
KEGG_ADHERENS_JUNCTION	67	-0.380791	-1.162149	0.19656786	0.72093356	1	4981 tags=27%, list=19%, signal=33%
REACTOME_IL_2_SIGNALING	37	-0.430282	-1.160902	0.23754153	0.72052556	1	6480 tags=38%, list=25%, signal=50%
BIOCARTA_BIOPEPTIDES_PATHWAY	40	-0.411656	-1.158987	0.24433658	0.72225493	1	6862 tags=38%, list=26%, signal=51%
REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	30	-0.438331	-1.152032	0.2647059	0.74115145	1	4077 tags=27%, list=15%, signal=32%
REACTOME_TOLL_RECEPTOR_CASCADES	109	-0.357632	-1.150022	0.19674556	0.7433869	1	6253 tags=30%, list=24%, signal=40%
KEGG_LYSOSOME	118	-0.353335	-1.149069	0.19242424	0.74178404	1	5849 tags=23%, list=22%, signal=29%
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	69	-0.381498	-1.148209	0.23076923	0.73972625	1	1553 tags=13%, list=6%, signal=14%
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	18	-0.486884	-1.148149	0.2757475	0.7351083	1	4235 tags=28%, list=16%, signal=33%
KEGG_ERBB_SIGNALING_PATHWAY	85	-0.365171	-1.147866	0.21374045	0.73138726	1	6566 tags=38%, list=25%, signal=50%
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	423	-0.307186	-1.147222	0.11411043	0.72878176	1	3831 tags=14%, list=15%, signal=16%
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	30	-0.44607	-1.146632	0.2766323	0.72599053	1	1622 tags=20%, list=6%, signal=21%
BIOCARTA_SPPA_PATHWAY	22	-0.469048	-1.144917	0.29382303	0.7270107	1	4844 tags=23%, list=18%, signal=28%
KEGG_TYROSINE_METABOLISM	37	-0.423779	-1.142651	0.25361156	0.7300049	1	3495 tags=24%, list=13%, signal=28%
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	27	-0.443527	-1.1418	0.2871795	0.7282337	1	4766 tags=48%, list=18%, signal=59%
REACTOME_PEROXISOMAL_LIPID_METABOLISM	20	-0.467319	-1.139136	0.29227942	0.7321875	1	621 tags=10%, list=2%, signal=10%
REACTOME_SMOOTH_MUSCLE_CONTRACTION	23	-0.462998	-1.137969	0.28793103	0.73155123	1	4742 tags=26%, list=18%, signal=32%
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	21	-0.461214	-1.137269	0.29491526	0.72931796	1	2168 tags=24%, list=8%, signal=26%
BIOCARTA_IL6_PATHWAY	22	-0.461359	-1.133624	0.30622008	0.7372247	1	6480 tags=50%, list=25%, signal=66%
REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	15	-0.502354	-1.133597	0.30579966	0.7328401	1	4766 tags=53%, list=18%, signal=65%
REACTOME_SIGNALING_BY_ERBB4	83	-0.360935	-1.129606	0.24255952	0.74122816	1	3070 tags=18%, list=12%, signal=20%
REACTOME_SIGNALING_BY_RHO_GTPASES	108	-0.345837	-1.129205	0.2124031	0.73813754	1	5358 tags=27%, list=20%, signal=34%
KEGG_DILATED_CARDIOMYOPATHY	79	-0.361684	-1.128316	0.24398074	0.73668855	1	2922 tags=15%, list=11%, signal=17%
REACTOME_AXON_GUIDANCE	229	-0.31938	-1.128182	0.18067227	0.7327694	1	4234 tags=21%, list=16%, signal=24%
KEGG_FOCAL_ADHESION	195	-0.324908	-1.125578	0.21015514	0.736648	1	3434 tags=18%, list=13%, signal=20%
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	64	-0.369712	-1.124119	0.26027396	0.7370253	1	5616 tags=30%, list=21%, signal=38%
BIOCARTA_ARAP_PATHWAY	17	-0.476105	-1.123621	0.30195382	0.7345249	1	7533 tags=53%, list=29%, signal=74%
REACTOME_ACTIVATED_TLR4_SIGNALLING	91	-0.35716	-1.120864	0.24525316	0.73924035	1	6253 tags=33%, list=24%, signal=43%
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	75	-0.363198	-1.119411	0.2625	0.7396301	1	5201 tags=27%, list=20%, signal=33%
REACTOME_DEVELOPMENTAL_BIOLOGY	352	-0.302477	-1.116717	0.17419355	0.7445016	1	4981 tags=21%, list=19%, signal=26%
KEGG_RIBOFLAVIN_METABOLISM	15	-0.498048	-1.116426	0.3180212	0.741229	1	3450 tags=27%, list=13%, signal=31%
REACTOME_SHC_MEDIATED_CASCADE	22	-0.452545	-1.11583	0.3127148	0.73895943	1	727 tags=14%, list=3%, signal=14%
BIOCARTA_TID_PATHWAY	18	-0.47043	-1.114746	0.33670035	0.73818344	1	6488 tags=44%, list=25%, signal=59%
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.402855	-1.113691	0.28180355	0.73754185	1	3108 tags=15%, list=12%, signal=17%
REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	49	-0.382016	-1.109528	0.28896105	0.7466562	1	709 tags=8%, list=3%, signal=8%
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI	17	-0.475561	-1.109029	0.32508835	0.744061	1	2405 tags=12%, list=9%, signal=13%
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	21	-0.460841	-1.106061	0.3327645	0.7496922	1	6823 tags=38%, list=26%, signal=51%
KEGG_PEROXISOME	75	-0.35989	-1.10458	0.27708977	0.7501747	1	5317 tags=24%, list=20%, signal=30%
KEGG_APOPTOSIS	82	-0.357582	-1.103944	0.26546004	0.7481164	1	5403 tags=29%, list=21%, signal=37%
KEGG_ARACHIDONIC_ACID_METABOLISM	47	-0.392646	-1.101704	0.31672025	0.7514869	1	2501 tags=19%, list=10%, signal=21%
REACTOME_GABA_B_RECEPTOR_ACTIVATION	36	-0.405134	-1.097469	0.30731708	0.760829	1	2164 tags=17%, list=8%, signal=18%
REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	18	-0.466839	-1.095395	0.3492908	0.763446	1	4739 tags=39%, list=18%, signal=47%
KEGG_GNRH_SIGNALING_PATHWAY	90	-0.346961	-1.094588	0.29192546	0.7620301	1	3890 tags=20%, list=15%, signal=23%
KEGG_CHEMOKINE_SIGNALING_PATHWAY	157	-0.322837	-1.0921	0.26742533	0.76617926	1	3105 tags=14%, list=12%, signal=16%
REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFATASE_ACTIVATION	22	-0.448219	-1.090684	0.36267605	0.7668015	1	4043 tags=23%, list=15%, signal=27%
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	164	-0.317092	-1.088324	0.2755102	0.770396	1	2164 tags=14%, list=8%, signal=15%
REACTOME_PHASE_II_CONJUGATION	57	-0.373722	-1.087618	0.30612245	0.76854956	1	1827 tags=5%, list=7%, signal=6%
KEGG_CELL_ADHESION_MOLECULES_CAMS	103	-0.34217	-1.086762	0.31595576	0.7672768	1	4818 tags=21%, list=18%, signal=26%
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN	28	-0.420192	-1.082592	0.34042552	0.77704287	1	3601 tags=18%, list=14%, signal=21%
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	231	-0.307106	-1.080781	0.26886144	0.7789143	1	3105 tags=17%, list=12%, signal=19%
REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	26	-0.423985	-1.080669	0.35845897	0.77521306	1	7274 tags=46%, list=28%, signal=64%
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	25	-0.435909	-1.078075	0.3633218	0.7794818	1	2261 tags=20%, list=9%, signal=22%
REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	15	-0.468428	-1.074455	0.36979166	0.78653187	1	2922 tags=33%, list=11%, signal=37%
BIOCARTA_PYK2_PATHWAY	28	-0.418457	-1.074136	0.3786885	0.7836074	1	6862 tags=39%, list=26%, signal=53%
KEGG_GLIOMA	65	-0.360542	-1.072786	0.3443163	0.78391975	1	3105 tags=18%, list=12%, signal=21%
REACTOME_HEMOSTASIS	412	-0.290213	-1.072567	0.2756005	0.78065574	1	3816 tags=17%, list=14%, signal=19%
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	36	-0.397405	-1.07231	0.37055016	0.777591	1	3444 tags=14%, list=13%, signal=16%
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	88	-0.342196	-1.070985	0.33385336	0.77793497	1	5368 tags=24%, list=20%, signal=30%
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	186	-0.307425	-1.069933	0.32753623	0.777454	1	5591 tags=24%, list=21%, signal=31%
KEGG_OLFACTORY_TRANSDUCTION	54	-0.3647	-1.069801	0.34557596	0.7741221	1	5433 tags=26%, list=21%, signal=33%
REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMATE_BINDING_AND_ACTIVATION	15	-0.481202	-1.068015	0.39482757	0.7758063	1	4427 tags=33%, list=17%, signal=40%
BIOCARTA_CSK_PATHWAY	19	-0.448484	-1.067694	0.40202704	0.7731771	1	1870 tags=11%, list=7%, signal=11%
KEGG_RETINOL_METABOLISM	49	-0.366475	-1.062678	0.36638656	0.7850447	1	5655 tags=27%, list=21%, signal=34%
REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLLAPSE	25	-0.425198	-1.059976	0.37277147	0.78971595	1	4434 tags=20%, list=17%, signal=24%
KEGG_SPHINGOLIPID_METABOLISM	33	-0.397509	-1.059961	0.38162544	0.78598195	1	3831 tags=27%, list=15%, signal=32%
BIOCARTA_EGF_PATHWAY	31	-0.395762	-1.05983	0.37310925	0.7827204	1	6862 tags=39%, list=26%, signal=52%
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	39	-0.38948	-1.059316	0.36717427	0.7807216	1	2023 tags=15%, list=8%, signal=17%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	24	-0.431522	-1.058164	0.4009901	0.78043896	1	7289 tags=38%, list=28%, signal=52%
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	54	-0.363954	-1.056472	0.37459284	0.78202313	1	2053 tags=13%, list=8%, signal=14%
REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	32	-0.394746	-1.054588	0.36900958	0.78408873	1	5587 tags=31%, list=21%, signal=40%
REACTOME_IL_RECEPTOR_SHC_SIGNALING	23	-0.429988	-1.054235	0.40418118	0.78158236	1	6480 tags=48%, list=25%, signal=63%
REACTOME_SIGNALING_BY_ERBB2	95	-0.337341	-1.053086	0.35642135	0.78144854	1	6539 tags=32%, list=25%, signal=42%
REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_D	22	-0.425474	-1.050892	0.41680396	0.7845178	1	4270 tags=23%, list=16%, signal=27%
REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	48	-0.371267	-1.050239	0.37710437	0.78304183	1	6272 tags=31%, list=24%, signal=41%
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	19	-0.439741	-1.049118	0.40784982	0.78279656	1	1870 tags=11%, list=7%, signal=11%
REACTOME_SIGNALING_BY_ROBO_RECEPTOR	27	-0.403975	-1.046489	0.40646258	0.7869555	1	7118 tags=41%, list=27%, signal=56%
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	461	-0.277909	-1.043586	0.32998747	0.7923186	1	3177 tags=14%, list=12%, signal=15%
KEGG_PATHWAYS_IN_CANCER	306	-0.287611	-1.042694	0.35019454	0.79143023	1	3934 tags=17%, list=15%, signal=20%
REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	28	-0.394428	-1.03851	0.39823008	0.8002342	1	6278 tags=46%, list=24%, signal=61%
KEGG_WNT_SIGNALING_PATHWAY	141	-0.305861	-1.037351	0.38737446	0.8001434	1	2705 tags=13%, list=10%, signal=15%
BIOCARTA_IL7_PATHWAY	17	-0.440964	-1.029858	0.4490501	0.8193822	1	1634 tags=18%, list=6%, signal=19%
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	128	-0.314224	-1.027249	0.40855458	0.823711	1	3686 tags=17%, list=14%, signal=20%

REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	15	-0.461327	-1.026605	0.4160839	0.82211566	1	2671 tags=20%, list=10%, signal=22%
BIOCARTA_STRESS_PATHWAY	25	-0.401921	-1.024659	0.42957747	0.8245845	1	6850 tags=36%, list=26%, signal=49%
REACTOME_PI3K_CASCADE	61	-0.34892	-1.022908	0.4276316	0.82618743	1	1062 tags=10%, list=4%, signal=10%
REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRCADIAN_EXPRESSION	32	-0.38259	-1.022207	0.45379537	0.8245961	1	4495 tags=19%, list=17%, signal=23%
BIOCARTA_IL2RB_PATHWAY	37	-0.369022	-1.0184	0.4318555	0.83267283	1	6418 tags=30%, list=24%, signal=39%
BIOCARTA_CREB_PATHWAY	26	-0.400414	-1.015524	0.4318182	0.8375507	1	4073 tags=23%, list=15%, signal=27%
KEGG_PROSTATE_CANCER	84	-0.324148	-1.015029	0.423676	0.83534473	1	3280 tags=19%, list=12%, signal=22%
KEGG_PHENYLALANINE_METABOLISM	17	-0.441631	-1.01288	0.4691358	0.8382717	1	7330 tags=47%, list=28%, signal=65%
REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR	88	-0.319855	-1.00757	0.42662632	0.8502989	1	5368 tags=24%, list=20%, signal=30%
BIOCARTA_UCALPAIN_PATHWAY	18	-0.42892	-1.007151	0.4373928	0.84802467	1	4844 tags=33%, list=18%, signal=41%
BIOCARTA_NFKB_PATHWAY	23	-0.40714	-1.006859	0.4707792	0.84534425	1	3798 tags=26%, list=14%, signal=30%
KEGG_NITROGEN_METABOLISM	19	-0.416498	-1.005705	0.47241378	0.84524524	1	5100 tags=53%, list=19%, signal=65%
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	60	-0.338627	-0.9979	0.47663552	0.8649375	1	5557 tags=30%, list=21%, signal=38%
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	122	-0.303337	-0.997392	0.45147058	0.8627702	1	2164 tags=11%, list=8%, signal=12%
BIOCARTA_IL12_PATHWAY	18	-0.42972	-0.99699	0.4637931	0.8603751	1	6760 tags=39%, list=26%, signal=52%
KEGG_ENDOCYTOSIS	166	-0.293188	-0.996893	0.47109827	0.8571567	1	4881 tags=22%, list=19%, signal=26%
REACTOME_STEROID_HORMONES	20	-0.405715	-0.995667	0.5016892	0.8573645	1	4270 tags=20%, list=16%, signal=24%
REACTOME_INTERFERON_SIGNALING	130	-0.30227	-0.995305	0.4704142	0.854938	1	2005 tags=11%, list=8%, signal=12%
BIOCARTA_STATHMIN_PATHWAY	17	-0.422552	-0.994141	0.46324787	0.8550238	1	6760 tags=41%, list=26%, signal=55%
BIOCARTA_CDMAC_PATHWAY	16	-0.422036	-0.989491	0.47079647	0.8655158	1	8158 tags=44%, list=31%, signal=63%
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	25	-0.38767	-0.985472	0.47692308	0.8735461	1	7117 tags=40%, list=27%, signal=55%
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	26	-0.38984	-0.984949	0.47972974	0.8717207	1	4767 tags=31%, list=18%, signal=38%
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	17	-0.4164	-0.984428	0.47256637	0.8698843	1	2671 tags=18%, list=10%, signal=20%
BIOCARTA_EPO_PATHWAY	19	-0.415681	-0.984374	0.48161122	0.8665662	1	7315 tags=47%, list=28%, signal=66%
KEGG_TYPE_I_DIABETES_MELLITUS	17	-0.423202	-0.983698	0.46600333	0.8652087	1	1775 tags=18%, list=7%, signal=19%
KEGG_INSULIN_SIGNALING_PATHWAY	128	-0.294664	-0.981374	0.47799698	0.8685403	1	3209 tags=15%, list=12%, signal=17%
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	103	-0.305519	-0.98069	0.49226007	0.8671191	1	6539 tags=31%, list=25%, signal=41%
REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY	20	-0.408346	-0.980473	0.4859038	0.86428964	1	3930 tags=20%, list=15%, signal=23%
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	77	-0.314286	-0.977748	0.49619484	0.86853796	1	1912 tags=12%, list=7%, signal=13%
BIOCARTA_PPARA_PATHWAY	53	-0.335633	-0.977053	0.4909091	0.86724347	1	5534 tags=23%, list=21%, signal=29%
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	37	-0.359991	-0.976842	0.49508196	0.86450714	1	4767 tags=24%, list=18%, signal=30%
REACTOME_CELL_JUNCTION_ORGANIZATION	70	-0.325101	-0.974479	0.50931674	0.8679328	1	4256 tags=19%, list=16%, signal=22%
BIOCARTA_MCALPAIN_PATHWAY	24	-0.394707	-0.973734	0.49832776	0.8667445	1	4152 tags=21%, list=16%, signal=25%
KEGG_PANCREATIC_CANCER	69	-0.320957	-0.97355	0.5007752	0.8640361	1	5358 tags=26%, list=20%, signal=33%
REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	43	-0.352566	-0.973351	0.5090016	0.8613724	1	7652 tags=40%, list=29%, signal=56%
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	96	-0.303812	-0.970412	0.5171386	0.86658883	1	6862 tags=28%, list=26%, signal=38%
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	29	-0.37387	-0.970017	0.48877373	0.8644045	1	5538 tags=34%, list=21%, signal=44%
REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULES	30	-0.370263	-0.968124	0.5240464	0.8663172	1	5966 tags=33%, list=23%, signal=43%
KEGG_VIBRIO_CHOLERAE_INFECTION	51	-0.338085	-0.967351	0.50333333	0.86529905	1	8459 tags=39%, list=32%, signal=58%
REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING	27	-0.376562	-0.966753	0.5188356	0.8638258	1	1213 tags=15%, list=5%, signal=16%
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	40	-0.349073	-0.965256	0.51869917	0.8647743	1	3638 tags=20%, list=14%, signal=23%
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	112	-0.29886	-0.959418	0.5184615	0.8783116	1	5739 tags=23%, list=22%, signal=30%
REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	20	-0.397064	-0.959247	0.5191257	0.875547	1	6155 tags=35%, list=23%, signal=46%
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	19	-0.398588	-0.958974	0.5487805	0.873155	1	1414 tags=11%, list=5%, signal=11%
REACTOME_CELL_CELL_COMMUNICATION	109	-0.297941	-0.957966	0.5576923	0.872777	1	5358 tags=26%, list=20%, signal=32%
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	41	-0.342085	-0.951345	0.5400641	0.8876153	1	3280 tags=15%, list=12%, signal=17%
BIOCARTA_WNT_PATHWAY	25	-0.371284	-0.950494	0.53511703	0.88675755	1	3916 tags=20%, list=15%, signal=23%
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	51	-0.328596	-0.941346	0.57475084	0.90888435	1	3310 tags=18%, list=13%, signal=20%
REACTOME_SIGNALING_BY_FGFR	100	-0.291437	-0.937592	0.5701358	0.91557664	1	6539 tags=28%, list=25%, signal=37%
KEGG_SMALL_CELL_LUNG_CANCER	84	-0.299333	-0.93309	0.57570976	0.9249822	1	3686 tags=19%, list=14%, signal=22%
BIOCARTA_TALL1_PATHWAY	15	-0.403121	-0.929959	0.5657439	0.93037456	1	5448 tags=33%, list=21%, signal=42%
REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_AND_AMINE_COMPOUNDS	71	-0.302237	-0.929949	0.5727136	0.927073	1	5242 tags=32%, list=20%, signal=40%
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	66	-0.303655	-0.928357	0.5967742	0.92813224	1	5393 tags=26%, list=20%, signal=32%
KEGG_MELANOGENESIS	94	-0.288658	-0.928119	0.5947136	0.925396	1	3280 tags=14%, list=12%, signal=16%
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	20	-0.383393	-0.927326	0.55499154	0.9243245	1	7425 tags=40%, list=28%, signal=56%
REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	24	-0.369736	-0.92684	0.5536627	0.9224184	1	6278 tags=46%, list=24%, signal=60%
REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	33	-0.345128	-0.925521	0.56462586	0.9228756	1	3559 tags=21%, list=14%, signal=24%
KEGG_ACUTE_MYELOID_LEUKEMIA	57	-0.313765	-0.919483	0.60131794	0.9361582	1	3336 tags=16%, list=13%, signal=18%
REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	81	-0.298237	-0.919468	0.60189575	0.9329173	1	6253 tags=31%, list=24%, signal=40%
BIOCARTA_PML_PATHWAY	16	-0.398835	-0.919363	0.5862676	0.9299402	1	1775 tags=13%, list=7%, signal=13%
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	29	-0.353615	-0.919361	0.5740132	0.9267176	1	5358 tags=34%, list=20%, signal=43%
KEGG_OTHER_GLYCAN_DEGRADATION	15	-0.403941	-0.919038	0.57698816	0.9244354	1	7417 tags=47%, list=28%, signal=65%
BIOCARTA_RAS_PATHWAY	23	-0.367113	-0.916198	0.6	0.92889714	1	5164 tags=26%, list=20%, signal=32%
REACTOME_FRS2_MEDIATED_CASCADE	30	-0.350287	-0.915986	0.6072607	0.9262509	1	3070 tags=17%, list=12%, signal=19%
BIOCARTA_CCR3_PATHWAY	22	-0.375975	-0.915522	0.55926543	0.92437094	1	206 tags=5%, list=1%, signal=5%
BIOCARTA_CK1_PATHWAY	16	-0.406379	-0.915239	0.55857384	0.92201066	1	1204 tags=13%, list=5%, signal=13%
BIOCARTA_BCR_PATHWAY	34	-0.343208	-0.915029	0.5872757	0.9193906	1	7468 tags=29%, list=28%, signal=41%
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	18	-0.386173	-0.911952	0.5810345	0.9244343	1	176 tags=6%, list=1%, signal=6%
BIOCARTA_ERK_PATHWAY	28	-0.350548	-0.909644	0.6141215	0.9273388	1	4844 tags=25%, list=18%, signal=31%
REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	114	-0.276842	-0.908834	0.6651852	0.92627156	1	5393 tags=22%, list=20%, signal=27%
KEGG_STEROID_HORMONE_BIOSYNTHESIS	40	-0.33188	-0.908547	0.6016	0.92397267	1	2711 tags=13%, list=10%, signal=14%
REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	98	-0.285312	-0.906375	0.64555055	0.92639303	1	2021 tags=8%, list=8%, signal=9%
KEGG_N_GLYCAN_BIOSYNTHESIS	46	-0.31481	-0.904099	0.6161137	0.92925847	1	7839 tags=28%, list=30%, signal=40%
REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_DAI	18	-0.384624	-0.903419	0.60600704	0.92788947	1	2855 tags=17%, list=11%, signal=19%
KEGG_CALCIUM_SIGNALING_PATHWAY	157	-0.267375	-0.901942	0.6842857	0.92857057	1	3478 tags=17%, list=13%, signal=19%
REACTOME_METABOLISM_OF_CARBOHYDRATES	216	-0.254042	-0.901876	0.7082192	0.9257069	1	3265 tags=13%, list=12%, signal=15%
REACTOME_MYOGENESIS	22	-0.363268	-0.901586	0.6035889	0.9234364	1	5274 tags=27%, list=20%, signal=34%
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	354	-0.244972	-0.898849	0.75252527	0.9274557	1	4787 tags=19%, list=18%, signal=23%
BIOCARTA_NO1_PATHWAY	28	-0.352593	-0.895925	0.62624586	0.93196553	1	4646 tags=21%, list=18%, signal=26%
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	-0.288271	-0.893742	0.66561514	0.9346101	1	4197 tags=18%, list=16%, signal=21%
REACTOME_SYNTHESIS_OF_PA	21	-0.366536	-0.892444	0.6016807	0.93485856	1	5823 tags=19%, list=22%, signal=24%
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	198	-0.257416	-0.891838	0.74852943	0.9333362	1	3898 tags=16%, list=15%, signal=18%
KEGG_GAP_JUNCTION	83	-0.285819	-0.891826	0.6731055	0.9303581	1	5616 tags=23%, list=21%, signal=29%
BIOCARTA_MTA3_PATHWAY	18	-0.37466	-0.891523	0.61538464	0.92809737	1	2869 tags=22%, list=11%, signal=25%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	24	-0.351269	-0.889553	0.62728786	0.93000877	1	4565 tags=21%, list=17%, signal=25%
REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	77	-0.288939	-0.886898	0.6666667	0.93375397	1	1062 tags=8%, list=4%, signal=8%
BIOCARTA_PTDINS_PATHWAY	23	-0.35316	-0.884236	0.62371135	0.9375235	1	2846 tags=17%, list=11%, signal=19%
REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	71	-0.287842	-0.883908	0.6656201	0.9353572	1	6207 tags=30%, list=24%, signal=39%
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	30	-0.33956	-0.882954	0.6405451	0.9347495	1	5100 tags=30%, list=19%, signal=37%
REACTOME_IL1_SIGNALING	38	-0.320468	-0.881789	0.6388443	0.9346897	1	2982 tags=21%, list=11%, signal=24%
BIOCARTA_CTCF_PATHWAY	23	-0.342085	-0.87897	0.6279864	0.93848604	1	3469 tags=13%, list=13%, signal=15%
REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING	31	-0.324893	-0.872905	0.64223385	0.9500606	1	727 tags=10%, list=3%, signal=10%
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	35	-0.322668	-0.872696	0.62335527	0.9475441	1	1213 tags=11%, list=5%, signal=12%
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	52	-0.303633	-0.872419	0.68237084	0.94532084	1	3025 tags=15%, list=11%, signal=17%
BIOCARTA_MAL_PATHWAY	19	-0.37153	-0.871729	0.64084506	0.9440538	1	2831 tags=16%, list=11%, signal=18%
REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE	44	-0.310571	-0.871623	0.6769984	0.9414122	1	727 tags=9%, list=3%, signal=9%
REACTOME_OLFACTORY_SIGNALING_PATHWAY	26	-0.338584	-0.868394	0.6293706	0.9464545	1	3182 tags=19%, list=12%, signal=22%
KEGG_LONG_TERM_DEPRESSION	58	-0.295502	-0.86833	0.6687403	0.94368446	1	5591 tags=24%, list=21%, signal=31%
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	61	-0.290956	-0.86615	0.70479137	0.9459052	1	4767 tags=18%, list=18%, signal=22%
REACTOME_SIGNALING_BY_NOTCH1	68	-0.286009	-0.865413	0.70689654	0.94463784	1	3916 tags=21%, list=15%, signal=24%
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	324	-0.235958	-0.864856	0.85714287	0.9430767	1	5295 tags=18%, list=20%, signal=22%
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	38	-0.316149	-0.864439	0.68634063	0.9412199	1	5564 tags=29%, list=21%, signal=37%
REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	26	-0.339884	-0.862133	0.6515913	0.9437745	1	3694 tags=23%, list=14%, signal=27%
KEGG_STARCH_AND_SUCROSE_METABOLISM	37	-0.315237	-0.859555	0.69204736	0.94692177	1	7327 tags=32%, list=28%, signal=45%
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	64	-0.286853	-0.851124	0.7245053	0.96352804	1	7369 tags=33%, list=28%, signal=45%
REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS	74	-0.275314	-0.85025	0.75911254	0.96255517	1	5823 tags=22%, list=22%, signal=28%
BIOCARTA_NDKDYNAMIN_PATHWAY	18	-0.354922	-0.850053	0.67128026	0.960145	1	1500 tags=11%, list=6%, signal=12%
REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	73	-0.277042	-0.849155	0.7515625	0.9593034	1	6207 tags=29%, list=24%, signal=38%
REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	16	-0.375218	-0.847394	0.6609589	0.9607268	1	5538 tags=38%, list=21%, signal=47%
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATION_OF_SECOND_MESSENGERS	29	-0.32621	-0.844104	0.6947195	0.9651501	1	3105 tags=14%, list=12%, signal=16%
KEGG_STEROID_BIOSYNTHESIS	16	-0.365819	-0.841367	0.6707317	0.9683478	1	3881 tags=25%, list=15%, signal=29%
REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDATION_IN_MUSCLE	18	-0.361928	-0.841157	0.6936027	0.965983	1	6620 tags=33%, list=25%, signal=45%

BIOCARTA_TNFR2_PATHWAY	17	-0.358643	-0.840572	0.6975089	0.96444815	1	6076	tags=35%, list=23%, signal=46%
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	75	-0.272335	-0.840185	0.76969695	0.96247953	1	6862	tags=27%, list=26%, signal=36%
REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	97	-0.266269	-0.835819	0.7688752	0.969041	1	1658	tags=8%, list=6%, signal=9%
KEGG_LINOLEIC_ACID_METABOLISM	21	-0.342658	-0.835478	0.6866197	0.96688944	1	2501	tags=19%, list=10%, signal=21%
REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSION_BY_REV_ERBA	22	-0.33763	-0.833088	0.7107843	0.9693053	1	1489	tags=9%, list=6%, signal=10%
BIOCARTA_TGFB_PATHWAY	19	-0.353558	-0.83244	0.7028862	0.96787065	1	245	tags=5%, list=1%, signal=5%
REACTOME_SIGNALING_BY_FGFR_MUTANTS	37	-0.306766	-0.830521	0.7436333	0.9693792	1	1516	tags=11%, list=6%, signal=11%
KEGG_NON_SMALL_CELL_LUNG_CANCER	54	-0.286865	-0.829239	0.76380366	0.9692649	1	5358	tags=28%, list=20%, signal=35%
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_DIFFERENTIATION	68	-0.27663	-0.828916	0.7890625	0.96714616	1	2021	tags=9%, list=8%, signal=10%
REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI	16	-0.360047	-0.828317	0.7118353	0.9656058	1	6669	tags=44%, list=25%, signal=59%
KEGG_NOTCH_SIGNALING_PATHWAY	45	-0.294104	-0.82822	0.73455757	0.9630474	1	6669	tags=29%, list=25%, signal=39%
BIOCARTA_PDGF_PATHWAY	32	-0.309869	-0.826372	0.72892565	0.9641185	1	6862	tags=34%, list=26%, signal=46%
KEGG_INOSITOL_PHOSPHATE_METABOLISM	53	-0.282578	-0.823173	0.7566719	0.96798134	1	6022	tags=25%, list=23%, signal=32%
BIOCARTA_RELA_PATHWAY	16	-0.358003	-0.818829	0.70950705	0.97405416	1	1775	tags=13%, list=7%, signal=13%
REACTOME_NOD1_2_SIGNALING_PATHWAY	29	-0.3119	-0.818237	0.73667204	0.9725515	1	6113	tags=41%, list=23%, signal=54%
KEGG_ARGININE_AND_PROLINE_METABOLISM	48	-0.286254	-0.817942	0.76311606	0.9703938	1	3368	tags=17%, list=13%, signal=19%
REACTOME_GRB2_SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTERGRINS_	15	-0.361969	-0.814879	0.7249135	0.97385645	1	4844	tags=33%, list=18%, signal=41%
BIOCARTA_NFAT_PATHWAY	49	-0.285716	-0.810478	0.771615	0.979536	1	5205	tags=18%, list=20%, signal=23%
REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	51	-0.278464	-0.808924	0.78617364	0.9798023	1	3055	tags=12%, list=12%, signal=13%
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	29	-0.308814	-0.807423	0.76831347	0.9799231	1	6707	tags=31%, list=25%, signal=42%
REACTOME_MUSCLE_CONTRACTION	42	-0.286873	-0.805901	0.7758064	0.98015654	1	4742	tags=19%, list=18%, signal=23%
REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BETA_PATHWAYS	61	-0.272941	-0.801092	0.82051283	0.9868251	1	3640	tags=18%, list=14%, signal=21%
REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	15	-0.35263	-0.800954	0.7469671	0.9843732	1	3070	tags=20%, list=12%, signal=23%
REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	58	-0.267838	-0.799385	0.8366013	0.9845476	1	7652	tags=34%, list=29%, signal=49%
REACTOME_L1CAM_INTERACTIONS	81	-0.25997	-0.798823	0.8290469	0.982935	1	3505	tags=21%, list=13%, signal=24%
BIOCARTA_DEATH_PATHWAY	33	-0.298858	-0.797016	0.7627119	0.9834328	1	5164	tags=27%, list=20%, signal=34%
REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION	23	-0.319153	-0.793654	0.75333333	0.9867346	1	1489	tags=9%, list=6%, signal=9%
KEGG_CARDIAC_MUSCLE_CONTRACTION	60	-0.265659	-0.793217	0.83702534	0.98490924	1	994	tags=7%, list=4%, signal=7%
KEGG_PYRUVATE_METABOLISM	36	-0.292576	-0.791954	0.797005	0.9844724	1	3025	tags=14%, list=11%, signal=16%
REACTOME_SIGNALING_BY_NOTCH	96	-0.245316	-0.788446	0.8905775	0.98791677	1	4499	tags=21%, list=17%, signal=25%
BIOCARTA_RAC1_PATHWAY	23	-0.315143	-0.786845	0.7590759	0.9880303	1	3107	tags=22%, list=12%, signal=25%
BIOCARTA_MAPK_PATHWAY	86	-0.251192	-0.78671	0.87218046	0.98560023	1	5274	tags=23%, list=20%, signal=29%
REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR7_8_OR_9_ACTIVATION	73	-0.257664	-0.786277	0.83975345	0.9837291	1	6207	tags=29%, list=24%, signal=38%
KEGG_ENDOMETRIAL_CANCER	51	-0.271208	-0.783971	0.8449612	0.9850497	1	5358	tags=22%, list=20%, signal=27%
REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE	130	-0.23649	-0.783665	0.9129129	0.98294854	1	6539	tags=28%, list=25%, signal=38%
REACTOME_REGULATION_OF_KIT_SIGNALING	16	-0.342657	-0.779914	0.771529	0.9864983	1	7315	tags=31%, list=28%, signal=43%
BIOCARTA_TOLL_PATHWAY	35	-0.288401	-0.779809	0.8033058	0.98401314	1	6253	tags=31%, list=24%, signal=41%
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	55	-0.265191	-0.779122	0.840694	0.98247427	1	5722	tags=25%, list=22%, signal=32%
BIOCARTA_MET_PATHWAY	37	-0.284058	-0.776431	0.80991733	0.9841659	1	5205	tags=27%, list=20%, signal=34%
REACTOME_DOWNSTREAM_TCR_SIGNALING	26	-0.308841	-0.775142	0.7859589	0.98361844	1	6760	tags=27%, list=26%, signal=36%
BIOCARTA_TNFR1_PATHWAY	29	-0.294989	-0.773944	0.8096055	0.98294705	1	2543	tags=14%, list=10%, signal=15%
REACTOME_IRON_UPTAKE_AND_TRANSPORT	35	-0.285336	-0.772704	0.8150573	0.98236006	1	3618	tags=14%, list=14%, signal=17%
REACTOME_SIGNALLING_BY_NGF	208	-0.219929	-0.771361	0.9681159	0.98192734	1	6420	tags=26%, list=24%, signal=35%
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	44	-0.273399	-0.767594	0.8681135	0.98518634	1	5133	tags=27%, list=19%, signal=34%
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	22	-0.317558	-0.763567	0.80263156	0.98878634	1	1536	tags=9%, list=6%, signal=10%
KEGG_TYPE_II_DIABETES_MELLITUS	41	-0.271944	-0.761836	0.84177214	0.98878396	1	3105	tags=15%, list=12%, signal=17%
BIOCARTA_HIVNEF_PATHWAY	57	-0.258927	-0.754752	0.892575	0.9966349	1	6205	tags=26%, list=24%, signal=34%
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	25	-0.29819	-0.753718	0.84148395	0.9955294	1	1536	tags=8%, list=6%, signal=8%
KEGG_TIGHT_JUNCTION	118	-0.228046	-0.752914	0.94505495	0.994138	1	5830	tags=20%, list=22%, signal=26%
REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	49	-0.261587	-0.752649	0.8668885	0.9919638	1	6207	tags=31%, list=24%, signal=40%
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	-0.285782	-0.752251	0.848537	0.9900048	1	5205	tags=27%, list=20%, signal=33%
REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	31	-0.283396	-0.750835	0.8374384	0.9895359	1	3741	tags=19%, list=14%, signal=23%
REACTOME_TCR_SIGNALING	42	-0.267511	-0.750226	0.8615137	0.9878649	1	6862	tags=26%, list=26%, signal=35%
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	43	-0.266125	-0.747889	0.8554622	0.98869973	1	4090	tags=19%, list=16%, signal=22%
KEGG_ETHER_LIPID_METABOLISM	23	-0.304153	-0.747638	0.8257191	0.98654205	1	2501	tags=13%, list=10%, signal=14%
KEGG_P53_SIGNALING_PATHWAY	65	-0.245901	-0.744358	0.9117175	0.98827136	1	2933	tags=12%, list=11%, signal=14%
REACTOME_RAP1_SIGNALLING	15	-0.331155	-0.741648	0.80475384	0.9893565	1	4646	tags=20%, list=18%, signal=24%
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	73	-0.240171	-0.737779	0.927357	0.9919728	1	8216	tags=30%, list=31%, signal=44%
BIOCARTA_PAR1_PATHWAY	36	-0.271609	-0.732786	0.8782051	0.9956565	1	3456	tags=14%, list=13%, signal=16%
KEGG_VEGF_SIGNALING_PATHWAY	68	-0.236793	-0.727109	0.92868215	1	1	5358	tags=21%, list=20%, signal=26%
REACTOME_PI_METABOLISM	45	-0.260084	-0.726579	0.88557214	0.998195	1	5358	tags=22%, list=20%, signal=28%
BIOCARTA_TPO_PATHWAY	24	-0.297025	-0.726117	0.86023295	0.996216	1	1780	tags=13%, list=7%, signal=13%
REACTOME_G_ALPHA1213_SIGNALLING_EVENTS	72	-0.238333	-0.725537	0.9379968	0.99439293	1	7652	tags=33%, list=29%, signal=47%
BIOCARTA_P38MAPK_PATHWAY	39	-0.262186	-0.725181	0.90222985	0.99234474	1	4929	tags=21%, list=19%, signal=25%
REACTOME_PKB_MEDIATED_EVENTS	28	-0.275173	-0.720198	0.8677966	0.9956074	1	1062	tags=7%, list=4%, signal=7%
REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKS_COMPLEX	23	-0.289513	-0.719935	0.8447099	0.9934394	1	5951	tags=30%, list=23%, signal=39%
REACTOME_ACYL_CHAIN_REMODELLING_OF_PC	18	-0.306466	-0.719349	0.8530885	0.99169576	1	4653	tags=22%, list=18%, signal=27%
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES	80	-0.229186	-0.714408	0.9517134	0.9944222	1	2279	tags=10%, list=9%, signal=11%
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	42	-0.254663	-0.70406	0.9101124	1	1	7674	tags=31%, list=29%, signal=44%
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	55	-0.235061	-0.695835	0.9536	1	1	4115	tags=16%, list=16%, signal=19%
BIOCARTA_FMLP_PATHWAY	36	-0.254409	-0.693637	0.9207921	1	1	4140	tags=17%, list=16%, signal=20%
REACTOME_SEMAPHORIN_INTERACTIONS	64	-0.234711	-0.691787	0.9520661	1	1	4434	tags=17%, list=17%, signal=21%
REACTOME_TRAF6_MEDIATED_NFKB_ACTIVATION	21	-0.277943	-0.684271	0.8867596	1	1	6830	tags=29%, list=26%, signal=39%
BIOCARTA_HIF_PATHWAY	15	-0.29801	-0.674291	0.8963093	1	1	3189	tags=13%, list=12%, signal=15%
BIOCARTA_IGF1_PATHWAY	21	-0.275373	-0.669566	0.9066901	1	1	6418	tags=33%, list=24%, signal=44%
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	85	-0.217427	-0.66905	0.9761194	1	1	1204	tags=7%, list=5%, signal=7%
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	31	-0.254936	-0.668436	0.9386107	1	1	6830	tags=35%, list=26%, signal=48%
BIOCARTA_INSULIN_PATHWAY	21	-0.2697	-0.656412	0.9230769	1	1	6418	tags=33%, list=24%, signal=44%
REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS	15	-0.285975	-0.650025	0.9095841	1	1	7117	tags=40%, list=27%, signal=55%
BIOCARTA_FAS_PATHWAY	29	-0.251391	-0.647725	0.9425287	1	1	6877	tags=34%, list=26%, signal=47%
BIOCARTA_CDC42RAC_PATHWAY	16	-0.281183	-0.640815	0.93867123	1	1	6566	tags=25%, list=25%, signal=33%
REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM	160	-0.187027	-0.633182	1	1	1	1489	tags=5%, list=6%, signal=5%
REACTOME_INSULIN_RECEPTOR_RECYCLING	21	-0.264602	-0.632493	0.9198036	1	1	3618	tags=14%, list=14%, signal=17%
REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB	15	-0.27982	-0.629977	0.9372822	1	1	6539	tags=20%, list=25%, signal=27%
REACTOME_SHC_MEDIATED_SIGNALLING	15	-0.272726	-0.626035	0.9296741	1	1	4197	tags=20%, list=16%, signal=24%
REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_TTP	17	-0.272981	-0.624461	0.93309224	1	1	3070	tags=12%, list=12%, signal=13%
REACTOME_ERK_MAPK_TARGETS	21	-0.259104	-0.624326	0.938918	1	1	4657	tags=24%, list=18%, signal=29%
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	98	-0.193901	-0.622105	0.9953775	1	1	5368	tags=16%, list=20%, signal=20%
BIOCARTA_SPRY_PATHWAY	18	-0.267853	-0.621607	0.9474606	1	1	6418	tags=33%, list=24%, signal=44%
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	-0.251366	-0.619613	0.9396552	1	1	4657	tags=21%, list=18%, signal=25%
REACTOME_TIE2_SIGNALING	17	-0.267448	-0.615089	0.9378151	1	1	3751	tags=18%, list=14%, signal=21%
BIOCARTA_MPR_PATHWAY	33	-0.225732	-0.60119	0.9708904	1	1	373	tags=3%, list=1%, signal=3%
KEGG_REGULATION_OF_AUTOPHAGY	20	-0.249276	-0.598798	0.96594983	1	1	6106	tags=30%, list=23%, signal=39%
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS	44	-0.210338	-0.595693	0.98489934	1	1	6113	tags=32%, list=23%, signal=41%
BIOCARTA_CALCINEURIN_PATHWAY	18	-0.248969	-0.594192	0.94690263	1	1	7468	tags=33%, list=28%, signal=47%
REACTOME_ACYL_CHAIN_REMODELLING_OF_PE	17	-0.254492	-0.589161	0.95304346	1	1	4340	tags=18%, list=16%, signal=21%
REACTOME_SHC_RELATED_EVENTS	16	-0.256555	-0.586447	0.9590444	1	1	4197	tags=19%, list=16%, signal=22%
REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	17	-0.251672	-0.582964	0.9635417	1	1	5951	tags=29%, list=23%, signal=38%
REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	38	-0.215507	-0.581605	0.98844886	1	1	6669	tags=32%, list=25%, signal=42%
BIOCARTA_NGF_PATHWAY	18	-0.247422	-0.577486	0.96034485	1	1	6862	tags=33%, list=26%, signal=45%
BIOCARTA_HCMV_PATHWAY	17	-0.242501	-0.567288	0.9754816	1	1	5164	tags=24%, list=20%, signal=29%
REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	36	-0.212319	-0.56572	0.98527	1	1	4743	tags=14%, list=18%, signal=17%
BIOCARTA_VIP_PATHWAY	25	-0.224004	-0.563269	0.97528833	0.99955255	1	8158	tags=32%, list=31%, signal=46%
BIOCARTA_SHH_PATHWAY	15	-0.242538	-0.556112	0.97192985	0.9988047	1	8873	tags=40%, list=34%, signal=60%
BIOCARTA_TCR_PATHWAY	44	-0.192701	-0.54268	0.99841774	0.9990657	1	6862	tags=25%, list=26%, signal=34%
BIOCARTA_CHEMICAL_PATHWAY	22	-0.218415	-0.531998	0.9811644	0.99852765	1	6420	tags=23%, list=24%, signal=30%
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	20	-0.218578	-0.518075	0.987931	0.9981213	1	1278	tags=5%, list=5%, signal=5%
BIOCARTA_NOS1_PATHWAY	20	-0.214896	-0.516349	0.9767442	0.9960512	1	7468	tags=25%, list=28%, signal=35%
BIOCARTA_GPCR_PATHWAY	33	-0.183025	-0.485667	0.99842024	0.99657464	1	7674	tags=27%, list=29%, signal=38%

Table S15

List of Aneuploidy-associated SASP genes and IFNA gene set

Aneuploidy-associated SASP	IFNa gene set
AREG	IFNA6
CCL2	IFNA8
CCL20	IFNA21
CCL3	IFNA5
CSF1	IFNA16
CSF2	IFNA10
CXCL1	IFNA2
CXCL2	IFNA1
EREG	IFNA7
FAS	IFNA14
FGF2	IFNA13
ICAM1	IFNA17
IGFBP2	IFNA4
IL1A	
IL1B	
IL6	
LIF	
MMP1	
MMP2	
CXCL8	

Table S16
GSEA Analysis on TCGA HNSC comparing tumors with or without 9p21.3 loss (arm or focal), Pathways Enriched

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX
REACTOME_TIGHT_JUNCTION_INTERACTIONS	29	0.731595	1.937374	0	0.012580046	0.014	2481
KEGG_STEROID_HORMONE_BIOSYNTHESIS	53	0.627997	1.870562	0	0.020422813	0.046	2543
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	68	0.591702	1.847079	0	0.026849346	0.09	2944
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM	17	0.776866	1.801386	0	0.041438803	0.171	2612
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION	16	0.793213	1.767101	0	0.05629256	0.279	1912
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	27	0.660126	1.751239	0.002347418	0.061124563	0.346	4018
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	64	0.556697	1.723256	0	0.08169483	0.476	6055
KEGG_SPLICEOSOME	114	0.496502	1.682155	0	0.12124397	0.678	5382
REACTOME_G2_M_CHECKPOINTS	35	0.60576	1.677029	0.007594937	0.115629055	0.706	4844
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	44	0.585492	1.670071	0.002518892	0.114482164	0.736	2867
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	27	0.632925	1.655855	0	0.12597407	0.798	4018
KEGG_PENTOSE_PHOSPHATE_PATHWAY	27	0.652271	1.653152	0.002325581	0.1201992	0.818	3301
REACTOME_DNA_STRAND_ELONGATION	30	0.611523	1.652916	0.011961723	0.11122398	0.818	6580
REACTOME_MITOTIC_PROMETAPHASE	85	0.501814	1.628538	0.003144654	0.137996	0.901	6171
REACTOME_G0_AND_EARLY_G1	23	0.662173	1.622311	0.011764706	0.13858844	0.919	5533
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROME RE	57	0.525434	1.608399	0.002832861	0.15199246	0.943	7465
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	27	0.61385	1.602984	0.011961723	0.15206027	0.949	4018
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	29	0.595557	1.577152	0.016908212	0.18990175	0.977	6041
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	24	0.626304	1.560452	0.02202643	0.21337499	0.986	6060
REACTOME_ACYL_CHAIN_REMODELLING_OF_PE	20	0.632811	1.552709	0.025700934	0.21794583	0.988	2471
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	33	0.576964	1.552093	0.012224939	0.20890135	0.988	5661
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	73	0.498068	1.551256	0.011730205	0.20077717	0.989	1911
REACTOME_TELOMERE_MAINTENANCE	72	0.489474	1.529162	0.008797654	0.23880161	0.998	7465
KEGG_OXIDATIVE_PHOSPHORYLATION	115	0.45428	1.524571	0.00330033	0.23887518	1	6881
REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	56	0.507398	1.524419	0.005797102	0.22957218	1	1318
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	27	0.587739	1.511676	0.01904762	0.24710564	1	4542
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	38	0.536955	1.509277	0.035989717	0.24349141	1	5272
REACTOME_CHROMOSOME_MAINTENANCE	113	0.445475	1.498398	0.003436426	0.25967848	1	7076
KEGG_DNA_REPLICATION	36	0.527896	1.493488	0.026455026	0.2627944	1	6580
KEGG_HUNTINGTONS_DISEASE	171	0.420808	1.487161	0	0.26902023	1	6057
REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS	81	0.470704	1.487103	0.014662757	0.26054007	1	2504
REACTOME_MICRORNA_MIRNA_BIOGENESIS	21	0.603113	1.482209	0.04235294	0.26454723	1	4299
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	32	0.537301	1.475403	0.04187192	0.27257213	1	4018
REACTOME_REGULATORY_RNA_PATHWAYS	24	0.583553	1.472286	0.037209302	0.27108842	1	5302
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	25	0.581981	1.464178	0.05035971	0.28124598	1	1789
REACTOME_GLYCOLYSIS	27	0.564647	1.45755	0.03827751	0.28957388	1	2314
REACTOME_PHASE_II_CONJUGATION	66	0.469397	1.455335	0.01734104	0.28655207	1	2742
REACTOME_ACYL_CHAIN_REMODELLING_OF_PC	21	0.592383	1.455084	0.046838406	0.27954417	1	2471
KEGG_BASAL_CELL_CARCINOMA	55	0.481133	1.449247	0.007978723	0.28553018	1	4751
BIOCARTA_PROTEASOME_PATHWAY	28	0.551761	1.442918	0.057142857	0.29271564	1	3381
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	126	0.424445	1.442356	0.003571429	0.28677234	1	5070
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	16	0.61387	1.429986	0.08571429	0.30779618	1	5533
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_CO UPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	80	0.448162	1.426655	0.028653296	0.30776942	1	6881
KEGG_NITROGEN_METABOLISM	23	0.569892	1.42509	0.05787037	0.30463615	1	1912
REACTOME_CELL_CYCLE	383	0.368736	1.415597	0	0.31906956	1	4975
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	24	0.566025	1.412331	0.051522247	0.31952226	1	2463
REACTOME_PACKAGING_OF_TELOMERE_ENDS	45	0.48265	1.404606	0.032432433	0.3319782	1	5293
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	27	0.55101	1.402627	0.05472637	0.32953778	1	1836
REACTOME_RNA_POL_I_PROMOTER_OPENING	55	0.464055	1.399151	0.038575668	0.33011863	1	7465
KEGG_PROTEIN_EXPORT	23	0.557454	1.395985	0.08035714	0.3309678	1	2613
KEGG_RETINOL_METABOLISM	63	0.453237	1.394337	0.034210525	0.3284775	1	4542
KEGG_PROPANOATE_METABOLISM	32	0.515513	1.389741	0.057416268	0.3328368	1	3568
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	194	0.386963	1.388923	0	0.32850027	1	2650
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	32	0.511934	1.385749	0.049382716	0.3294784	1	3783
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	101	0.418881	1.384567	0.04054054	0.32613602	1	5760
REACTOME_GLUCONEOGENESIS	31	0.532402	1.382815	0.06763285	0.32408944	1	2640
REACTOME_EXTENSION_OF_TELOMERES	27	0.533759	1.381572	0.0942029	0.32128483	1	6580
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	27	0.529097	1.363635	0.07908163	0.35594237	1	5821
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	49	0.464115	1.362024	0.06738544	0.3534123	1	5095
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	342	0.357445	1.350516	0.017964073	0.3746983	1	6507
KEGG_CELL_CYCLE	118	0.400024	1.345178	0.028368793	0.38154948	1	4919
REACTOME_ELONGATION_ARREST_AND_RECOVERY	31	0.493588	1.338579	0.09113924	0.39163804	1	5342
REACTOME_CELL_CYCLE_MITOTIC	297	0.353336	1.332688	0.010928961	0.40019646	1	4975
REACTOME_BIOLOGICAL_OXIDATIONS	133	0.386936	1.328012	0.015151516	0.4055522	1	4034
REACTOME_METABOLISM_OF_NON_CODING_RNA	47	0.464246	1.326035	0.086021505	0.40403816	1	4185
KEGG_HOMOLOGOUS_RECOMBINATION	26	0.515085	1.321215	0.09615385	0.41030538	1	4635
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	70	0.417166	1.311047	0.05730659	0.4299129	1	4319
REACTOME_LAGGING_STRAND_SYNTHESIS	19	0.552533	1.305082	0.13053612	0.43809763	1	6580
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	0.433488	1.303883	0.07387863	0.4348693	1	4498
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	39	0.459458	1.286923	0.08900524	0.4737907	1	2463
REACTOME_ACYL_CHAIN_REMODELLING_OF_PG	15	0.557415	1.284614	0.15982722	0.4732179	1	239
REACTOME_MRNA_PROCESSING	146	0.365392	1.282844	0.02189781	0.47113022	1	5070
REACTOME_MEIOSIS	105	0.383462	1.277822	0.07590759	0.47797194	1	5388
REACTOME_SIGNALING_BY_NODAL	18	0.552595	1.274693	0.15366973	0.4802905	1	5639
REACTOME_MRNA_SPLICING	97	0.387636	1.273288	0.064935066	0.47753182	1	5070
BIOCARTA_TEL_PATHWAY	18	0.541751	1.269439	0.17078651	0.48196858	1	4951
REACTOME_SHC_MEDIATED_CASCADE	28	0.492176	1.2676	0.11899313	0.48080614	1	1918
REACTOME_DNA_REPLICATION	181	0.34717	1.251494	0.06278027	0.51838845	1	4869
REACTOME_MEIOTIC_RECOMBINATION	77	0.392278	1.248173	0.10240964	0.5214553	1	5388
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	44	0.436557	1.246712	0.11989796	0.51927465	1	6900
REACTOME_XENOBIOTICS	15	0.551258	1.243008	0.19058296	0.52420986	1	5729
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	52	0.418242	1.238474	0.1661891	0.53148407	1	3911
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	49	0.430308	1.238347	0.123324394	0.5253171	1	2880
REACTOME_OXYGEN_DEPENDENT_PROLINE_HYDROXYLATION_OF_HYPOXIA_INDUCIBLE_FAC TOR_ALPHA	16	0.546064	1.235674	0.1812227	0.52652085	1	16
REACTOME_TRANSCRIPTION	190	0.343518	1.231759	0.04385965	0.5314193	1	5694
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	34	0.452835	1.229493	0.1768868	0.5313684	1	559
REACTOME_MEIOTIC_SYNAPSIS	68	0.405055	1.22628	0.1300813	0.5344407	1	5293
KEGG_SELENOAMINO_ACID_METABOLISM	26	0.470336	1.222632	0.17889908	0.5387358	1	2794
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	19	0.511249	1.217668	0.21108742	0.54609907	1	6155
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	59	0.392549	1.210494	0.1697128	0.56037223	1	3911
REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULES	30	0.463462	1.206891	0.17548077	0.5646048	1	1290
REACTOME_CELL_JUNCTION_ORGANIZATION	77	0.378193	1.204704	0.12571429	0.56448364	1	1318
REACTOME_BASE_EXCISION_REPAIR	19	0.508803	1.204557	0.2290749	0.55892617	1	5510
KEGG_RNA_POLYMERASE	29	0.445648	1.18019	0.22361809	0.62433726	1	3089
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	116	0.350878	1.176271	0.13422818	0.62924725	1	6055
KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	16	0.507947	1.173251	0.24842106	0.632226	1	613
REACTOME_MITOTIC_M_M_G1_PHASES	161	0.333364	1.169098	0.10869565	0.6385114	1	4844

REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	16	0.515232	1.165831	0.26593408	0.6416897	1	2047
REACTOME_MITOTIC_G1_G1_S_PHASES	124	0.341468	1.162278	0.14285715	0.64573264	1	4869
REACTOME_DNA_REPAIR	105	0.347631	1.162071	0.13988096	0.6399325	1	4869
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	59	0.37491	1.155053	0.19220056	0.6560755	1	4816
KEGG_ARGININE_AND_PROLINE_METABOLISM	54	0.390149	1.154455	0.19498608	0.65141696	1	1932
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	113	0.338842	1.153986	0.14666666	0.6463826	1	7013
REACTOME_REGULATION_OF_HYPOXIA_INDUCIBLE_FACTOR_HIF_BY_OXYGEN	23	0.466436	1.153464	0.24561404	0.6418129	1	3969
REACTOME_UNFOLDED_PROTEIN_RESPONSE	76	0.361685	1.146071	0.16847827	0.6584646	1	2473
REACTOME_GLUCURONIDATION	17	0.495726	1.13961	0.30155212	0.6720791	1	4542
BIOCARTA_MTA3_PATHWAY	19	0.47931	1.139373	0.29175946	0.6666161	1	4126
REACTOME_GLUCOSE_TRANSPORT	38	0.41316	1.137177	0.23076923	0.666868	1	4018
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	62	0.371932	1.128806	0.22727273	0.6868023	1	3657
KEGG_LYSINE_DEGRADATION	44	0.398221	1.127503	0.24804178	0.6843904	1	3239
REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	22	0.45927	1.125402	0.32568806	0.6847514	1	5111
REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	19	0.469904	1.124272	0.295302	0.68199813	1	2026
REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT	23	0.450697	1.120996	0.30044842	0.6860982	1	5342
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	22	0.452686	1.118459	0.27751195	0.68793905	1	1319
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	43	0.392792	1.118448	0.27083334	0.6820265	1	4816
KEGG_WNT_SIGNALING_PATHWAY	150	0.321772	1.117483	0.176259	0.6789583	1	2933
REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	15	0.497611	1.116165	0.30669546	0.6768199	1	7187
KEGG_BETA_ALANINE_METABOLISM	22	0.449009	1.114676	0.31083843	0.67562157	1	1992
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	44	0.3837	1.113756	0.27296588	0.6727489	1	5051
REACTOME_CELL_CYCLE_CHECKPOINTS	105	0.339055	1.11369	0.22377622	0.66745716	1	3381
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	15	0.486061	1.109881	0.33043477	0.6731648	1	1363
REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_AND_AMINE_COMPOUNDS	88	0.338847	1.101902	0.2681388	0.6909867	1	2294
BIOCARTA_WNT_PATHWAY	26	0.427415	1.098744	0.32705882	0.694597	1	2840
KEGG_PARKINSONS_DISEASE	112	0.320134	1.096466	0.1978022	0.69582236	1	6055
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	27	0.428458	1.094774	0.2908654	0.69546854	1	1476
REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY	17	0.467064	1.094246	0.33653846	0.69135207	1	5471
REACTOME_MITOTIC_G2_G2_M_PHASES	74	0.346027	1.08996	0.26764706	0.6989223	1	6253
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	40	0.390194	1.089626	0.3048499	0.6945307	1	5637
REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION	22	0.452718	1.086998	0.3470716	0.69667506	1	1918
REACTOME_RNA_POL_I_TRANSCRIPTION	80	0.333245	1.085781	0.28391168	0.6950611	1	7013
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	34	0.399695	1.083854	0.34390244	0.69558835	1	1089
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_7ALPHA_HYDROXYCHOLESTEROL	15	0.481914	1.078246	0.3783784	0.70742035	1	613
REACTOME_LIPOPROTEIN_METABOLISM	28	0.414907	1.078164	0.3245033	0.7023376	1	2587
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS	26	0.432023	1.077969	0.35664335	0.6975479	1	4143
REACTOME_GLUTATHIONE_CONJUGATION	22	0.434459	1.077681	0.37762237	0.6932578	1	2742
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	44	0.369276	1.075254	0.32352942	0.6951179	1	2434
REACTOME_RNA_POL_II_TRANSCRIPTION	93	0.325147	1.074769	0.26865673	0.6914292	1	5669
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	31	0.409882	1.071933	0.3626943	0.69464755	1	1156
KEGG_GLUTATHIONE_METABOLISM	47	0.371118	1.067101	0.34554973	0.70409197	1	4443
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	49	0.369822	1.066347	0.35368958	0.70129776	1	3815
REACTOME_MRNA_CAPPING	29	0.40772	1.066307	0.38084114	0.69641143	1	4816
REACTOME_FRS2_MEDIATED_CASCADE	36	0.385356	1.060881	0.35189873	0.7074293	1	5110
REACTOME_FORMATION_OF_TRANSCRIPTION_COUPLED_NER_TC_NER_REPAIR_COMPLEX	29	0.407986	1.058849	0.3642534	0.7082965	1	3370
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_2_PROMOTER	23	0.427321	1.054061	0.4	0.71737957	1	6641
REACTOME_NEPHRIN_INTERACTIONS	19	0.437956	1.049091	0.3859275	0.72712964	1	3242
REACTOME_S_PHASE	100	0.31463	1.048791	0.33962265	0.72301555	1	3159
KEGG_ALZHEIMERS_DISEASE	157	0.298572	1.041275	0.30487806	0.7406412	1	4329
REACTOME_PERK_REGULATED_GENE_EXPRESSION	27	0.405554	1.036667	0.42298287	0.7502836	1	3744
REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	16	0.463596	1.034631	0.42163354	0.7517098	1	5533
KEGG_STARCH_AND_SUCROSE_METABOLISM	49	0.351626	1.025531	0.38666666	0.77479464	1	2463
BIOCARTA_CARM_ER_PATHWAY	35	0.368926	1.024147	0.37783375	0.7737518	1	3388
REACTOME_LIGAND_GATED_ION_CHANNEL_TRANSPORT	20	0.425578	1.017647	0.4617117	0.78852326	1	3871
REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS	68	0.320712	1.016078	0.398374	0.7881051	1	3815
KEGG_BUTANOATE_METABOLISM	33	0.370561	1.014631	0.43466666	0.7874925	1	4441
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	24	0.404609	1.013765	0.42212188	0.7848635	1	3744
REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING	36	0.369814	1.009808	0.46354166	0.79198605	1	4650
REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	50	0.341554	1.004981	0.44215938	0.80202067	1	2789
REACTOME_POTASSIUM_CHANNELS	96	0.307	1.003621	0.43434343	0.8011494	1	1776
KEGG_GLYCEROLIPID_METABOLISM	46	0.345488	1.003504	0.43544304	0.7964616	1	2574
REACTOME_G1_S_TRANSITION	100	0.301022	1.002224	0.4358108	0.7954422	1	4869
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	44	0.354108	1.00194	0.4292683	0.7912264	1	2433
REACTOME_FANCONI_ANEMIA_PATHWAY	21	0.414743	1.001584	0.4415011	0.787136	1	4028
BIOCARTA_P53_PATHWAY	16	0.441658	1.001503	0.47679326	0.78254896	1	684
REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	52	0.337654	0.995529	0.43065694	0.7955234	1	4224
REACTOME_CHOLESTEROL_BIOSYNTHESIS	21	0.41229	0.991344	0.48165137	0.8034694	1	8633
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	19	0.414067	0.989686	0.48451328	0.8035045	1	613
KEGG_LINOLEIC_ACID_METABOLISM	25	0.402058	0.988766	0.44630072	0.8014953	1	5133
REACTOME_GLUCOSE_METABOLISM	64	0.320735	0.978132	0.51675975	0.8293507	1	2640
BIOCARTA_ATRBRCA_PATHWAY	21	0.394427	0.976125	0.47544643	0.8310718	1	4028
REACTOME_DIABETES_PATHWAYS	128	0.289629	0.975713	0.5183824	0.8272935	1	2651
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	237	0.26387	0.972984	0.5613208	0.83055127	1	3151
REACTOME_RNA_POL_III_TRANSCRIPTION	33	0.369032	0.972124	0.5035629	0.8282725	1	3089
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	461	0.2492	0.967108	0.5905512	0.83856595	1	3902
REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	18	0.413466	0.961843	0.5273523	0.85008353	1	5434
KEGG_BLADDER_CANCER	42	0.335801	0.960972	0.5150754	0.8477198	1	4566
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	34	0.35668	0.960596	0.5277778	0.844105	1	860
REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	104	0.290461	0.960383	0.55172414	0.83993083	1	6164
REACTOME_SYNTHESIS_OF_PA	26	0.371261	0.953761	0.52459013	0.854709	1	2504
REACTOME_FORMATION_OF_THE_HIV1_EARLY_ELONGATION_COMPLEX	33	0.355385	0.953419	0.53517586	0.8510297	1	5342
KEGG_BASE_EXCISION_REPAIR	33	0.352858	0.952546	0.5282555	0.8490838	1	6749
REACTOME_HDL_MEDIATED_LIPID_TRANSPORT	15	0.433687	0.951593	0.5264271	0.84729934	1	1623
REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	17	0.405387	0.949598	0.5365854	0.8486941	1	1089
REACTOME_ACTIVATED_POINT_MUTANTS_OF_FGFR2	16	0.419438	0.945625	0.53205127	0.8558732	1	1725
BIOCARTA_G2_PATHWAY	24	0.373212	0.944103	0.56790125	0.8553196	1	4845
REACTOME_PYRUVATE_METABOLISM	18	0.410111	0.94348	0.54565215	0.8525426	1	2242
REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS	84	0.293628	0.94256	0.5692308	0.8504494	1	2945
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	49	0.322148	0.940269	0.5653333	0.8522396	1	4869
REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_D	34	0.3405	0.938249	0.5644769	0.85376334	1	3815
KEGG_FATTY_ACID_METABOLISM	40	0.338508	0.931914	0.57894737	0.86810976	1	1992
REACTOME_SYNTHESIS_OF_PC	18	0.395451	0.928496	0.5756208	0.87347245	1	5808
BIOCARTA_EIF_PATHWAY	16	0.410007	0.92828	0.56828195	0.8695432	1	3268
KEGG_PURINE_METABOLISM	156	0.263846	0.926423	0.6755725	0.8702519	1	3759
KEGG_INOSITOL_PHOSPHATE_METABOLISM	54	0.310306	0.921167	0.5966851	0.8809193	1	1195
KEGG_VIBRIO_CHOLERAE_INFECTION	53	0.306187	0.919337	0.6318681	0.8814977	1	2010
REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM	167	0.261872	0.918386	0.6574803	0.8798024	1	3121
BIOCARTA_CHREBP2_PATHWAY	42	0.319756	0.914832	0.5862069	0.88562834	1	2607
CANCER-TESTIS-ANTIGEN	180	0.254253	0.914292	0.770751	0.8827372	1	2219
REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY	19	0.379663	0.911497	0.60337555	0.88612616	1	6221
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	44	0.312864	0.910398	0.6380697	0.8847371	1	2874

KEGG_BASAL_TRANSCRIPTION_FACTORS	34	0.325361	0.903558	0.6112532	0.8989622	1	6119
REACTOME_SIGNALING_BY_ROBO_RECEPTOR	29	0.340909	0.89683	0.6340326	0.9136431	1	3995
REACTOME_G1_PHASE	35	0.323864	0.896035	0.64028776	0.9114048	1	6312
REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	21	0.369118	0.895043	0.60954446	0.9094593	1	3562
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	23	0.359846	0.89421	0.6270023	0.9073314	1	3827
BIOCARTA_P53HYPOXIA_PATHWAY	22	0.368836	0.893575	0.6273148	0.9045066	1	1501
REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	21	0.365477	0.892616	0.61777776	0.90262	1	583
REACTOME_KINESINS	23	0.358895	0.888883	0.6218679	0.90824825	1	9101
REACTOME_METABOLISM_OF_POLYAMINES	15	0.395075	0.883043	0.6231884	0.9194484	1	688
KEGG_PHENYLALANINE_METABOLISM	18	0.379926	0.881748	0.63053095	0.9186142	1	4676
REACTOME_METABOLISM_OF_PROTEINS	421	0.226706	0.88063	0.94074076	0.9170738	1	4530
REACTOME_STEROID_HORMONES	28	0.338296	0.878596	0.62690353	0.91781265	1	567
REACTOME_RNA_POL_III_TRANSCRIPTION_TERMINATION	19	0.360596	0.877485	0.64444447	0.91631633	1	6458
BIOCARTA_MITOCHONDRIA_PATHWAY	21	0.353299	0.877229	0.6396396	0.9127416	1	2470
REACTOME_SULFUR_AMINO_ACID_METABOLISM	24	0.352228	0.876941	0.63752663	0.9092441	1	795
REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	15	0.387488	0.875552	0.6272727	0.9087133	1	5036
KEGG_TASTE_TRANSDUCTION	44	0.299893	0.874578	0.6968912	0.90697443	1	3726
REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_ACTIVITY_BY_INSULIN_LIKE_GROWTH_FACTOR_BINDING_PROTEINS_IGFBPS	16	0.375159	0.873693	0.6332623	0.9049986	1	1572
REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION	24	0.345304	0.871394	0.6595289	0.9063157	1	5049
REACTOME_HIV_LIFE_CYCLE	114	0.259519	0.871377	0.81528664	0.90222454	1	4103
REACTOME_PLATELET_SENSITIZATION_BY_LDL	16	0.386782	0.869662	0.6260504	0.9021305	1	1916
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	16	0.384878	0.864637	0.6515151	0.91033673	1	57
REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION_INDEPENDENT_DOUBLE_STRAND_BREAKS	16	0.372275	0.862205	0.66317993	0.91178536	1	4366
REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT	16	0.380346	0.862128	0.6292373	0.9079215	1	2587
REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	20	0.360113	0.860327	0.67264575	0.9080713	1	5111
REACTOME_INFLUENZA_LIFE_CYCLE	136	0.250668	0.860059	0.8722628	0.9046037	1	4103
REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	18	0.362619	0.850298	0.6731602	0.9231615	1	4189
BIOCARTA_CELLCYCLE_PATHWAY	23	0.338512	0.848326	0.6989011	0.92342734	1	930
REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION	27	0.323538	0.83762	0.7083333	0.9434212	1	1753
KEGG_MELANOMA	71	0.271067	0.83679	0.82058823	0.9411162	1	3820
BIOCARTA_ATM_PATHWAY	20	0.348762	0.836148	0.7256637	0.9382481	1	663
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	38	0.302018	0.83443	0.7582697	0.93781126	1	2611
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	64	0.272018	0.830339	0.8060109	0.9422419	1	320
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION	21	0.332772	0.823584	0.72789115	0.9522546	1	3370
KEGG_MISMATCH_REPAIR	23	0.328809	0.820438	0.7256637	0.95464194	1	3384
KEGG_THYROID_CANCER	29	0.311783	0.816313	0.7791262	0.9586997	1	5177
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	25	0.322651	0.810479	0.7710843	0.96577865	1	2271
BIOCARTA_ACTINY_PATHWAY	20	0.339542	0.809163	0.75838923	0.9641299	1	3294
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	60	0.261314	0.805983	0.8518519	0.9662671	1	3029
REACTOME_SIGNALING_BY_CONSTITUTIVELY_ACTIVE_EGFR	17	0.344139	0.798326	0.75789475	0.976252	1	2531
REACTOME_ZINC_TRANSPORTERS	15	0.345745	0.7953	0.7694013	0.97761196	1	3133
REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	15	0.350117	0.790896	0.76626015	0.9812927	1	1089
BIOCARTA_ERK_PATHWAY	28	0.304815	0.78599	0.82988507	0.9856851	1	5036
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	179	0.21791	0.782628	0.99615383	0.98714775	1	4324
KEGG_PROSTATE_CANCER	88	0.238026	0.768428	0.9478528	1	1	3034
BIOCARTA_AMI_PATHWAY	20	0.313301	0.767067	0.8198198	1	1	4906
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	22	0.309711	0.763524	0.8249453	1	1	4366
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	23	0.317277	0.763391	0.8149883	1	1	6132
BIOCARTA_PITX2_PATHWAY	15	0.343267	0.758531	0.8097448	1	1	6152
REACTOME_RNA_POL_III_CHAIN_ELONGATION	17	0.329405	0.754798	0.8314351	1	1	6458
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN	28	0.288774	0.751642	0.85131896	1	1	1530
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	21	0.302184	0.739707	0.86206895	1	1	2333
REACTOME_PI_3K_CASCADE	54	0.247967	0.732334	0.9587912	1	1	3488
REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	104	0.214653	0.72562	0.9755245	1	1	3268
REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI	17	0.317487	0.718085	0.8532495	1	1	5578
REACTOME_PURINE_METABOLISM	33	0.265501	0.711552	0.9110577	1	1	3467
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	25	0.281972	0.707454	0.8727273	1	1	6239
BIOCARTA_HIF_PATHWAY	15	0.318605	0.70286	0.87142855	1	1	6268
BIOCARTA_G1_PATHWAY	28	0.266252	0.702377	0.91079813	1	1	5574
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_SYNTHESIS	25	0.279409	0.698494	0.9166667	1	1	994
REACTOME_HS_GAG_DEGRADATION	20	0.287705	0.693345	0.9031532	1	1	3526
REACTOME_CIRCADIAN_CLOCK	51	0.237343	0.69305	0.9506493	1	1	6362
REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRCADIAN_EXPRESSION	35	0.252101	0.690605	0.9514563	1	1	4899
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	26	0.26938	0.686316	0.9320843	1	1	6458
REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	42	0.242959	0.68472	0.97783935	1	1	2531
REACTOME_DEADENYLATION_OF_MRNA	19	0.281857	0.671377	0.9273128	1	1	4664
KEGG_O_GLYCAN_BIOSYNTHESIS	29	0.253753	0.668192	0.9649123	1	1	3404
REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	84	0.207176	0.667062	0.99680513	1	1	3268
REACTOME_TRANSLATION	147	0.187013	0.652252	1	1	1	3509
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	47	0.228047	0.650082	0.984252	1	1	1168
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	0.220619	0.642355	0.9727723	1	1	6900
KEGG_ONE_CARBON_POOL_BY_FOLATE	17	0.275636	0.638603	0.9252137	1	1	7894
REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSION_BY_REV_ERBA	23	0.255637	0.634617	0.95681816	1	1	4899
BIOCARTA_SHH_PATHWAY	16	0.273708	0.629782	0.9413043	1	1	4751
REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	24	0.248904	0.621073	0.96803653	1	1	4666
REACTOME_SHC_MEDIATED_SIGNALLING	15	0.271423	0.611833	0.9527027	1	1	1655
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	36	0.218394	0.603626	0.99731183	1	1	6239
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	110	0.175991	0.589149	1	1	1	2081
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	102	0.170044	0.568726	1	1	1	2081
REACTOME_SHC_RELATED_EVENTS	17	0.245577	0.565353	0.9774775	1	1	1655
BIOCARTA_BARRESTIN_SRC_PATHWAY	15	0.243879	0.54886	0.98004436	1	1	6303
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	18	0.222638	0.51956	0.9912088	1	1	2333
REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	16	0.210932	0.484911	0.9843049	1	1	6152
BIOCARTA_CERAMIDE_PATHWAY	22	0.194343	0.4739	0.9977064	1	1	5983
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	15	0.204606	0.455568	0.9958592	1	1	6952
REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	17	0.154424	0.362149	1	0.9999491	1	7332

Table S17
GSEA Analysis on TCGA HNSC comparing tumors with or without 9p21.3 loss (arm or focal), Pathways Depleted

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX	LEADING EDGE
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	56	-0.88129	-2.38407	0	0	0	972	tags=68%, list=5%, signal=71%
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	251	-0.71899	-2.31727	0	0	0	1910	tags=37%, list=10%, signal=41%
REACTOME_INTERFERON_SIGNALING	132	-0.77057	-2.31291	0	0	0	1492	tags=38%, list=8%, signal=41%
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	239	-0.7151	-2.31163	0	0	0	1910	tags=33%, list=10%, signal=36%
KEGG_CHEMOKINE_SIGNALING_PATHWAY	188	-0.7295	-2.27369	0	0	0	1671	tags=34%, list=9%, signal=37%
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	92	-0.7739	-2.25952	0	0	0	1232	tags=28%, list=6%, signal=30%
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	53	-0.85367	-2.2581	0	0	0	1208	tags=58%, list=6%, signal=62%
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	117	-0.75887	-2.25312	0	0	0	1066	tags=38%, list=6%, signal=40%
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	492	-0.66865	-2.24365	0	0	0	1433	tags=23%, list=7%, signal=24%
REACTOME_INTERFERON_GAMMA_SIGNALING	48	-0.85238	-2.22763	0	0	0	1492	tags=54%, list=8%, signal=59%
REACTOME_INNATE_IMMUNE_SYSTEM	225	-0.69491	-2.21964	0	0	0	1723	tags=28%, list=9%, signal=31%
KEGG_HEMATOPOIETIC_CELL_LINEAGE	78	-0.7758	-2.21824	0	0	0	1864	tags=50%, list=10%, signal=55%
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	47	-0.84793	-2.21126	0	0	0	2176	tags=70%, list=11%, signal=79%
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	55	-0.82553	-2.20098	0	0	0	1559	tags=47%, list=8%, signal=51%
KEGG_LEISHMANIA_INFECTION	57	-0.79586	-2.1717	0	0	0	1310	tags=37%, list=7%, signal=39%
KEGG_PRIMARY_IMMUNODEFICIENCY	35	-0.86759	-2.16638	0	0	0	867	tags=51%, list=4%, signal=54%
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	55	-0.81376	-2.14652	0	0	0	945	tags=33%, list=5%, signal=34%
BIOCARTA_NKT_PATHWAY	28	-0.88958	-2.12785	0	0	0	1310	tags=68%, list=7%, signal=73%
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	107	-0.72051	-2.11518	0	0	0	1038	tags=28%, list=5%, signal=29%
REACTOME_TCR_SIGNALING	44	-0.82009	-2.1106	0	0	0	945	tags=43%, list=5%, signal=45%
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	45	-0.80223	-2.09554	0	0	0	1860	tags=40%, list=10%, signal=44%
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	68	-0.76012	-2.08702	0	0	0	1622	tags=37%, list=8%, signal=40%
BIOCARTA_IL12_PATHWAY	21	-0.90825	-2.06528	0	0	0	963	tags=62%, list=5%, signal=65%
KEGG_JAK_STAT_SIGNALING_PATHWAY	141	-0.66424	-2.0568	0	0	0	2958	tags=40%, list=15%, signal=47%
KEGG_GRAFT_VERSUS_HOST_DISEASE	19	-0.93079	-2.04262	0	0	0	683	tags=74%, list=4%, signal=76%
KEGG_TYPE_I_DIABETES_MELLITUS	23	-0.89297	-2.03758	0	0	0	683	tags=43%, list=4%, signal=45%
KEGG_ALLOGRAFT_REJECTION	16	-0.92231	-2.02832	0	0	0	683	tags=69%, list=4%, signal=71%
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	182	-0.6412	-2.02527	0	0	0	1992	tags=26%, list=10%, signal=29%
BIOCARTA_NO2IL12_PATHWAY	17	-0.93158	-2.0245	0	0	0	963	tags=82%, list=5%, signal=87%
KEGG_CELL_ADHESION_MOLECULES_CAMS	113	-0.66905	-1.98807	0	3.66E-05	0.001	1106	tags=26%, list=6%, signal=27%
BIOCARTA_CTLA4_PATHWAY	17	-0.90947	-1.97798	0	3.55E-05	0.001	945	tags=71%, list=5%, signal=74%
KEGG_AUTOIMMUNE_THYROID_DISEASE	20	-0.87474	-1.97205	0	3.43E-05	0.001	1976	tags=75%, list=10%, signal=83%
BIOCARTA_DC_PATHWAY	20	-0.87232	-1.97035	0	6.57E-05	0.002	1864	tags=75%, list=10%, signal=83%
REACTOME_DOWNSTREAM_TCR_SIGNALING	27	-0.82933	-1.96325	0	6.38E-05	0.002	945	tags=37%, list=5%, signal=39%
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	275	-0.59893	-1.95624	0	6.19E-05	0.002	2311	tags=28%, list=12%, signal=32%
REACTOME_TOLL_RECEPTOR_CASCADES	113	-0.6563	-1.949	0	9.10E-05	0.003	1723	tags=24%, list=9%, signal=26%
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	20	-0.86947	-1.94802	0	8.85E-05	0.003	847	tags=65%, list=4%, signal=68%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	112	-0.65667	-1.944	0	8.62E-05	0.003	747	tags=19%, list=4%, signal=19%
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	33	-0.79583	-1.93411	0	1.12E-04	0.004	2233	tags=61%, list=12%, signal=68%
REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BETA_PATHWAYS	62	-0.7003	-1.92249	0	1.89E-04	0.007	1723	tags=27%, list=9%, signal=30%
BIOCARTA_CSK_PATHWAY	20	-0.85138	-1.9213	0	1.84E-04	0.007	1291	tags=45%, list=7%, signal=48%
BIOCARTA_STATHMIN_PATHWAY	19	-0.86694	-1.91596	0	2.31E-04	0.009	1291	tags=42%, list=7%, signal=45%
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	176	-0.60812	-1.90971	0	3.24E-04	0.013	2268	tags=30%, list=12%, signal=33%
SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE	59	-0.70552	-1.90742	0	3.41E-04	0.014	1687	tags=31%, list=9%, signal=33%
REACTOME_IL_3_5_AND_GM_CSF_SIGNALING	42	-0.73327	-1.8865	0	5.44E-04	0.023	2592	tags=48%, list=13%, signal=55%
REACTOME_SIGNALING_BY_RHO_GTPASES	108	-0.63372	-1.88476	0	5.55E-04	0.024	2741	tags=33%, list=14%, signal=39%
BIOCARTA_INFLAM_PATHWAY	25	-0.81122	-1.87436	0	6.35E-04	0.028	1976	tags=56%, list=10%, signal=62%
REACTOME_COMPLEMENT_CASCADE	29	-0.76737	-1.86738	0	8.46E-04	0.038	1622	tags=41%, list=8%, signal=45%
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	95	-0.6426	-1.86411	0	9.40E-04	0.043	1418	tags=25%, list=7%, signal=27%
BIOCARTA_TOB1_PATHWAY	18	-0.8575	-1.86206	0	0.001006359	0.047	1976	tags=67%, list=10%, signal=74%
BIOCARTA_TH1TH2_PATHWAY	16	-0.86896	-1.85621	0	0.001195527	0.056	1976	tags=75%, list=10%, signal=83%
BIOCARTA_COMP_PATHWAY	18	-0.85604	-1.85099	0	0.001235158	0.059	1300	tags=56%, list=7%, signal=60%
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	75	-0.65642	-1.84817	0	0.001353928	0.066	2176	tags=35%, list=11%, signal=39%
BIOCARTA_TCR_PATHWAY	44	-0.72791	-1.8479	0	0.001328855	0.066	2592	tags=45%, list=13%, signal=52%
REACTOME_SIGNALING_BY_ILS	104	-0.63166	-1.84632	0	0.001363088	0.068	3175	tags=37%, list=16%, signal=43%
BIOCARTA_NKCELLS_PATHWAY	19	-0.82744	-1.84028	0	0.001433716	0.073	945	tags=47%, list=5%, signal=50%
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	30	-0.7514	-1.82911	0	0.001857374	0.097	1723	tags=33%, list=9%, signal=37%
BIOCARTA_IL2RB_PATHWAY	38	-0.73952	-1.82869	0	0.001843708	0.098	2242	tags=39%, list=12%, signal=45%
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	61	-0.67656	-1.82386	0	0.002087271	0.11	2406	tags=31%, list=12%, signal=35%
BIOCARTA_CASPASE_PATHWAY	23	-0.77833	-1.82094	0	0.002211541	0.117	553	tags=22%, list=3%, signal=22%
REACTOME_MUSCLE_CONTRACTION	46	-0.69319	-1.81864	0	0.002385665	0.128	2987	tags=61%, list=15%, signal=72%
BIOCARTA_CYTOKINE_PATHWAY	18	-0.82608	-1.8163	0	0.00252008	0.137	2363	tags=61%, list=12%, signal=70%
BIOCARTA_TOLL_PATHWAY	37	-0.71953	-1.81094	0	0.002703568	0.149	2098	tags=27%, list=11%, signal=30%
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	62	-0.66234	-1.81054	0	0.002661324	0.149	1892	tags=26%, list=10%, signal=29%
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	67	-0.6532	-1.80038	0	0.003096168	0.176	852	tags=24%, list=4%, signal=25%
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	31	-0.74602	-1.78726	0	0.004059102	0.229	1354	tags=39%, list=7%, signal=42%
REACTOME_IL_RECEPTOR_SHC_SIGNALING	26	-0.7585	-1.78376	0.001788909	0.00433516	0.248	2374	tags=50%, list=12%, signal=57%
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	20	-0.79695	-1.77603	0.001848429	0.005045717	0.284	1723	tags=35%, list=9%, signal=38%
REACTOME_STRIATED_MUSCLE_CONTRACTION	27	-0.75046	-1.75865	0	0.006631577	0.351	2865	tags=81%, list=15%, signal=96%
REACTOME_GPCR_LIGAND_BINDING	373	-0.52618	-1.75112	0	0.007407473	0.392	2270	tags=23%, list=12%, signal=26%
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	30	-0.71335	-1.74308	0.005059022	0.008603484	0.433	2115	tags=33%, list=11%, signal=37%
REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC	15	-0.82831	-1.74253	0	0.008499135	0.434	926	tags=27%, list=5%, signal=28%
REACTOME_HEMOSTASIS	435	-0.52101	-1.7372	0	0.009193953	0.467	2190	tags=23%, list=11%, signal=26%
KEGG_VIRAL_MYOCARDITIS	50	-0.64382	-1.72107	0.001574803	0.011974846	0.571	2860	tags=50%, list=15%, signal=59%
BIOCARTA_UCALPAIN_PATHWAY	18	-0.78188	-1.71809	0.005444646	0.012454872	0.587	2744	tags=50%, list=14%, signal=58%
BIOCARTA_CCR5_PATHWAY	17	-0.79031	-1.71494	0.001855288	0.013000839	0.608	3263	tags=53%, list=17%, signal=64%
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	79	-0.60256	-1.70779	0.001457726	0.014531474	0.656	3421	tags=41%, list=18%, signal=49%
BIOCARTA_INTEGRIN_PATHWAY	38	-0.67396	-1.70591	0.001658375	0.014884696	0.671	2593	tags=37%, list=13%, signal=42%
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATION_OF_SECOND_MESSENGERS	29	-0.71361	-1.70181	0	0.015597886	0.688	2592	tags=48%, list=13%, signal=56%
REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS	26	-0.71821	-1.68344	0.006666667	0.020272084	0.777	1671	tags=35%, list=9%, signal=38%
BIOCARTA_PML_PATHWAY	17	-0.78662	-1.67779	0.005444646	0.021681372	0.804	1223	tags=29%, list=6%, signal=31%
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	228	-0.52368	-1.6747	0	0.02233385	0.814	1182	tags=14%, list=6%, signal=14%
BIOCARTA_TID_PATHWAY	19	-0.75917	-1.67468	0.001834862	0.022064766	0.814	273	tags=16%, list=1%, signal=16%
BIOCARTA_CTCF_PATHWAY	23	-0.73198	-1.67016	0.005415163	0.02324353	0.83	2026	tags=43%, list=10%, signal=49%
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	195	-0.53253	-1.66973	0	0.02313292	0.832	2817	tags=33%, list=15%, signal=38%
BIOCARTA_IL22BP_PATHWAY	16	-0.78906	-1.66745	0.003683241	0.023565525	0.843	3152	tags=63%, list=16%, signal=75%
REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_DAI	18	-0.76572	-1.66616	0.001862197	0.02357832	0.844	1603	tags=28%, list=8%, signal=30%
REACTOME_ACTIVATED_TLR4_SIGNALLING	90	-0.57253	-1.65523	0.001449275	0.027322618	0.888	2213	tags=20%, list=11%, signal=22%
BIOCARTA_IL2_PATHWAY	22	-0.72885	-1.65498	0.006956522	0.027123075	0.888	2242	tags=41%, list=12%, signal=46%
REACTOME_IL_2_SIGNALING	40	-0.65066	-1.65411	0.004893964	0.02716778	0.892	2374	tags=40%, list=12%, signal=46%
KEGG_ECM_RECEPTOR_INTERACTION	83	-0.57727	-1.65361	0.002976191	0.026963385	0.892	4292	tags=47%, list=22%, signal=60%
REACTOME_TRAF6_MEDIATED_NFKB_ACTIVATION	21	-0.72552	-1.65316	0.003546099	0.026867772	0.895	1460	tags=19%, list=8%, signal=21%
REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS	16	-0.76703	-1.65083	0.015009381	0.027686479	0.905	885	tags=38%, list=5%, signal=39%
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	19	-0.74841	-1.6368	0.010657194	0.032896098	0.949	1314	tags=32%, list=7%, signal=34%
KEGG_DILATED_CARDIOMYOPATHY	90	-0.5584	-1.63486	0	0.03342955	0.954	2865	tags=40%, list=15%, signal=47%
BIOCARTA_GH_PATHWAY	28	-0.68473	-1.63421	0.003466205	0.03332589	0.955	3152	tags=43%, list=16%, signal=51%
KEGG_PRION_DISEASES	35	-0.66205	-1.63216	0.005008347	0.033900417	0.957	1842	tags=26%, list=10%, signal=28%
REACTOME_CTLA4_INHIBITORY_SIGNALING	21	-0.72054	-1.63172	0.019963702	0.03375156	0.957	847	tags=19%, list=4%, signal=20%
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS	44	-0.63266	-1.63059	0.011627907	0.033971325	0.961	1719	tags=20%, list=9%, signal=22%
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	21	-0.70673	-1.62068	0.011152417	0.037814215	0.969	945	tags=24%, list=5%, signal=25%
BIOCARTA_TALL1_PATHWAY	15	-0.77869	-1.61791	0.011320755	0.038598724	0.972	2935	tags=40%, list=15%, signal=47%
BIOCARTA_BIOPEPTIDES_PATHWAY	42	-0.62497	-1.61711	0.008347246	0.03854585	0.973	2592	tags=29%, list=13%, signal=33%
BIOCARTA_PTEN_PATHWAY	18	-0.73536	-1.61593	0.010695187	0.03870017	0.974	1587	tags=22%, list=8%, signal=24%
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	84	-0.57045	-1.60925	0	0.041452266	0.984	1331	tags=21%, list=7%, signal=23%
BIOCARTA_LAIR_PATHWAY	17	-0.74867	-1.60838	0.011516315	0.041382767	0.984	1687	tags=41%, list=9%, signal=45%

BIOCARTA_IL7_PATHWAY	17	-0.73814	-1.6073	0.011363637	0.041492388	0.984	2592	tags=59%, list=13%, signal=68%
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	65	-0.58798	-1.60416	0.001589825	0.042649403	0.986	1698	tags=22%, list=9%, signal=24%
BIOCARTA_BCR_PATHWAY	34	-0.64961	-1.60357	0.015100671	0.04262433	0.988	2467	tags=35%, list=13%, signal=40%
KEGG_FOCAL_ADHESION	198	-0.51327	-1.60263	0	0.042892095	0.99	3421	tags=37%, list=18%, signal=44%
REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR7_8_OR_9_ACTIVATION	74	-0.56425	-1.60166	0.007278021	0.042962354	0.992	1460	tags=16%, list=8%, signal=17%
BIOCARTA_TPO_PATHWAY	24	-0.69538	-1.60071	0.010452962	0.043028116	0.992	2572	tags=46%, list=13%, signal=53%
REACTOME_INFLAMMASOMES	16	-0.75178	-1.59516	0.013059702	0.045470864	0.992	1719	tags=31%, list=9%, signal=34%
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	23	-0.6936	-1.59152	0.007272727	0.046942748	0.995	3152	tags=39%, list=16%, signal=47%
REACTOME_CD28_CO_STIMULATION	31	-0.67081	-1.58769	0.005025126	0.048862904	0.996	945	tags=23%, list=5%, signal=24%
BIOCARTA_EGF_PATHWAY	31	-0.65007	-1.58128	0.014234875	0.05215741	0.998	3473	tags=45%, list=18%, signal=55%
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	114	-0.53648	-1.57626	0.001386963	0.054470047	0.998	2467	tags=29%, list=13%, signal=33%
BIOCARTA_NTHI_PATHWAY	24	-0.66726	-1.57493	0.02189781	0.054842927	0.998	2935	tags=29%, list=15%, signal=34%
REACTOME_PI_METABOLISM	47	-0.60614	-1.57274	0.013050571	0.055687133	0.998	1587	tags=21%, list=8%, signal=23%
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	74	-0.55532	-1.5669	0.006097561	0.05864361	0.999	2772	tags=35%, list=14%, signal=41%
KEGG_GALACTOSE_METABOLISM	26	-0.65692	-1.56306	0.016393442	0.060442973	0.999	654	tags=15%, list=3%, signal=16%
BIOCARTA_HSP27_PATHWAY	15	-0.76026	-1.55748	0.0331384	0.06364752	0.999	995	tags=27%, list=5%, signal=28%
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	83	-0.55476	-1.55634	0.005925926	0.06387288	0.999	3616	tags=46%, list=19%, signal=56%
REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	72	-0.55703	-1.55579	0.009160305	0.06373554	0.999	1723	tags=18%, list=9%, signal=20%
BIOCARTA_FAS_PATHWAY	30	-0.63535	-1.55078	0.015706806	0.06695809	0.999	909	tags=17%, list=5%, signal=17%
REACTOME_G_ALPHA1213_SIGNALLING_EVENTS	73	-0.55162	-1.5498	0.011182109	0.06713592	0.999	3620	tags=36%, list=19%, signal=44%
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	209	-0.48263	-1.54784	0.002590674	0.067890204	0.999	3421	tags=32%, list=18%, signal=38%
BIOCARTA_PDGF_PATHWAY	32	-0.63812	-1.54731	0.01610018	0.0677601	0.999	2572	tags=38%, list=13%, signal=43%
BIOCARTA_IL10_PATHWAY	17	-0.71624	-1.54371	0.021543985	0.0697721	1	2242	tags=53%, list=12%, signal=60%
REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	70	-0.55376	-1.54343	0.010835913	0.06941369	1	1460	tags=16%, list=8%, signal=17%
KEGG_LYSOSOME	121	-0.51853	-1.54075	0.007163324	0.0705837	1	2892	tags=29%, list=15%, signal=34%
BIOCARTA_NFKB_PATHWAY	23	-0.67854	-1.53967	0.03499079	0.07082099	1	409	tags=13%, list=2%, signal=13%
BIOCARTA_ECM_PATHWAY	24	-0.64988	-1.53958	0.024263432	0.07034273	1	2609	tags=38%, list=13%, signal=43%
BIOCARTA_GLEEVEC_PATHWAY	23	-0.66395	-1.53662	0.02877698	0.07173622	1	2242	tags=30%, list=12%, signal=34%
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	47	-0.5899	-1.52891	0.018181818	0.07680433	1	852	tags=21%, list=4%, signal=22%
BIOCARTA_KERATINOCYTE_PATHWAY	46	-0.58596	-1.52674	0.009787928	0.07788599	1	1418	tags=15%, list=7%, signal=16%
REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	80	-0.52906	-1.52508	0.01065449	0.07843293	1	1460	tags=15%, list=8%, signal=16%
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	47	-0.58321	-1.52028	0.022764228	0.08165027	1	1572	tags=23%, list=8%, signal=25%
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	28	-0.63473	-1.51828	0.015929203	0.08266418	1	935	tags=25%, list=5%, signal=26%
BIOCARTA_CARDIACEGF_PATHWAY	18	-0.6946	-1.50876	0.03125	0.089585185	1	2467	tags=39%, list=13%, signal=45%
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	126	-0.49323	-1.50457	0.004195804	0.0921735	1	1658	tags=16%, list=9%, signal=17%
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	121	-0.49937	-1.50129	0.007022472	0.09443483	1	2062	tags=20%, list=11%, signal=22%
BIOCARTA_MCALPAIN_PATHWAY	25	-0.64036	-1.49823	0.028119508	0.0965824	1	1776	tags=20%, list=9%, signal=22%
KEGG_APOPTOSIS	86	-0.51994	-1.49185	0.012195122	0.101696916	1	2935	tags=22%, list=15%, signal=26%
BIOCARTA_MET_PATHWAY	37	-0.5925	-1.48956	0.033898305	0.10305829	1	2572	tags=30%, list=13%, signal=34%
BIOCARTA_TNFR2_PATHWAY	18	-0.68468	-1.48917	0.048387095	0.10270173	1	3223	tags=33%, list=17%, signal=40%
BIOCARTA_IL1R_PATHWAY	33	-0.60224	-1.48195	0.030100334	0.1091399	1	3223	tags=30%, list=17%, signal=36%
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	114	-0.49328	-1.47206	0.011428571	0.11858773	1	1658	tags=13%, list=9%, signal=14%
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	38	-0.58129	-1.46852	0.039473683	0.121698014	1	4006	tags=37%, list=21%, signal=46%
REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKS_COMPLEX	23	-0.6365	-1.46757	0.060606062	0.1219591	1	1460	tags=17%, list=8%, signal=19%
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	73	-0.51627	-1.46287	0.011713031	0.126043	1	1418	tags=21%, list=7%, signal=22%
BIOCARTA_IL6_PATHWAY	22	-0.64098	-1.46277	0.048561152	0.12533534	1	4417	tags=50%, list=23%, signal=65%
REACTOME_ER_PHAGOSOME_PATHWAY	53	-0.54696	-1.45503	0.014876033	0.132285	1	852	tags=19%, list=4%, signal=20%
REACTOME_DAG_AND_IP3_SIGNALING	31	-0.59524	-1.45109	0.050251257	0.13578802	1	2673	tags=39%, list=14%, signal=45%
REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	28	-0.61	-1.44629	0.050522648	0.14089368	1	1354	tags=18%, list=7%, signal=19%
REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	17	-0.66913	-1.44359	0.05954466	0.14329226	1	1043	tags=18%, list=5%, signal=19%
REACTOME_PLC_BETA_MEDIATED_EVENTS	42	-0.55168	-1.44253	0.06902087	0.14357544	1	2673	tags=31%, list=14%, signal=36%
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	31	-0.59447	-1.43951	0.05392157	0.14615779	1	2018	tags=23%, list=10%, signal=25%
BIOCARTA_ACH_PATHWAY	16	-0.67165	-1.43193	0.06607143	0.1538326	1	945	tags=19%, list=5%, signal=20%
REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	33	-0.58053	-1.43047	0.061359867	0.15475708	1	3266	tags=30%, list=17%, signal=36%
REACTOME_NOD1_2_SIGNALING_PATHWAY	29	-0.59001	-1.42731	0.06013746	0.15777755	1	1413	tags=17%, list=7%, signal=19%
BIOCARTA_HIVNEF_PATHWAY	58	-0.53218	-1.42688	0.032496307	0.15734582	1	1120	tags=10%, list=6%, signal=11%
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	79	-0.50051	-1.42504	0.02293578	0.15845026	1	3421	tags=41%, list=18%, signal=49%
REACTOME_SMOOTH_MUSCLE_CONTRACTION	23	-0.62454	-1.42176	0.063716814	0.16142774	1	3410	tags=43%, list=18%, signal=53%
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	25	-0.6146	-1.41693	0.055846423	0.16683668	1	1669	tags=28%, list=9%, signal=31%
REACTOME_REGULATION_OF_KIT_SIGNALING	16	-0.66186	-1.41511	0.08073395	0.16805407	1	2592	tags=38%, list=13%, signal=43%
REACTOME_ERK_MAPK_TARGETS	21	-0.63702	-1.41297	0.06654344	0.16956486	1	3858	tags=33%, list=20%, signal=42%
REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING	27	-0.59744	-1.40982	0.07664884	0.17233373	1	3421	tags=33%, list=18%, signal=40%
REACTOME_DEFENSINS	16	-0.6732	-1.4098	0.0707635	0.17132692	1	2459	tags=44%, list=13%, signal=50%
BIOCARTA_GSK3_PATHWAY	27	-0.59844	-1.40843	0.056410257	0.17201912	1	1932	tags=22%, list=10%, signal=25%
KEGG_PROTEASOME	44	-0.54284	-1.40779	0.054054055	0.17180924	1	852	tags=18%, list=4%, signal=19%
BIOCARTA_AKT_PATHWAY	22	-0.62538	-1.40583	0.092334494	0.17331165	1	945	tags=14%, list=5%, signal=14%
REACTOME_SIGNALING_BY_SCF_KIT	75	-0.50881	-1.40337	0.043343652	0.1755187	1	2607	tags=25%, list=13%, signal=29%
BIOCARTA_PGC1A_PATHWAY	22	-0.60432	-1.40286	0.072463766	0.17514205	1	2139	tags=32%, list=11%, signal=36%
KEGG_TGF_BETA_SIGNALING_PATHWAY	85	-0.49165	-1.40221	0.03323263	0.1749865	1	3101	tags=27%, list=16%, signal=32%
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	196	-0.44129	-1.40056	0.009259259	0.1762752	1	1322	tags=11%, list=7%, signal=12%
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	79	-0.49707	-1.39894	0.03671072	0.17735271	1	2729	tags=19%, list=14%, signal=22%
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	119	-0.4707	-1.39713	0.026239067	0.17864181	1	1010	tags=13%, list=5%, signal=14%
BIOCARTA_RHO_PATHWAY	32	-0.56923	-1.39486	0.07020548	0.18096122	1	3622	tags=44%, list=19%, signal=54%
REACTOME_APOPTOSIS	143	-0.45351	-1.39132	0.016064256	0.18453173	1	1174	tags=12%, list=6%, signal=13%
REACTOME_INTRINSIC_PATHWAY	16	-0.64863	-1.38406	0.10243055	0.19312055	1	2018	tags=25%, list=10%, signal=28%
BIOCARTA_41BB_PATHWAY	16	-0.66362	-1.38394	0.09622642	0.19223826	1	1976	tags=19%, list=10%, signal=21%
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	61	-0.50739	-1.38132	0.0576	0.19493109	1	852	tags=15%, list=4%, signal=15%
BIOCARTA_FCER1_PATHWAY	38	-0.55232	-1.37638	0.0738255	0.20098257	1	2467	tags=32%, list=13%, signal=36%
BIOCARTA_CREB_PATHWAY	27	-0.57186	-1.37449	0.080617495	0.20256326	1	1291	tags=15%, list=7%, signal=16%
BIOCARTA_ERK5_PATHWAY	17	-0.63938	-1.36948	0.09074074	0.20877425	1	1118	tags=24%, list=6%, signal=25%
BIOCARTA_CD40_PATHWAY	15	-0.64787	-1.36885	0.103053436	0.20856829	1	3223	tags=33%, list=17%, signal=40%
BIOCARTA_PAR1_PATHWAY	37	-0.54104	-1.35724	0.078947365	0.22456856	1	1630	tags=22%, list=8%, signal=24%
REACTOME_SEMAPHORIN_INTERACTIONS	63	-0.49542	-1.35502	0.074554294	0.22680357	1	1776	tags=17%, list=9%, signal=19%
REACTOME_RAP1_SIGNALLING	16	-0.63022	-1.3521	0.13059033	0.23001947	1	1524	tags=31%, list=8%, signal=34%
KEGG_RENIN_ANGIOTENSIN_SYSTEM	17	-0.63126	-1.35177	0.10526316	0.22936721	1	3025	tags=53%, list=16%, signal=63%
REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	43	-0.52694	-1.34763	0.065989845	0.23458724	1	3505	tags=33%, list=18%, signal=40%
REACTOME_SIGNALLING_BY_NGF	211	-0.42028	-1.34405	0.019582245	0.23885489	1	2820	tags=21%, list=15%, signal=25%
KEGG_ENDOCYTOSIS	174	-0.43195	-1.34359	0.026957639	0.23842333	1	2930	tags=21%, list=15%, signal=24%
KEGG_CALCIUM_SIGNALING_PATHWAY	176	-0.42987	-1.33975	0.02745098	0.24363297	1	2847	tags=28%, list=15%, signal=32%
BIOCARTA_TGFB_PATHWAY	19	-0.60054	-1.33678	0.12037037	0.24697156	1	2274	tags=26%, list=12%, signal=30%
REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	30	-0.54405	-1.3354	0.08963093	0.24795371	1	1572	tags=20%, list=8%, signal=22%
REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	15	-0.6274	-1.33316	0.13513513	0.2502373	1	1562	tags=27%, list=8%, signal=29%
REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	16	-0.64133	-1.3282	0.13756613	0.2571202	1	2190	tags=56%, list=11%, signal=63%
REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	79	-0.47404	-1.32542	0.06495468	0.26070696	1	3505	tags=25%, list=18%, signal=31%
BIOCARTA_EDG1_PATHWAY	27	-0.5556	-1.32289	0.1366782	0.26373544	1	1573	tags=22%, list=8%, signal=24%
BIOCARTA_CCR3_PATHWAY	23	-0.58348	-1.32003	0.12920354	0.2671532	1	3545	tags=43%, list=18%, signal=53%
BIOCARTA_HDAC_PATHWAY	28	-0.5577	-1.31857	0.11655405	0.2684265	1	2999	tags=36%, list=16%, signal=42%
BIOCARTA_RAS_PATHWAY	23	-0.56721	-1.31815	0.124333926	0.26783422	1	1418	tags=17%, list=7%, signal=19%
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	111	-0.44418	-1.30959	0.06716418	0.28089088	1	2062	tags=23%, list=11%, signal=25%
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES	91	-0.44803	-1.30374	0.07173601	0.28965765	1	2030	tags=20%, list=11%, signal=22%
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	53	-0.49349	-1.30148	0.09538461	0.29238114	1	1932	tags=15%, list=10%, signal=17%
REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI	16	-0.60647	-1.29972	0.16176471	0.2941084	1	1564	tags=25%, list=8%, signal=27%
KEGG_ABC_TRANSPORTERS	44	-0.50413	-1.29616	0.13001606	0.29889083	1	2435	tags=27%, list=13%, signal=31%
REACTOME_PEROXISOMAL_LIPID_METABOLISM	20	-0.57286	-1.29401	0.1534196	0.30145493	1	2206	tags=30%, list=11%, signal=34%
BIOCARTA_RAC1_PATHWAY	23	-0.56337	-1.29148	0.12956205	0.3048008	1	3311	tags=43%, list=17%, signal=52%
KEGG_ACUTE_MYELOID_LEUKEMIA	57	-0.48241	-1.28941	0.10272873	0.3071172	1	2473	tags=25%, list=13%, signal=28%
KEGG_MTOR_SIGNALING_PATHWAY	51	-0.4809	-1.28637	0.1008	0.31120983	1	2999	tags=24%, list=16%, signal=28%
REACTOME_REGULATION_OF_APOPTOSIS	56	-0.46911	-1.28541	0.1072	0.31169832	1	1117	tags=16%, list=6%, signal=17%
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI	18	-0.58927	-1.28299	0.16635513	0.31455255	1	2764	tags=28%, list=14%, signal=32%
REACTOME_REGULATION_OF_INSULIN_SECRETION	89	-0.43988	-1.28237	0.095729016	0.31417465	1	3464	tags=26%, list=18%, signal=31%

REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	15	-0.60517	-1.282	0.1782364	0.3132764	1	3421	tags=40%, list=18%, signal=49%
KEGG_COLORECTAL_CANCER	62	-0.47074	-1.28118	0.116099074	0.31344253	1	2098	tags=27%, list=11%, signal=31%
REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	30	-0.53183	-1.27682	0.1669506	0.3198087	1	2894	tags=30%, list=15%, signal=35%
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	107	-0.42981	-1.2756	0.0882353	0.32055068	1	2268	tags=21%, list=12%, signal=24%
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	92	-0.44349	-1.27477	0.086330935	0.32061067	1	1038	tags=12%, list=5%, signal=13%
REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	58	-0.47318	-1.27423	0.12068965	0.32023352	1	3505	tags=26%, list=18%, signal=31%
BIOCARTA_ETS_PATHWAY	18	-0.58478	-1.27348	0.18232045	0.32016128	1	668	tags=17%, list=3%, signal=17%
KEGG_ADHERENS_JUNCTION	73	-0.45292	-1.27102	0.12557428	0.32322794	1	2739	tags=26%, list=14%, signal=30%
BIOCARTA_RELA_PATHWAY	16	-0.58949	-1.26768	0.17818181	0.32811418	1	273	tags=6%, list=1%, signal=6%
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	18	-0.58614	-1.2628	0.17196262	0.33602273	1	2592	tags=39%, list=13%, signal=45%
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	49	-0.48158	-1.26258	0.12903225	0.33497807	1	902	tags=16%, list=5%, signal=17%
REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	174	-0.4075	-1.26143	0.08222812	0.33590478	1	2637	tags=24%, list=14%, signal=28%
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	-0.44761	-1.2569	0.11649016	0.34284976	1	1831	tags=16%, list=9%, signal=18%
BIOCARTA_NFAT_PATHWAY	52	-0.47357	-1.25451	0.15728477	0.34607357	1	2400	tags=27%, list=12%, signal=31%
REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	16	-0.58429	-1.25227	0.18426104	0.34924883	1	2062	tags=19%, list=11%, signal=21%
REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE	133	-0.40963	-1.25132	0.08531468	0.34963796	1	2685	tags=23%, list=14%, signal=26%
KEGG_INSULIN_SIGNALING_PATHWAY	136	-0.41344	-1.24991	0.09348442	0.35101572	1	2171	tags=15%, list=11%, signal=16%
BIOCARTA_INSULIN_PATHWAY	22	-0.55872	-1.24711	0.19081272	0.35486224	1	4417	tags=50%, list=23%, signal=65%
BIOCARTA_VIP_PATHWAY	26	-0.53233	-1.24667	0.18848167	0.35412142	1	3988	tags=38%, list=21%, signal=48%
REACTOME_GRB2_SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTERGRINS_	15	-0.58932	-1.2458	0.19144982	0.35424277	1	2676	tags=33%, list=14%, signal=39%
REACTOME_PLATELET_HOMEOSTASIS	76	-0.44259	-1.24554	0.112426035	0.35330582	1	2190	tags=29%, list=11%, signal=33%
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	49	-0.47414	-1.24525	0.15422885	0.3523944	1	852	tags=14%, list=4%, signal=15%
REACTOME_SIGNALING_BY_FGFR1_FUSION_MUTANTS	17	-0.57473	-1.24451	0.21121496	0.35234126	1	3152	tags=35%, list=16%, signal=42%
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	-0.53746	-1.24054	0.18560606	0.35902485	1	3858	tags=29%, list=20%, signal=36%
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	76	-0.43521	-1.23826	0.12518854	0.36205995	1	2554	tags=20%, list=13%, signal=23%
REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	21	-0.56058	-1.23733	0.1802974	0.362371	1	1669	tags=24%, list=9%, signal=26%
BIOCARTA_BAD_PATHWAY	25	-0.53426	-1.22777	0.19689119	0.3802463	1	3988	tags=40%, list=21%, signal=50%
BIOCARTA_NO1_PATHWAY	30	-0.51197	-1.22626	0.20462634	0.38163978	1	4051	tags=43%, list=21%, signal=55%
BIOCARTA_CHEMICAL_PATHWAY	22	-0.5387	-1.22123	0.21376811	0.3907922	1	553	tags=14%, list=3%, signal=14%
KEGG_REGULATION_OF_AUTOPHAGY	24	-0.53093	-1.2169	0.22727273	0.39816353	1	1061	tags=17%, list=5%, signal=18%
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	27	-0.51279	-1.21669	0.19170985	0.39696258	1	1605	tags=19%, list=8%, signal=20%
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	44	-0.46879	-1.2164	0.18876755	0.39597782	1	3374	tags=36%, list=17%, signal=44%
BIOCARTA_ALK_PATHWAY	36	-0.48467	-1.21418	0.18892509	0.39919814	1	3051	tags=31%, list=16%, signal=36%
BIOCARTA_MYOSIN_PATHWAY	31	-0.50034	-1.21135	0.21207178	0.40353394	1	3263	tags=29%, list=17%, signal=35%
BIOCARTA_EPO_PATHWAY	19	-0.55358	-1.21081	0.20145191	0.40309677	1	2467	tags=32%, list=13%, signal=36%
REACTOME_IL1_SIGNALING	38	-0.47167	-1.20865	0.2	0.4061188	1	1525	tags=11%, list=8%, signal=11%
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK	195	-0.38083	-1.20747	0.12073491	0.40693814	1	2685	tags=23%, list=14%, signal=26%
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	-0.5077	-1.19963	0.23076923	0.42238954	1	1680	tags=17%, list=9%, signal=18%
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	16	-0.56538	-1.19607	0.24399261	0.42855814	1	557	tags=19%, list=3%, signal=19%
REACTOME_CA_DEPENDENT_EVENTS	29	-0.49063	-1.19425	0.23333333	0.43083113	1	2673	tags=34%, list=14%, signal=40%
KEGG_LONG_TERM_POTENTIATION	70	-0.42605	-1.19265	0.18307692	0.43266615	1	2139	tags=20%, list=11%, signal=22%
KEGG_TYPE_II_DIABETES_MELLITUS	47	-0.46621	-1.1926	0.19713831	0.43106586	1	1528	tags=17%, list=8%, signal=18%
REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	49	-0.4491	-1.19122	0.18979266	0.43261576	1	3464	tags=33%, list=18%, signal=40%
REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS	42	-0.46768	-1.1906	0.22310127	0.43227586	1	3464	tags=36%, list=18%, signal=43%
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	48	-0.44709	-1.18729	0.19129083	0.4377797	1	852	tags=15%, list=4%, signal=15%
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	81	-0.42039	-1.18608	0.19664635	0.43888155	1	1328	tags=15%, list=7%, signal=16%
REACTOME_HIV_INFECTION	192	-0.3767	-1.18522	0.12646675	0.43912345	1	1314	tags=10%, list=7%, signal=11%
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	46	-0.44855	-1.18517	0.20757826	0.43751043	1	852	tags=15%, list=4%, signal=16%
BIOCARTA_IGF1_PATHWAY	21	-0.52206	-1.18318	0.24783362	0.44030806	1	4417	tags=48%, list=23%, signal=62%
REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS	15	-0.56045	-1.17879	0.2843691	0.44868076	1	1605	tags=20%, list=8%, signal=22%
REACTOME_SYNTHESIS_SECRETION_AND_DEACYLATION_OF_GHRELIN	16	-0.54097	-1.17647	0.27037036	0.45213827	1	2999	tags=31%, list=16%, signal=37%
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	35	-0.47206	-1.17283	0.24342105	0.4588489	1	2018	tags=26%, list=10%, signal=29%
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	50	-0.43813	-1.1728	0.20983607	0.45719346	1	852	tags=14%, list=4%, signal=15%
REACTOME_SIGNALING_BY_WNT	63	-0.42554	-1.17034	0.21301775	0.46097407	1	852	tags=11%, list=4%, signal=12%
BIOCARTA_CDMAC_PATHWAY	16	-0.55015	-1.1678	0.2945591	0.46494156	1	2098	tags=19%, list=11%, signal=21%
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	47	-0.44783	-1.16722	0.2353896	0.46468318	1	852	tags=15%, list=4%, signal=16%
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	29	-0.48934	-1.16646	0.27457628	0.4646717	1	2392	tags=17%, list=12%, signal=20%
BIOCARTA_BCELLSURVIVAL_PATHWAY	16	-0.54802	-1.16554	0.3074074	0.46485034	1	2098	tags=31%, list=11%, signal=35%
KEGG_GLIOMA	65	-0.42345	-1.16058	0.2124031	0.4739986	1	1587	tags=15%, list=8%, signal=17%
REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	26	-0.48662	-1.15792	0.2452174	0.4781692	1	3976	tags=35%, list=21%, signal=44%
BIOCARTA_MEF2D_PATHWAY	18	-0.52158	-1.1574	0.2983725	0.47763416	1	2139	tags=22%, list=11%, signal=25%
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	48	-0.43892	-1.15613	0.23692308	0.4788525	1	852	tags=15%, list=4%, signal=15%
BIOCARTA_CDC42RAC_PATHWAY	16	-0.5389	-1.15375	0.2829861	0.48275363	1	1350	tags=19%, list=7%, signal=20%
BIOCARTA_PYK2_PATHWAY	28	-0.47165	-1.15113	0.26508227	0.48701096	1	4723	tags=43%, list=24%, signal=57%
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	43	-0.44555	-1.14859	0.2599681	0.49110186	1	2966	tags=21%, list=15%, signal=25%
BIOCARTA_GPCR_PATHWAY	34	-0.4619	-1.14735	0.25827813	0.492149	1	4451	tags=47%, list=23%, signal=61%
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	48	-0.42602	-1.14474	0.24960254	0.49633008	1	852	tags=15%, list=4%, signal=15%
REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	33	-0.46843	-1.14446	0.27022377	0.49519563	1	2229	tags=24%, list=12%, signal=27%
REACTOME_OPIOID_SIGNALLING	77	-0.40577	-1.14351	0.23846154	0.49554121	1	2139	tags=21%, list=11%, signal=23%
BIOCARTA_MAL_PATHWAY	19	-0.51046	-1.1429	0.30198914	0.49521983	1	3337	tags=37%, list=17%, signal=44%
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	256	-0.35622	-1.14255	0.1731493	0.49426484	1	2958	tags=21%, list=15%, signal=25%
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	64	-0.41691	-1.14198	0.23993559	0.49378467	1	1182	tags=13%, list=6%, signal=13%
BIOCARTA_EIF4_PATHWAY	24	-0.49992	-1.14102	0.3046595	0.49428186	1	2530	tags=21%, list=13%, signal=24%
BIOCARTA_IGF1MTOR_PATHWAY	20	-0.50843	-1.1397	0.3139746	0.49563426	1	3101	tags=35%, list=16%, signal=42%
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	37	-0.45347	-1.1394	0.28525123	0.49465773	1	3994	tags=41%, list=21%, signal=51%
REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB	17	-0.52749	-1.13786	0.31918818	0.49641228	1	3988	tags=47%, list=21%, signal=59%
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	53	-0.42288	-1.13553	0.2676282	0.49995267	1	852	tags=13%, list=4%, signal=14%
KEGG_TRYPTOPHAN_METABOLISM	40	-0.44267	-1.13383	0.26923078	0.5021059	1	2520	tags=23%, list=13%, signal=26%
BIOCARTA_GATA3_PATHWAY	15	-0.53218	-1.13352	0.29885057	0.5011967	1	4493	tags=40%, list=23%, signal=52%
REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	49	-0.42652	-1.13303	0.2819237	0.5005583	1	1118	tags=12%, list=6%, signal=13%
KEGG_RENAL_CELL_CARCINOMA	70	-0.4034	-1.13077	0.23916294	0.50391567	1	1524	tags=16%, list=8%, signal=17%
REACTOME_SIGNAL_AMPLIFICATION	31	-0.46818	-1.12595	0.285956	0.513404	1	1669	tags=19%, list=9%, signal=21%
KEGG_PANCREATIC_CANCER	70	-0.40194	-1.12522	0.25597748	0.51334333	1	1418	tags=16%, list=7%, signal=17%
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	134	-0.37146	-1.12411	0.24128312	0.51430994	1	2725	tags=22%, list=14%, signal=26%
BIOCARTA_HER2_PATHWAY	22	-0.48598	-1.12372	0.29982364	0.51354915	1	2805	tags=32%, list=15%, signal=37%
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	105	-0.37939	-1.12165	0.25779036	0.51679695	1	3014	tags=22%, list=16%, signal=26%
REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	37	-0.44744	-1.12032	0.29432014	0.5181331	1	3445	tags=27%, list=18%, signal=33%
REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_LIKE_PEPTIDE1	42	-0.43227	-1.11679	0.26755852	0.5245072	1	3464	tags=31%, list=18%, signal=38%
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	77	-0.38651	-1.10764	0.2684049	0.5444874	1	1182	tags=10%, list=6%, signal=11%
REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS	16	-0.5246	-1.10732	0.33460075	0.5434403	1	4583	tags=44%, list=24%, signal=57%
REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE	25	-0.4666	-1.10569	0.32020548	0.5456256	1	3374	tags=36%, list=17%, signal=44%
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	33	-0.45028	-1.10452	0.3293919	0.5465768	1	3732	tags=39%, list=19%, signal=49%
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	65	-0.40475	-1.10347	0.2891374	0.5472487	1	1182	tags=12%, list=6%, signal=13%
BIOCARTA_NOS1_PATHWAY	21	-0.48449	-1.09803	0.32667875	0.5582356	1	2139	tags=24%, list=11%, signal=27%
KEGG_PATHWAYS_IN_CANCER	324	-0.33129	-1.09363	0.2529976	0.5673041	1	2628	tags=18%, list=14%, signal=20%
BIOCARTA_CXCR4_PATHWAY	24	-0.48422	-1.09202	0.33333334	0.56935143	1	3263	tags=29%, list=17%, signal=35%
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	108	-0.36943	-1.08939	0.30477527	0.5737248	1	3259	tags=28%, list=17%, signal=33%
REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_TTP	17	-0.50125	-1.08634	0.3600713	0.5792045	1	2862	tags=29%, list=15%, signal=34%
REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1	17	-0.51208	-1.08551	0.3710575	0.5791926	1	2298	tags=24%, list=12%, signal=27%
KEGG_CITRATE_CYCLE_TCA_CYCLE	30	-0.44827	-1.08464	0.33616298	0.57938045	1	649	tags=10%, list=3%, signal=10%
KEGG_AXON_GUIDANCE	129	-0.35543	-1.07864	0.30307263	0.5917833	1	2963	tags=22%, list=15%, signal=25%
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	20	-0.48488	-1.07669	0.36044362	0.59468526	1	2510	tags=35%, list=13%, signal=40%
REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	26	-0.45633	-1.07556	0.3560477	0.59564686	1	2894	tags=23%, list=15%, signal=27%
REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	17	-0.50568	-1.07434	0.37360594	0.5966488	1	1280	tags=18%, list=7%, signal=19%
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	91	-0.36845	-1.07325	0.33049646	0.59748554	1	2789	tags=24%, list=14%, signal=28%
BIOCARTA_MTOR_PATHWAY	23	-0.46896	-1.07224	0.37477148	0.59802073	1	3101	tags=26%, list=16%, signal=31%
REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLP1	17	-0.48843	-1.07197	0.38204226	0.5968647	1	1932	tags=18%, list=10%, signal=20%
REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	18	-0.48619	-1.0704	0.3775701	0.59894425	1	366	tags=6%, list=2%, signal=6%
BIOCARTA_AT1R_PATHWAY	32	-0.43254	-1.06885	0.38704318	0.60075295	1	4417	tags=41%, list=23%, signal=53%
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	23	-0.46704	-1.06877	0.36541888	0.5991086	1	2190	tags=30%, list=11%, signal=34%
BIOCARTA_LONGEVITY_PATHWAY	15	-0.51412	-1.06781	0.38715595	0.5995915	1	4396	tags=53%, list=23%, signal=69%

REACTOME_SIGNALING_BY_FGFR1_MUTANTS	28	-0.44297	-1.06311	0.37237763	0.6089822	1	3336	tags=32%, list=17%, signal=39%
KEGG_ENDOMETRIAL_CANCER	52	-0.39635	-1.06116	0.37345678	0.61168253	1	2003	tags=23%, list=10%, signal=26%
BIOCARTA_AKAPCENTROSOME_PATHWAY	15	-0.50398	-1.06103	0.41142857	0.6101208	1	1291	tags=13%, list=7%, signal=14%
REACTOME_AXON_GUIDANCE	240	-0.33064	-1.06022	0.3324905	0.6101723	1	3546	tags=26%, list=18%, signal=32%
KEGG_ERBB_SIGNALING_PATHWAY	87	-0.36631	-1.06022	0.3447251	0.60834825	1	2467	tags=17%, list=13%, signal=20%
REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	41	-0.41234	-1.05954	0.3592233	0.60808563	1	1564	tags=15%, list=8%, signal=16%
BIOCARTA_TFF_PATHWAY	21	-0.46959	-1.05831	0.4074703	0.60933304	1	2958	tags=29%, list=15%, signal=34%
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	53	-0.39475	-1.05716	0.3736434	0.61032057	1	852	tags=11%, list=4%, signal=12%
KEGG_HISTIDINE_METABOLISM	29	-0.43754	-1.0536	0.37755102	0.6170027	1	1629	tags=21%, list=8%, signal=23%
REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLLAPSE	24	-0.45114	-1.05328	0.39790577	0.6159382	1	3796	tags=33%, list=20%, signal=41%
KEGG_GAP_JUNCTION	87	-0.36242	-1.05309	0.36652237	0.6145149	1	1830	tags=13%, list=9%, signal=14%
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS	30	-0.4347	-1.05307	0.37414965	0.61279315	1	4148	tags=40%, list=21%, signal=51%
REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	32	-0.43016	-1.05139	0.3808725	0.6149446	1	3374	tags=34%, list=17%, signal=42%
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	56	-0.39004	-1.05061	0.38271606	0.6150553	1	1182	tags=13%, list=6%, signal=13%
REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	116	-0.35441	-1.04829	0.3797654	0.6186792	1	3464	tags=22%, list=18%, signal=27%
BIOCARTA_HCMV_PATHWAY	17	-0.48431	-1.04811	0.4223485	0.61727715	1	945	tags=12%, list=5%, signal=12%
KEGG_MAPK_SIGNALING_PATHWAY	261	-0.32314	-1.04113	0.37918216	0.63230014	1	2789	tags=20%, list=14%, signal=23%
KEGG_N_GLYCAN_BIOSYNTHESIS	46	-0.40012	-1.04101	0.41576508	0.6307737	1	817	tags=9%, list=4%, signal=9%
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA	20	-0.47045	-1.04101	0.41573033	0.6289607	1	1669	tags=20%, list=9%, signal=22%
BIOCARTA_SPPA_PATHWAY	22	-0.45638	-1.04007	0.3975265	0.62937105	1	1562	tags=18%, list=8%, signal=20%
BIOCARTA_NGF_PATHWAY	18	-0.4772	-1.03914	0.40714285	0.62977487	1	2467	tags=28%, list=13%, signal=32%
REACTOME_PI3K_AKT_ACTIVATION	36	-0.41861	-1.03789	0.410596	0.63085747	1	2607	tags=17%, list=13%, signal=19%
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	59	-0.38729	-1.03345	0.39263803	0.63971907	1	852	tags=12%, list=4%, signal=12%
BIOCARTA_ARF_PATHWAY	17	-0.47702	-1.03329	0.43263757	0.6382466	1	1658	tags=18%, list=9%, signal=19%
REACTOME_NETRIN1_SIGNALING	38	-0.40571	-1.0325	0.42326334	0.63819087	1	2943	tags=32%, list=15%, signal=37%
REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	25	-0.43852	-1.03081	0.39590445	0.6401993	1	1931	tags=28%, list=10%, signal=31%
REACTOME_CGMP_EFFECTS	19	-0.46223	-1.02839	0.43362832	0.64408195	1	1931	tags=32%, list=10%, signal=35%
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	42	-0.39648	-1.02576	0.43290734	0.64844304	1	2328	tags=24%, list=12%, signal=27%
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	62	-0.37504	-1.02267	0.44	0.65378255	1	852	tags=10%, list=4%, signal=10%
BIOCARTA_GCR_PATHWAY	19	-0.46206	-1.02263	0.41361257	0.65202475	1	3345	tags=32%, list=17%, signal=38%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	15	-0.49009	-1.02152	0.45419848	0.6528178	1	139	tags=7%, list=1%, signal=7%
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	134	-0.33443	-1.02061	0.4135021	0.6530756	1	525	tags=4%, list=3%, signal=5%
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	57	-0.38075	-1.01819	0.44094488	0.65690666	1	852	tags=12%, list=4%, signal=13%
REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT	25	-0.43389	-1.01771	0.43432575	0.65624344	1	1148	tags=8%, list=6%, signal=8%
REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE	53	-0.37913	-1.0157	0.4347158	0.6592243	1	3464	tags=32%, list=18%, signal=39%
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	183	-0.32216	-1.01448	0.41560102	0.6602969	1	2725	tags=21%, list=14%, signal=24%
REACTOME_GABA_B_RECEPTOR_ACTIVATION	38	-0.40448	-1.01114	0.45261437	0.66630566	1	3374	tags=32%, list=17%, signal=38%
REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	19	-0.4523	-1.00732	0.45233968	0.6733332	1	4693	tags=47%, list=24%, signal=62%
REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	17	-0.46405	-1.00492	0.47079647	0.6770823	1	1224	tags=12%, list=6%, signal=13%
REACTOME_PYRIMIDINE_METABOLISM	24	-0.43264	-1.00469	0.44542253	0.67578757	1	931	tags=13%, list=5%, signal=13%
REACTOME_APOPTOTIC_EXECUTION_PHASE	52	-0.37612	-1.0034	0.453125	0.6769484	1	3245	tags=23%, list=17%, signal=28%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	26	-0.4263	-0.99945	0.47887325	0.6845421	1	379	tags=8%, list=2%, signal=8%
BIOCARTA_MAPK_PATHWAY	86	-0.34769	-0.99938	0.44903988	0.6828819	1	2098	tags=14%, list=11%, signal=16%
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	67	-0.35989	-0.99928	0.4747634	0.681236	1	783	tags=6%, list=4%, signal=6%
BIOCARTA_INTRINSIC_PATHWAY	23	-0.43147	-0.99893	0.45189002	0.68016875	1	798	tags=9%, list=4%, signal=9%
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	20	-0.451	-0.99549	0.45698926	0.6863754	1	3301	tags=25%, list=17%, signal=30%
BIOCARTA_CALCINEURIN_PATHWAY	18	-0.4519	-0.99488	0.46494466	0.68602693	1	2467	tags=28%, list=13%, signal=32%
REACTOME_SIGNALING_BY_PDGF	118	-0.33278	-0.99462	0.4695652	0.6848026	1	2790	tags=24%, list=14%, signal=28%
BIOCARTA_ARAP_PATHWAY	17	-0.463	-0.99136	0.48126233	0.6905384	1	213	tags=6%, list=1%, signal=6%
REACTOME_G_PROTEIN_ACTIVATION	27	-0.41063	-0.99037	0.47584972	0.6910474	1	1669	tags=15%, list=9%, signal=16%
REACTOME_BASIGIN_INTERACTIONS	24	-0.42933	-0.98572	0.47124305	0.7002208	1	257	tags=8%, list=1%, signal=8%
BIOCARTA_P38MAPK_PATHWAY	39	-0.38403	-0.98266	0.4819672	0.70573217	1	1831	tags=15%, list=9%, signal=17%
REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	121	-0.32642	-0.97807	0.50977653	0.714472	1	3464	tags=23%, list=18%, signal=28%
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	24	-0.4133	-0.97541	0.4784946	0.7190132	1	2843	tags=33%, list=15%, signal=39%
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.37775	-0.97458	0.50248754	0.71900946	1	1680	tags=12%, list=9%, signal=13%
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	21	-0.43641	-0.97254	0.5306859	0.72187024	1	2504	tags=19%, list=13%, signal=22%
REACTOME_M_G1_TRANSITION	72	-0.34299	-0.96413	0.5212121	0.7399528	1	852	tags=10%, list=4%, signal=10%
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	23	-0.41678	-0.96286	0.5034602	0.74110746	1	1669	tags=17%, list=9%, signal=19%
REACTOME_AMYLOIDS	75	-0.33648	-0.95757	0.534375	0.75160736	1	385	tags=4%, list=2%, signal=4%
REACTOME_GAP_JUNCTION_TRAFFICKING	26	-0.4005	-0.95666	0.5366667	0.7518404	1	2719	tags=19%, list=14%, signal=22%
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	84	-0.33499	-0.95596	0.53914326	0.751548	1	2999	tags=24%, list=16%, signal=28%
REACTOME_NEURONAL_SYSTEM	273	-0.2962	-0.95367	0.5871446	0.7549438	1	2769	tags=21%, list=14%, signal=24%
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	23	-0.41179	-0.95341	0.54545456	0.7536127	1	2746	tags=22%, list=14%, signal=25%
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	404	-0.28393	-0.95203	0.6284404	0.75486547	1	2673	tags=17%, list=14%, signal=19%
REACTOME_MYOGENESIS	26	-0.40144	-0.95065	0.53125	0.75619334	1	4645	tags=46%, list=24%, signal=61%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	-0.45014	-0.94607	0.54347825	0.7651418	1	3319	tags=47%, list=17%, signal=56%
KEGG_PYRIMIDINE_METABOLISM	97	-0.3221	-0.94526	0.5760234	0.7649674	1	931	tags=8%, list=5%, signal=9%
BIOCARTA_RARRXR_PATHWAY	15	-0.4464	-0.94455	0.5591603	0.7646661	1	652	tags=7%, list=3%, signal=7%
KEGG_GNRH_SIGNALING_PATHWAY	96	-0.32344	-0.9442	0.5660377	0.76352286	1	4074	tags=31%, list=21%, signal=39%
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRANE	17	-0.43943	-0.94329	0.56078434	0.7636385	1	2115	tags=18%, list=11%, signal=20%
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	80	-0.3297	-0.94319	0.5601783	0.76198745	1	2764	tags=14%, list=14%, signal=16%
REACTOME_TRNA_AMINOACYLATION	42	-0.36928	-0.93842	0.5504886	0.7709711	1	1680	tags=12%, list=9%, signal=13%
KEGG_RIBOFLAVIN_METABOLISM	16	-0.43728	-0.93761	0.5368421	0.77091503	1	3579	tags=31%, list=19%, signal=38%
REACTOME_ARMS_MEDIATED_ACTIVATION	17	-0.42649	-0.93731	0.55128205	0.76967824	1	1524	tags=24%, list=8%, signal=26%
REACTOME_METABOLISM_OF_MRNA	209	-0.29624	-0.93631	0.62531644	0.76993567	1	2622	tags=13%, list=14%, signal=15%
REACTOME_DEVELOPMENTAL_BIOLOGY	380	-0.27934	-0.93417	0.65501165	0.77282923	1	3468	tags=22%, list=18%, signal=26%
REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS	26	-0.39237	-0.93401	0.5523156	0.7713084	1	3452	tags=19%, list=18%, signal=23%
BIOCARTA_FMLP_PATHWAY	36	-0.37193	-0.92955	0.5738255	0.7797162	1	2139	tags=19%, list=11%, signal=22%
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	-0.37939	-0.92873	0.5584192	0.77963483	1	3858	tags=27%, list=20%, signal=33%
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	27	-0.39	-0.92555	0.5659051	0.7848831	1	3732	tags=37%, list=19%, signal=46%
REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	26	-0.39624	-0.92336	0.5767285	0.78795546	1	3181	tags=23%, list=16%, signal=28%
REACTOME_SIGNALLING_TO_ERKS	35	-0.36988	-0.92095	0.5869565	0.79149157	1	1524	tags=17%, list=8%, signal=19%
BIOCARTA_PTDINS_PATHWAY	23	-0.40606	-0.91935	0.5763889	0.79309994	1	3293	tags=26%, list=17%, signal=31%
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	27	-0.38689	-0.9182	0.5833333	0.79368114	1	2340	tags=22%, list=12%, signal=25%
REACTOME_BOTULINUM_NEUROTOXICITY	18	-0.41906	-0.91777	0.53417265	0.79271364	1	2497	tags=22%, list=13%, signal=25%
REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	20	-0.41554	-0.91366	0.5885417	0.7998652	1	1932	tags=15%, list=10%, signal=17%
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	86	-0.31574	-0.91218	0.62852895	0.8012333	1	4714	tags=47%, list=24%, signal=61%
BIOCARTA_DEATH_PATHWAY	33	-0.36682	-0.91048	0.5852459	0.8029996	1	3245	tags=24%, list=17%, signal=29%
REACTOME_ION_CHANNEL_TRANSPORT	53	-0.3457	-0.91012	0.6061093	0.80190223	1	2600	tags=19%, list=13%, signal=22%
KEGG_OTHER_GLYCAN_DEGRADATION	16	-0.42187	-0.90802	0.6076642	0.8046742	1	4871	tags=44%, list=25%, signal=58%
REACTOME_SIGNALLING_TO_RAS	27	-0.38307	-0.90792	0.57876104	0.8029504	1	1418	tags=15%, list=7%, signal=16%
REACTOME_CELL_CELL_COMMUNICATION	118	-0.30147	-0.90175	0.6704708	0.814687	1	2421	tags=18%, list=13%, signal=20%
REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	25	-0.38153	-0.90135	0.61669505	0.8136744	1	1509	tags=12%, list=8%, signal=13%
REACTOME_SYNTHESIS_OF_DNA	84	-0.31635	-0.90135	0.6432836	0.8117498	1	852	tags=8%, list=4%, signal=9%
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	28	-0.36993	-0.9011	0.60583943	0.81035864	1	4262	tags=54%, list=22%, signal=69%
REACTOME_SIGNALING_BY_NOTCH	99	-0.30641	-0.89705	0.6706056	0.81760097	1	2038	tags=12%, list=11%, signal=13%
BIOCARTA_AGR_PATHWAY	36	-0.35651	-0.89636	0.6143791	0.817105	1	2085	tags=22%, list=11%, signal=25%
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	49	-0.33816	-0.89399	0.65008295	0.82043767	1	2466	tags=10%, list=13%, signal=12%
KEGG_LONG_TERM_DEPRESSION	64	-0.32751	-0.89258	0.64777946	0.8216702	1	1830	tags=16%, list=9%, signal=17%
REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR	97	-0.31125	-0.89155	0.67	0.8220171	1	2673	tags=20%, list=14%, signal=23%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	26	-0.37793	-0.89133	0.61646235	0.8205685	1	4756	tags=46%, list=25%, signal=61%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	-0.39244	-0.88817	0.6263538	0.82571125	1	4693	tags=45%, list=24%, signal=60%
KEGG_STEROID_BIOSYNTHESIS	16	-0.40466	-0.88177	0.59778595	0.8376459	1	2698	tags=19%, list=14%, signal=22%
REACTOME_SIGNALING_BY_ERBB4	86	-0.30552	-0.88073	0.69185185	0.8378848	1	3152	tags=16%, list=16%, signal=19%
REACTOME_GABA_RECEPTOR_ACTIVATION	51	-0.33842	-0.87958	0.6613924	0.8384876	1	3374	tags=27%, list=17%, signal=33%
REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPORTERS	16	-0.41592	-0.87822	0.64363635	0.83949834	1	3181	tags=25%, list=16%, signal=30%
REACTOME_MEMBRANE_TRAFFICKING	125	-0.28892	-0.87608	0.7452693	0.84203553	1	2930	tags=14%, list=15%, signal=17%
KEGG_PPAR_SIGNALING_PATHWAY	68	-0.31356	-0.87572	0.6842878	0.84082204	1	2739	tags=18%, list=14%, signal=20%
REACTOME_SPHINGOLIPID_METABOLISM	62	-0.3181	-0.87293	0.6697966	0.84475327	1	2799	tags=21%, list=14%, signal=24%
KEGG_NON_SMALL_CELL_LUNG_CANCER	54	-0.32998	-0.87288	0.64763457	0.842946	1	1418	tags=13%, list=7%, signal=14%
BIOCARTA_IGF1R_PATHWAY	23	-0.37774	-0.87001	0.64223385	0.8469804	1	1418	tags=13%, list=7%, signal=14%
KEGG_RNA_DEGRADATION	57	-0.31804	-0.86279	0.71755725	0.86032057	1	1224	tags=11%, list=6%, signal=11%

REACTOME_NCAM1_INTERACTIONS	39	-0.34344	-0.86214	0.6672326	0.85972756	1	4697	tags=49%, list=24%, signal=64%
BIOCARTA_TNFR1_PATHWAY	29	-0.35561	-0.86062	0.6903973	0.86088467	1	137	tags=3%, list=1%, signal=3%
REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	19	-0.38629	-0.85795	0.638448	0.8645512	1	1669	tags=16%, list=9%, signal=17%
REACTOME_METAL_ION_SLC_TRANSPORTERS	22	-0.37986	-0.85794	0.66603774	0.8626386	1	3635	tags=36%, list=19%, signal=45%
REACTOME_SIGNALING_BY_ERBB2	97	-0.29437	-0.85455	0.743553	0.8678439	1	2673	tags=20%, list=14%, signal=23%
REACTOME_SIGNALING_BY_BMP	22	-0.37253	-0.85006	0.66488415	0.8751827	1	2639	tags=23%, list=14%, signal=26%
BIOCARTA_PPARA_PATHWAY	57	-0.31447	-0.849	0.7269985	0.8752869	1	2375	tags=16%, list=12%, signal=18%
REACTOME_SIGNALING_BY_FGFR	108	-0.28634	-0.8478	0.77648765	0.875675	1	3464	tags=22%, list=18%, signal=27%
KEGG_NOTCH_SIGNALING_PATHWAY	47	-0.32044	-0.84663	0.73021	0.8761328	1	2038	tags=13%, list=11%, signal=14%
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	17	-0.39223	-0.84384	0.693032	0.87996256	1	3732	tags=41%, list=19%, signal=51%
REACTOME_EICOSANOID_LIGAND_BINDING_RECEPTORS	15	-0.40121	-0.8425	0.65555555	0.88078606	1	1832	tags=33%, list=9%, signal=37%
REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	19	-0.38722	-0.8423	0.6893382	0.87920743	1	2467	tags=26%, list=13%, signal=30%
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIV ATED_HUMAN_TAK1	16	-0.39571	-0.83961	0.6912879	0.882498	1	1043	tags=13%, list=5%, signal=13%
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	53	-0.31417	-0.83959	0.74390244	0.88059974	1	2338	tags=15%, list=12%, signal=17%
REACTOME_METABOLISM_OF_RNA	253	-0.26045	-0.83933	0.86107635	0.8791593	1	1404	tags=7%, list=7%, signal=8%
REACTOME_METABOLISM_OF_CARBOHYDRATES	234	-0.26229	-0.83649	0.86895674	0.88290745	1	3169	tags=20%, list=16%, signal=23%
KEGG_TIGHT_JUNCTION	132	-0.27641	-0.83491	0.8134864	0.8843102	1	2943	tags=23%, list=15%, signal=27%
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	33	-0.34192	-0.83439	0.71896553	0.8833936	1	3988	tags=36%, list=21%, signal=46%
REACTOME_GAP_JUNCTION_ASSEMBLY	17	-0.39056	-0.83265	0.6898496	0.8847223	1	2719	tags=18%, list=14%, signal=21%
REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	38	-0.33013	-0.8315	0.7350993	0.8850418	1	1721	tags=8%, list=9%, signal=9%
REACTOME_PHOSPHOLIPID_METABOLISM	189	-0.26503	-0.83128	0.8443038	0.883497	1	2799	tags=17%, list=14%, signal=20%
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	31	-0.35074	-0.82906	0.716263	0.8856862	1	2062	tags=16%, list=11%, signal=18%
REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	33	-0.33912	-0.8272	0.7358804	0.8872433	1	2234	tags=18%, list=12%, signal=21%
BIOCARTA_VEGF_PATHWAY	29	-0.34675	-0.82593	0.7239583	0.8877883	1	2527	tags=21%, list=13%, signal=24%
KEGG_VEGF_SIGNALING_PATHWAY	72	-0.29232	-0.82375	0.8026101	0.89001334	1	1760	tags=15%, list=9%, signal=17%
KEGG_PEROXISOME	77	-0.29061	-0.82254	0.80505955	0.8903713	1	2299	tags=14%, list=12%, signal=16%
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	44	-0.3152	-0.82071	0.7575251	0.89173585	1	2561	tags=18%, list=13%, signal=21%
KEGG_DORSO_VENTRAL_AXIS_FORMATION	24	-0.35542	-0.81685	0.7225131	0.8971873	1	1842	tags=17%, list=10%, signal=18%
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	33	-0.32991	-0.81517	0.7447496	0.8983627	1	1967	tags=15%, list=10%, signal=17%
KEGG_OLFACTORY_TRANSDUCTION	118	-0.27125	-0.81487	0.8628258	0.8969892	1	3490	tags=14%, list=18%, signal=16%
REACTOME_GLYCOSPHINGOLIPID_METABOLISM	37	-0.3207	-0.81416	0.7389771	0.8964723	1	3164	tags=30%, list=16%, signal=35%
REACTOME_GAB1_SIGNALOSOME	36	-0.32246	-0.80998	0.7746711	0.90221566	1	2607	tags=14%, list=13%, signal=16%
KEGG_ARACHIDONIC_ACID_METABOLISM	52	-0.30446	-0.80746	0.7792	0.9047429	1	2032	tags=15%, list=11%, signal=17%
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	47	-0.3154	-0.80621	0.79008263	0.90507406	1	3547	tags=28%, list=18%, signal=34%
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	19	-0.36635	-0.80204	0.76132405	0.9108608	1	501	tags=5%, list=3%, signal=5%
REACTOME_IRON_UPTAKE_AND_TRANSPORT	35	-0.32017	-0.80016	0.78849405	0.9123846	1	3870	tags=31%, list=20%, signal=39%
KEGG_SMALL_CELL_LUNG_CANCER	84	-0.27973	-0.79791	0.8502994	0.91427726	1	3421	tags=21%, list=18%, signal=26%
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AN D_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	57	-0.29947	-0.79762	0.8097484	0.91288483	1	2530	tags=11%, list=13%, signal=12%
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	31	-0.32531	-0.79609	0.75382006	0.9135153	1	1979	tags=19%, list=10%, signal=22%
BIOCARTA_MPR_PATHWAY	34	-0.32125	-0.79345	0.7893836	0.9161346	1	4723	tags=29%, list=24%, signal=39%
REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	51	-0.29534	-0.77929	0.83307576	0.93805486	1	3259	tags=24%, list=17%, signal=28%
BIOCARTA_SPRY_PATHWAY	18	-0.35646	-0.77915	0.7788104	0.9363085	1	4723	tags=44%, list=24%, signal=59%
REACTOME_SIGNAL_TRANSDUCTION_BY_L1	34	-0.31256	-0.7777	0.80690736	0.9367625	1	3014	tags=21%, list=16%, signal=24%
KEGG_P53_SIGNALING_PATHWAY	67	-0.27603	-0.77461	0.8946541	0.9397649	1	2659	tags=19%, list=14%, signal=22%
REACTOME_TIE2_SIGNALING	17	-0.36146	-0.77438	0.7714808	0.938198	1	1253	tags=18%, list=6%, signal=19%
REACTOME_COLLAGEN_FORMATION	58	-0.28888	-0.77262	0.8520249	0.9389126	1	5661	tags=59%, list=29%, signal=83%
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	44	-0.29951	-0.77164	0.8309179	0.9384914	1	2759	tags=20%, list=14%, signal=24%
REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	59	-0.28516	-0.77098	0.8605769	0.9376244	1	4589	tags=32%, list=24%, signal=42%
KEGG_ETHER_LIPID_METABOLISM	29	-0.31945	-0.76902	0.80213904	0.93868595	1	2656	tags=21%, list=14%, signal=24%
KEGG_MELANOGENESIS	101	-0.25954	-0.76259	0.90603083	0.9464696	1	2673	tags=19%, list=14%, signal=22%
REACTOME_PKB_MEDIATED_EVENTS	28	-0.31988	-0.75942	0.81803006	0.94912356	1	2171	tags=11%, list=11%, signal=12%
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	25	-0.32541	-0.75544	0.8158784	0.9528494	1	1669	tags=16%, list=9%, signal=17%
KEGG_TYROSINE_METABOLISM	42	-0.29166	-0.75381	0.8592965	0.9532121	1	1738	tags=17%, list=9%, signal=18%
KEGG_RIBOSOME	87	-0.25721	-0.74144	0.92444444	0.96795696	1	4274	tags=20%, list=22%, signal=25%
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	25	-0.31605	-0.73705	0.8448276	0.9716282	1	1979	tags=16%, list=10%, signal=18%
REACTOME_EGFR_DOWNREGULATION	24	-0.31912	-0.73209	0.8428835	0.97604215	1	3014	tags=21%, list=16%, signal=25%
REACTOME_PEPTIDE_CHAIN_ELONGATION	86	-0.25354	-0.7264	0.94345236	0.9809963	1	4274	tags=17%, list=22%, signal=22%
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	67	-0.25996	-0.72525	0.9323077	0.9803565	1	3870	tags=25%, list=20%, signal=32%
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	24	-0.30767	-0.71985	0.87068963	0.9845443	1	1737	tags=13%, list=9%, signal=14%
REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	15	-0.34428	-0.71956	0.8485981	0.9828752	1	3312	tags=33%, list=17%, signal=40%
BIOCARTA_STRESS_PATHWAY	25	-0.30837	-0.71812	0.8691099	0.98245335	1	3473	tags=16%, list=18%, signal=19%
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	43	-0.27887	-0.71588	0.8912	0.9828526	1	2769	tags=21%, list=14%, signal=24%
REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMATE_BINDING_AND_ACTIVATION	15	-0.34142	-0.71222	0.81395346	0.9846603	1	3994	tags=40%, list=21%, signal=50%
REACTOME_SIGNALING_BY_FGFR_MUTANTS	42	-0.27738	-0.71084	0.92087543	0.98411727	1	3377	tags=26%, list=17%, signal=32%
KEGG_PYRUVATE_METABOLISM	40	-0.27677	-0.70434	0.9253247	0.9887999	1	1465	tags=10%, list=8%, signal=11%
REACTOME_L1CAM_INTERACTIONS	84	-0.24668	-0.69905	0.9710145	0.9919589	1	3749	tags=25%, list=19%, signal=31%
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	34	-0.28215	-0.69829	0.9221658	0.9907497	1	876	tags=6%, list=5%, signal=6%
REACTOME_SIGNALING_BY_HIPPO	18	-0.32312	-0.69581	0.8786765	0.9909677	1	4132	tags=39%, list=21%, signal=49%
REACTOME_MRNA_3_END_PROCESSING	25	-0.29413	-0.68934	0.92805755	0.994676	1	299	tags=4%, list=2%, signal=4%
REACTOME_SIGNALING_BY_NOTCH1	68	-0.25083	-0.68801	0.951952	0.9938265	1	3088	tags=16%, list=16%, signal=19%
KEGG_CARDIAC_MUSCLE_CONTRACTION	73	-0.24776	-0.68661	0.96520424	0.99308455	1	2865	tags=21%, list=15%, signal=24%
BIOCARTA_RACCYCD_PATHWAY	26	-0.29388	-0.68545	0.9070175	0.9921643	1	1418	tags=12%, list=7%, signal=12%
REACTOME_GLOBAL_GENOMIC_NER_GG_NER	33	-0.27767	-0.685	0.9313894	0.9906309	1	2504	tags=12%, list=13%, signal=14%
KEGG_SPHINGOLIPID_METABOLISM	39	-0.27233	-0.68375	0.94262296	0.98983693	1	1573	tags=13%, list=8%, signal=14%
REACTOME_PROTEIN_FOLDING	49	-0.25577	-0.68278	0.9350238	0.9887805	1	2320	tags=10%, list=12%, signal=12%
REACTOME_METABOLISM_OF_NUCLEOTIDES	71	-0.2451	-0.6765	0.9666161	0.99178255	1	3630	tags=23%, list=19%, signal=28%
KEGG_OOCYTE_MEIOSIS	111	-0.22513	-0.67646	0.9941945	0.98988813	1	3187	tags=18%, list=16%, signal=21%
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_DIFFERENTIATION	72	-0.23714	-0.66306	0.9836553	0.99761534	1	2726	tags=13%, list=14%, signal=14%
REACTOME_HS_GAG_BIOSYNTHESIS	30	-0.27677	-0.66016	0.9274874	0.99752676	1	3169	tags=30%, list=16%, signal=36%
REACTOME_DARPP_32_EVENTS	24	-0.28861	-0.65682	0.9362832	0.9977627	1	3988	tags=29%, list=21%, signal=37%
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	106	-0.22253	-0.65512	0.99158484	0.99693424	1	2622	tags=10%, list=14%, signal=12%
REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING	36	-0.26278	-0.65389	0.9433657	0.9957696	1	2607	tags=14%, list=13%, signal=16%
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	15	-0.3089	-0.64915	0.92	0.9967483	1	3732	tags=33%, list=19%, signal=41%
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	30	-0.26147	-0.63981	0.9567474	0.99988985	1	2445	tags=17%, list=13%, signal=19%
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	22	-0.28346	-0.63642	0.9365942	0.9997659	1	2050	tags=9%, list=11%, signal=10%
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	40	-0.24818	-0.63457	0.96935487	0.99879885	1	1803	tags=10%, list=9%, signal=11%
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	105	-0.21132	-0.62576	0.997093	1	1	4274	tags=18%, list=22%, signal=23%
REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	52	-0.23355	-0.6206	0.9793978	1	1	4589	tags=29%, list=24%, signal=38%
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	24	-0.26434	-0.61629	0.9494774	1	1	2662	tags=17%, list=14%, signal=19%
REACTOME_RNA_POL_I_TRANSCRIPTION_INITIATION	24	-0.26641	-0.61426	0.9534483	1	1	2504	tags=17%, list=13%, signal=19%
REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFATASE_AC TIVATION	26	-0.2503	-0.58873	0.97815126	1	1	3022	tags=23%, list=16%, signal=27%
BIOCARTA_NDKDYNAMIN_PATHWAY	18	-0.26502	-0.58724	0.95729536	1	1	2821	tags=28%, list=15%, signal=32%
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	21	-0.2644	-0.58091	0.96276593	1	1	2274	tags=14%, list=12%, signal=16%
REACTOME_ENOS_ACTIVATION_AND_REGULATION	19	-0.258	-0.57596	0.97307	1	1	2062	tags=16%, list=11%, signal=18%
REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	15	-0.26677	-0.56081	0.96461827	1	1	2072	tags=13%, list=11%, signal=15%
REACTOME_INSULIN_RECEPTOR_RECYCLING	22	-0.23593	-0.54501	0.9929701	1	1	3870	tags=32%, list=20%, signal=40%
REACTOME_PI3K_CASCADE	68	-0.19414	-0.54125	0.9985119	1	1	3377	tags=16%, list=17%, signal=20%
REACTOME_RECYCLING_PATHWAY_OF_L1	27	-0.23218	-0.54069	0.9896194	1	1	4723	tags=33%, list=24%, signal=44%
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	-0.24859	-0.53439	0.9873188	1	1	2761	tags=18%, list=14%, signal=21%
REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	27	-0.22191	-0.52206	0.9896194	1	1	2607	tags=11%, list=13%, signal=13%
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	16	-0.24537	-0.51852	0.979206	1	1	2761	tags=19%, list=14%, signal=22%
REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDATION_IN_MUSCLE	18	-0.22866	-0.50246	0.99813783	1	1	5797	tags=56%, list=30%, signal=79%
BIOCARTA_CK1_PATHWAY	17	-0.2326	-0.49618	0.9860384	0.9996151	1	4441	tags=29%, list=23%, signal=38%
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	19	-0.22022	-0.4859	0.9908925	0.99848694	1	2761	tags=16%, list=14%, signal=18%
REACTOME_OLFACTORY_SIGNALING_PATHWAY	80	-0.16243	-0.46205	1	0.9979781	1	3427	tags=10%, list=18%, signal=12%

Table S18
GSEA Analysis on TCGA HNSC comparing tumors with or without 9p loss, Pathways Enriched

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX
REACTOME_TIGHT_JUNCTION_INTERACTIONS	29	0.744469	1.990204	0	0.005779869	0.007	2678
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM	17	0.772985	1.820285	0	0.07345401	0.162	2072
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION	16	0.754271	1.804531	0.002227172	0.064499	0.212	1989
KEGG_PENTOSE_PHOSPHATE_PATHWAY	27	0.671001	1.754012	0	0.10669811	0.397	498
REACTOME_G2_M_CHECKPOINTS	35	0.592935	1.636803	0.002518892	0.36997345	0.89	4758
REACTOME_G0_AND_EARLY_G1	23	0.643359	1.622941	0.011961723	0.3564944	0.922	3403
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	24	0.635988	1.619449	0.018561484	0.3149564	0.927	5191
REACTOME_CHROMOSOME_MAINTENANCE	113	0.470117	1.608263	0.003436426	0.31060007	0.947	6314
KEGG_STEROID_HORMONE_BIOSYNTHESIS	53	0.538139	1.606151	0.002906977	0.28188443	0.951	3107
REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	56	0.523243	1.58059	0.007874016	0.33056882	0.981	3159
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTRO MERE	57	0.513974	1.554163	0.014705882	0.38473693	0.995	6043
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	27	0.599734	1.551954	0.024813896	0.36081663	0.995	2581
REACTOME_TELOMERE_MAINTENANCE	72	0.494805	1.54986	0.005882353	0.3394294	0.995	6043
REACTOME_DNA_STRAND_ELONGATION	30	0.578035	1.540739	0.019900497	0.34447914	0.998	6617
KEGG_BASAL_CELL_CARCINOMA	55	0.509389	1.533305	0.005524862	0.34387925	0.999	3455
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	44	0.529691	1.510558	0.016304348	0.39402822	0.999	2261
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	342	0.388317	1.509678	0	0.373362	0.999	5195
REACTOME_MITOTIC_PROMETAPHASE	85	0.458019	1.505124	0.003076923	0.3665125	0.999	4978
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	38	0.525139	1.49041	0.027363185	0.39108586	0.999	4736
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	29	0.560934	1.489218	0.041162226	0.37520856	1	4758
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	27	0.564765	1.484658	0.02955665	0.37173638	1	3302
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	27	0.564175	1.483022	0.024449877	0.35974577	1	1911
REACTOME_REGULATORY_RNA_PATHWAYS	24	0.569636	1.468085	0.050808314	0.38389334	1	5000
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	68	0.471634	1.451819	0.017910447	0.41597393	1	3298
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	64	0.46992	1.451584	0.022151899	0.40008813	1	6994
KEGG_NITROGEN_METABOLISM	23	0.570332	1.451303	0.055155877	0.38550952	1	609
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	24	0.567412	1.448607	0.057077624	0.37942195	1	2581
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	44	0.501236	1.445079	0.033613447	0.37668124	1	4406
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	16	0.616578	1.438762	0.06888361	0.38217095	1	3052
REACTOME_MICRORNA_MIRNA_BIOGENESIS	21	0.577986	1.436202	0.059496567	0.37645003	1	4953
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	101	0.421926	1.434335	0.006849315	0.3695635	1	4551
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	73	0.452898	1.422202	0.009036144	0.38855878	1	1624
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	25	0.552229	1.417456	0.052109182	0.39005306	1	2244
REACTOME_PACKAGING_OF_TELOMERE_ENDS	45	0.48476	1.403306	0.055263158	0.4174984	1	6043
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	27	0.526827	1.400447	0.075566754	0.41343737	1	3302
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	27	0.538892	1.382722	0.08728179	0.4532529	1	3302
REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS	81	0.425247	1.381851	0.032352943	0.44370967	1	1487
KEGG_SPLICEOSOME	114	0.395888	1.372023	0.027874565	0.46206927	1	6440
REACTOME_EXTENSION_OF_TELOMERES	27	0.535793	1.370199	0.0775	0.45532677	1	5621
KEGG_DNA_REPLICATION	36	0.487688	1.367819	0.050377835	0.45065007	1	4758
REACTOME_SIGNALING_BY_NODAL	18	0.565818	1.366919	0.06960557	0.44248798	1	2321
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCR IPT	33	0.49558	1.365701	0.0952381	0.43524164	1	3525
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	52	0.451442	1.359278	0.051212937	0.4426986	1	3978
REACTOME_FORMATION_OF_TRANSCRIPTION_COUPLED_NER_TC_NER_REPAIR_COMPLEX	29	0.506592	1.359012	0.085642315	0.4334041	1	4406
REACTOME_GLYCOLYSIS	27	0.525602	1.356746	0.0890411	0.43015242	1	3064
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION	21	0.54133	1.352144	0.10514019	0.43338698	1	3066
REACTOME_MEIOSIS	105	0.398394	1.347094	0.03642384	0.43827873	1	4792
REACTOME_GLUCONEOGENESIS	31	0.510309	1.344982	0.087765954	0.4344647	1	3497
REACTOME_CELL_CYCLE	383	0.348901	1.342342	0	0.43278584	1	3449
REACTOME_MRNA_CAPPING	29	0.495742	1.335254	0.09466019	0.4438303	1	4406
BIOCARTA_PROTEASOME_PATHWAY	28	0.507821	1.333742	0.096244134	0.43911052	1	3924
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROT EINS	26	0.510817	1.331693	0.121559635	0.43596074	1	2244
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	22	0.529485	1.331193	0.11709602	0.42918408	1	1911
REACTOME_MEIOTIC_SYNAPSIS	68	0.413451	1.317808	0.036516853	0.4570916	1	6272
KEGG_HOMOLOGOUS_RECOMBINATION	26	0.495414	1.315251	0.08292683	0.45556173	1	4758
KEGG_LYSINE_DEGRADATION	44	0.448461	1.310573	0.072386056	0.4601787	1	2513
KEGG_CELL_CYCLE	118	0.382232	1.308353	0.046428572	0.4581629	1	3236
REACTOME_LAGGING_STRAND_SYNTHESIS	19	0.539117	1.307171	0.10933941	0.45358637	1	6314
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	59	0.428268	1.304326	0.06534091	0.45397985	1	3978
REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_ACTIVITY_BY_INSULIN _LIKE_GROWTH_FACTOR_BINDING_PROTEINS_IGFBPS	16	0.554565	1.293414	0.1670282	0.47628373	1	995
KEGG_PROTEIN_EXPORT	23	0.51472	1.286959	0.14460784	0.48619547	1	4075
REACTOME_MEIOTIC_RECOMBINATION	77	0.391311	1.27459	0.08580858	0.51301116	1	6043
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	32	0.467966	1.273838	0.123222746	0.5069786	1	2081
KEGG_SELENOAMINO_ACID_METABOLISM	26	0.496606	1.273712	0.1632653	0.49942473	1	2835
REACTOME_CELL_CYCLE_MITOTIC	297	0.333541	1.272762	0.01875	0.49444774	1	3449
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	43	0.432903	1.271266	0.13279133	0.4910057	1	4492
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	40	0.441022	1.268302	0.13402061	0.49203792	1	4406
KEGG_HUNTINGTONS_DISEASE	171	0.3474	1.263819	0.035433073	0.49631965	1	6222
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC _COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	80	0.387381	1.25821	0.08219178	0.5045358	1	7307
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	194	0.348618	1.25726	0.03524229	0.49985874	1	1786
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	59	0.401989	1.254399	0.1184573	0.50049335	1	4492
REACTOME_RNA_POL_I_PROMOTER_OPENING	55	0.409388	1.253909	0.10985915	0.49480057	1	6043
REACTOME_CELL_JUNCTION_ORGANIZATION	77	0.391752	1.249594	0.08637874	0.49944216	1	2678
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	0.404384	1.237569	0.13235295	0.5257196	1	3116
KEGG_PROPANOATE_METABOLISM	32	0.458385	1.235043	0.15085158	0.52609235	1	2642
REACTOME_UNFOLDED_PROTEIN_RESPONSE	76	0.382918	1.234179	0.109467454	0.52139395	1	5260
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	27	0.466655	1.231966	0.18588236	0.5206718	1	3303
REACTOME_METABOLISM_OF_POLYAMINES	15	0.544115	1.23108	0.19058296	0.5164101	1	863
REACTOME_BASE_EXCISION_REPAIR	19	0.507749	1.228468	0.20422535	0.5169191	1	5621
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	44	0.418758	1.225326	0.15789473	0.5189514	1	1609
KEGG_RETINOL_METABOLISM	63	0.394028	1.224087	0.15406163	0.5156455	1	3107
REACTOME_DNA_REPAIR	105	0.362235	1.218511	0.10410095	0.524834	1	4927
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	126	0.347566	1.215245	0.061594203	0.5279289	1	5339
REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLA CEMENT_PATHWAY	17	0.509374	1.213993	0.21609196	0.5249476	1	5621
REACTOME_ACYL_CHAIN_REMODELLING_OF_PE	20	0.503063	1.213893	0.23058252	0.51892704	1	3329
KEGG_OXIDATIVE_PHOSPHORYLATION	115	0.356955	1.213812	0.09057971	0.513168	1	5779
REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY	19	0.504338	1.205789	0.22168675	0.52926254	1	3195
REACTOME_ELONGATION_ARREST_AND_RECOVERY	31	0.445456	1.197419	0.1925	0.5453977	1	4492
REACTOME_MRNA_PROCESSING	146	0.337529	1.195317	0.08949416	0.54487246	1	4426
REACTOME_MITOTIC_G2_G2_M_PHASES	74	0.376253	1.184525	0.13953489	0.5678652	1	3978
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	43	0.402855	1.175429	0.17369728	0.5875978	1	1089
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	34	0.42784	1.175268	0.2141058	0.5816419	1	863
REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION	22	0.468084	1.167145	0.23222749	0.59814787	1	2698
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	86	0.359569	1.160832	0.1572327	0.6096992	1	1259

BIOCARTA_P53_PATHWAY	16	0.498629	1.160097	0.25438598	0.6052775	1	3052
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	32	0.424128	1.151165	0.24878049	0.6257995	1	3913
REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	15	0.509374	1.138852	0.28117913	0.6563644	1	5621
REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	16	0.482899	1.135183	0.29816514	0.6611266	1	3052
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	49	0.380104	1.131793	0.24736843	0.66524714	1	4834
KEGG_BASAL_TRANSCRIPTION_FACTORS	34	0.413228	1.129502	0.27664974	0.6657761	1	5014
REACTOME_FORMATION_OF_THE_HIV1_EARLY_ELONGATION_COMPLEX	33	0.408307	1.125877	0.2542373	0.67047995	1	4492
REACTOME_XENOBIOTICS	15	0.486943	1.124997	0.30866808	0.6666722	1	6678
REACTOME_PHASE_II_CONJUGATION	66	0.358581	1.124717	0.23876405	0.661171	1	2581
REACTOME_ACYL_CHAIN_REMODELLING_OF_PC	21	0.452965	1.124669	0.2809524	0.6549925	1	3329
REACTOME_SYNTHESIS_OF_PC	18	0.473533	1.121387	0.29017857	0.6583885	1	3480
REACTOME_GLUCURONIDATION	17	0.475855	1.120457	0.31042653	0.6548902	1	2581
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	28	0.419382	1.11529	0.2880562	0.6637588	1	709
REACTOME_GLUCOSE_TRANSPORT	38	0.394369	1.112752	0.28133705	0.6650571	1	4020
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	27	0.424622	1.111834	0.297561	0.66151386	1	5186
REACTOME_METABOLISM_OF_NON_CODING_RNA	47	0.369424	1.111236	0.25721785	0.65725917	1	3688
REACTOME_TRANSCRIPTION	190	0.303531	1.106215	0.17167382	0.6660766	1	6054
REACTOME_DIABETES_PATHWAYS	128	0.31322	1.099687	0.22743683	0.6792083	1	3822
REACTOME_DNA_REPLICATION	181	0.304012	1.098963	0.16751269	0.67532194	1	4978
REACTOME_REGULATION_OF_HYPOXIA_INDUCIBLE_FACTOR_HIF_BY_OXYGEN	23	0.433352	1.097669	0.33169532	0.6730995	1	3193
KEGG_TASTE_TRANSDUCTION	44	0.368503	1.096223	0.28607595	0.671238	1	5188
KEGG_ARGININE_AND_PROLINE_METABOLISM	54	0.364787	1.088569	0.28198433	0.6884457	1	2925
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	31	0.398347	1.081509	0.3385013	0.703489	1	471
REACTOME_EICOSANOID_LIGAND_BINDING_RECEPTORS	15	0.481041	1.07589	0.36123347	0.7143605	1	0
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	25	0.415199	1.068972	0.35391924	0.7288076	1	3454
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_2_PROMOTER	23	0.419298	1.068591	0.34068626	0.7238975	1	4406
REACTOME_RNA_POL_I_TRANSCRIPTION	80	0.333346	1.06784	0.292517	0.7201482	1	6043
BIOCARTA_AMI_PATHWAY	20	0.4361	1.062654	0.38495576	0.7301452	1	1259
REACTOME_BIOLOGICAL_OXIDATIONS	133	0.30272	1.061914	0.30291972	0.7264611	1	3298
REACTOME_OXYGEN_DEPENDENT_PROLINE_HYDROXYLATION_OF_HYPOXIA_INDUCIBLE_FACTOR_ALPHA	16	0.454593	1.060467	0.3696145	0.7250355	1	122
KEGG_BASE_EXCISION_REPAIR	33	0.395671	1.059627	0.3641161	0.72178364	1	4312
REACTOME_MITOTIC_G1_G1_S_PHASES	124	0.302284	1.05884	0.29166666	0.71828187	1	3449
REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	52	0.353335	1.058677	0.328	0.7130874	1	4209
BIOCARTA_TEL_PATHWAY	18	0.442547	1.05806	0.38530067	0.7094418	1	5040
CANCER-TESTIS-ANTIGEN	181	0.291198	1.057468	0.27391306	0.70584095	1	3297
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	113	0.309121	1.054978	0.28125	0.70800716	1	6043
REACTOME_MRNA_SPLICING	97	0.315989	1.052909	0.31864408	0.70851976	1	4736
BIOCARTA_MITOCHONDRIA_PATHWAY	21	0.421195	1.051973	0.36533958	0.7058145	1	2371
REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT	23	0.404627	1.042317	0.38340807	0.7300632	1	4492
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	34	0.387352	1.041426	0.37823835	0.72719455	1	1621
REACTOME_ACTIVATED_POINT_MUTANTS_OF_FGFR2	16	0.442842	1.039995	0.38105726	0.7262017	1	1887
KEGG_BUTANOATE_METABOLISM	33	0.376909	1.036567	0.4	0.7311825	1	2563
REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	18	0.434887	1.030435	0.42572063	0.7442996	1	1911
REACTOME_RNA_POL_II_TRANSCRIPTION	93	0.309598	1.029647	0.36363637	0.74141645	1	4603
REACTOME_MITOTIC_M_M_G1_PHASES	161	0.286625	1.028148	0.356	0.7405512	1	4878
REACTOME_HS_GAG_DEGRADATION	20	0.415496	1.022314	0.42890996	0.75293446	1	1151
REACTOME_PERK_REGULATED_GENE_EXPRESSION	27	0.396599	1.017121	0.42959428	0.762969	1	3689
REACTOME_SHC_MEDIATED_CASCADE	28	0.39188	1.012554	0.42079207	0.77165455	1	2705
REACTOME_HIV_LIFE_CYCLE	114	0.292255	1.012313	0.4219858	0.7670901	1	4551
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	62	0.325021	1.010487	0.4224138	0.7673913	1	3064
REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI	17	0.432357	1.008101	0.44956142	0.76951927	1	5146
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	23	0.402055	1.000032	0.46853146	0.78857654	1	1857
REACTOME_COLLAGEN_FORMATION	58	0.326608	0.999177	0.43681318	0.7858907	1	1259
REACTOME_SIGNALING_BY_ROBO_RECEPTOR	29	0.373237	0.997076	0.42092457	0.7869743	1	3151
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	34	0.365623	0.996021	0.45360824	0.7848939	1	754
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	60	0.31985	0.994718	0.4570637	0.7837735	1	3454
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	116	0.289213	0.994178	0.4377224	0.7803863	1	5434
KEGG_WNT_SIGNALING_PATHWAY	150	0.274418	0.992862	0.48165137	0.77932763	1	2060
BIOCARTA_HIF_PATHWAY	15	0.428567	0.992227	0.475162	0.7761364	1	3886
REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING	36	0.353624	0.986051	0.48387095	0.789064	1	5085
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	24	0.385663	0.986046	0.43822843	0.7839888	1	2523
REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	16	0.420319	0.982688	0.47865167	0.7888228	1	2232
BIOCARTA_G2_PATHWAY	24	0.382497	0.979773	0.4648526	0.79233956	1	2297
REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS	84	0.297055	0.978795	0.5	0.790272	1	3455
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	49	0.32987	0.97875	0.49739584	0.78545034	1	5557
BIOCARTA_MTA3_PATHWAY	19	0.403958	0.977572	0.49881235	0.78406703	1	2861
REACTOME_FRS2_MEDIATED_CASCADE	36	0.342776	0.972825	0.495	0.7933777	1	4473
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	70	0.302006	0.972159	0.49853373	0.79055154	1	3298
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	36	0.346814	0.958524	0.5108108	0.82492536	1	3454
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	21	0.381987	0.956026	0.54126215	0.8276218	1	5433
KEGG_GLYCEROLIPID_METABOLISM	46	0.323655	0.955341	0.5322129	0.82457787	1	738
REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	15	0.421576	0.955314	0.5112613	0.81969064	1	4366
KEGG_LINOLEIC_ACID_METABOLISM	25	0.361673	0.949713	0.5113636	0.8313427	1	2544
KEGG_RNA_POLYMERASE	29	0.362615	0.939144	0.5620438	0.8571947	1	4406
BIOCARTA_WNT_PATHWAY	26	0.364475	0.936769	0.5547786	0.8590811	1	1633
KEGG_O_GLYCAN_BIOSYNTHESIS	29	0.344952	0.931148	0.5616798	0.87120837	1	3971
REACTOME_SULFUR_AMINO_ACID_METABOLISM	24	0.367656	0.922133	0.5867347	0.8929253	1	1364
BIOCARTA_CELLCYCLE_PATHWAY	23	0.365613	0.921159	0.569378	0.8907336	1	3163
REACTOME_NCAM1_INTERACTIONS	39	0.317753	0.920723	0.5775	0.8869109	1	1259
REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION_INDEPENDENT_DOUBLE_STRAND_BREAKS	16	0.386723	0.911633	0.57236844	0.9084052	1	59
REACTOME_RNA_POL_III_TRANSCRIPTION	33	0.325866	0.902181	0.6265664	0.92992073	1	4406
REACTOME_SYNTHESIS_OF_PA	26	0.352203	0.901481	0.6271605	0.9267157	1	1410
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	179	0.252157	0.900406	0.82464457	0.9244282	1	3980
REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_AND_AMINE_COMPOUNDS	88	0.271652	0.899739	0.70858896	0.92118245	1	908
BIOCARTA_ATM_PATHWAY	20	0.36158	0.896343	0.60879123	0.9257578	1	457
BIOCARTA_ERK_PATHWAY	28	0.33737	0.892673	0.64903843	0.9305332	1	3770
REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	19	0.369568	0.891776	0.63377196	0.92797184	1	3980
REACTOME_FANCONI_ANEMIA_PATHWAY	21	0.358745	0.887294	0.6277372	0.9348472	1	1397
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	0.303766	0.886371	0.6855524	0.9320441	1	5640
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	19	0.369792	0.882046	0.600907	0.93827474	1	3296
REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULES	30	0.328166	0.878619	0.6555024	0.9421511	1	621
KEGG_MELANOGENESIS	101	0.261361	0.878538	0.79288024	0.93724436	1	2890
KEGG_STARCH_AND_SUCROSE_METABOLISM	49	0.295334	0.87435	0.6997245	0.9428191	1	2960
REACTOME_POTASSIUM_CHANNELS	96	0.263865	0.869481	0.7719298	0.95022833	1	2299
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	49	0.292578	0.860825	0.7431694	0.9669832	1	1784
KEGG_INOSITOL_PHOSPHATE_METABOLISM	54	0.29122	0.859633	0.7262248	0.96477616	1	1991
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	47	0.295858	0.858736	0.7154696	0.9619552	1	1151
KEGG_ALZHEIMERS_DISEASE	157	0.237874	0.855002	0.8951311	0.96611816	1	5779
REACTOME_RNA_POL_I_TRANSCRIPTION_INITIATION	24	0.330953	0.85416	0.7108168	0.96310514	1	3066
REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS	68	0.26743	0.846828	0.8017493	0.9753736	1	3210
KEGG_GLUTATHIONE_METABOLISM	47	0.290415	0.846241	0.7709497	0.9717664	1	3298
KEGG_ONE_CARBON_POOL_BY_FOLATE	17	0.356406	0.844241	0.675174	0.9712819	1	4998
KEGG_MELANOMA	71	0.262912	0.842789	0.7993421	0.970009	1	4138

REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_SYNTHESIS	25	0.32839	0.838496	0.7311321	0.974537	1	1151
REACTOME_GLUCOSE_METABOLISM	64	0.269366	0.83769	0.81556195	0.9713127	1	3497
KEGG_PURINE_METABOLISM	156	0.232621	0.834497	0.9366516	0.9738739	1	4431
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	16	0.367397	0.833408	0.6859504	0.9713969	1	1211
BIOCARTA_G1_PATHWAY	28	0.31768	0.832433	0.73965937	0.9688097	1	3052
REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	15	0.366501	0.822135	0.7120879	0.9857624	1	754
REACTOME_KINESINS	23	0.324903	0.821806	0.72596157	0.98155564	1	8375
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	22	0.327565	0.821786	0.7278761	0.9768117	1	59
KEGG_SPHINGOLIPID_METABOLISM	39	0.291055	0.821786	0.8109589	0.9720699	1	3709
REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	15	0.356468	0.821719	0.7	0.96753186	1	4473
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	39	0.285283	0.816964	0.78446114	0.97232	1	3223
REACTOME_DARPP_32_EVENTS	24	0.318266	0.811709	0.77261615	0.97792643	1	949
KEGG_SMALL_CELL_LUNG_CANCER	84	0.248463	0.810873	0.88387096	0.97491497	1	3664
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	18	0.338813	0.810336	0.7201835	0.97126454	1	5433
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	21	0.32006	0.798857	0.7644445	0.9878821	1	4774
KEGG_MISMATCH_REPAIR	23	0.308993	0.794459	0.7701422	0.9909085	1	4758
REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	21	0.325317	0.793601	0.75296915	0.98770875	1	2998
REACTOME_GLUTATHIONE_CONJUGATION	22	0.315715	0.788675	0.8053528	0.9916118	1	5216
REACTOME_G1_PHASE	35	0.282498	0.787875	0.83937824	0.98849857	1	3163
REACTOME_RNA_POL_III_TRANSCRIPTION_TERMINATION	19	0.328696	0.787057	0.78483605	0.9853419	1	4406
REACTOME_ZINC_TRANSPORTERS	15	0.343266	0.780698	0.7827051	0.9911039	1	4637
REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFATASE_ACTIVATION	26	0.304187	0.779905	0.81113803	0.9878738	1	1559
REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM	167	0.215497	0.776877	0.9834025	0.9880686	1	3371
BIOCARTA_PITX2_PATHWAY	15	0.338221	0.771901	0.77102804	0.9913178	1	1633
REACTOME_RNA_POL_III_CHAIN_ELONGATION	17	0.326992	0.768899	0.81100476	0.9911907	1	4406
REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_D	34	0.273971	0.764574	0.8682927	0.9930346	1	1822
BIOCARTA_ATRBRCA_PATHWAY	21	0.309393	0.760355	0.79334915	0.99437445	1	2328
KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	16	0.322802	0.750778	0.81400967	1	1	5074
KEGG_BETA_ALANINE_METABOLISM	22	0.299269	0.745157	0.85091746	1	1	2261
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	30	0.271046	0.734404	0.90076333	1	1	901
KEGG_OOCYTE_MEIOSIS	111	0.215373	0.728819	0.9895105	1	1	5205
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	25	0.278434	0.7208	0.89772725	1	1	3296
KEGG_PROSTATE_CANCER	88	0.221018	0.718948	0.990625	1	1	4208
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	64	0.227021	0.71584	0.96438354	1	1	3886
REACTOME_GLOBAL_GENOMIC_NER_GG_NER	33	0.259129	0.711103	0.89646465	1	1	4834
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN	28	0.271005	0.701739	0.9147465	1	1	3001
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	16	0.301917	0.701196	0.86946905	1	1	5433
REACTOME_ACYL_CHAIN_REMODELLING_OF_PG	15	0.301446	0.688813	0.87782806	1	1	1410
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	24	0.266147	0.686114	0.94183445	1	1	4774
BIOCARTA_CARM_ER_PATHWAY	35	0.243743	0.67777	0.95595855	1	1	4511
REACTOME_PYRUVATE_METABOLISM	18	0.283381	0.674789	0.9057971	1	1	4520
REACTOME_STEROID_HORMONES	28	0.258219	0.671929	0.9443038	1	1	386
REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	22	0.263886	0.663835	0.9413093	1	1	6560
KEGG_OTHER_GLYCAN_DEGRADATION	16	0.286161	0.660193	0.8975501	1	1	1205
BIOCARTA_EIF_PATHWAY	16	0.28344	0.656585	0.93453723	1	1	1474
KEGG_BLADDER_CANCER	42	0.229964	0.651932	0.97461927	1	1	3770
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	49	0.222539	0.649809	0.9848101	1	1	2834
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	0.279755	0.647967	0.92410713	1	1	5433
REACTOME_PI_3K_CASCADE	54	0.213189	0.645941	0.98559076	1	1	5381
BIOCARTA_AGR_PATHWAY	36	0.229651	0.635679	0.97105265	1	1	3135
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_7ALPHA_HYDROXYCHOLESTEROL	15	0.278441	0.630066	0.9263158	1	1	5600
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	19	0.262629	0.629567	0.947619	0.99813354	1	5433
BIOCARTA_NDKDYNAMIN_PATHWAY	18	0.269743	0.625561	0.94725275	0.9957655	1	3132
REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	104	0.187198	0.625293	1	0.99188656	1	3371
REACTOME_INFLUENZA_LIFE_CYCLE	136	0.175907	0.621058	1	0.98961276	1	4617
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	19	0.253764	0.617989	0.9675174	0.9868294	1	5600
REACTOME_SHC_MEDIATED_SIGNALLING	15	0.262253	0.584576	0.9622222	0.992697	1	4473
BIOCARTA_SHH_PATHWAY	16	0.25386	0.584095	0.96351933	0.9888904	1	3455
REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	50	0.18014	0.540497	0.99710983	0.9927477	1	3207

Table S19

GSEA Analysis on TCGA HNSC comparing tumors with or without 9p loss, Pathways Depleted

NAME	SIZE	ES	NES	NOM p-Value	FDR q-Value	FWER p-Value	RANK AT MAX	LEADING EDGE
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	56	-0.869116	-2.350486	0	0	0	1030	tags=66%, list=5%, signal=70%
REACTOME_INTERFERON_SIGNALING	132	-0.772164	-2.343878	0	0	0	1711	tags=40%, list=9%, signal=44%
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	239	-0.710653	-2.307	0	0	0	2444	tags=36%, list=13%, signal=41%
REACTOME_INNATE_IMMUNE_SYSTEM	225	-0.699494	-2.281682	0	0	0	1856	tags=32%, list=10%, signal=35%
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	47	-0.853878	-2.281531	0	0	0	1636	tags=64%, list=8%, signal=70%
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	53	-0.83499	-2.268407	0	0	0	1071	tags=53%, list=6%, signal=56%
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	492	-0.657706	-2.252617	0	0	0	1671	tags=24%, list=9%, signal=26%
KEGG_CHEMOKINE_SIGNALING_PATHWAY	188	-0.692527	-2.22282	0	0	0	2311	tags=39%, list=12%, signal=44%
REACTOME_INTERFERON_GAMMA_SIGNALING	48	-0.833213	-2.216742	0	0	0	1345	tags=50%, list=7%, signal=54%
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	251	-0.685151	-2.216012	0	0	0	2441	tags=40%, list=13%, signal=45%
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	117	-0.718913	-2.19441	0	0	0	1959	tags=41%, list=10%, signal=45%
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	55	-0.812068	-2.183908	0	0	0	1739	tags=51%, list=9%, signal=56%
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	55	-0.794671	-2.169345	0	0	0	890	tags=31%, list=5%, signal=32%
KEGG_PRIMARY_IMMUNODEFICIENCY	35	-0.859444	-2.147169	0	0	0	1537	tags=54%, list=8%, signal=59%
KEGG_HEMATOPOIETIC_CELL_LINEAGE	78	-0.753137	-2.142935	0	0	0	2463	tags=55%, list=13%, signal=63%
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	92	-0.731235	-2.141147	0	0	0	1929	tags=30%, list=10%, signal=34%
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	107	-0.707181	-2.12383	0	0	0	932	tags=24%, list=5%, signal=25%
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	45	-0.807007	-2.117807	0	0	0	1929	tags=40%, list=10%, signal=44%
BIOCARTA_NKT_PATHWAY	28	-0.864645	-2.097821	0	0	0	1739	tags=68%, list=9%, signal=74%
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	182	-0.647675	-2.080307	0	0	0	1739	tags=25%, list=9%, signal=27%
KEGG_TYPE_I_DIABETES_MELLITUS	23	-0.889874	-2.076309	0	0	0	841	tags=43%, list=4%, signal=45%
BIOCARTA_NO2IL12_PATHWAY	17	-0.923158	-2.066802	0	0	0	780	tags=76%, list=4%, signal=80%
REACTOME_TCR_SIGNALING	44	-0.777201	-2.066168	0	0	0	890	tags=36%, list=5%, signal=38%
KEGG_GRAFT_VERSUS_HOST_DISEASE	19	-0.920166	-2.055185	0	0	0	1030	tags=74%, list=5%, signal=78%
REACTOME_TOLL_RECEPTOR_CASCADES	113	-0.680383	-2.054488	0	0	0	1825	tags=27%, list=9%, signal=30%
KEGG_ALLOGRAFT_REJECTION	16	-0.924073	-2.02582	0	0	0	932	tags=69%, list=5%, signal=72%
BIOCARTA_IL12_PATHWAY	21	-0.881223	-1.996621	0	0	0	780	tags=52%, list=4%, signal=55%
REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BETA_PATHWAYS	62	-0.722306	-1.991175	0	0	0	1856	tags=32%, list=10%, signal=36%
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	68	-0.703895	-1.990424	0	0	0	1819	tags=32%, list=9%, signal=36%
KEGG_LEISHMANIA_INFECTION	57	-0.728278	-1.980061	0	3.71E-05	0.001	1799	tags=33%, list=9%, signal=37%
KEGG_JAK_STAT_SIGNALING_PATHWAY	141	-0.632564	-1.968745	0	1.41E-04	0.004	3004	tags=37%, list=16%, signal=43%
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	20	-0.862575	-1.960871	0	2.41E-04	0.007	612	tags=60%, list=3%, signal=62%
BIOCARTA_CTLA4_PATHWAY	17	-0.892696	-1.958768	0	2.33E-04	0.007	890	tags=65%, list=5%, signal=68%
BIOCARTA_DC_PATHWAY	20	-0.850226	-1.956722	0	2.59E-04	0.008	1799	tags=65%, list=9%, signal=72%
KEGG_AUTOIMMUNE_THYROID_DISEASE	20	-0.845982	-1.94481	0	3.16E-04	0.01	2248	tags=70%, list=12%, signal=79%
KEGG_CELL_ADHESION_MOLECULES_CAMS	113	-0.632158	-1.935789	0	3.38E-04	0.011	1421	tags=26%, list=7%, signal=28%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	112	-0.635545	-1.928255	0	5.08E-04	0.017	967	tags=19%, list=5%, signal=20%
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	176	-0.601418	-1.917536	0	6.71E-04	0.023	1887	tags=25%, list=10%, signal=27%
BIOCARTA_TH1TH2_PATHWAY	16	-0.860797	-1.910659	0	6.83E-04	0.024	958	tags=56%, list=5%, signal=59%
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	75	-0.662279	-1.903115	0	8.59E-04	0.03	1959	tags=32%, list=10%, signal=35%
REACTOME_SIGNALING_BY_ILS	104	-0.623844	-1.892084	0	8.92E-04	0.032	3159	tags=36%, list=16%, signal=42%
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	33	-0.750861	-1.884971	0	9.48E-04	0.035	1717	tags=48%, list=9%, signal=53%
REACTOME_SIGNALING_BY_RHO_GTPASES	108	-0.628163	-1.881929	0	0.001054762	0.04	3086	tags=37%, list=16%, signal=44%
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	275	-0.573736	-1.879084	0	0.001056181	0.041	3123	tags=32%, list=16%, signal=38%
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	84	-0.632128	-1.876887	0	0.00103271	0.041	1315	tags=21%, list=7%, signal=23%
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	67	-0.659035	-1.87427	0	0.001057406	0.043	820	tags=22%, list=4%, signal=23%
REACTOME_DOWNSTREAM_TCR_SIGNALING	27	-0.786962	-1.871522	0	0.00108205	0.045	2089	tags=41%, list=11%, signal=46%
SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE	59	-0.673285	-1.856776	0	0.001570316	0.066	1783	tags=25%, list=9%, signal=28%
BIOCARTA_COMP_PATHWAY	18	-0.839016	-1.849997	0	0.002129027	0.091	964	tags=50%, list=5%, signal=53%
BIOCARTA_CASPASE_PATHWAY	23	-0.790808	-1.846258	0	0.002283952	0.1	1540	tags=30%, list=8%, signal=33%
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	61	-0.680118	-1.844575	0	0.002328683	0.104	1929	tags=34%, list=10%, signal=38%
BIOCARTA_CSK_PATHWAY	20	-0.809049	-1.83767	0	0.002652555	0.121	612	tags=35%, list=3%, signal=36%
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	30	-0.746213	-1.837412	0.001628664	0.002602507	0.121	1856	tags=37%, list=10%, signal=40%
REACTOME_IL_3_5_AND_GM_CSF_SIGNALING	42	-0.711101	-1.834649	0	0.002658453	0.125	2981	tags=52%, list=15%, signal=62%
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	95	-0.623841	-1.828931	0	0.003013594	0.142	2990	tags=41%, list=15%, signal=48%
BIOCARTA_STATHMIN_PATHWAY	19	-0.818664	-1.82303	0	0.003399384	0.161	1593	tags=42%, list=8%, signal=46%
REACTOME_ACTIVATED_TLR4_SIGNALLING	90	-0.611289	-1.814779	0	0.003825968	0.177	1799	tags=21%, list=9%, signal=23%
BIOCARTA_TCR_PATHWAY	44	-0.695158	-1.811989	0	0.003875283	0.183	1959	tags=34%, list=10%, signal=38%
REACTOME_COMPLEMENT_CASCADE	29	-0.741896	-1.808679	0.001610306	0.003960451	0.189	1454	tags=38%, list=8%, signal=41%
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	20	-0.796378	-1.808078	0.001727116	0.003931359	0.191	1808	tags=40%, list=9%, signal=44%
BIOCARTA_IL2RB_PATHWAY	38	-0.713299	-1.800782	0	0.004467059	0.214	2993	tags=47%, list=15%, signal=56%
BIOCARTA_INFLAM_PATHWAY	25	-0.741069	-1.788001	0.001633987	0.005563226	0.261	2292	tags=52%, list=12%, signal=59%
BIOCARTA_TOB1_PATHWAY	18	-0.808262	-1.781485	0	0.006323382	0.297	762	tags=44%, list=4%, signal=46%
REACTOME_TRAF6_MEDIATED_NFKB_ACTIVATION	21	-0.763401	-1.77945	0	0.006468802	0.305	1808	tags=29%, list=9%, signal=31%
BIOCARTA_NKCELLS_PATHWAY	19	-0.776211	-1.765751	0	0.008267257	0.372	1021	tags=42%, list=5%, signal=44%
REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	28	-0.723174	-1.763099	0	0.008600952	0.393	1510	tags=25%, list=8%, signal=27%
BIOCARTA_TOLL_PATHWAY	37	-0.689104	-1.748946	0	0.010515982	0.461	1799	tags=27%, list=9%, signal=30%
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	31	-0.708779	-1.748077	0.001686341	0.01049268	0.466	1952	tags=39%, list=10%, signal=43%
BIOCARTA_IL22BP_PATHWAY	16	-0.812189	-1.742459	0.001798561	0.011230485	0.494	3004	tags=75%, list=16%, signal=89%
REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_DAI	18	-0.784574	-1.738733	0.003690037	0.011751955	0.511	1298	tags=28%, list=7%, signal=30%
REACTOME_HEMOSTASIS	435	-0.514187	-1.737394	0	0.01175891	0.516	2922	tags=25%, list=15%, signal=29%
REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS	26	-0.716209	-1.733789	0.005050505	0.012227139	0.541	2153	tags=35%, list=11%, signal=39%
KEGG_PRION_DISEASES	35	-0.674075	-1.732322	0	0.012196067	0.547	2346	tags=29%, list=12%, signal=32%
BIOCARTA_CYTOKINE_PATHWAY	18	-0.768104	-1.723848	0	0.013607052	0.593	1636	tags=44%, list=8%, signal=49%
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	30	-0.713334	-1.723348	0	0.013527392	0.595	1797	tags=30%, list=9%, signal=33%
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	65	-0.614541	-1.721204	0.001557632	0.013776516	0.607	2400	tags=28%, list=12%, signal=32%
REACTOME_G_ALPHA1213_SIGNALLING_EVENTS	73	-0.607388	-1.719922	0.001569859	0.013913425	0.619	3869	tags=40%, list=20%, signal=49%
KEGG_GALACTOSE_METABOLISM	26	-0.73107	-1.71633	0.003305785	0.014523762	0.634	1316	tags=15%, list=7%, signal=16%
BIOCARTA_TPO_PATHWAY	24	-0.735488	-1.713744	0.001672241	0.014917967	0.644	2993	tags=54%, list=15%, signal=64%
REACTOME_IL_RECEPTOR_SHC_SIGNALING	26	-0.726457	-1.713449	0.003418803	0.01478733	0.644	2902	tags=54%, list=15%, signal=63%
REACTOME_IL_2_SIGNALING	40	-0.654866	-1.702102	0	0.017232409	0.706	2902	tags=48%, list=15%, signal=56%
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	228	-0.521247	-1.691175	0	0.019884635	0.769	1653	tags=16%, list=9%, signal=18%
BIOCARTA_PDGF_PATHWAY	32	-0.682933	-1.686341	0.003262643	0.020749256	0.787	2993	tags=50%, list=15%, signal=59%
REACTOME_INFLAMMASOMES	16	-0.790511	-1.683136	0.003502627	0.021610424	0.807	1386	tags=38%, list=7%, signal=40%
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATION_OF_SECOND_MESSENGERS	29	-0.69078	-1.683077	0.005050505	0.0213692	0.807	1853	tags=38%, list=10%, signal=42%
REACTOME_GPCR_LIGAND_BINDING	373	-0.49792	-1.682918	0	0.021146933	0.807	3123	tags=28%, list=16%, signal=33%
BIOCARTA_PML_PATHWAY	17	-0.772409	-1.68076	0.007194245	0.021657968	0.82	1595	tags=35%, list=8%, signal=38%
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS	44	-0.652872	-1.679662	0.003115265	0.021778492	0.824	1439	tags=23%, list=7%, signal=24%
BIOCARTA_TID_PATHWAY	19	-0.757272	-1.676231	0.003546099	0.022546018	0.841	336	tags=16%, list=2%, signal=16%
REACTOME_CTLA4_INHIBITORY_SIGNALING	21	-0.721011	-1.676145	0.005454545	0.022333067	0.841	1952	tags=24%, list=10%, signal=26%
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	62	-0.602147	-1.67329	0.00152439	0.022775525	0.855	2311	tags=26%, list=12%, signal=29%
REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR7_8_OR_9_ACTIVATION	74	-0.589748	-1.673101	0	0.022587378	0.855	1749	tags=19%, list=9%, signal=21%
BIOCARTA_CCR5_PATHWAY	17	-0.763804	-1.672047	0.005747126	0.022791214	0.859	3604	tags=71%, list=19%, signal=87%
REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	72	-0.590597	-1.670697	0	0.022953946	0.862	3899	tags=36%, list=20%, signal=45%
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	28	-0.694809	-1.666072	0.006768189	0.024315672	0.881	983	tags=25%, list=5%, signal=26%
BIOCARTA_HSP27_PATHWAY	15	-0.775351	-1.65773	0.011257036	0.02708117	0.908	1365	tags=27%, list=7%, signal=29%
BIOCARTA_EGF_PATHWAY	31	-0.66982	-1.656311	0.006557377	0.027206492	0.91	2993	tags=48%, list=15%, signal=57%
REACTOME_STRIATED_MUSCLE_CONTRACTION	27	-0.686262	-1.646475	0.001818182	0.03078658	0.937	3830	tags=78%, list=20%, signal=97%
REACTOME_MUSCLE_CONTRACTION	46	-0.617548	-1.645426	0	0.030921647	0.94	3838	tags=61%, list=20%, signal=76%
REACTOME_ER_PHAGOSOME_PATHWAY	53	-0.603181	-1.640086	0.007530121	0.03282088	0.946	820	tags=19%, list=4%, signal=20%
BIOCARTA_IL7_PATHWAY	17	-0.7411	-1.638306	0.015789473	0.03323781	0.948	2815	tags=59%, list=15%, signal=69%
BIOCARTA_RHO_PATHWAY	32	-0.659662	-1.637801	0.004815409	0.03315181	0.948	3621	tags=44%, list=19%, signal=54%
KEGG_PROTEASOME	44	-0.621915	-1.636757	0.003164557	0.033303253	0.949	820	tags=18%, list=4%, signal=19%

REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	80	-0.564222	-1.630875	0.004405286	0.03567982	0.962	2089 tags=19%, list=11%, signal=21%
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	25	-0.682217	-1.62821	0.007017544	0.036540147	0.968	983 tags=24%, list=5%, signal=25%
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	121	-0.535368	-1.627943	0.001390821	0.036289915	0.968	1853 tags=19%, list=10%, signal=21%
REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	70	-0.574078	-1.627014	0.010463378	0.036397215	0.968	3899 tags=34%, list=20%, signal=43%
REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS	16	-0.737304	-1.622997	0.005681818	0.037775196	0.976	2584 tags=56%, list=13%, signal=65%
REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC	15	-0.770422	-1.619174	0.01208981	0.03917201	0.978	1104 tags=27%, list=6%, signal=28%
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	19	-0.718272	-1.617806	0.015679443	0.039420284	0.978	2699 tags=37%, list=14%, signal=43%
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	195	-0.496988	-1.61204	0	0.04168021	0.984	2404 tags=25%, list=12%, signal=28%
KEGG_VIRAL_MYOCARDITIS	50	-0.599472	-1.608672	0.004731861	0.042994224	0.986	2956 tags=36%, list=15%, signal=42%
BIOCARTA_INTEGRIN_PATHWAY	38	-0.622647	-1.604079	0.006589786	0.0447313	0.989	4276 tags=50%, list=22%, signal=64%
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	47	-0.604444	-1.599438	0.006462036	0.046823163	0.992	820 tags=19%, list=4%, signal=20%
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	23	-0.678346	-1.598023	0.019264448	0.04722039	0.992	2998 tags=35%, list=16%, signal=41%
BIOCARTA_IL2_PATHWAY	22	-0.687488	-1.597744	0.012195122	0.04695609	0.992	2993 tags=50%, list=15%, signal=59%
BIOCARTA_IL10_PATHWAY	17	-0.726151	-1.592678	0.012867647	0.04947176	0.995	2918 tags=59%, list=15%, signal=69%
BIOCARTA_UCALPAIN_PATHWAY	18	-0.717973	-1.590131	0.020761246	0.05054621	0.996	3843 tags=56%, list=20%, signal=69%
BIOCARTA_NFKB_PATHWAY	23	-0.666574	-1.577803	0.012455516	0.05701198	0.999	1344 tags=17%, list=7%, signal=19%
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	73	-0.553711	-1.576912	0.013782542	0.05690473	0.999	2981 tags=34%, list=15%, signal=40%
BIOCARTA_GSK3_PATHWAY	27	-0.65877	-1.569909	0.015050167	0.0606932	0.999	2589 tags=33%, list=13%, signal=38%
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	114	-0.521166	-1.565062	0.002777778	0.06337483	1	2630 tags=32%, list=14%, signal=36%
REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	37	-0.613186	-1.556774	0.014876033	0.06824078	1	3159 tags=27%, list=16%, signal=32%
REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_TTP	17	-0.706063	-1.555331	0.019011406	0.06869463	1	1438 tags=29%, list=7%, signal=32%
REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKS_COMPLEX	23	-0.671273	-1.551425	0.030612245	0.070871115	1	2089 tags=22%, list=11%, signal=24%
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	114	-0.511651	-1.550038	0.005524862	0.071236216	1	1636 tags=12%, list=8%, signal=13%
BIOCARTA_GLEEVEC_PATHWAY	23	-0.669223	-1.549953	0.01923077	0.07072742	1	2993 tags=43%, list=15%, signal=51%
REACTOME_DEFENSINS	16	-0.722661	-1.546132	0.022346368	0.07321512	1	2807 tags=50%, list=15%, signal=58%
BIOCARTA_GH_PATHWAY	28	-0.649963	-1.545028	0.021594685	0.073530264	1	2998 tags=39%, list=16%, signal=46%
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	61	-0.558532	-1.537392	0.01076923	0.078868	1	820 tags=15%, list=4%, signal=15%
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	21	-0.672945	-1.534892	0.026785715	0.08033656	1	890 tags=19%, list=5%, signal=20%
BIOCARTA_BCR_PATHWAY	34	-0.612928	-1.533976	0.016583748	0.08044347	1	2993 tags=38%, list=15%, signal=45%
BIOCARTA_CTCF_PATHWAY	23	-0.657701	-1.530421	0.03220339	0.08270369	1	2427 tags=48%, list=13%, signal=55%
REACTOME_PI_METABOLISM	47	-0.573576	-1.529009	0.013931888	0.08346217	1	3142 tags=30%, list=16%, signal=35%
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	79	-0.530861	-1.520515	0.005873715	0.08954203	1	3991 tags=37%, list=21%, signal=46%
REACTOME_SEMAPHORIN_INTERACTIONS	63	-0.543348	-1.518001	0.021052632	0.090820186	1	1649 tags=19%, list=9%, signal=21%
KEGG_FOCAL_ADHESION	198	-0.471257	-1.513862	0	0.09359371	1	2762 tags=25%, list=14%, signal=29%
REACTOME_APOPTOSIS	143	-0.485368	-1.513064	0.00273224	0.09356832	1	1540 tags=15%, list=8%, signal=16%
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	209	-0.468593	-1.50954	0.002560825	0.0962108	1	2106 tags=20%, list=11%, signal=22%
BIOCARTA_FAS_PATHWAY	30	-0.616195	-1.50564	0.02725724	0.09899269	1	1540 tags=23%, list=8%, signal=25%
BIOCARTA_CARDIACEGF_PATHWAY	18	-0.675138	-1.504872	0.038800705	0.099036075	1	3604 tags=44%, list=19%, signal=55%
REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	43	-0.574834	-1.500318	0.01904762	0.10240781	1	3869 tags=37%, list=20%, signal=46%
REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	79	-0.518999	-1.499489	0.013595167	0.10236732	1	2089 tags=18%, list=11%, signal=20%
BIOCARTA_BIOPEPTIDES_PATHWAY	42	-0.581654	-1.499306	0.020733653	0.10182743	1	3049 tags=36%, list=16%, signal=42%
BIOCARTA_IL6_PATHWAY	22	-0.65129	-1.49522	0.033210333	0.10492127	1	4276 tags=55%, list=22%, signal=70%
BIOCARTA_KERATINOCYTE_PATHWAY	46	-0.572068	-1.495008	0.02208202	0.1044167	1	1409 tags=17%, list=7%, signal=19%
REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLLAPSE	24	-0.638089	-1.493908	0.048695654	0.1047384	1	4625 tags=50%, list=24%, signal=66%
BIOCARTA_ECM_PATHWAY	24	-0.641173	-1.492213	0.03716814	0.10564375	1	2753 tags=42%, list=14%, signal=49%
REACTOME_NOD1_2_SIGNALING_PATHWAY	29	-0.603927	-1.487711	0.0302521	0.10927103	1	2089 tags=21%, list=11%, signal=23%
BIOCARTA_RAC1_PATHWAY	23	-0.637418	-1.484654	0.037102472	0.11161195	1	2493 tags=43%, list=13%, signal=50%
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	81	-0.50172	-1.483289	0.019345239	0.112302326	1	1717 tags=17%, list=9%, signal=19%
BIOCARTA_TALL1_PATHWAY	15	-0.6893	-1.479781	0.05172414	0.11499211	1	3219 tags=40%, list=17%, signal=48%
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	38	-0.57837	-1.475651	0.033980582	0.11835511	1	3283 tags=34%, list=17%, signal=41%
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	92	-0.503849	-1.474688	0.010852713	0.11861005	1	820 tags=12%, list=4%, signal=12%
REACTOME_SIGNALLING_BY_NGF	211	-0.454749	-1.473987	0.001261034	0.118487716	1	2990 tags=25%, list=15%, signal=29%
REACTOME_REGULATION_OF_APOPTOSIS	56	-0.538055	-1.473477	0.02715655	0.11820131	1	885 tags=16%, list=5%, signal=17%
REACTOME_ERK_MAPK_TARGETS	21	-0.64962	-1.472352	0.04152249	0.11848707	1	4636 tags=48%, list=24%, signal=63%
REACTOME_CD28_CO_STIMULATION	31	-0.585541	-1.471156	0.045	0.1188705	1	1952 tags=23%, list=10%, signal=25%
REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	17	-0.669579	-1.470044	0.04882155	0.11932435	1	2089 tags=24%, list=11%, signal=26%
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	196	-0.456033	-1.46721	0.001257862	0.12156089	1	1653 tags=14%, list=9%, signal=15%
BIOCARTA_LAIR_PATHWAY	17	-0.675817	-1.460044	0.05667276	0.12843052	1	2798 tags=53%, list=14%, signal=62%
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	79	-0.505519	-1.458801	0.022255193	0.12920308	1	2838 tags=20%, list=15%, signal=24%
BIOCARTA_ACH_PATHWAY	16	-0.676868	-1.457335	0.04681648	0.1299313	1	890 tags=19%, list=5%, signal=20%
BIOCARTA_TNFR2_PATHWAY	18	-0.657583	-1.455786	0.057040997	0.13076808	1	3726 tags=44%, list=19%, signal=55%
REACTOME_RAP1_SIGNALLING	16	-0.680654	-1.455701	0.05212355	0.13004996	1	2278 tags=31%, list=12%, signal=35%
REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1	17	-0.658853	-1.446016	0.06017699	0.13995105	1	1438 tags=24%, list=7%, signal=25%
BIOCARTA_PTEN_PATHWAY	18	-0.651397	-1.443811	0.07205624	0.14140975	1	1960 tags=22%, list=10%, signal=25%
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	126	-0.466329	-1.443507	0.012261581	0.1408948	1	2089 tags=17%, list=11%, signal=19%
KEGG_ACUTE_MYELOID_LEUKEMIA	57	-0.526154	-1.437697	0.040880505	0.14628333	1	1959 tags=23%, list=10%, signal=25%
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	47	-0.533791	-1.43624	0.042071197	0.1472831	1	2051 tags=21%, list=11%, signal=24%
KEGG_DILATED_CARDIOMYOPATHY	90	-0.492872	-1.435782	0.01884058	0.14702868	1	4572 tags=48%, list=24%, signal=62%
BIOCARTA_HIVNEF_PATHWAY	58	-0.52224	-1.434266	0.027190333	0.14796565	1	1344 tags=14%, list=7%, signal=15%
KEGG_LYSOSOME	121	-0.4705	-1.434113	0.009681881	0.1473337	1	2472 tags=25%, list=13%, signal=28%
REACTOME_SIGNALING_BY_FGFR1_FUSION_MUTANTS	17	-0.661084	-1.43252	0.06423611	0.14844228	1	2896 tags=35%, list=15%, signal=41%
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	31	-0.58123	-1.428352	0.05496454	0.1524117	1	2779 tags=29%, list=14%, signal=34%
REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPORTERS	16	-0.656155	-1.427336	0.091726616	0.1527956	1	860 tags=19%, list=4%, signal=20%
BIOCARTA_MCALPAIN_PATHWAY	25	-0.601431	-1.42516	0.07130435	0.15454417	1	2753 tags=36%, list=14%, signal=42%
BIOCARTA_IL1R_PATHWAY	33	-0.566475	-1.425075	0.042071197	0.15376356	1	5008 tags=45%, list=26%, signal=61%
REACTOME_SIGNALING_BY_SCF_KIT	75	-0.503685	-1.422455	0.02818991	0.15587553	1	3173 tags=28%, list=16%, signal=33%
BIOCARTA_EDG1_PATHWAY	27	-0.58765	-1.422225	0.07401033	0.15531148	1	1490 tags=22%, list=8%, signal=24%
BIOCARTA_AKT_PATHWAY	22	-0.613502	-1.41747	0.07789855	0.159965	1	1409 tags=18%, list=7%, signal=20%
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	-0.598059	-1.412556	0.08170515	0.16505802	1	1640 tags=21%, list=8%, signal=23%
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	49	-0.528515	-1.411684	0.037369207	0.16523215	1	1139 tags=16%, list=6%, signal=17%
BIOCARTA_41BB_PATHWAY	16	-0.651436	-1.40875	0.077617325	0.16764918	1	2499 tags=31%, list=13%, signal=36%
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	119	-0.467956	-1.408106	0.020949721	0.16756864	1	1139 tags=13%, list=6%, signal=13%
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	74	-0.494712	-1.40557	0.04524887	0.16994016	1	4572 tags=46%, list=24%, signal=60%
KEGG_APOPTOSIS	86	-0.47672	-1.403205	0.026049204	0.17207631	1	2911 tags=20%, list=15%, signal=23%
REACTOME_CELL_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	58	-0.513134	-1.401793	0.043806646	0.17292574	1	3869 tags=29%, list=20%, signal=37%
BIOCARTA_NTHI_PATHWAY	24	-0.586702	-1.398633	0.082585275	0.17611833	1	2427 tags=25%, list=13%, signal=29%
BIOCARTA_MET_PATHWAY	37	-0.547936	-1.394814	0.071875	0.18045294	1	4276 tags=49%, list=22%, signal=62%
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	49	-0.529087	-1.394146	0.0543131	0.1803631	1	820 tags=14%, list=4%, signal=15%
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	111	-0.458826	-1.388501	0.01830986	0.18686262	1	2818 tags=26%, list=15%, signal=30%
BIOCARTA_MAL_PATHWAY	19	-0.615713	-1.38844	0.094642855	0.1859517	1	2656 tags=42%, list=14%, signal=49%
KEGG_ADHERENS_JUNCTION	73	-0.488278	-1.382735	0.057017542	0.1926856	1	3211 tags=26%, list=17%, signal=31%
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	50	-0.513594	-1.376384	0.073131956	0.20096269	1	820 tags=14%, list=4%, signal=15%
REACTOME_SIGNALING_BY_WNT	63	-0.494325	-1.375181	0.052790347	0.20167176	1	1409 tags=14%, list=7%, signal=15%
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	48	-0.510588	-1.374033	0.07582939	0.20214328	1	820 tags=15%, list=4%, signal=15%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	15	-0.648768	-1.373066	0.13271028	0.20243108	1	11 tags=7%, list=0%, signal=7%
KEGG_ECM_RECEPTOR_INTERACTION	83	-0.475144	-1.364917	0.04500703	0.21318299	1	4013 tags=36%, list=21%, signal=45%
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	48	-0.51405	-1.364512	0.068910256	0.21271677	1	820 tags=15%, list=4%, signal=15%
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	47	-0.516053	-1.36277	0.06230032	0.21402381	1	820 tags=15%, list=4%, signal=16%
REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	21	-0.595343	-1.361002	0.10175438	0.21543892	1	983 tags=19%, list=5%, signal=20%
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	27	-0.563152	-1.361	0.07719928	0.21439414	1	1432 tags=22%, list=7%, signal=24%
BIOCARTA_FCER1_PATHWAY	38	-0.527862	-1.355709	0.07472178	0.2208842	1	2993 tags=37%, list=15%, signal=44%
REACTOME_DAG_AND_IP3_SIGNALING	31	-0.554655	-1.352903	0.10344828	0.22367045	1	2896 tags=42%, list=15%, signal=49%
KEGG_ENDOCYTOSIS	174	-0.424034	-1.352513	0.022486772	0.22318594	1	3256 tags=25%, list=17%, signal=29%
REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING	27	-0.566669	-1.352234	0.09090909	0.22258541	1	2386 tags=22%, list=12%, signal=25%
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	46	-0.519698	-1.349389	0.090189874	0.22599693	1	820 tags=15%, list=4%, signal=16%

BIOCARTA_PAR1_PATHWAY	37	-0.529076	-1.348802	0.09421488	0.22582231	1	2630 tags=27%, list=14%, signal=31%
REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE	133	-0.432042	-1.348743	0.044382803	0.22483273	1	3396 tags=29%, list=18%, signal=35%
REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS	15	-0.635669	-1.347212	0.124542125	0.22612949	1	1432 tags=27%, list=7%, signal=29%
BIOCARTA_ETS_PATHWAY	18	-0.611349	-1.347151	0.10526316	0.225178	1	845 tags=17%, list=4%, signal=17%
REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS	42	-0.515979	-1.346821	0.08429752	0.22457954	1	2967 tags=33%, list=15%, signal=39%
REACTOME_INTRINSIC_PATHWAY	16	-0.619516	-1.342105	0.104395606	0.23016319	1	2779 tags=31%, list=14%, signal=36%
REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	26	-0.562742	-1.338263	0.11363637	0.23482876	1	1195 tags=15%, list=6%, signal=16%
BIOCARTA_GATA3_PATHWAY	15	-0.621308	-1.329665	0.13962264	0.24693629	1	4870 tags=53%, list=25%, signal=71%
REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	16	-0.619799	-1.325737	0.12857144	0.2521072	1	2675 tags=56%, list=14%, signal=65%
REACTOME_SIGNALING_BY_FGFR1_MUTANTS	28	-0.541531	-1.323681	0.106712565	0.25427416	1	3056 tags=25%, list=16%, signal=30%
REACTOME_BASIGIN_INTERACTIONS	24	-0.563201	-1.320575	0.13400336	0.25816503	1	263 tags=8%, list=1%, signal=8%
REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	49	-0.497878	-1.319936	0.1109375	0.25798762	1	4645 tags=41%, list=24%, signal=54%
REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI	16	-0.615788	-1.318249	0.14788732	0.25982502	1	2624 tags=38%, list=14%, signal=43%
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	53	-0.481389	-1.317523	0.071428575	0.25987753	1	2185 tags=19%, list=11%, signal=21%
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	79	-0.45662	-1.314858	0.07473841	0.2633522	1	3635 tags=35%, list=19%, signal=43%
REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	33	-0.526159	-1.312966	0.11165048	0.26540828	1	2569 tags=21%, list=13%, signal=24%
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	48	-0.496954	-1.312726	0.10172144	0.26463386	1	1051 tags=17%, list=5%, signal=18%
REACTOME_IL1_SIGNALING	38	-0.518323	-1.312306	0.108589955	0.264173	1	3159 tags=21%, list=16%, signal=25%
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	83	-0.46016	-1.311722	0.07634731	0.26395765	1	4572 tags=48%, list=24%, signal=63%
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	107	-0.437418	-1.310797	0.07072136	0.2642939	1	3302 tags=29%, list=17%, signal=35%
REACTOME_PLC_BETA_MEDIATED_EVENTS	42	-0.50569	-1.309305	0.11690363	0.26558837	1	1934 tags=29%, list=10%, signal=32%
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	91	-0.445231	-1.308869	0.062222224	0.26521984	1	2990 tags=27%, list=15%, signal=32%
KEGG_MTOR_SIGNALING_PATHWAY	51	-0.482143	-1.306556	0.10608424	0.2677	1	3684 tags=29%, list=19%, signal=36%
BIOCARTA_MTOR_PATHWAY	23	-0.555443	-1.306151	0.13089006	0.26720783	1	2910 tags=35%, list=15%, signal=41%
REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	15	-0.601853	-1.300385	0.15469614	0.2756086	1	2386 tags=27%, list=12%, signal=30%
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	-0.566559	-1.298571	0.15265866	0.2775748	1	4636 tags=42%, list=24%, signal=55%
BIOCARTA_CCR3_PATHWAY	23	-0.567766	-1.293182	0.13344887	0.28559133	1	2656 tags=35%, list=14%, signal=40%
REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	49	-0.488089	-1.290568	0.11908397	0.28858665	1	2967 tags=29%, list=15%, signal=34%
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI	18	-0.585527	-1.287595	0.16159695	0.29274893	1	1656 tags=17%, list=9%, signal=18%
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	53	-0.478668	-1.287236	0.11323764	0.29212165	1	820 tags=13%, list=4%, signal=14%
REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT	25	-0.537469	-1.285064	0.14031972	0.2947779	1	970 tags=8%, list=5%, signal=8%
BIOCARTA_CXCR4_PATHWAY	24	-0.548062	-1.281627	0.16370107	0.29979274	1	3036 tags=33%, list=16%, signal=39%
KEGG_ABC_TRANSPORTERS	44	-0.486895	-1.280628	0.13207547	0.30035752	1	3569 tags=34%, list=18%, signal=42%
REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	30	-0.527297	-1.274863	0.15423729	0.309519	1	1981 tags=20%, list=10%, signal=22%
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	59	-0.461191	-1.267315	0.10719755	0.32147902	1	820 tags=12%, list=4%, signal=12%
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	64	-0.454145	-1.266313	0.10823171	0.32199603	1	1539 tags=14%, list=8%, signal=15%
KEGG_TGF_BETA_SIGNALING_PATHWAY	85	-0.433946	-1.264616	0.10364964	0.32369214	1	3630 tags=32%, list=19%, signal=39%
REACTOME_SYNTHESIS_SECRETION_AND_DEACYLATION_OF_GHRELIN	16	-0.594184	-1.257823	0.19238095	0.3353633	1	3516 tags=31%, list=18%, signal=38%
BIOCARTA_MYOSIN_PATHWAY	31	-0.507223	-1.256609	0.1660959	0.3364648	1	2204 tags=23%, list=11%, signal=25%
KEGG_GNRH_SIGNALING_PATHWAY	96	-0.426723	-1.255974	0.0997191	0.33645004	1	3899 tags=32%, list=20%, signal=40%
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.486335	-1.253398	0.16256158	0.34005457	1	1640 tags=17%, list=8%, signal=19%
REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	174	-0.400889	-1.253351	0.07783641	0.33878747	1	3124 tags=25%, list=16%, signal=29%
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	15	-0.594406	-1.25235	0.17712177	0.33945122	1	2962 tags=20%, list=15%, signal=24%
BIOCARTA_IGF1MTOR_PATHWAY	20	-0.553424	-1.248414	0.17335767	0.34549713	1	2669 tags=30%, list=14%, signal=35%
KEGG_ENDOMETRIAL_CANCER	52	-0.462834	-1.246144	0.15301391	0.348686	1	2046 tags=23%, list=11%, signal=26%
REACTOME_PLATELET_HOMEOSTASIS	76	-0.433546	-1.240847	0.1179941	0.35751912	1	2920 tags=32%, list=15%, signal=37%
REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	33	-0.499988	-1.239814	0.19224283	0.35820496	1	3859 tags=42%, list=20%, signal=53%
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	57	-0.45496	-1.239538	0.14976598	0.35737166	1	820 tags=12%, list=4%, signal=13%
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	43	-0.470991	-1.238576	0.16693419	0.35780096	1	3450 tags=26%, list=18%, signal=31%
BIOCARTA_CHEMICAL_PATHWAY	22	-0.543596	-1.237627	0.19836065	0.35808736	1	1574 tags=18%, list=8%, signal=20%
BIOCARTA_CREB_PATHWAY	27	-0.502824	-1.237537	0.18675722	0.3568724	1	2721 tags=22%, list=14%, signal=26%
BIOCARTA_VIP_PATHWAY	26	-0.517181	-1.233403	0.19415808	0.36370715	1	4834 tags=50%, list=25%, signal=67%
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	44	-0.472256	-1.230593	0.1768595	0.36799517	1	2920 tags=27%, list=15%, signal=32%
BIOCARTA_EPO_PATHWAY	19	-0.542645	-1.230016	0.20379965	0.36762264	1	2993 tags=42%, list=15%, signal=50%
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	-0.502105	-1.228915	0.20751634	0.3685568	1	3710 tags=37%, list=19%, signal=45%
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	56	-0.444258	-1.227202	0.14837712	0.37078333	1	1539 tags=14%, list=8%, signal=15%
KEGG_RENIN_ANGIOTENSIN_SYSTEM	17	-0.5681	-1.226523	0.21841155	0.37063247	1	5264 tags=76%, list=27%, signal=105%
BIOCARTA_CD40_PATHWAY	15	-0.55952	-1.224082	0.25493717	0.37393573	1	3605 tags=33%, list=19%, signal=41%
REACTOME_SIGNALING_BY_ERBB4	86	-0.418949	-1.223097	0.13245997	0.3746556	1	3159 tags=19%, list=16%, signal=22%
BIOCARTA_AKAPCENTROSOME_PATHWAY	15	-0.561865	-1.219214	0.24862888	0.38092867	1	2721 tags=27%, list=14%, signal=31%
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	18	-0.547053	-1.218209	0.22852233	0.381411	1	1853 tags=33%, list=10%, signal=37%
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES	91	-0.414956	-1.217491	0.14532374	0.38119635	1	3040 tags=26%, list=16%, signal=31%
KEGG_INSULIN_SIGNALING_PATHWAY	136	-0.394799	-1.216631	0.11813187	0.3814145	1	3152 tags=20%, list=16%, signal=24%
BIOCARTA_HDAC_PATHWAY	28	-0.5032	-1.214114	0.21186441	0.38519466	1	3927 tags=39%, list=20%, signal=49%
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	53	-0.449124	-1.213851	0.18140244	0.38429752	1	820 tags=11%, list=4%, signal=12%
REACTOME_TRNA_AMINOACYLATION	42	-0.46432	-1.213314	0.16037735	0.38395813	1	1640 tags=17%, list=8%, signal=18%
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	105	-0.403336	-1.211554	0.1315029	0.38589543	1	3733 tags=29%, list=19%, signal=35%
BIOCARTA_CDC42RAC_PATHWAY	16	-0.558753	-1.21049	0.24744028	0.38646945	1	3621 tags=38%, list=19%, signal=46%
KEGG_REGULATION_OF_AUTOPHAGY	24	-0.515278	-1.208515	0.21105528	0.38894904	1	1929 tags=17%, list=10%, signal=18%
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	49	-0.457763	-1.205677	0.20032051	0.39316493	1	5022 tags=27%, list=26%, signal=36%
REACTOME_METABOLISM_OF_MRNA	209	-0.370765	-1.203969	0.10654686	0.39533567	1	2388 tags=13%, list=12%, signal=15%
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK	195	-0.375563	-1.203913	0.11398964	0.39404377	1	2768 tags=21%, list=14%, signal=24%
KEGG_ETHER_LIPID_METABOLISM	29	-0.49299	-1.203567	0.21105528	0.39333156	1	2267 tags=31%, list=12%, signal=35%
REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_LIKE_PEPTIDE1	42	-0.46243	-1.202642	0.19808307	0.39391297	1	3966 tags=36%, list=21%, signal=45%
REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	16	-0.551864	-1.201885	0.22179732	0.39413396	1	2046 tags=19%, list=11%, signal=21%
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRANE	17	-0.538971	-1.2005	0.2659176	0.39560804	1	3142 tags=35%, list=16%, signal=42%
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TAK1	16	-0.541091	-1.200007	0.21428572	0.39526874	1	4645 tags=44%, list=24%, signal=58%
BIOCARTA_IGF1_PATHWAY	21	-0.520212	-1.199615	0.2195122	0.39474693	1	4276 tags=48%, list=22%, signal=61%
BIOCARTA_EIF4_PATHWAY	24	-0.510014	-1.198354	0.2231834	0.3960357	1	2388 tags=21%, list=12%, signal=24%
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	65	-0.431772	-1.19677	0.17121212	0.39772838	1	1539 tags=14%, list=8%, signal=15%
BIOCARTA_ERK5_PATHWAY	17	-0.551653	-1.196603	0.23792486	0.3966698	1	4233 tags=53%, list=22%, signal=68%
REACTOME_GABA_RECEPTOR_ACTIVATION	51	-0.4424	-1.191136	0.21550387	0.4061978	1	1418 tags=14%, list=7%, signal=15%
KEGG_COLORECTAL_CANCER	62	-0.43759	-1.190489	0.19728915	0.4061456	1	2427 tags=26%, list=13%, signal=29%
BIOCARTA_BAD_PATHWAY	25	-0.497711	-1.190409	0.25044405	0.40492043	1	4233 tags=44%, list=22%, signal=56%
BIOCARTA_NFAT_PATHWAY	52	-0.443644	-1.186351	0.19968304	0.41193023	1	2721 tags=27%, list=14%, signal=31%
BIOCARTA_INSULIN_PATHWAY	22	-0.521656	-1.184521	0.24310344	0.41456413	1	4276 tags=45%, list=22%, signal=58%
REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	17	-0.547856	-1.184095	0.26534295	0.41398814	1	1438 tags=12%, list=7%, signal=13%
REACTOME_ION_CHANNEL_TRANSPORT	53	-0.43707	-1.183815	0.21324718	0.41315666	1	2604 tags=21%, list=13%, signal=24%
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	29	-0.490361	-1.180163	0.23271501	0.419371	1	868 tags=10%, list=4%, signal=11%
REACTOME_PEPTIDE_CHAIN_ELONGATION	86	-0.401661	-1.179916	0.17492712	0.4185144	1	4604 tags=24%, list=24%, signal=32%
BIOCARTA_RAS_PATHWAY	23	-0.50728	-1.178676	0.25778547	0.41956806	1	2656 tags=22%, list=14%, signal=25%
REACTOME_GRB2_SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTERGRINS_	15	-0.553555	-1.178307	0.28782287	0.4189364	1	2386 tags=27%, list=12%, signal=30%
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	35	-0.470688	-1.177057	0.2369281	0.42001158	1	2386 tags=23%, list=12%, signal=26%
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	27	-0.486061	-1.172882	0.25255972	0.42711508	1	3923 tags=33%, list=20%, signal=42%
REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	121	-0.381973	-1.171958	0.1859155	0.42778665	1	3056 tags=21%, list=16%, signal=25%
REACTOME_GABA_B_RECEPTOR_ACTIVATION	38	-0.460019	-1.171852	0.23027375	0.42662457	1	4523 tags=42%, list=23%, signal=55%
BIOCARTA_LONGEVITY_PATHWAY	15	-0.553298	-1.171669	0.27686703	0.4256604	1	3684 tags=47%, list=19%, signal=58%
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	24	-0.501294	-1.170116	0.27347612	0.4276773	1	3379 tags=42%, list=17%, signal=50%
REACTOME_PYRIMIDINE_METABOLISM	24	-0.502444	-1.169623	0.2767857	0.42736745	1	862 tags=13%, list=4%, signal=13%
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA	20	-0.525042	-1.167846	0.24416517	0.42957047	1	983 tags=15%, list=5%, signal=16%
REACTOME_SMOOTH_MUSCLE_CONTRACTION	23	-0.498259	-1.166904	0.26565143	0.43016514	1	3838 tags=43%, list=20%, signal=54%
REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	30	-0.477934	-1.166327	0.24278438	0.42995536	1	2515 tags=23%, list=13%, signal=27%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	26	-0.484949	-1.164944	0.2688356	0.4315122	1	245 tags=8%, list=1%, signal=8%
REACTOME_SIGNAL_AMPLIFICATION	31	-0.471238	-1.163617	0.24177632	0.43273607	1	983 tags=13%, list=5%, signal=14%
REACTOME_OPIOID_SIGNALLING	77	-0.404717	-1.160969	0.20833333	0.43682313	1	1934 tags=19%, list=10%, signal=22%
REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	15	-0.540435	-1.159139	0.27407408	0.43916756	1	3685 tags=40%, list=19%, signal=49%
REACTOME_REGULATION_OF_INSULIN_SECRETION	89	-0.39597	-1.158422	0.21438849	0.4393503	1	3809 tags=27%, list=20%, signal=33%
KEGG_AXON_GUIDANCE	129	-0.374491	-1.157026	0.1819464	0.44078305	1	2368 tags=19%, list=12%, signal=22%

KEGG_HISTIDINE_METABOLISM	29	-0.467329	-1.150798	0.25441697	0.45255965	1	3335 tags=38%, list=17%, signal=46%
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	62	-0.415042	-1.149797	0.23851852	0.45328403	1	820 tags=10%, list=4%, signal=10%
REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS	26	-0.476979	-1.146056	0.28764805	0.45972762	1	2418 tags=23%, list=13%, signal=26%
REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT	16	-0.522324	-1.145357	0.2936803	0.45985156	1	2649 tags=31%, list=14%, signal=36%
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	76	-0.397928	-1.144513	0.22852984	0.46022892	1	3396 tags=25%, list=18%, signal=30%
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	134	-0.374362	-1.143553	0.2077748	0.4607476	1	3875 tags=28%, list=20%, signal=35%
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	-0.398552	-1.142645	0.23065476	0.4612747	1	2815 tags=21%, list=15%, signal=24%
BIOCARTA_MAPK_PATHWAY	86	-0.392296	-1.142227	0.24	0.4607375	1	3932 tags=29%, list=20%, signal=36%
KEGG_STEROID_BIOSYNTHESIS	16	-0.521368	-1.140953	0.30851063	0.46204227	1	1718 tags=13%, list=9%, signal=14%
KEGG_ERBB_SIGNALING_PATHWAY	87	-0.391355	-1.139518	0.23211679	0.46349436	1	2990 tags=22%, list=15%, signal=26%
REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	116	-0.378	-1.139385	0.20949721	0.46236178	1	3809 tags=24%, list=20%, signal=30%
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	20	-0.497961	-1.137611	0.30879712	0.46469513	1	2258 tags=30%, list=12%, signal=34%
KEGG_PANCREATIC_CANCER	70	-0.401129	-1.136404	0.23148148	0.4658127	1	2427 tags=19%, list=13%, signal=21%
REACTOME_PEROXISOMAL_LIPID_METABOLISM	20	-0.497443	-1.130559	0.31760436	0.47708046	1	4241 tags=40%, list=22%, signal=51%
REACTOME_SIGNALING_BY_PDGF	118	-0.374744	-1.129946	0.24606581	0.47687495	1	4357 tags=34%, list=23%, signal=43%
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	24	-0.485185	-1.127698	0.30860034	0.4804133	1	2670 tags=21%, list=14%, signal=24%
REACTOME_M_G1_TRANSITION	72	-0.399309	-1.127564	0.24960998	0.47925723	1	820 tags=10%, list=4%, signal=10%
REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS	16	-0.514847	-1.124945	0.34719712	0.48351282	1	4510 tags=44%, list=23%, signal=57%
REACTOME_HIV_INFECTION	192	-0.353748	-1.124035	0.20905459	0.48408	1	2726 tags=16%, list=14%, signal=19%
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	33	-0.450326	-1.122781	0.31051752	0.48539734	1	3809 tags=33%, list=20%, signal=41%
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	77	-0.393313	-1.119893	0.2607362	0.4904094	1	1539 tags=12%, list=8%, signal=13%
REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB	17	-0.510874	-1.11872	0.31944445	0.49133405	1	2818 tags=35%, list=15%, signal=41%
REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	41	-0.430646	-1.118707	0.29069766	0.48989108	1	2624 tags=22%, list=14%, signal=25%
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	106	-0.37287	-1.115636	0.27194244	0.49510694	1	4604 tags=24%, list=24%, signal=31%
REACTOME_APOPTOTIC_EXECUTION_PHASE	52	-0.413811	-1.115057	0.2830769	0.49498874	1	3283 tags=25%, list=17%, signal=30%
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	37	-0.434915	-1.11411	0.3091537	0.49564764	1	3514 tags=35%, list=18%, signal=43%
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	57	-0.405814	-1.112627	0.27613103	0.49732012	1	5055 tags=28%, list=26%, signal=38%
REACTOME_CA_DEPENDENT_EVENTS	29	-0.464687	-1.112312	0.3301282	0.4965644	1	2818 tags=38%, list=15%, signal=44%
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	23	-0.480586	-1.112227	0.33333334	0.49528688	1	1358 tags=22%, list=7%, signal=23%
KEGG_LONG_TERM_POTENTIATION	70	-0.39075	-1.110117	0.29456192	0.4985281	1	3538 tags=24%, list=18%, signal=30%
BIOCARTA_HCMV_PATHWAY	17	-0.501166	-1.109465	0.33559322	0.49850267	1	1344 tags=18%, list=7%, signal=19%
REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE	25	-0.476211	-1.108476	0.32225913	0.4993672	1	3809 tags=36%, list=20%, signal=45%
REACTOME_REGULATION_OF_KIT_SIGNALING	16	-0.503751	-1.107359	0.34686348	0.50036967	1	3173 tags=38%, list=16%, signal=45%
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	256	-0.337356	-1.106807	0.23188406	0.49997652	1	3123 tags=21%, list=16%, signal=25%
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	16	-0.51707	-1.105278	0.3470483	0.5017767	1	440 tags=19%, list=2%, signal=19%
BIOCARTA_TNFR1_PATHWAY	29	-0.462595	-1.104239	0.33552632	0.50269186	1	1344 tags=14%, list=7%, signal=15%
BIOCARTA_PTDINS_PATHWAY	23	-0.474425	-1.104193	0.3293919	0.50136846	1	2981 tags=30%, list=15%, signal=36%
BIOCARTA_PYK2_PATHWAY	28	-0.449802	-1.100692	0.31647635	0.5076949	1	4870 tags=50%, list=25%, signal=67%
KEGG_LONG_TERM_DEPRESSION	64	-0.397104	-1.100001	0.31268436	0.5077271	1	2656 tags=23%, list=14%, signal=27%
KEGG_GLIOMA	65	-0.39348	-1.097129	0.28998506	0.5124475	1	1959 tags=15%, list=10%, signal=17%
KEGG_NOTCH_SIGNALING_PATHWAY	47	-0.419176	-1.096718	0.33873582	0.5118793	1	1099 tags=11%, list=6%, signal=11%
REACTOME_METABOLISM_OF_RNA	253	-0.334426	-1.096622	0.24632353	0.51062983	1	1447 tags=9%, list=7%, signal=10%
BIOCARTA_PGC1A_PATHWAY	22	-0.475156	-1.095482	0.3457627	0.5117489	1	4866 tags=55%, list=25%, signal=73%
REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	19	-0.476785	-1.095473	0.34234235	0.5103461	1	2912 tags=37%, list=15%, signal=43%
KEGG_PPAR_SIGNALING_PATHWAY	68	-0.390824	-1.094451	0.2996988	0.51108366	1	2419 tags=19%, list=13%, signal=22%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	26	-0.464463	-1.093581	0.3321492	0.51159096	1	2538 tags=35%, list=13%, signal=40%
REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	18	-0.487044	-1.093115	0.33507854	0.5111199	1	184 tags=6%, list=1%, signal=6%
KEGG_TYPE_II_DIABETES_MELLITUS	47	-0.416686	-1.089206	0.31861198	0.5181733	1	1797 tags=15%, list=9%, signal=16%
BIOCARTA_PPARA_PATHWAY	57	-0.392948	-1.085892	0.32394367	0.523908	1	2815 tags=25%, list=15%, signal=29%
KEGG_RIBOSOME	87	-0.371166	-1.085585	0.3190883	0.5231396	1	4604 tags=23%, list=24%, signal=30%
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	33	-0.436159	-1.085148	0.33816424	0.5226871	1	4074 tags=30%, list=21%, signal=38%
KEGG_PYRIMIDINE_METABOLISM	97	-0.363398	-1.084785	0.3252841	0.52203506	1	1862 tags=10%, list=10%, signal=11%
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	404	-0.317065	-1.081011	0.255441	0.52888036	1	2985 tags=20%, list=15%, signal=23%
REACTOME_SYNTHESIS_OF_DNA	84	-0.371862	-1.080351	0.31355932	0.5289308	1	820 tags=8%, list=4%, signal=9%
REACTOME_G_PROTEIN_ACTIVATION	27	-0.452733	-1.071306	0.36038962	0.54668665	1	983 tags=11%, list=5%, signal=12%
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	23	-0.457677	-1.070851	0.3602812	0.5462377	1	3809 tags=30%, list=20%, signal=38%
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	25	-0.457172	-1.070849	0.37611407	0.54477334	1	983 tags=12%, list=5%, signal=13%
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	108	-0.35609	-1.070815	0.33898306	0.5433858	1	2258 tags=19%, list=12%, signal=22%
REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	32	-0.420069	-1.069748	0.35562807	0.5442626	1	4413 tags=41%, list=23%, signal=53%
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	105	-0.358764	-1.067869	0.34081346	0.54704005	1	4604 tags=24%, list=24%, signal=31%
REACTOME_AXON_GUIDANCE	240	-0.328534	-1.067239	0.30226701	0.5469455	1	3462 tags=23%, list=18%, signal=27%
BIOCARTA_RELA_PATHWAY	16	-0.494571	-1.064334	0.39488116	0.55155075	1	336 tags=6%, list=2%, signal=6%
REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	26	-0.452353	-1.063771	0.3916811	0.5513399	1	2515 tags=19%, list=13%, signal=22%
KEGG_CALCIUM_SIGNALING_PATHWAY	176	-0.337285	-1.062221	0.33200532	0.5533128	1	3628 tags=29%, list=19%, signal=35%
KEGG_N_GLYCAN_BIOSYNTHESIS	46	-0.398898	-1.059284	0.365105	0.5580384	1	1656 tags=11%, list=9%, signal=12%
REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRCADIAN_EXPRESSION	35	-0.428123	-1.057949	0.37460318	0.55956787	1	5020 tags=46%, list=26%, signal=62%
BIOCARTA_P38MAPK_PATHWAY	39	-0.417989	-1.0578	0.3729097	0.5584405	1	2656 tags=23%, list=14%, signal=27%
BIOCARTA_RARRXR_PATHWAY	15	-0.492446	-1.056043	0.40036562	0.56087255	1	2670 tags=20%, list=14%, signal=23%
BIOCARTA_ARF_PATHWAY	17	-0.471814	-1.055033	0.3882784	0.56169415	1	1307 tags=18%, list=7%, signal=19%
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	44	-0.404463	-1.054895	0.36741215	0.5605588	1	1497 tags=18%, list=8%, signal=20%
REACTOME_TIE2_SIGNALING	17	-0.482759	-1.054886	0.3958724	0.5591161	1	2656 tags=29%, list=14%, signal=34%
BIOCARTA_HER2_PATHWAY	22	-0.461691	-1.054484	0.3927928	0.5585103	1	4276 tags=50%, list=22%, signal=64%
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	67	-0.377427	-1.053861	0.38271606	0.5584472	1	2762 tags=15%, list=14%, signal=17%
BIOCARTA_CDMAC_PATHWAY	16	-0.481448	-1.051808	0.41476274	0.56160456	1	4233 tags=38%, list=22%, signal=48%
REACTOME_SIGNALING_BY_ERBB2	97	-0.353557	-1.049357	0.37518036	0.56541425	1	2990 tags=21%, list=15%, signal=24%
BIOCARTA_GPCR_PATHWAY	34	-0.41603	-1.048439	0.39765102	0.56589085	1	4834 tags=50%, list=25%, signal=67%
REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE	53	-0.384905	-1.042973	0.37360892	0.5766309	1	3970 tags=34%, list=21%, signal=43%
KEGG_MAPK_SIGNALING_PATHWAY	261	-0.317284	-1.038492	0.36887255	0.58499134	1	3352 tags=23%, list=17%, signal=27%
BIOCARTA_NGF_PATHWAY	18	-0.459649	-1.03081	0.43806103	0.6000782	1	4276 tags=50%, list=22%, signal=64%
KEGG_TRYPTOPHAN_METABOLISM	40	-0.400247	-1.028785	0.41867954	0.6030014	1	938 tags=10%, list=5%, signal=10%
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS	30	-0.415101	-1.026478	0.42611682	0.6067225	1	4378 tags=43%, list=23%, signal=56%
REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	17	-0.480522	-1.025088	0.44122967	0.60815364	1	3569 tags=29%, list=18%, signal=36%
REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	19	-0.453022	-1.020847	0.42293906	0.6161227	1	983 tags=11%, list=5%, signal=11%
REACTOME_MEMBRANE_TRAFFICKING	125	-0.335665	-1.019346	0.4220963	0.61784196	1	3612 tags=22%, list=19%, signal=26%
REACTOME_SIGNALING_BY_NOTCH	99	-0.34091	-1.016574	0.41949153	0.6223086	1	3159 tags=19%, list=16%, signal=23%
REACTOME_SIGNALING_BY_FGFR_MUTANTS	42	-0.385512	-1.016126	0.43275863	0.62184525	1	3994 tags=31%, list=21%, signal=39%
KEGG_VEGF_SIGNALING_PATHWAY	72	-0.354863	-1.013895	0.44285715	0.6251812	1	2656 tags=22%, list=14%, signal=26%
REACTOME_S_PHASE	100	-0.338898	-1.010254	0.44701087	0.6316583	1	820 tags=8%, list=4%, signal=8%
BIOCARTA_VEGF_PATHWAY	29	-0.414285	-1.006754	0.46231157	0.6377051	1	2896 tags=24%, list=15%, signal=28%
KEGG_PATHWAYS_IN_CANCER	324	-0.299321	-1.001483	0.48341233	0.64806145	1	3292 tags=20%, list=17%, signal=24%
KEGG_RNA_DEGRADATION	57	-0.364341	-1.000042	0.45619336	0.6497503	1	2015 tags=16%, list=10%, signal=18%
KEGG_RENAL_CELL_CARCINOMA	70	-0.353747	-0.997239	0.47058824	0.6545211	1	2292 tags=16%, list=12%, signal=18%
KEGG_GAP_JUNCTION	87	-0.341918	-0.997061	0.4594203	0.6533123	1	4276 tags=29%, list=22%, signal=37%
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	183	-0.313626	-0.994515	0.46700507	0.6574292	1	3875 tags=26%, list=20%, signal=32%
REACTOME_MRNA_3_END_PROCESSING	25	-0.420299	-0.992634	0.47517732	0.66009074	1	39 tags=4%, list=0%, signal=4%
REACTOME_METABOLISM_OF_NUCLEOTIDES	71	-0.348037	-0.992489	0.45454547	0.65880483	1	2001 tags=14%, list=10%, signal=16%
REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR	97	-0.332678	-0.986434	0.4797601	0.6707273	1	4344 tags=31%, list=22%, signal=40%
REACTOME_SIGNALING_BY_HIPPO	18	-0.4481	-0.986207	0.5036232	0.6696511	1	3502 tags=33%, list=18%, signal=41%
REACTOME_LIGAND_GATED_ION_CHANNEL_TRANSPORT	20	-0.431206	-0.985841	0.49468085	0.6688357	1	214 tags=5%, list=1%, signal=5%
BIOCARTA_TFF_PATHWAY	21	-0.431958	-0.982473	0.48404256	0.67491245	1	2998 tags=29%, list=16%, signal=34%
REACTOME_SIGNALLING_TO_ERKS	35	-0.381799	-0.977621	0.5	0.68443096	1	3380 tags=29%, list=17%, signal=35%
KEGG_DORSO_VENTRAL_AXIS_FORMATION	24	-0.42114	-0.977245	0.4851658	0.68365556	1	1081 tags=13%, list=6%, signal=13%
BIOCARTA_BCELLSURVIVAL_PATHWAY	16	-0.451405	-0.976417	0.5207207	0.68388087	1	890 tags=19%, list=5%, signal=20%
REACTOME_CELL_CELL_COMMUNICATION	118	-0.324869	-0.975049	0.5088677	0.6852273	1	3485 tags=27%, list=18%, signal=33%

REACTOME_ARMS_MEDIATED_ACTIVATION	17	-0.445623	-0.970375	0.5045872	0.6940878	1	2656 tags=29%, list=14%, signal=34%
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	33	-0.38322	-0.968216	0.48013246	0.6972836	1	3514 tags=33%, list=18%, signal=41%
KEGG_NON_SMALL_CELL_LUNG_CANCER	54	-0.353092	-0.968044	0.5101404	0.6960412	1	2896 tags=22%, list=15%, signal=26%
REACTOME_PLATELET_SENSITIZATION_BY_LDL	16	-0.446553	-0.964688	0.5244755	0.7018641	1	1409 tags=19%, list=7%, signal=20%
REACTOME_SIGNALING_BY_FGFR	108	-0.321006	-0.964462	0.5129683	0.7007499	1	3970 tags=26%, list=21%, signal=32%
REACTOME_BOTULINUM_NEUROTOXICITY	18	-0.432385	-0.962706	0.5391791	0.70293224	1	4510 tags=39%, list=23%, signal=51%
BIOCARTA_AT1R_PATHWAY	32	-0.391861	-0.960235	0.5551948	0.70693296	1	4276 tags=44%, list=22%, signal=56%
REACTOME_PI3K_AKT_ACTIVATION	36	-0.377461	-0.959666	0.51602024	0.7065133	1	2990 tags=17%, list=15%, signal=20%
BIOCARTA_GCR_PATHWAY	19	-0.423312	-0.954876	0.5257353	0.71546537	1	3396 tags=32%, list=18%, signal=38%
REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	51	-0.356865	-0.954564	0.5321101	0.71446073	1	2164 tags=20%, list=11%, signal=22%
BIOCARTA_NO1_PATHWAY	30	-0.388464	-0.95295	0.53872055	0.7165132	1	3712 tags=37%, list=19%, signal=45%
REACTOME_PROTEIN_FOLDING	49	-0.353858	-0.943082	0.5670262	0.7369504	1	2418 tags=18%, list=13%, signal=21%
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	31	-0.387811	-0.942353	0.5555556	0.7369288	1	4737 tags=42%, list=25%, signal=55%
REACTOME_CIRCADIAN_CLOCK	51	-0.351092	-0.941849	0.551447	0.7362477	1	5020 tags=39%, list=26%, signal=53%
REACTOME_PKB_MEDIATED_EVENTS	28	-0.387509	-0.939345	0.5557432	0.7401274	1	3622 tags=29%, list=19%, signal=35%
REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	16	-0.425899	-0.937692	0.5727612	0.7421494	1	3537 tags=31%, list=18%, signal=38%
REACTOME_NEURONAL_SYSTEM	273	-0.281988	-0.93718	0.6326034	0.7415921	1	3568 tags=23%, list=18%, signal=28%
REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	18	-0.423878	-0.936198	0.5637584	0.7421517	1	1386 tags=11%, list=7%, signal=12%
REACTOME_HDL_MEDIATED_LIPID_TRANSPORT	15	-0.434654	-0.936025	0.56499135	0.74090046	1	1311 tags=27%, list=7%, signal=29%
REACTOME_NETRIN1_SIGNALING	38	-0.364688	-0.935823	0.56856185	0.73964256	1	3144 tags=26%, list=16%, signal=31%
REACTOME_AMYLOIDS	75	-0.325659	-0.932441	0.5936556	0.745424	1	371 tags=4%, list=2%, signal=4%
KEGG_CITRATE_CYCLE_TCA_CYCLE	30	-0.379963	-0.932182	0.5618557	0.7443212	1	1067 tags=10%, list=6%, signal=11%
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	42	-0.357327	-0.928301	0.5711974	0.75106597	1	3859 tags=36%, list=20%, signal=45%
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	44	-0.349697	-0.924223	0.5897858	0.7584087	1	2234 tags=18%, list=12%, signal=21%
BIOCARTA_TGFB_PATHWAY	19	-0.40907	-0.923902	0.5681416	0.757426	1	3350 tags=26%, list=17%, signal=32%
BIOCARTA_NOS1_PATHWAY	21	-0.409491	-0.92378	0.54810995	0.7560048	1	4834 tags=48%, list=25%, signal=63%
BIOCARTA_INTRINSIC_PATHWAY	23	-0.390224	-0.922436	0.5566836	0.7571662	1	1057 tags=9%, list=5%, signal=9%
BIOCARTA_CALCINEURIN_PATHWAY	18	-0.409531	-0.922382	0.5539305	0.7556222	1	5409 tags=61%, list=28%, signal=85%
REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMATE_BINDING_AND_ACTIVATION	15	-0.433948	-0.920882	0.5810565	0.7570674	1	4957 tags=53%, list=26%, signal=72%
REACTOME_DEVELOPMENTAL_BIOLOGY	380	-0.271707	-0.917886	0.7146226	0.76204854	1	3516 tags=20%, list=18%, signal=24%
REACTOME_GAP_JUNCTION_TRAFFICKING	26	-0.383465	-0.916733	0.5962838	0.7628464	1	3464 tags=27%, list=18%, signal=33%
REACTOME_IRON_UPTAKE_AND_TRANSPORT	35	-0.355064	-0.916582	0.5973378	0.7614731	1	1985 tags=17%, list=10%, signal=19%
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	237	-0.280097	-0.910289	0.7023661	0.7735486	1	2051 tags=14%, list=11%, signal=15%
REACTOME_CGMP_EFFECTS	19	-0.406029	-0.906732	0.6028881	0.77939636	1	1678 tags=26%, list=9%, signal=29%
REACTOME_METABOLISM_OF_CARBOHYDRATES	234	-0.278408	-0.90519	0.6936488	0.7810137	1	2299 tags=15%, list=12%, signal=16%
REACTOME_PHOSPHOLIPID_METABOLISM	189	-0.282042	-0.903595	0.706258	0.78255063	1	2412 tags=17%, list=12%, signal=20%
REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	26	-0.372977	-0.898469	0.57719296	0.7919067	1	3099 tags=23%, list=16%, signal=27%
BIOCARTA_STRESS_PATHWAY	25	-0.37541	-0.898422	0.6016667	0.79024804	1	5008 tags=40%, list=26%, signal=54%
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	34	-0.358597	-0.897113	0.6299841	0.7912585	1	606 tags=6%, list=3%, signal=6%
KEGG_TIGHT_JUNCTION	132	-0.291938	-0.894528	0.6864407	0.79504424	1	3069 tags=23%, list=16%, signal=27%
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	44	-0.338545	-0.894328	0.6259905	0.7937518	1	1447 tags=14%, list=7%, signal=15%
BIOCARTA_IGF1R_PATHWAY	23	-0.385855	-0.89196	0.63468015	0.79695755	1	4276 tags=39%, list=22%, signal=50%
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	80	-0.306387	-0.886686	0.68136555	0.806062	1	3689 tags=20%, list=19%, signal=25%
REACTOME_SPHINGOLIPID_METABOLISM	62	-0.319659	-0.881528	0.6651652	0.8151163	1	2412 tags=21%, list=12%, signal=24%
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	134	-0.285087	-0.879148	0.7170596	0.81836677	1	1545 tags=7%, list=8%, signal=8%
REACTOME_G1_S_TRANSITION	100	-0.297324	-0.87738	0.7152875	0.8203834	1	820 tags=6%, list=4%, signal=6%
BIOCARTA_SPPA_PATHWAY	22	-0.376874	-0.873499	0.6469565	0.82673436	1	353 tags=9%, list=2%, signal=9%
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	31	-0.354414	-0.872449	0.65384614	0.82720834	1	983 tags=10%, list=5%, signal=10%
KEGG_ARACHIDONIC_ACID_METABOLISM	52	-0.320204	-0.868166	0.6818898	0.8344223	1	2148 tags=17%, list=11%, signal=19%
REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	17	-0.395942	-0.867998	0.62593985	0.83301467	1	1381 tags=24%, list=7%, signal=25%
BIOCARTA_DEATH_PATHWAY	33	-0.343652	-0.866823	0.6586621	0.8335814	1	3920 tags=30%, list=20%, signal=38%
REACTOME_CELL_CYCLE_CHECKPOINTS	105	-0.287915	-0.862334	0.73399717	0.841165	1	1539 tags=10%, list=8%, signal=10%
REACTOME_SIGNALING_BY_NOTCH1	68	-0.303303	-0.860368	0.7279522	0.8435582	1	3159 tags=18%, list=16%, signal=21%
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	47	-0.320603	-0.856963	0.7156398	0.84890324	1	3620 tags=28%, list=19%, signal=34%
REACTOME_LIPOPROTEIN_METABOLISM	28	-0.35804	-0.856519	0.67450273	0.84793144	1	1311 tags=18%, list=7%, signal=19%
REACTOME_GLYCOSPHINGOLIPID_METABOLISM	37	-0.336066	-0.85444	0.6896552	0.8504125	1	2412 tags=27%, list=12%, signal=31%
REACTOME_HS_GAG_BIOSYNTHESIS	30	-0.356622	-0.852934	0.6828859	0.85142523	1	2164 tags=27%, list=11%, signal=30%
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	23	-0.369259	-0.852754	0.6695502	0.8500207	1	4158 tags=35%, list=22%, signal=44%
BIOCARTA_FMLP_PATHWAY	36	-0.340408	-0.848916	0.6955782	0.85592735	1	3396 tags=25%, list=18%, signal=30%
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	53	-0.31447	-0.846977	0.7362805	0.8578314	1	1245 tags=9%, list=6%, signal=10%
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	84	-0.292357	-0.84612	0.73631126	0.85779506	1	3684 tags=25%, list=19%, signal=31%
BIOCARTA_MEF2D_PATHWAY	18	-0.384372	-0.844088	0.68904597	0.8601148	1	4834 tags=44%, list=25%, signal=59%
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	25	-0.35681	-0.84242	0.6863085	0.86166286	1	3809 tags=28%, list=20%, signal=35%
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	38	-0.33196	-0.841664	0.71666664	0.8614031	1	3299 tags=24%, list=17%, signal=29%
REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSION_BY_REV_ERBA	23	-0.358683	-0.840125	0.6678832	0.8626311	1	5020 tags=39%, list=26%, signal=53%
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	461	-0.245098	-0.837695	0.91799545	0.8656167	1	3045 tags=16%, list=16%, signal=19%
REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	59	-0.306786	-0.836995	0.758567	0.86517835	1	3612 tags=25%, list=19%, signal=31%
BIOCARTA_ALK_PATHWAY	36	-0.331712	-0.834148	0.71828663	0.86889523	1	3478 tags=33%, list=18%, signal=41%
REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	52	-0.308819	-0.828382	0.73748106	0.87815934	1	3612 tags=23%, list=19%, signal=28%
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	67	-0.29311	-0.826474	0.7687688	0.8798793	1	3907 tags=27%, list=20%, signal=34%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	-0.388997	-0.823883	0.72924185	0.8830593	1	1923 tags=27%, list=10%, signal=30%
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_DIFFERENTIATION	72	-0.293074	-0.823771	0.7837838	0.8814764	1	2765 tags=15%, list=14%, signal=18%
KEGG_RIBOFLAVIN_METABOLISM	16	-0.381305	-0.823631	0.69055945	0.8799664	1	2828 tags=19%, list=15%, signal=22%
KEGG_PEROXISOME	77	-0.289162	-0.822847	0.7990798	0.8796867	1	2977 tags=16%, list=15%, signal=18%
REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	25	-0.337739	-0.807737	0.7314189	0.905947	1	3258 tags=20%, list=17%, signal=24%
KEGG_TYROSINE_METABOLISM	42	-0.3094	-0.807263	0.7852459	0.90497744	1	2202 tags=17%, list=11%, signal=19%
KEGG_PHENYLALANINE_METABOLISM	18	-0.366754	-0.803018	0.7395105	0.910497	1	2202 tags=22%, list=11%, signal=25%
KEGG_FATTY_ACID_METABOLISM	40	-0.309703	-0.801484	0.7986577	0.9114154	1	2150 tags=15%, list=11%, signal=17%
REACTOME_NEPHRIN_INTERACTIONS	19	-0.35611	-0.798169	0.7395264	0.9153925	1	3485 tags=37%, list=18%, signal=45%
BIOCARTA_CHREBP2_PATHWAY	42	-0.298881	-0.786037	0.8085443	0.93395734	1	4344 tags=24%, list=22%, signal=31%
BIOCARTA_ARAP_PATHWAY	17	-0.362499	-0.785083	0.76731795	0.9336748	1	315 tags=6%, list=2%, signal=6%
REACTOME_GAP_JUNCTION_ASSEMBLY	17	-0.359771	-0.784586	0.7447619	0.9326489	1	3464 tags=24%, list=18%, signal=29%
REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	25	-0.327569	-0.782257	0.78797996	0.9349113	1	1678 tags=20%, list=9%, signal=22%
KEGG_CARDIAC_MUSCLE_CONTRACTION	73	-0.270239	-0.77037	0.8690293	0.95224786	1	4671 tags=33%, list=24%, signal=43%
REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	33	-0.308056	-0.770083	0.8160535	0.95074993	1	3569 tags=24%, list=18%, signal=30%
REACTOME_CHOLESTEROL_BIOSYNTHESIS	21	-0.326952	-0.769279	0.7993139	0.9500953	1	1494 tags=5%, list=8%, signal=5%
KEGG_P53_SIGNALING_PATHWAY	67	-0.272832	-0.764343	0.8852459	0.9557723	1	4491 tags=34%, list=23%, signal=45%
KEGG_PARKINSONS_DISEASE	113	-0.24915	-0.763139	0.9366906	0.9557083	1	1601 tags=5%, list=8%, signal=6%
REACTOME_EGFR_DOWNREGULATION	24	-0.327482	-0.760683	0.79422385	0.95744157	1	3583 tags=21%, list=19%, signal=26%
KEGG_THYROID_CANCER	29	-0.31501	-0.759661	0.82434785	0.95703655	1	3277 tags=24%, list=17%, signal=29%
BIOCARTA_CERAMIDE_PATHWAY	22	-0.325695	-0.758563	0.79122806	0.9567969	1	4233 tags=32%, list=22%, signal=41%
REACTOME_MYOGENESIS	26	-0.320043	-0.756724	0.81219906	0.95765746	1	2046 tags=15%, list=11%, signal=17%
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	27	-0.310829	-0.756071	0.8238342	0.9567992	1	4957 tags=44%, list=26%, signal=60%
REACTOME_GAB1_SIGNALOSOME	36	-0.291817	-0.753247	0.84210527	0.958943	1	3733 tags=22%, list=19%, signal=27%
REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION	24	-0.325288	-0.752397	0.83716816	0.95822674	1	5020 tags=38%, list=26%, signal=51%
REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING	36	-0.293664	-0.749966	0.86023295	0.9597224	1	2990 tags=14%, list=15%, signal=16%
REACTOME_SIGNAL_TRANSDUCTION_BY_L1	34	-0.296101	-0.746702	0.8444816	0.9622165	1	4233 tags=26%, list=22%, signal=34%
REACTOME_SIGNALLING_TO_RAS	27	-0.309243	-0.743087	0.8662207	0.96515465	1	4344 tags=33%, list=22%, signal=43%
BIOCARTA_MPR_PATHWAY	34	-0.29558	-0.738817	0.8447412	0.9687628	1	3712 tags=26%, list=19%, signal=33%
KEGG_PYRUVATE_METABOLISM	40	-0.281557	-0.73252	0.88412696	0.974995	1	3335 tags=20%, list=17%, signal=24%
REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	21	-0.314665	-0.731361	0.8581436	0.9745677	1	1523 tags=14%, list=8%, signal=15%
REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	38	-0.28415	-0.727653	0.87122416	0.97704875	1	774 tags=5%, list=4%, signal=5%
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	44	-0.28045	-0.726944	0.89891136	0.97597516	1	39 tags=2%, list=0%, signal=2%
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	44	-0.277938	-0.726369	0.88584477	0.9748169	1	1290 tags=7%, list=7%, signal=7%
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	17	-0.336341	-0.726304	0.8576923	0.97303367	1	4957 tags=53%, list=26%, signal=71%
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	22	-0.311671	-0.72618	0.8521257	0.97134197	1	1644 tags=9%, list=9%, signal=10%
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	102	-0.244219	-0.724692	0.95522386	0.9712469	1	4608 tags=22%, list=24%, signal=28%
REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION	27	-0.300795	-0.723559	0.8689655	0.97073364	1	716 tags=7%, list=4%, signal=8%
BIOCARTA_SPRY_PATHWAY	18	-0.322004	-0.718511	0.8350877	0.9747039	1	2656 tags=22%, list=14%, signal=26%

REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	20	-0.320024	-0.715567	0.8460177	0.9760173	1	4503	tags=30%, list=23%, signal=39%
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	15	-0.335895	-0.714253	0.83302754	0.9755561	1	2148	tags=33%, list=11%, signal=37%
REACTOME_METAL_ION_SLC_TRANSPORTERS	22	-0.309791	-0.71005	0.8894831	0.9782005	1	1683	tags=14%, list=9%, signal=15%
REACTOME_PI3K_CASCADE	68	-0.249406	-0.706686	0.9582043	0.9797577	1	3970	tags=24%, list=21%, signal=30%
REACTOME_L1CAM_INTERACTIONS	84	-0.24142	-0.705869	0.9636099	0.97878844	1	3352	tags=19%, list=17%, signal=23%
REACTOME_SIGNALING_BY_BMP	22	-0.30503	-0.703371	0.8705674	0.9793487	1	3409	tags=27%, list=18%, signal=33%
REACTOME_DEADENYLATION_OF_MRNA	19	-0.312823	-0.699452	0.8938849	0.98124206	1	3622	tags=32%, list=19%, signal=39%
REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	104	-0.232768	-0.698298	0.9818689	0.98050326	1	4344	tags=27%, list=22%, signal=35%
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	21	-0.301442	-0.692932	0.9027778	0.9836121	1	2407	tags=19%, list=12%, signal=22%
KEGG_VIBRIO_CHOLERAE_INFECTION	53	-0.254406	-0.690984	0.9330065	0.9835881	1	1852	tags=13%, list=10%, signal=15%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	-0.297505	-0.684483	0.91071427	0.9872328	1	1999	tags=18%, list=10%, signal=20%
REACTOME_ENOS_ACTIVATION_AND_REGULATION	19	-0.302111	-0.679006	0.90575916	0.9898656	1	269	tags=5%, list=1%, signal=5%
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	23	-0.284239	-0.66762	0.902439	0.9963672	1	2875	tags=30%, list=15%, signal=36%
REACTOME_TRANSLATION	147	-0.21329	-0.663994	0.9945726	0.9971091	1	3977	tags=16%, list=21%, signal=20%
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	26	-0.278229	-0.661865	0.9394464	0.9966464	1	171	tags=4%, list=1%, signal=4%
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	110	-0.217884	-0.65727	0.9958449	0.9978254	1	3977	tags=16%, list=21%, signal=20%
REACTOME_PURINE_METABOLISM	33	-0.262993	-0.656635	0.950764	0.9964178	1	3856	tags=30%, list=20%, signal=38%
REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	84	-0.226203	-0.655465	0.99277455	0.99537104	1	4344	tags=26%, list=22%, signal=34%
BIOCARTA_RACCYCD_PATHWAY	26	-0.2737	-0.65368	0.9324547	0.9946653	1	2656	tags=15%, list=14%, signal=18%
BIOCARTA_ACTINY_PATHWAY	20	-0.295755	-0.649893	0.91943955	0.99524635	1	3621	tags=30%, list=19%, signal=37%
REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	19	-0.289207	-0.645917	0.94727594	0.99582535	1	4786	tags=42%, list=25%, signal=56%
REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDATION_IN_MUSCLE	18	-0.28986	-0.638158	0.9381818	0.99837476	1	3070	tags=28%, list=16%, signal=33%
REACTOME_INSULIN_RECEPTOR_RECYCLING	22	-0.275272	-0.634939	0.9300341	0.99821424	1	5227	tags=45%, list=27%, signal=62%
REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	42	-0.241929	-0.632374	0.9549249	0.9977341	1	3733	tags=17%, list=19%, signal=21%
REACTOME_METABOLISM_OF_PROTEINS	421	-0.185197	-0.630972	1	0.99663234	1	3701	tags=16%, list=19%, signal=19%
BIOCARTA_CK1_PATHWAY	17	-0.288032	-0.623582	0.914611	0.998367	1	5505	tags=47%, list=28%, signal=66%
REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	17	-0.282806	-0.61727	0.9310987	0.9994191	1	3070	tags=29%, list=16%, signal=35%
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	19	-0.267336	-0.599544	0.9607843	1	1	5253	tags=32%, list=27%, signal=43%
REACTOME_SIGNALING_BY_CONSTITUTIVELY_ACTIVE_EGFR	17	-0.265338	-0.588285	0.9634146	1	1	4276	tags=29%, list=22%, signal=38%
BIOCARTA_BARRESTIN_SRC_PATHWAY	15	-0.276628	-0.584767	0.9669725	1	1	2656	tags=27%, list=14%, signal=31%
REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	24	-0.246405	-0.57551	0.97727275	1	1	5227	tags=46%, list=27%, signal=63%
REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	15	-0.265094	-0.558964	0.9715808	1	1	2081	tags=13%, list=11%, signal=15%
KEGG_OLFACTORY_TRANSDUCTION	118	-0.183274	-0.553515	1	1	1	5426	tags=21%, list=28%, signal=29%
REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLP1	17	-0.253845	-0.544989	0.96892136	1	1	3220	tags=18%, list=17%, signal=21%
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	40	-0.204317	-0.534722	0.996748	1	1	3887	tags=18%, list=20%, signal=22%
REACTOME_SHC_RELATED_EVENTS	17	-0.242006	-0.532551	0.97806215	1	1	4344	tags=41%, list=22%, signal=53%
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	15	-0.24108	-0.519183	0.9842209	1	1	4957	tags=47%, list=26%, signal=63%
REACTOME_RECYCLING_PATHWAY_OF_L1	27	-0.210367	-0.504187	0.9935065	1	1	5710	tags=37%, list=30%, signal=52%
REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	20	-0.221099	-0.497781	0.9894921	1	1	3220	tags=15%, list=17%, signal=18%
REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	27	-0.203992	-0.485553	0.99823636	1	1	5180	tags=26%, list=27%, signal=35%
REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	20	-0.214823	-0.479978	0.9893617	1	1	4344	tags=30%, list=22%, signal=39%
BIOCARTA_P53HYPOXIA_PATHWAY	22	-0.208517	-0.476881	0.9929453	0.99877846	1	4807	tags=27%, list=25%, signal=36%
REACTOME_OLFACTORY_SIGNALING_PATHWAY	80	-0.150169	-0.427563	1	0.99907035	1	4055	tags=11%, list=21%, signal=14%

Table S20
Association between SASP signature pathway and copy number alterations in HPV-negative HNSC cell lines.

S20A
Logistic Regression for the prediction of SASP enrichment in HNSC cell lines (CCLE) - after separating arm-level and focal-level loss at 9p21.3
Distinction between tumors showing arm-only, focal-only events and a combination of both.

SASP enrichment
Top and bottom 35% of the distributions were considered.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 Loss: ARM	-3.465736	-2.619891	0.008796	0.017592	0.03125	binary
9p21.3 Loss: FOCAL	-2.772589	-1.711297	0.087026	0.087026	0.0625	binary

For each copy number event, we used copy number values after standardization.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 copy number ARM Level	0.7924514	1.646595	0.099641	0.199283	2.208804	continuous
9p21.3 copy number FOCAL Level	-34.3869968	-0.006174	0.995074	0.995074	1.16E-15	continuous

SASP enrichment
Top and bottom 50% of the distributions were considered.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 Loss: ARM	-1.856298	-2.155478	0.031124	0.062249	0.15625	binary
9p21.3 Loss: FOCAL	-1.974081	-1.552584	0.120523	0.120523	0.138889	binary

For each copy number event, we used copy number values after standardization.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 copy number ARM Level	0.4695842	1.186006	0.23562	0.47124	1.599329	continuous
9p21.3 copy number FOCAL Level	-33.6715041	-0.006905	0.994491	0.994491	2.38E-15	continuous

SASP enrichment
Top and bottom 35% of the distributions were considered.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 Loss: ARM	-4.852692	-2.509997	0.012073	0.03622	0.007807	binary
9p21.3 Loss: FOCAL	-4.884157	-2.112046	0.034683	0.052024	0.007565	binary
SCNA level	-1.531852	-1.718469	0.085711	0.085711	0.216135	continuous

For each copy number event, we used copy number values after standardization.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
9p21.3 copy number ARM Level	0.8971552	1.763381	0.077836	0.233509	2.452616	continuous
9p21.3 copy number FOCAL Level	-34.017447	-0.005999	0.995214	0.995214	1.68E-15	continuous
SCNA level	-0.6681904	-1.22247	0.22153	0.332295	0.512635	continuous

S20B
Logistic Regression for the prediction of SASP enrichment in HNSC cell lines (CCLE) - after separating arm-level and focal-level loss at 3p14.
Distinction between tumors showing arm-only, focal-only events and a combination of both.

SASP enrichment
Top and bottom 35% of the distributions were considered.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss: ARM	-0.5596158	-0.420888	0.673837	0.673837	0.571429	binary
3p14 Loss: FOCAL	-1.7917595	-1.064464	0.287118	0.574237	0.166667	binary

For each copy number event, we used copy number values after standardization.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 copy number ARM Level	-0.3296374	-0.64421	0.519439	0.519439	0.719184	continuous
3p14 copy number FOCAL Level	0.9255492	1.015226	0.309998	0.519439	2.523254	continuous

SASP enrichment
Top and bottom 50% of the distributions were considered.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss: ARM	-0.2231436	-0.221307	0.824853	0.824853	0.8	binary
3p14 Loss: FOCAL	-1.7917595	-1.241368	0.21447	0.42894	0.166667	binary

For each copy number event, we used copy number values after standardization.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 copy number ARM Level	-0.4207858	-0.964783	0.334654	0.334654	0.656531	continuous
3p14 copy number FOCAL Level	0.9358364	1.08422	0.278267	0.334654	2.549345	continuous

SASP enrichment
Top and bottom 35% of the distributions were considered.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 Loss: ARM	-0.5015306	-0.373447	0.708816	0.708816	0.605603	binary
3p14 Loss: FOCAL	-1.733305	-1.017104	0.309104	0.563351	0.176699	binary
SCNA level	-0.4339868	-0.886093	0.375568	0.563351	0.647921	continuous

For each copy number event, we used copy number values after standardization.

	β coefficient	z value	Pr(>|z|)	FDR	OR	
3p14 copy number ARM Level	-0.1552262	-0.287761	0.77353	0.77353	0.856221	continuous
3p14 copy number FOCAL Level	1.2632036	1.188531	0.234624	0.383654	3.536734	continuous
SCNA level	-0.6588638	-1.136447	0.255769	0.383654	0.517439	continuous

Table S21

GSEA Analysis on TCGA HNSC comparing tumors with or without 9p21.3 focal loss, Pathways Depleted

NAME	SIZE	ES	NES	NOM p-value	FDR q-value	FWER p-value	RANK AT MAX
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	264	-0.742234	-2.292991	0	0	0	2613
KEGG_CHEMOKINE_SIGNALING_PATHWAY	188	-0.749268	-2.251939	0	0	0	2153
KEGG_HEMATOPOIETIC_CELL_LINEAGE	81	-0.802782	-2.217916	0	0	0	2503
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	55	-0.851982	-2.217695	0	0	0	1297
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	108	-0.76475	-2.189447	0	0	0	2196
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	56	-0.829581	-2.170076	0	0	0	956
REACTOME_TCR_SIGNALING	44	-0.846303	-2.125368	0	0	0	2043
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	127	-0.73128	-2.105545	0	0	0	2417
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	291	-0.673445	-2.102669	0	0	0	2168
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	68	-0.771634	-2.081329	0	0	0	2398
KEGG_AUTOIMMUNE_THYROID_DISEASE	32	-0.874516	-2.076328	0	0	0	729
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	189	-0.683625	-2.073621	0	0	0	2399
REACTOME_IL_3_5_AND_GM_CSF_SIGNALING	43	-0.818815	-2.061079	0	0	0	2196
BIOCARTA_NKT_PATHWAY	29	-0.885884	-2.060921	0	0	0	962
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	95	-0.72968	-2.046607	0	0	0	2370
KEGG_PRIMARY_IMMUNODEFICIENCY	35	-0.844103	-2.043252	0	0	0	1293
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	75	-0.746561	-2.039286	0	0	0	2012
REACTOME_SIGNALING_BY_ILS	105	-0.713522	-2.028774	0	0	0	2639
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	181	-0.672615	-2.02734	0	0	0	2168
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	494	-0.635082	-2.019429	0	0	0	2386
KEGG_CELL_ADHESION_MOLECULES_CAMS	113	-0.703601	-2.019334	0	0	0	2142
KEGG_LEISHMANIA_INFECTION	58	-0.769515	-2.01745	0	0	0	2695
REACTOME_SIGNALING_BY_RHO_GTPASES	108	-0.702615	-2.01603	0	0	0	2485
BIOCARTA_DC_PATHWAY	22	-0.906632	-2.012431	0	0	0	1523
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	55	-0.770181	-1.999051	0	0	0	2196
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	115	-0.700603	-1.998796	0	0	0	2386
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	31	-0.84926	-1.997065	0	0	0	2196
KEGG_JAK_STAT_SIGNALING_PATHWAY	155	-0.67441	-1.989023	0	0	0	2591
BIOCARTA_IL12_PATHWAY	21	-0.906364	-1.988609	0	0	0	1011
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	195	-0.659439	-1.986084	0	3.5319E-05	0.001	2216
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	63	-0.74603	-1.985421	0	3.418E-05	0.001	2366
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	84	-0.71434	-1.978127	0	3.3111E-05	0.001	2012
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	20	-0.906687	-1.976623	0	3.2108E-05	0.001	1134
BIOCARTA_TCR_PATHWAY	44	-0.777444	-1.974054	0	3.1164E-05	0.001	1068
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	102	-0.704237	-1.968291	0	3.0273E-05	0.001	2033
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	34	-0.804833	-1.967404	0	2.9432E-05	0.001	2095
REACTOME_DOWNSTREAM_TCR_SIGNALING	27	-0.852225	-1.952277	0	2.8637E-05	0.001	1978
BIOCARTA_NO2IL12_PATHWAY	17	-0.917641	-1.948843	0	2.7883E-05	0.001	1011
REACTOME_IL_2_SIGNALING	41	-0.769562	-1.937786	0	2.7168E-05	0.001	2133
REACTOME_INNATE_IMMUNE_SYSTEM	245	-0.634177	-1.936764	0	2.6489E-05	0.001	2731
REACTOME_IL_RECEPTOR_SHC_SIGNALING	27	-0.842633	-1.936123	0	2.5843E-05	0.001	2120
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	251	-0.626084	-1.934381	0	2.5228E-05	0.001	3229
REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS	26	-0.831642	-1.91976	0	4.8178E-05	0.002	2196
BIOCARTA_TOB1_PATHWAY	19	-0.88697	-1.908442	0	9.4987E-05	0.004	552
KEGG_ALLOGRAFT_REJECTION	17	-0.895781	-1.903015	0	0.00011609	0.005	729
REACTOME_INTERFERON_GAMMA_SIGNALING	48	-0.744522	-1.895014	0	0.00015934	0.007	1772
BIOCARTA_CTLA4_PATHWAY	17	-0.910292	-1.891062	0	0.00020061	0.009	737
KEGG_FOCAL_ADHESION	198	-0.62096	-1.887991	0	0.00024078	0.011	3400
BIOCARTA_IL2RB_PATHWAY	38	-0.76146	-1.884378	0	0.00025781	0.012	2695
KEGG_TYPE_I_DIABETES_MELLITUS	23	-0.841885	-1.881528	0	0.00029511	0.014	2274
BIOCARTA_INFLAM_PATHWAY	27	-0.819869	-1.880547	0	0.00033169	0.016	2572
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	79	-0.693618	-1.870394	0	0.00040671	0.02	2302
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	57	-0.713458	-1.869709	0	0.00039903	0.02	3494
REACTOME_GPCR_LIGAND_BINDING	392	-0.589916	-1.869605	0	0.00039164	0.02	2168
REACTOME_DEFENSINS	26	-0.809382	-1.868269	0	0.00044243	0.023	2061
SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE	60	-0.706388	-1.868164	0	0.00043453	0.023	3028
REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS	16	-0.898091	-1.865408	0	0.00046301	0.025	1624
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	30	-0.79269	-1.864714	0	0.00047263	0.026	2657
REACTOME_HEMOSTASIS	446	-0.585125	-1.860758	0	0.00051856	0.029	2229
REACTOME_TOLL_RECEPTOR_CASCADES	113	-0.642552	-1.860327	0	0.00050992	0.029	2033
KEGG_GRAFT_VERSUS_HOST_DISEASE	19	-0.863988	-1.854514	0	0.00050156	0.029	2274
BIOCARTA_IL17_PATHWAY	15	-0.906131	-1.849743	0	0.00054389	0.032	956
BIOCARTA_COMP_PATHWAY	18	-0.864405	-1.841274	0	0.00073451	0.044	2293
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATION_OF_SECOND_MESSENGERS	29	-0.787253	-1.83993	0	0.00073953	0.045	2196
BIOCARTA_BCR_PATHWAY	34	-0.77032	-1.838327	0	0.00072815	0.045	1077
BIOCARTA_INTEGRIN_PATHWAY	38	-0.747978	-1.833357	0	0.0007969	0.05	2982
REACTOME_COMPLEMENT_CASCADE	29	-0.769795	-1.826173	0	0.00089633	0.057	2293
BIOCARTA_MAL_PATHWAY	19	-0.840702	-1.822159	0	0.00105282	0.066	104
BIOCARTA_CYTOKINE_PATHWAY	21	-0.826564	-1.821488	0	0.00105249	0.067	2572
BIOCARTA_CSK_PATHWAY	20	-0.821244	-1.818392	0	0.00109602	0.071	737
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	77	-0.662961	-1.811923	0	0.00127123	0.082	2196
BIOCARTA_LAIR_PATHWAY	17	-0.853393	-1.80988	0	0.00132686	0.086	2302
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	28	-0.766864	-1.79482	0	0.0018527	0.123	897
BIOCARTA_TH1TH2_PATHWAY	17	-0.847456	-1.788309	0.00169779	0.00209621	0.141	2226
BIOCARTA_GH_PATHWAY	28	-0.754163	-1.780022	0	0.00243321	0.161	2946
BIOCARTA_PDGF_PATHWAY	32	-0.73942	-1.77919	0.00149925	0.0024012	0.161	3033
BIOCARTA_EDG1_PATHWAY	27	-0.754652	-1.778589	0	0.00242428	0.164	1070
REACTOME_BETA_DEFENSINS	20	-0.816018	-1.778012	0.00166667	0.00242013	0.166	1493
BIOCARTA_KERATINOCYTE_PATHWAY	46	-0.696477	-1.777099	0	0.0024287	0.168	3033
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_	19	-0.820607	-1.775206	0	0.002478	0.174	2193
BIOCARTA_IL10_PATHWAY	17	-0.83126	-1.766941	0.00170648	0.00280661	0.201	2255
KEGG_ECM_RECEPTOR_INTERACTION	83	-0.640653	-1.766569	0	0.00278564	0.201	3507
REACTOME_PI_METABOLISM	47	-0.693876	-1.762804	0	0.00291711	0.213	2657
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	55	-0.675039	-1.760272	0	0.00316895	0.227	2421
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	25	-0.754909	-1.754906	0.00163399	0.00347986	0.25	897
BIOCARTA_CCR3_PATHWAY	23	-0.779055	-1.754422	0.00166389	0.0034764	0.252	360
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	114	-0.60954	-1.746453	0	0.00419487	0.293	1716
BIOCARTA_TPO_PATHWAY	24	-0.759864	-1.745161	0.00336134	0.00419426	0.296	2695
BIOCARTA_STATHMIN_PATHWAY	19	-0.796134	-1.744099	0.00167504	0.00424101	0.3	488
REACTOME_G_ALPHA1213_SIGNALLING_EVENTS	73	-0.643407	-1.742479	0	0.00428799	0.306	2485
BIOCARTA_NKCELLS_PATHWAY	19	-0.794392	-1.733895	0.0017301	0.00506039	0.353	1872
BIOCARTA_CARDIACEGF_PATHWAY	18	-0.794438	-1.733457	0	0.00503932	0.356	986
BIOCARTA_CCR5_PATHWAY	17	-0.826707	-1.729567	0.00165289	0.00535783	0.377	847
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	79	-0.62681	-1.727778	0.00133511	0.00550039	0.39	4250
REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	28	-0.736586	-1.72768	0.00335008	0.00544249	0.39	2816
BIOCARTA_RAS_PATHWAY	23	-0.770531	-1.72661	0.00172414	0.00548279	0.393	347
BIOCARTA_ECM_PATHWAY	24	-0.766203	-1.72522	0	0.00561046	0.403	2639
BIOCARTA_IL22BP_PATHWAY	16	-0.824661	-1.7242	0	0.00561661	0.407	2255
BIOCARTA_IL7_PATHWAY	17	-0.80047	-1.721741	0	0.00582518	0.419	3229
BIOCARTA_IL1R_PATHWAY	33	-0.715325	-1.720954	0	0.0058399	0.422	3033
KEGG_APOPTOSIS	87	-0.615936	-1.709869	0	0.00703405	0.493	2455
BIOCARTA_TOLL_PATHWAY	37	-0.693246	-1.697251	0.00149925	0.0088153	0.57	3033
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	113	-0.596236	-1.695772	0	0.00899513	0.582	2865
REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	79	-0.612834	-1.688733	0	0.01018093	0.632	2485
BIOCARTA_TALL1_PATHWAY	15	-0.817322	-1.688689	0	0.0100941	0.632	1722
BIOCARTA_EGF_PATHWAY	31	-0.707932	-1.686926	0.00155763	0.01019553	0.639	3033
KEGG_ASTHMA	16	-0.808934	-1.686909	0.00343053	0.01011026	0.639	2127
REACTOME_INTERFERON_SIGNALING	142	-0.57273	-1.683359	0	0.0107059	0.664	3214
BIOCARTA_IL2_PATHWAY	22	-0.777284	-1.679677	0.00170648	0.01128868	0.687	2695
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	210	-0.55336	-1.679506	0	0.01118606	0.687	2845
BIOCARTA_FCER1_PATHWAY	38	-0.679379	-1.678671	0	0.01130165	0.695	2695
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	21	-0.758414	-1.678311	0	0.01128558	0.698	3094
BIOCARTA_CTCF_PATHWAY	23	-0.758626	-1.677733	0.00321027	0.01137063	0.706	2990
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	18	-0.792905	-1.675924	0.00170358	0.01160292	0.712	2587
BIOCARTA_PAR1_PATHWAY	37	-0.683886	-1.67538	0	0.01159248	0.713	1872

KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	62	-0.630392	-1.671431	0	0.01233345	0.736	3360
KEGG_DILATED_CARDIOMYOPATHY	90	-0.59619	-1.668399	0	0.0128125	0.749	4338
REACTOME_MUSCLE_CONTRACTION	46	-0.646011	-1.652671	0.00465839	0.01629043	0.842	5139
BIOCARTA_BIOPEPTIDES_PATHWAY	42	-0.67045	-1.652132	0.00296736	0.01626728	0.842	2639
BIOCARTA_MET_PATHWAY	37	-0.669912	-1.646509	0.00458716	0.01763634	0.874	2695
BIOCARTA_IL3_PATHWAY	15	-0.801685	-1.643559	0.00175747	0.0182464	0.883	2695
BIOCARTA_HSP27_PATHWAY	15	-0.787767	-1.641959	0.00362319	0.01841535	0.884	1716
BIOCARTA_UCALPAIN_PATHWAY	18	-0.764903	-1.633432	0.00537634	0.02072281	0.917	2216
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	126	-0.563503	-1.632505	0.00126103	0.02083539	0.919	3033
REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	43	-0.650854	-1.630501	0.00286944	0.02129059	0.922	2875
REACTOME_SEMAPHORIN_INTERACTIONS	63	-0.606604	-1.629019	0.00143885	0.0214959	0.924	2943
BIOCARTA_NTHI_PATHWAY	24	-0.718644	-1.628111	0.00642055	0.02161578	0.926	2274
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	83	-0.591253	-1.627239	0	0.02168313	0.927	4338
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	53	-0.626244	-1.618171	0.00421348	0.02425834	0.954	883
REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING	27	-0.699539	-1.617699	0.00813008	0.02415294	0.954	2216
BIOCARTA_HDAC_PATHWAY	28	-0.695341	-1.61651	0.00624025	0.02430492	0.956	2417
REACTOME_STRIATED_MUSCLE_CONTRACTION	27	-0.69255	-1.607475	0.00651466	0.02722768	0.971	5139
REACTOME_REGULATION_OF_KIT_SIGNALING	16	-0.75361	-1.606755	0.00874126	0.02723465	0.971	2300
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	74	-0.595791	-1.605957	0.0027137	0.02734423	0.971	4338
KEGG_LYSOSOME	121	-0.5561	-1.604335	0.00128205	0.0276439	0.971	2612
KEGG_COLORECTAL_CANCER	62	-0.598733	-1.601968	0.0058309	0.02827909	0.974	602
REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT	16	-0.760536	-1.60002	0.01016949	0.02891152	0.978	1981
REACTOME_CD28_CO_STIMULATION	31	-0.66871	-1.598181	0.00453172	0.02934243	0.979	2196
BIOCARTA_TFF_PATHWAY	21	-0.72556	-1.597179	0.00943396	0.02958937	0.98	602
BIOCARTA_PML_PATHWAY	17	-0.743112	-1.59675	0.01039861	0.02954267	0.981	1716
REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLLAPSE	24	-0.710219	-1.5967	0.0064	0.02937017	0.981	2802
BIOCARTA_GLEEVEC_PATHWAY	23	-0.720289	-1.596598	0.00796178	0.02917836	0.981	3033
BIOCARTA_INSULIN_PATHWAY	22	-0.712828	-1.596073	0.01954397	0.02924681	0.982	2695
KEGG_PRION_DISEASES	35	-0.65215	-1.595044	0.01550388	0.02941279	0.983	4098
KEGG_VIRAL_MYOCARDITIS	50	-0.613213	-1.594547	0.00596125	0.02941425	0.983	2392
BIOCARTA_PYK2_PATHWAY	28	-0.683245	-1.585683	0.00794913	0.03281055	0.99	79
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK	198	-0.517379	-1.583484	0	0.03341423	0.992	2188
BIOCARTA_IL6_PATHWAY	22	-0.696846	-1.578147	0.01680672	0.03570303	0.995	4501
KEGG_ADHERENS_JUNCTION	73	-0.57823	-1.569133	0.01068091	0.03933208	0.998	3053
REACTOME_PLC_BETA_MEDIATED_EVENTS	42	-0.619745	-1.566345	0.01517451	0.04043821	0.998	1681
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	24	-0.695275	-1.559209	0.01451613	0.04347286	0.999	2946
REACTOME_CTLA4_INHIBITORY_SIGNALING	21	-0.718799	-1.558378	0.01967213	0.04364198	0.999	2825
REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	177	-0.528994	-1.55823	0.00120482	0.04343182	0.999	2412
BIOCARTA_STEM_PATHWAY	15	-0.760411	-1.557504	0.01960784	0.04350454	0.999	534
BIOCARTA_CDMAC_PATHWAY	16	-0.741458	-1.55729	0.02076125	0.04332513	0.999	3002
KEGG_ENDOCYTOSIS	174	-0.518822	-1.555011	0	0.04416064	0.999	1934
REACTOME_SIGNALLING_BY_NGF	212	-0.51087	-1.554184	0	0.04425851	0.999	2990
REACTOME_SIGNALING_BY_PDGF	118	-0.544624	-1.553788	0.0025974	0.04417202	0.999	3400
BIOCARTA_CXCR4_PATHWAY	24	-0.681266	-1.550176	0.01442308	0.04580964	0.999	847
REACTOME_INTRINSIC_PATHWAY	16	-0.745222	-1.544655	0.02430556	0.04875248	0.999	3000
BIOCARTA_CDC42RAC_PATHWAY	16	-0.743383	-1.544123	0.02241379	0.04881601	0.999	1872
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	44	-0.613608	-1.539838	0.02228826	0.05094184	0.999	2246
REACTOME_REGULATION_OF_IFNA_SIGNALING	24	-0.680989	-1.533255	0.02725724	0.05446777	0.999	2255
BIOCARTA_PTDINS_PATHWAY	23	-0.686619	-1.53231	0.01525424	0.05467153	0.999	179
REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC	15	-0.759429	-1.530927	0.03071672	0.05521235	0.999	3268
REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	58	-0.58473	-1.530603	0.00728863	0.05501143	0.999	3515
BIOCARTA_IGF1_PATHWAY	21	-0.698162	-1.52935	0.01311475	0.05538808	0.999	2695
REACTOME_REGULATION_OF_INSULIN_SECRETION	90	-0.545244	-1.525665	0.00801068	0.05712585	0.999	1681
BIOCARTA_RHO_PATHWAY	32	-0.644173	-1.524865	0.01421801	0.05732876	0.999	2216
BIOCARTA_CASPASE_PATHWAY	23	-0.672076	-1.524113	0.02931596	0.05741806	0.999	2261
REACTOME_PEPTIDE_CHAIN_ELONGATION	86	-0.546961	-1.524042	0.00536193	0.05711947	0.999	3614
KEGG_ACUTE_MYELOID_LEUKEMIA	57	-0.57766	-1.520186	0.00957592	0.05905014	0.999	3181
REACTOME_ACTIVATED_TLR4_SIGNALLING	90	-0.545749	-1.514908	0.00265604	0.06201743	1	4206
KEGG_ENDOMETRIAL_CANCER	52	-0.582613	-1.509277	0.01402525	0.06538955	1	2743
BIOCARTA_RACCYCD_PATHWAY	26	-0.64753	-1.508626	0.02664577	0.06542542	1	10
BIOCARTA_NGF_PATHWAY	18	-0.699714	-1.50815	0.03367003	0.06535196	1	2695
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	270	-0.486279	-1.504829	0.00111359	0.06745562	1	2437
KEGG_TYPE_II_DIABETES_MELLITUS	47	-0.600031	-1.504452	0.01603499	0.06729527	1	1991
BIOCARTA_ERYTH_PATHWAY	15	-0.71924	-1.498394	0.03773585	0.07112219	1	2329
BIOCARTA_AT1R_PATHWAY	32	-0.623603	-1.495185	0.02515723	0.07307788	1	4501
BIOCARTA_SPRY_PATHWAY	18	-0.692277	-1.490389	0.0281457	0.07611768	1	2639
REACTOME_IL1_SIGNALING	38	-0.604657	-1.489283	0.02006173	0.07652487	1	3007
KEGG_TGF_BETA_SIGNALING_PATHWAY	85	-0.540917	-1.489261	0.00534759	0.07611807	1	3919
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	30	-0.637896	-1.488961	0.03692762	0.07593893	1	4206
REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR7_8_OR_9_ACTIVATION	74	-0.550616	-1.487663	0.01664355	0.07652906	1	3330
BIOCARTA_FMLP_PATHWAY	36	-0.610087	-1.486546	0.03560372	0.07695738	1	3033
BIOCARTA_BAD_PATHWAY	26	-0.656272	-1.475254	0.03015873	0.08520204	1	2639
KEGG_RENIN_ANGIOTENSIN_SYSTEM	17	-0.700428	-1.474358	0.04240283	0.08537347	1	3306
BIOCARTA_41BB_PATHWAY	17	-0.709863	-1.471852	0.057041	0.08676319	1	3033
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	21	-0.670164	-1.470981	0.02970297	0.08703759	1	2196
REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	17	-0.689733	-1.4706	0.0552677	0.08687951	1	3007
KEGG_RIBOSOME	87	-0.525062	-1.468272	0.01340483	0.08820937	1	3044
REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE	25	-0.634253	-1.468232	0.0477707	0.08780106	1	1180
REACTOME_DAG_AND_IP3_SIGNALING	31	-0.622538	-1.46808	0.04287902	0.0874513	1	2271
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	44	-0.586523	-1.467525	0.01911765	0.08742791	1	1265
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	-0.529474	-1.466076	0.01778386	0.08809236	1	3148
KEGG_GLIOMA	65	-0.544722	-1.463146	0.01793104	0.08985844	1	2639
BIOCARTA_HER2_PATHWAY	22	-0.654092	-1.461824	0.03934426	0.09062172	1	4405
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	86	-0.529561	-1.460863	0.01560468	0.09095229	1	3722
REACTOME_SIGNALING_BY_SCF_KIT	75	-0.534468	-1.460757	0.0125	0.09059791	1	2990
REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	31	-0.612682	-1.459642	0.04231975	0.09109361	1	2428
KEGG_ERBB_SIGNALING_PATHWAY	87	-0.51999	-1.45674	0.01324503	0.0930089	1	2677
REACTOME_SMOOTH_MUSCLE_CONTRACTION	23	-0.640687	-1.454758	0.04444445	0.09426531	1	4250
BIOCARTA_BARRESTIN_SRC_PATHWAY	15	-0.719809	-1.454427	0.03832753	0.0940964	1	838
BIOCARTA_AKAPCENTROSOME_PATHWAY	15	-0.698637	-1.454059	0.06187291	0.09402178	1	2
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	31	-0.621148	-1.453834	0.0304	0.09375476	1	2075
REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	33	-0.611713	-1.450963	0.0462963	0.09565572	1	3373
REACTOME_SIGNALING_BY_FGFR1_FUSION_MUTANTS	17	-0.690503	-1.448701	0.06434783	0.09723327	1	2423
BIOCARTA_GSK3_PATHWAY	27	-0.61822	-1.44846	0.04	0.09700345	1	3002
KEGG_LONG_TERM_DEPRESSION	67	-0.532496	-1.447143	0.02272727	0.09760033	1	2825
REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	80	-0.527053	-1.446895	0.0171278	0.0973765	1	4162
BIOCARTA_VIP_PATHWAY	26	-0.635477	-1.440786	0.05076923	0.10225481	1	4968
BIOCARTA_NFKB_PATHWAY	23	-0.654547	-1.434301	0.03896104	0.1076555	1	3033
BIOCARTA_MCALPAIN_PATHWAY	25	-0.626379	-1.429929	0.0464	0.11117759	1	4320
KEGG_RENAL_CELL_CARCINOMA	70	-0.537984	-1.429312	0.0286123	0.11128471	1	2639
REACTOME_LIPOPROTEIN_METABOLISM	28	-0.614669	-1.42589	0.05993691	0.11424387	1	3302
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_	44	-0.569577	-1.425133	0.04090909	0.1145151	1	3360
BIOCARTA_ERK5_PATHWAY	17	-0.678648	-1.423893	0.07653061	0.1151104	1	2639
BIOCARTA_NFAT_PATHWAY	52	-0.547859	-1.422375	0.04608939	0.11601607	1	2639
REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	38	-0.572784	-1.421529	0.0436747	0.11633328	1	3979
REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE	134	-0.484946	-1.420308	0.01629073	0.11690541	1	1948
KEGG_CALCIUM_SIGNALING_PATHWAY	177	-0.470897	-1.417636	0.00722022	0.11888433	1	2782
REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_DAI	18	-0.665963	-1.41645	0.08390411	0.11951831	1	3986
BIOCARTA_EPO_PATHWAY	19	-0.657005	-1.415127	0.06365159	0.12039886	1	2695
BIOCARTA_GPCR_PATHWAY	34	-0.581975	-1.414589	0.0398773	0.120334	1	4937
REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	21	-0.645281	-1.411477	0.06456953	0.12283492	1	897
REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	70	-0.52411	-1.411338	0.02545969	0.12242872	1	4098
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	71	-0.523833	-1.410038	0.02920723	0.12301318	1	2058
BIOCARTA_SPPA_PATHWAY	22	-0.639598	-1.409903	0.06844741	0.12259563	1	1788
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	121	-0.493094	-1.409348	0.02080624	0.12255239	1	2223
REACTOME_TRAF6_MEDIATED_NFKB_ACTIVATION	21	-0.638124	-1.408014	0.06810631	0.12338173	1	3803
BIOCARTA_HIVNEF_PATHWAY	58	-0.541892	-1.404606	0.03268945	0.12614371	1	3594
BIOCARTA_CALCINEURIN_PATHWAY	18	-0.650399	-1.404346	0.07532957	0.1259413	1	4937
BIOCARTA_AKT_PATHWAY	22	-0.626818	-1.403329	0.05948553	0.12645933	1	3810

REACTOME_GRB2_SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTERGRINS_	15	-0.676475	-1.403101	0.08798646	0.1261541	1	2216
REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	15	-0.686568	-1.402283	0.07597173	0.1264311	1	2216
KEGG_VEGF_SIGNALING_PATHWAY	74	-0.519611	-1.401256	0.02881844	0.12699646	1	2063
REACTOME_RAP1_SIGNALLING	16	-0.663652	-1.401175	0.08241759	0.12653409	1	2319
BIOCARTA_TNFR2_PATHWAY	18	-0.662195	-1.400087	0.08034188	0.1271186	1	3033
BIOCARTA_TID_PATHWAY	19	-0.644629	-1.398608	0.07068966	0.12810019	1	3002
REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLP1	18	-0.664004	-1.392044	0.07304348	0.13455933	1	602
REACTOME_BASIGIN_INTERACTIONS	24	-0.61007	-1.386966	0.05762712	0.13931361	1	144
KEGG_AXON_GUIDANCE	129	-0.478732	-1.386269	0.02075702	0.13951808	1	2677
REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BETA_PATHWAYS	72	-0.506172	-1.383998	0.03688525	0.14142068	1	3986
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	91	-0.491519	-1.383062	0.0379085	0.14189608	1	2990
KEGG_INSULIN_SIGNALING_PATHWAY	137	-0.470689	-1.38066	0.0163728	0.14392315	1	2639
BIOCARTA_RAC1_PATHWAY	23	-0.61323	-1.380163	0.0862069	0.14389111	1	4772
BIOCARTA_PTEN_PATHWAY	18	-0.640367	-1.377446	0.10291595	0.14647594	1	4405
REACTOME_SYNTHESIS_SECRETION_AND_DEACYLATION_OF_GHRELIN	16	-0.648734	-1.376775	0.11599297	0.14658041	1	1285
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	35	-0.577083	-1.376367	0.07255521	0.14651522	1	2216
KEGG_GAP_JUNCTION	87	-0.488525	-1.372932	0.03571429	0.14983837	1	3396
KEGG_GNRH_SIGNALING_PATHWAY	99	-0.486207	-1.370995	0.03041825	0.15138744	1	3148
KEGG_NON_SMALL_CELL_LUNG_CANCER	54	-0.525878	-1.370919	0.06530612	0.15087222	1	585
BIOCARTA_MYOSIN_PATHWAY	31	-0.570239	-1.364864	0.08782743	0.15745035	1	1789
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	229	-0.442985	-1.361626	0.01144165	0.16074342	1	2470
REACTOME_SIGNAL_AMPLIFICATION	31	-0.572429	-1.360704	0.08201893	0.16114871	1	1117
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	49	-0.533103	-1.360428	0.05685131	0.1608802	1	2428
REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	72	-0.500562	-1.358764	0.04946524	0.1620556	1	4206
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	42	-0.545588	-1.357354	0.07993967	0.16328141	1	2810
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	105	-0.480236	-1.356628	0.0448718	0.16348232	1	2271
REACTOME_AXON_GUIDANCE	240	-0.440711	-1.353653	0.01363636	0.16631845	1	4184
BIOCARTA_LONGEVITY_PATHWAY	15	-0.670164	-1.353421	0.09189189	0.16596876	1	2946
REACTOME_INFLAMMASOMES	16	-0.65491	-1.352921	0.11245675	0.16599296	1	3175
REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKS_COMPLEX	23	-0.605562	-1.351722	0.09983897	0.1668208	1	3803
BIOCARTA_MEF2D_PATHWAY	18	-0.62936	-1.349735	0.10452962	0.16866305	1	1226
REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	117	-0.470399	-1.348675	0.02688861	0.16942467	1	1681
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	28	-0.58343	-1.347267	0.09448819	0.17048049	1	2980
BIOCARTA_MAPK_PATHWAY	86	-0.489233	-1.341992	0.04133333	0.17633894	1	3033
REACTOME_COLLAGEN_FORMATION	58	-0.513114	-1.341962	0.07103064	0.1757147	1	3639
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	64	-0.506361	-1.341512	0.06388889	0.17565094	1	3586
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	76	-0.485196	-1.339685	0.05858311	0.17720528	1	1991
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	106	-0.467711	-1.332455	0.05026455	0.18576458	1	718
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	67	-0.487176	-1.331703	0.0545977	0.1860832	1	2386
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	120	-0.465933	-1.330693	0.04805195	0.18666625	1	2437
KEGG_MAPK_SIGNALING_PATHWAY	264	-0.431245	-1.330207	0.01791713	0.1865704	1	2845
REACTOME_OPIOID_SIGNALLING	77	-0.488637	-1.328747	0.07047872	0.18788747	1	2417
REACTOME_NCAM1_INTERACTIONS	39	-0.542983	-1.327029	0.09531014	0.1894384	1	3539
BIOCARTA_PPARA_PATHWAY	57	-0.511913	-1.325489	0.08333334	0.1908556	1	3167
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES	93	-0.469313	-1.324817	0.06048387	0.19098964	1	2428
BIOCARTA_VEGF_PATHWAY	29	-0.567646	-1.324392	0.10485133	0.19090568	1	2283
BIOCARTA_ACH_PATHWAY	16	-0.638592	-1.320373	0.13485114	0.19546348	1	3810
BIOCARTA_CREB_PATHWAY	27	-0.56702	-1.314695	0.12779553	0.20220733	1	2639
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	38	-0.542303	-1.312887	0.11463047	0.20398279	1	3586
BIOCARTA_GATA3_PATHWAY	16	-0.628329	-1.310165	0.12937063	0.20704578	1	4320
BIOCARTA_HCMV_PATHWAY	17	-0.619141	-1.304941	0.14814815	0.21377745	1	3033
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	-0.623344	-1.301784	0.16725352	0.21735898	1	2612
BIOCARTA_TGFB_PATHWAY	19	-0.603919	-1.301084	0.14770798	0.21772127	1	2639
KEGG_MELANOGENESIS	101	-0.460751	-1.300573	0.05687831	0.21776713	1	1424
REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS	15	-0.620569	-1.293704	0.14736842	0.22696872	1	1414
KEGG_LONG_TERM_POTENTIATION	70	-0.478561	-1.293567	0.09090909	0.22636777	1	2680
BIOCARTA_PGC1A_PATHWAY	22	-0.583046	-1.293469	0.14808652	0.22577326	1	5206
REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	16	-0.620704	-1.291015	0.15734266	0.22853851	1	3703
REACTOME_SIGNALLING_TO_RAS	27	-0.558403	-1.290244	0.14330709	0.2288405	1	47
REACTOME_CA_DEPENDENT_EVENTS	29	-0.554131	-1.288672	0.14084508	0.23024108	1	2271
REACTOME_PEROXISOMAL_LIPID_METABOLISM	20	-0.582756	-1.28592	0.13770492	0.23352738	1	3167
REACTOME_SIGNALING_BY_BMP	22	-0.582696	-1.284128	0.13804714	0.23553315	1	4511
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS	31	-0.540186	-1.283441	0.14045802	0.23579419	1	3010
REACTOME_PLATELET_HOMEOSTASIS	76	-0.468918	-1.283215	0.10410959	0.23541388	1	2825
KEGG_GALACTOSE_METABOLISM	26	-0.563879	-1.282154	0.13015874	0.23606321	1	441
REACTOME_NOD1_2_SIGNALING_PATHWAY	29	-0.549308	-1.281645	0.13354531	0.23599133	1	3360
KEGG_PANCREATIC_CANCER	70	-0.474035	-1.280383	0.10183875	0.2371502	1	1991
BIOCARTA_IGF1R_PATHWAY	23	-0.578317	-1.277966	0.15024233	0.24000019	1	4405
REACTOME_ARMS_MEDIATED_ACTIVATION	17	-0.599615	-1.277275	0.17574692	0.24018042	1	2639
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	110	-0.449113	-1.276241	0.08333334	0.24099831	1	718
REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	19	-0.585949	-1.275418	0.16442953	0.2413654	1	2639
REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	15	-0.613584	-1.269209	0.19081272	0.2500821	1	1903
BIOCARTA_ALK_PATHWAY	36	-0.521489	-1.268469	0.13656388	0.25042248	1	4186
REACTOME_GLYCOSPHINGOLIPID_METABOLISM	37	-0.518536	-1.266861	0.12480974	0.25201067	1	3462
KEGG_OTHER_GLYCAN_DEGRADATION	16	-0.611397	-1.265828	0.17171717	0.25268817	1	2612
REACTOME_EICOSANOID_LIGAND_BINDING_RECEPTORS	15	-0.619944	-1.265708	0.18620689	0.25203535	1	3774
REACTOME_HDL_MEDIATED_LIPID_TRANSPORT	15	-0.620119	-1.262366	0.17352416	0.25644755	1	3302
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	80	-0.458405	-1.261563	0.10597826	0.25693303	1	3373
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	27	-0.549562	-1.260549	0.15714286	0.2577905	1	2816
KEGG_CITRATE_CYCLE_TCA_CYCLE	30	-0.529634	-1.260297	0.17209302	0.25740466	1	143
KEGG_PROSTATE_CANCER	88	-0.453998	-1.25979	0.10981912	0.25735897	1	3148
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	27	-0.527331	-1.257478	0.16020235	0.26019296	1	1414
REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	30	-0.533447	-1.256256	0.15384616	0.26124233	1	3431
REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	27	-0.539108	-1.253556	0.17377567	0.26486662	1	4724
REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	32	-0.526318	-1.253159	0.15846154	0.26463485	1	1788
KEGG_TIGHT_JUNCTION	132	-0.429163	-1.251461	0.08226221	0.26644322	1	2954
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	30	-0.52539	-1.25102	0.15562403	0.26627702	1	4511
BIOCARTA_ETS_PATHWAY	18	-0.588958	-1.24732	0.16958041	0.27119863	1	584
REACTOME_APOPTOTIC_EXECUTION_PHASE	52	-0.479891	-1.243537	0.14623338	0.27658632	1	3803
BIOCARTA_CD40_PATHWAY	15	-0.605888	-1.241347	0.19190142	0.27919662	1	3033
REACTOME_G_PROTEIN_ACTIVATION	27	-0.534634	-1.240828	0.17100978	0.27913794	1	897
REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS	43	-0.488746	-1.238196	0.16966967	0.28265092	1	2059
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	34	-0.512285	-1.235043	0.1734375	0.2869616	1	487
REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPORTERS	17	-0.582856	-1.230295	0.20797227	0.29402646	1	3251
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	23	-0.548609	-1.228177	0.21357615	0.296763	1	2412
REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	33	-0.510166	-1.227828	0.1858006	0.29641423	1	3009
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	23	-0.552578	-1.222878	0.19306931	0.30418253	1	2193
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	108	-0.429331	-1.221075	0.12710765	0.3063593	1	3532
REACTOME_SIGNALING_BY_ERBB2	97	-0.430912	-1.21992	0.124834	0.30727828	1	2271
REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	50	-0.482964	-1.218749	0.15797317	0.30841628	1	2059
REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	26	-0.530694	-1.217765	0.22258064	0.3091604	1	4134
REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	21	-0.561757	-1.215004	0.20330578	0.31312087	1	602
KEGG_PATHWAYS_IN_CANCER	324	-0.389079	-1.213604	0.06229508	0.31452727	1	2849
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNA	135	-0.415627	-1.210643	0.13032581	0.31895775	1	2511
REACTOME_GABA_RECEPTOR_ACTIVATION	52	-0.465173	-1.208345	0.18518518	0.32217667	1	2135
BIOCARTA_NOS1_PATHWAY	21	-0.540757	-1.204061	0.22442244	0.32874063	1	2417
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	37	-0.492976	-1.203331	0.18769716	0.3291522	1	2754
REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDATION_IN_MUSCLE	18	-0.55886	-1.202586	0.23965517	0.32958728	1	1294
REACTOME_SIGNALLING_TO_ERKS	36	-0.498677	-1.202453	0.20029673	0.32885185	1	1510
KEGG_TYROSINE_METABOLISM	42	-0.479913	-1.20167	0.21028744	0.32932892	1	1621
REACTOME_ION_CHANNEL_TRANSPORT	54	-0.457738	-1.19897	0.17945008	0.3330815	1	3009
REACTOME_PI3K_AKT_ACTIVATION	36	-0.502116	-1.193607	0.22290076	0.34174278	1	1872
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	33	-0.497246	-1.189302	0.22762951	0.34862608	1	2816
KEGG_ARACHIDONIC_ACID_METABOLISM	56	-0.448221	-1.187871	0.19027181	0.35014957	1	3098
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	44	-0.470558	-1.185269	0.19642857	0.3537875	1	2440
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	80	-0.432201	-1.184505	0.18588874	0.35400024	1	3268
REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	15	-0.571378	-1.183018	0.24828768	0.35564417	1	10
KEGG_PPAR_SIGNALING_PATHWAY	69	-0.437442	-1.182956	0.16867469	0.35474482	1	2992
REACTOME_GABA_B_RECEPTOR_ACTIVATION	38	-0.481458	-1.181055	0.23088455	0.3572038	1	2135

REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFATASE_ACTIVATION	26	-0.510059	-1.180783	0.22955975	0.35671353	1	3000
BIOCARTA_STRESS_PATHWAY	25	-0.52063	-1.179367	0.24132231	0.35817626	1	4501
BIOCARTA_ARAP_PATHWAY	17	-0.557737	-1.176027	0.28428093	0.36346	1	258
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	45	-0.467991	-1.174302	0.22385861	0.36574054	1	2045
BIOCARTA_GCR_PATHWAY	19	-0.53773	-1.171616	0.2591362	0.369762	1	2038
REACTOME_PLATELET_SENSITIZATION_BY_LDL	16	-0.559624	-1.161094	0.27040815	0.38849932	1	1558
KEGG_MTOR_SIGNALING_PATHWAY	52	-0.448288	-1.156717	0.22401172	0.39613065	1	2639
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	53	-0.448011	-1.156424	0.2514535	0.3955733	1	2417
REACTOME_DEVELOPMENTAL_BIOLOGY	381	-0.367468	-1.155941	0.12982832	0.39545703	1	3586
BIOCARTA_EIF4_PATHWAY	24	-0.508947	-1.155087	0.2676282	0.3960253	1	2639
BIOCARTA_NDKDYNAMIN_PATHWAY	18	-0.542122	-1.152949	0.30232558	0.39908817	1	5276
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	184	-0.383384	-1.152885	0.18757467	0.39813858	1	2816
REACTOME_SPHINGOLIPID_METABOLISM	62	-0.436384	-1.15015	0.24005681	0.4023613	1	3462
REACTOME_SIGNALING_BY_ERBB4	87	-0.410334	-1.146043	0.24059139	0.40933985	1	3515
BIOCARTA_FAS_PATHWAY	30	-0.485659	-1.145231	0.26412213	0.409845	1	2289
BIOCARTA_PITX2_PATHWAY	15	-0.555044	-1.145179	0.29982045	0.40885967	1	2442
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	22	-0.519989	-1.143813	0.28341386	0.41039833	1	1691
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA	20	-0.519487	-1.141396	0.29666665	0.41404873	1	897
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	49	-0.442791	-1.138842	0.25267994	0.41778284	1	5815
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	19	-0.529266	-1.13516	0.30541873	0.4238665	1	11
REACTOME_NETRIN1_SIGNALING	38	-0.458852	-1.132752	0.29312977	0.42778936	1	4967
REACTOME_TIE2_SIGNALING	17	-0.530023	-1.130045	0.32569557	0.43196282	1	2675
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	125	-0.386936	-1.128765	0.22822087	0.43332684	1	1242
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRANE	17	-0.52696	-1.128397	0.3106961	0.43305033	1	62
REACTOME_NEURONAL_SYSTEM	276	-0.363204	-1.126892	0.21931818	0.43499562	1	2816
REACTOME_CELL_CELL_COMMUNICATION	118	-0.391045	-1.125205	0.23449132	0.4373017	1	3265
REACTOME_SHC_MEDIATED_SIGNALLING	15	-0.55198	-1.124991	0.31964287	0.43661845	1	10
KEGG_HISTIDINE_METABOLISM	29	-0.465533	-1.124376	0.28478965	0.4366905	1	2344
REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	49	-0.438483	-1.124257	0.28843337	0.4357912	1	4098
REACTOME_GAP_JUNCTION_TRAFFICKING	27	-0.488409	-1.123088	0.29372936	0.43706924	1	2310
REACTOME_SHC_RELATED_EVENTS	17	-0.528249	-1.114076	0.31871837	0.45399114	1	1285
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	102	-0.395233	-1.111468	0.28047183	0.45841122	1	718
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	24	-0.490736	-1.109422	0.32279533	0.46144217	1	2570
REACTOME_APOPTOSIS	143	-0.377532	-1.103649	0.26814267	0.4719735	1	2289
BIOCARTA_CHEMICAL_PATHWAY	22	-0.49977	-1.103446	0.32387313	0.47119123	1	2261
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	37	-0.451892	-1.102159	0.31329113	0.47263697	1	2816
REACTOME_ERK_MAPK_TARGETS	21	-0.499577	-1.101871	0.3529412	0.47192708	1	5533
REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_LIKE_PEPTIDE1	42	-0.439514	-1.097561	0.3247734	0.4797411	1	1681
REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	19	-0.500522	-1.094318	0.35332254	0.485379	1	3532
REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	20	-0.506904	-1.093729	0.34228188	0.48555037	1	10
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	180	-0.360303	-1.090858	0.26985982	0.49022737	1	3000
KEGG_REGULATION_OF_AUTOPHAGY	34	-0.448654	-1.090748	0.31202435	0.48918316	1	1285
REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	25	-0.479399	-1.090447	0.33711508	0.48857057	1	2684
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	197	-0.360001	-1.089015	0.2875895	0.4902774	1	2223
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	40	-0.430997	-1.086736	0.32618684	0.49400613	1	143
REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	22	-0.490278	-1.083428	0.35655057	0.49953002	1	10
REACTOME_TRANSLATION	147	-0.367158	-1.080565	0.308933	0.5042483	1	718
REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	121	-0.37277	-1.080146	0.31410256	0.5039138	1	3053
REACTOME_CGMP_EFFECTS	19	-0.500533	-1.077817	0.3763251	0.5076945	1	2319
BIOCARTA_INTRINSIC_PATHWAY	23	-0.478813	-1.076024	0.36453202	0.5103518	1	4209
REACTOME_EGFR_DOWNREGULATION	24	-0.473935	-1.075652	0.36201298	0.50986826	1	1599
REACTOME_PHOSPHOLIPID_METABOLISM	190	-0.355885	-1.073965	0.30741626	0.51209503	1	2657
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	105	-0.379716	-1.07261	0.33858266	0.51366884	1	718
BIOCARTA_RARRXR_PATHWAY	15	-0.515969	-1.071966	0.40034965	0.51374876	1	89
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	119	-0.371692	-1.071148	0.33846155	0.51429045	1	2307
REACTOME_MYOGENESIS	26	-0.46237	-1.068068	0.3515249	0.51941365	1	4011
REACTOME_SIGNALLING_TO_P38_VIA_RIT_AND_RIN	15	-0.522675	-1.061588	0.40388006	0.53184944	1	1445
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	60	-0.401952	-1.054974	0.38428572	0.5446754	1	268
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	85	-0.377863	-1.052649	0.37617135	0.5483477	1	2308
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	17	-0.495977	-1.050987	0.4338983	0.550471	1	2511
REACTOME_HS_GAG_DEGRADATION	20	-0.475265	-1.047161	0.4086207	0.5573639	1	56
BIOCARTA_AGR_PATHWAY	36	-0.43657	-1.045393	0.40273556	0.5599241	1	4254
BIOCARTA_CERAMIDE_PATHWAY	22	-0.472882	-1.042876	0.40239727	0.5640151	1	10
BIOCARTA_NO1_PATHWAY	30	-0.448508	-1.042647	0.40438873	0.5631154	1	4320
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	44	-0.411666	-1.041444	0.39513677	0.5643657	1	2945
KEGG_N_GLYCAN_BIOSYNTHESIS	46	-0.408228	-1.038548	0.39786586	0.5695733	1	2930
REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	18	-0.485105	-1.038076	0.4449918	0.5693325	1	4605
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	47	-0.407639	-1.029374	0.41185412	0.58706975	1	2223
BIOCARTA_ERK_PATHWAY	28	-0.448267	-1.028398	0.41455695	0.5878648	1	10
BIOCARTA_ACTINY_PATHWAY	20	-0.464374	-1.02287	0.43278688	0.5984815	1	1648
REACTOME_DIABETES_PATHWAYS	128	-0.356789	-1.022741	0.4205845	0.5973586	1	3031
BIOCARTA_P38MAPK_PATHWAY	39	-0.416178	-1.022295	0.4370258	0.59697944	1	4213
REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS	16	-0.490097	-1.02131	0.453125	0.5977925	1	4108
KEGG_ETHER_LIPID_METABOLISM	31	-0.431394	-1.020884	0.44117647	0.5972762	1	2370
KEGG_PEROXISOME	77	-0.371251	-1.019677	0.4225352	0.59843576	1	1787
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	464	-0.318204	-1.014204	0.42154813	0.6089496	1	2122
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	16	-0.486723	-1.011922	0.4567063	0.6125199	1	3381
KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	16	-0.476014	-1.009657	0.46376812	0.6161091	1	3661
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	23	-0.442012	-1.002374	0.46469623	0.6306414	1	1117
REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR	97	-0.352799	-1.00097	0.47182176	0.6321925	1	3053
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	-0.445719	-0.996776	0.46153846	0.6398733	1	659
BIOCARTA_BCELLSURVIVAL_PATHWAY	16	-0.479923	-0.99566	0.46931407	0.64091307	1	2695
REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	51	-0.387637	-0.992919	0.46438748	0.64547664	1	3532
REACTOME_SIGNALING_BY_FGFR	108	-0.346887	-0.991704	0.50449294	0.64657694	1	3053
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	409	-0.313225	-0.989029	0.5054466	0.6511014	1	3036
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	16	-0.474718	-0.981818	0.47863248	0.6654674	1	1587
KEGG_BLADDER_CANCER	42	-0.39286	-0.979746	0.50454545	0.66864955	1	3006
REACTOME_MEMBRANE_TRAFFICKING	126	-0.336886	-0.975737	0.5031686	0.6759006	1	2465
REACTOME_INSULIN_RECEPTOR_RECYCLING	23	-0.439658	-0.972901	0.5269168	0.6805923	1	4220
KEGG_ABC_TRANSPORTERS	44	-0.385633	-0.972134	0.5053599	0.6806894	1	2986
KEGG_O_GLYCAN_BIOSYNTHESIS	30	-0.412399	-0.967704	0.5211931	0.68875945	1	2633
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI	18	-0.452655	-0.966405	0.5362832	0.69006693	1	2930
REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	19	-0.450696	-0.9632	0.53266335	0.69546586	1	2364
REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE	53	-0.370636	-0.96127	0.5329513	0.6981216	1	2271
KEGG_MELANOMA	71	-0.35599	-0.958863	0.53150684	0.7019308	1	3053
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	31	-0.406731	-0.958671	0.52782196	0.70077825	1	897
BIOCARTA_DEATH_PATHWAY	33	-0.406603	-0.958544	0.51816744	0.6994775	1	4234
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	68	-0.352793	-0.955947	0.54442877	0.7036691	1	3010
KEGG_CARDIAC_MUSCLE_CONTRACTION	73	-0.347703	-0.949057	0.5390946	0.71718985	1	4343
BIOCARTA_RELA_PATHWAY	16	-0.452674	-0.948809	0.55516636	0.71618736	1	3986
REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	21	-0.432106	-0.947858	0.56543624	0.7166736	1	494
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	47	-0.369097	-0.945038	0.5647744	0.72101814	1	3979
REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	53	-0.361594	-0.943663	0.5538922	0.7224496	1	2633
KEGG_FATTY_ACID_METABOLISM	40	-0.38591	-0.943147	0.55572754	0.7220158	1	3821
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	47	-0.373115	-0.942815	0.5688351	0.72112715	1	3786
REACTOME_SIGNALING_BY_NOTCH1	68	-0.355048	-0.939093	0.55739975	0.7276962	1	4280
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	16	-0.444202	-0.934685	0.5698052	0.73537534	1	109
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	-0.412026	-0.934166	0.57283145	0.73496556	1	5533
REACTOME_POTASSIUM_CHANNELS	98	-0.327598	-0.931684	0.6016043	0.738905	1	2327
REACTOME_GAP_JUNCTION_ASSEMBLY	18	-0.438652	-0.929294	0.5671141	0.7425801	1	2310
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	27	-0.403749	-0.928515	0.5501672	0.74257225	1	4550
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	23	-0.415103	-0.927098	0.56143343	0.7440591	1	3955
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	50	-0.358479	-0.924069	0.5914286	0.7488627	1	4340
REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_TTP	17	-0.429226	-0.922459	0.58303887	0.7506229	1	3717
REACTOME_METABOLISM_OF_MRNA	209	-0.30318	-0.922049	0.64878047	0.74978137	1	2223
REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB	17	-0.441574	-0.920397	0.60720414	0.7516098	1	1681
REACTOME_IRON_UPTAKE_AND_TRANSPORT	36	-0.376395	-0.916191	0.5822785	0.7589386	1	3010
REACTOME_DEADENYLATION_OF_MRNA	19	-0.418399	-0.91467	0.58347106	0.76049614	1	164
REACTOME_METABOLISM_OF_CARBOHYDRATES	234	-0.297727	-0.914618	0.6943182	0.75900227	1	3532

REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	19	-0.41498	-0.909393	0.58894646	0.7684364	1	109
BIOCARTA_ARF_PATHWAY	17	-0.428125	-0.908937	0.6299484	0.76785415	1	2990
REACTOME_METABOLISM_OF_PROTEINS	422	-0.285477	-0.907225	0.7312296	0.76974905	1	3044
KEGG_TASTE_TRANSDUCTION	51	-0.348326	-0.904195	0.63338304	0.774478	1	2098
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_LL(	28	-0.394092	-0.901959	0.6196513	0.777535	1	3344
REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI	16	-0.438637	-0.900337	0.62432915	0.7793128	1	3431
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	19	-0.413569	-0.898448	0.6211382	0.78149563	1	3661
REACTOME_UNFOLDED_PROTEIN_RESPONSE	76	-0.330674	-0.894229	0.6526459	0.78860307	1	2440
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	61	-0.343775	-0.893682	0.6495957	0.7881682	1	2223
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	62	-0.330653	-0.89146	0.6680441	0.791114	1	2345
REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS	69	-0.331164	-0.891285	0.6676301	0.7898373	1	3661
REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	19	-0.413617	-0.889327	0.6471572	0.7922459	1	897
REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	26	-0.385801	-0.888512	0.6286201	0.79226935	1	3431
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	25	-0.394867	-0.888414	0.62222224	0.79085326	1	1117
KEGG_WNT_SIGNALING_PATHWAY	150	-0.300921	-0.887246	0.72095805	0.79167455	1	2949
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	92	-0.31852	-0.886073	0.65539664	0.7922254	1	2223
REACTOME_AMYLOIDS	76	-0.326171	-0.884749	0.66944444	0.7933415	1	2394
REACTOME_BOTULINUM_NEUROTOXICITY	18	-0.420018	-0.884047	0.62051284	0.79310703	1	2065
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	24	-0.392834	-0.882619	0.6628478	0.7942912	1	3368
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUB	57	-0.336226	-0.877202	0.66248256	0.8036385	1	5815
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	-0.409407	-0.876864	0.63468015	0.8026842	1	109
KEGG_BETA_ALANINE_METABOLISM	22	-0.393923	-0.87537	0.65139115	0.80404234	1	3821
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	26	-0.38109	-0.875035	0.63857377	0.8030728	1	3235
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	-0.369852	-0.872363	0.64162755	0.8066701	1	5935
REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	59	-0.329536	-0.868586	0.68265164	0.812729	1	4072
KEGG_BUTANOATE_METABOLISM	34	-0.359569	-0.864747	0.68621236	0.81886595	1	1896
REACTOME_ENDOGENOUS_STEROLS	15	-0.408557	-0.860498	0.66972476	0.8254858	1	4340
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.345852	-0.859603	0.7016743	0.82561976	1	659
KEGG_NOTCH_SIGNALING_PATHWAY	47	-0.33385	-0.859478	0.69777775	0.8242276	1	988
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	67	-0.322748	-0.859392	0.7197279	0.82274824	1	1716
KEGG_SPHINGOLIPID_METABOLISM	39	-0.342416	-0.851348	0.70750386	0.8364014	1	2626
REACTOME_TRNA_AMINOACYLATION	42	-0.340455	-0.847261	0.71080667	0.84269583	1	659
BIOCARTA_IGF1MTOR_PATHWAY	20	-0.391613	-0.845424	0.68585527	0.84451026	1	2825
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	81	-0.30738	-0.845097	0.7455296	0.843501	1	2223
REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_	89	-0.304972	-0.844614	0.7520107	0.84270555	1	3349
KEGG_PHENYLALANINE_METABOLISM	18	-0.390474	-0.843251	0.679868	0.8436651	1	2344
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	240	-0.271032	-0.833869	0.837963	0.8594955	1	2512
KEGG_P53_SIGNALING_PATHWAY	67	-0.308986	-0.833002	0.7479893	0.8593835	1	1892
KEGG_VIBRIO_CHOLERAE_INFECTION	54	-0.319407	-0.828957	0.754173	0.8653242	1	1626
REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	52	-0.323384	-0.82626	0.7684515	0.868613	1	4072
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	31	-0.345383	-0.826066	0.74615383	0.8672585	1	2135
REACTOME_CELL_JUNCTION_ORGANIZATION	77	-0.299217	-0.826025	0.79727894	0.865639	1	3265
KEGG_SMALL_CELL_LUNG_CANCER	84	-0.299082	-0.821688	0.7911051	0.87196344	1	3594
REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	17	-0.394891	-0.821045	0.71428573	0.8713924	1	3753
REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1	17	-0.382653	-0.819127	0.714527	0.8729953	1	3717
KEGG_INOSITOL_PHOSPHATE_METABOLISM	54	-0.310626	-0.810317	0.80780345	0.88664806	1	2523
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	65	-0.303413	-0.808838	0.8175389	0.8874882	1	1577
KEGG_STARCH_AND_SUCROSE_METABOLISM	49	-0.319043	-0.808484	0.7796374	0.8864626	1	3408
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	25	-0.35546	-0.807793	0.7451613	0.8859923	1	2135
REACTOME_DARPP_32_EVENTS	24	-0.349892	-0.80476	0.7580645	0.88959426	1	5094
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	33	-0.330969	-0.803665	0.7816265	0.88978523	1	1475
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHAS	18	-0.376164	-0.803664	0.7361111	0.88808715	1	109
REACTOME_SIGNALING_BY_NOTCH	99	-0.284701	-0.802705	0.85128206	0.8880725	1	3515
REACTOME_SIGNALING_BY_FGFR1_MUTANTS	28	-0.342527	-0.801833	0.7755102	0.887816	1	3053
REACTOME_NEPHRIN_INTERACTIONS	19	-0.369823	-0.798597	0.7350877	0.89163345	1	5792
BIOCARTA_AMI_PATHWAY	20	-0.374604	-0.794875	0.7615894	0.8960689	1	4830
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	20	-0.361479	-0.79047	0.7436333	0.9015925	1	2955
REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION	27	-0.339037	-0.788273	0.7752066	0.9033928	1	89
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	21	-0.353711	-0.787033	0.7561779	0.9037108	1	14
REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	16	-0.376249	-0.78695	0.76584506	0.90215254	1	602
BIOCARTA_MTA3_PATHWAY	19	-0.359245	-0.784736	0.7740303	0.90410954	1	4105
REACTOME_XENOBIOTICS	15	-0.375519	-0.784479	0.7474403	0.90286434	1	4760
KEGG_SELENOAMINO_ACID_METABOLISM	26	-0.340402	-0.784298	0.79375	0.90146804	1	1889
BIOCARTA_MPR_PATHWAY	34	-0.326529	-0.784008	0.7893916	0.90026	1	4320
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	-0.341931	-0.776564	0.779661	0.91003215	1	3498
REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	16	-0.373035	-0.774704	0.7804878	0.9113505	1	1197
REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	17	-0.365823	-0.77086	0.8044218	0.91568774	1	5158
REACTOME_METAL_ION_SLC_TRANSPORTERS	22	-0.343155	-0.770264	0.8039867	0.9148409	1	2378
REACTOME_PURINE_METABOLISM	33	-0.319243	-0.768295	0.796875	0.9161606	1	1796
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	116	-0.26631	-0.7652	0.9070064	0.91889834	1	290
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	34	-0.313967	-0.764318	0.84326017	0.91844934	1	3753
REACTOME_SIGNALING_BY_ROBO_RECEPTOR	29	-0.318613	-0.757674	0.83548385	0.926346	1	4671
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	33	-0.315015	-0.755597	0.8539157	0.92767715	1	1681
REACTOME_REGULATION_OF_APOPTOSIS	56	-0.289258	-0.755315	0.8809182	0.92639977	1	2223
REACTOME_SIGNAL_TRANSDUCTION_BY_L1	34	-0.311378	-0.75415	0.84076434	0.92633367	1	4665
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	43	-0.301416	-0.750408	0.8781575	0.92968476	1	1606
REACTOME_INFLUENZA_LIFE_CYCLE	136	-0.255666	-0.742948	0.9520295	0.93770105	1	718
REACTOME_GAB1_SIGNALOSOME	36	-0.300756	-0.739129	0.8556391	0.9408471	1	3307
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	134	-0.252953	-0.733906	0.9455006	0.94553185	1	1927
BIOCARTA_TNFR1_PATHWAY	29	-0.308342	-0.730797	0.86846274	0.94763726	1	4095
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	21	-0.326935	-0.724071	0.8598616	0.95381194	1	268
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	44	-0.284287	-0.718413	0.9138973	0.9584092	1	1997
REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_ACTIVITY_BY_INSULIN_LIKE_GROWTH_FACT(	16	-0.341021	-0.718235	0.83779263	0.95690286	1	2729
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	17	-0.344082	-0.718169	0.840604	0.95527446	1	3098
REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRCADIAN_EXPRESSION	36	-0.290552	-0.714093	0.9050536	0.9580055	1	3598
REACTOME_GLUCOSE_METABOLISM	64	-0.268994	-0.713682	0.9374131	0.95675236	1	1197
REACTOME_ACYL_CHAIN_REMODELLING_OF_PG	16	-0.345389	-0.713307	0.82807016	0.9554501	1	2063
KEGG_OLFACTORY_TRANSDUCTION	346	-0.225016	-0.708377	1	0.95884	1	5777
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	24	-0.307222	-0.707935	0.8982512	0.95757556	1	268
REACTOME_LIGAND_GATED_ION_CHANNEL_TRANSPORT	21	-0.316712	-0.701207	0.86551726	0.96255654	1	2898
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_SYNTHESIS	25	-0.301313	-0.69909	0.88611543	0.96281976	1	4068
KEGG_ALZHEIMERS_DISEASE	157	-0.232236	-0.69564	0.9891957	0.96431965	1	2680
REACTOME_OLFACTORY_SIGNALING_PATHWAY	284	-0.220622	-0.687443	1	0.96970683	1	6781
REACTOME_L1CAM_INTERACTIONS	84	-0.247201	-0.683925	0.9699864	0.97100705	1	4184
KEGG_LINOLEIC_ACID_METABOLISM	27	-0.292624	-0.682039	0.9052133	0.97083235	1	4812
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	29	-0.28749	-0.67827	0.92948717	0.9721099	1	5157
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TA	16	-0.32721	-0.674352	0.8863262	0.9732686	1	4095
KEGG_RNA_DEGRADATION	57	-0.25107	-0.664339	0.9739508	0.9784989	1	3822
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	27	-0.286761	-0.663613	0.9411765	0.9772409	1	3661
REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	25	-0.293277	-0.660608	0.928115	0.97747743	1	5607
REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	41	-0.258487	-0.657469	0.96879643	0.9778058	1	2980
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	44	-0.263583	-0.654998	0.9571865	0.9776515	1	89
REACTOME_CIRCADIAN_CLOCK	52	-0.24377	-0.64542	0.98107713	0.9816033	1	3961
REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	17	-0.301432	-0.643621	0.93085104	0.98083603	1	539
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	28	-0.277462	-0.642456	0.94548285	0.9797443	1	4440
KEGG_PYRUVATE_METABOLISM	40	-0.257954	-0.64213	0.9618768	0.9781831	1	2249
REACTOME_STEROID_HORMONES	29	-0.260786	-0.606871	0.9649123	0.9915026	1	3302
KEGG_DORSO_VENTRAL_AXIS_FORMATION	24	-0.26424	-0.598832	0.966129	0.99247366	1	3148
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_7ALPHA_HYDROXYCHOLESTEROL	15	-0.286393	-0.583332	0.95614034	0.99505955	1	3661
REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_D	35	-0.229453	-0.55668	0.9985251	0.9988997	1	3302
REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	38	-0.22488	-0.554937	0.9939302	0.99749184	1	4177
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	23	-0.249986	-0.554803	0.98489934	0.9957926	1	2499
REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	18	-0.245262	-0.518613	0.989547	0.9985278	1	3405
BIOCARTA_MTOR_PATHWAY	23	-0.231662	-0.518345	0.9967051	0.99685454	1	2825
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	15	-0.248614	-0.512436	0.9876543	0.9956517	1	2511

Table S22

GSEA Analysis on HNSC cancer cell lines comparing cell lines with or without 9p21.3 focal loss, Pathways Depleted

NAME	SIZE	ES	NES	NOM p-value	FDR q-value	FWER p-value	RANK AT MAX
KEGG_OLFACTORY_TRANSDUCTION	384	-0.966582	-1.570215	0	0	0	1460
REACTOME_OLFACTORY_SIGNALING_PATHWAY	322	-0.966583	-1.519536	0	0.00181627	0.003	1460
REACTOME_METABOLISM_OF_RNA	282	-0.958056	-1.501448	0	0.002426551	0.007	1565
REACTOME_METABOLISM_OF_MRNA	237	-0.958109	-1.486494	0	0.003849077	0.016	1553
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	135	-0.969243	-1.411333	0.010224949	0.065579645	0.295	1352
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	135	-0.971784	-1.38709	0.015151516	0.11254018	0.529	1242
REACTOME_INFLUENZA_LIFE_CYCLE	163	-0.947652	-1.377813	0.02504817	0.12453453	0.62	1394
REACTOME_PEPTIDE_CHAIN_ELONGATION	114	-0.979871	-1.351344	0.017408123	0.21148005	0.842	886
REACTOME_CELL_CYCLE_CHECKPOINTS	112	-0.954638	-1.338975	0.063432835	0.255265	0.917	1498
REACTOME_MEIOSIS	109	-0.968374	-1.336612	0.03018868	0.2445696	0.929	1326
REACTOME_TRANSLATION	176	-0.895932	-1.3313	0.065298505	0.25445583	0.945	1315
KEGG_OXIDATIVE_PHOSPHORYLATION	101	-0.96227	-1.319854	0.068716094	0.30401286	0.975	1656
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	130	-0.954472	-1.318634	0.06212425	0.28751013	0.977	886
REACTOME_MRNA_PROCESSING	153	-0.902436	-1.303765	0.09665427	0.35262087	0.992	1444
KEGG_LYSOSOME	119	-0.933274	-1.289031	0.09811321	0.43243542	0.997	745
REACTOME_MEIOTIC_RECOMBINATION	82	-0.97877	-1.282584	0.033771105	0.45758796	0.999	858
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	133	-0.902451	-1.279398	0.106343284	0.4559873	0.999	1444
KEGG_RIBOSOME	88	-0.962032	-1.278651	0.12723657	0.4363941	0.999	886
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	137	-0.891906	-1.277578	0.11005693	0.42162213	0.999	1315
REACTOME_M_G1_TRANSITION	79	-0.966037	-1.271325	0.123809524	0.44969657	1	1498
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	69	-0.987022	-1.264915	0.024029575	0.48383516	1	343
KEGG_PARKINSONS_DISEASE	100	-0.946655	-1.261275	0.1302682	0.4932273	1	1611
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	106	-0.917339	-1.25705	0.12660551	0.5055512	1	1167
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	117	-0.880353	-1.242042	0.16666667	0.62274367	1	1416
REACTOME_MEIOTIC_SYNAPSIS	70	-0.969883	-1.240017	0.12641509	0.61825067	1	1326
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUB SEQUENT_BINDING_TO_43S	68	-0.971781	-1.237979	0.13518198	0.61422616	1	1242
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	82	-0.940749	-1.233865	0.18410853	0.63091195	1	1498
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	66	-0.966025	-1.233612	0.16759777	0.6107023	1	1498
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	78	-0.950323	-1.230189	0.18878505	0.6243817	1	1498
REACTOME_TRANSCRIPTION	195	-0.829107	-1.229017	0.15313654	0.6146667	1	1444
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	117	-0.886442	-1.227058	0.18426104	0.6130133	1	1498
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	63	-0.966004	-1.22657	0.21003717	0.59813327	1	1498
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	64	-0.966026	-1.226354	0.2021858	0.5818355	1	1498
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	235	-0.8086	-1.226095	0.14314516	0.5669874	1	1655
KEGG_PPAR_SIGNALING_PATHWAY	67	-0.962528	-1.222725	0.25703564	0.577399	1	1644
REACTOME_RNA_POL_I_PROMOTER_OPENING	61	-0.980558	-1.219392	0.10159363	0.587706	1	858
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	66	-0.963283	-1.21815	0.2326923	0.58088434	1	1611
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	66	-0.949807	-1.213854	0.24770643	0.5996209	1	1498
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	62	-0.965959	-1.212812	0.23597679	0.591823	1	1498
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	60	-0.979851	-1.211938	0.1009009	0.5826653	1	886
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	65	-0.966484	-1.209872	0.20907298	0.5825583	1	1256
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	59	-0.975384	-1.209434	0.14857143	0.5715179	1	536
REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS	64	-0.964541	-1.206815	0.24452555	0.57914436	1	1555
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	61	-0.965275	-1.202766	0.24904214	0.59427947	1	1532
REACTOME_CHROMOSOME_MAINTENANCE	116	-0.869715	-1.19787	0.2041237	0.61800873	1	1532
KEGG_P53_SIGNALING_PATHWAY	65	-0.932707	-1.196858	0.2818533	0.61229575	1	1509
KEGG_RNA_DEGRADATION	56	-0.962447	-1.19032	0.30952382	0.64977884	1	1553
BIOCARTA_HIVNEF_PATHWAY	57	-0.967859	-1.18836	0.23782772	0.6511815	1	1413
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	55	-0.978574	-1.185622	0.14492753	0.6624674	1	946
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	55	-0.96601	-1.180831	0.27376425	0.6880872	1	1498
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEI NS_IN_LATE_MITOSIS_EARLY_G1	65	-0.940632	-1.178563	0.3012939	0.69476277	1	1498
REACTOME_HIV_INFECTION	185	-0.794107	-1.177431	0.19361277	0.6912573	1	1498
REACTOME_REGULATION_OF_APOPTOSIS	57	-0.96363	-1.176976	0.3126177	0.68258864	1	1498
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	54	-0.965988	-1.176359	0.30215827	0.67477626	1	1498
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	51	-0.964266	-1.173971	0.36452243	0.68148255	1	1352
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	52	-0.962495	-1.172961	0.3339383	0.67901456	1	1647
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	51	-0.966013	-1.172326	0.29009008	0.6724569	1	1498
REACTOME_SIGNALING_BY_WNT	63	-0.942804	-1.171382	0.330855	0.6681148	1	1498
REACTOME_ER_PHAGOSOME_PATHWAY	54	-0.966011	-1.169294	0.3	0.6743329	1	1498
REACTOME_PACKAGING_OF_TELOMERE_ENDS	48	-0.984584	-1.169184	0.11615245	0.66402787	1	680
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	54	-0.965965	-1.164918	0.3134058	0.6877373	1	1498
REACTOME_RNA_POL_I_TRANSCRIPTION	85	-0.886983	-1.161842	0.29704797	0.7029846	1	858
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	48	-0.96597	-1.161087	0.36050725	0.6975247	1	1498
KEGG_STEROID_HORMONE_BIOSYNTHESIS	52	-0.966241	-1.159654	0.32688588	0.69901687	1	1482
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	49	-0.966015	-1.159284	0.30922243	0.6908135	1	1498
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	47	-0.965971	-1.1577	0.35728157	0.6944802	1	1498
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	50	-0.965991	-1.157087	0.33716476	0.68804353	1	1498
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	402	-0.709214	-1.155713	0.17669903	0.68793213	1	1510
SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE	56	-0.939241	-1.155076	0.36753732	0.68371826	1	712
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	48	-0.96597	-1.153195	0.35365853	0.68906426	1	1498
REACTOME_MRNA_SPLICING	105	-0.834715	-1.152429	0.2919132	0.6864178	1	1444
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	48	-0.964531	-1.150882	0.33273703	0.6906865	1	1555
KEGG_N_GLYCAN_BIOSYNTHESIS	46	-0.969603	-1.150278	0.30072463	0.6858194	1	1336
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	48	-0.965993	-1.150106	0.3631068	0.67773026	1	1498
REACTOME_G2_M_CHECKPOINTS	41	-0.967095	-1.149411	0.3697632	0.67409104	1	1452
REACTOME_CELL_JUNCTION_ORGANIZATION	69	-0.899918	-1.144182	0.34593573	0.7033701	1	1100
KEGG_ABC_TRANSPORTERS	42	-0.969446	-1.143148	0.34649912	0.7028204	1	1342
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	47	-0.958232	-1.14198	0.46494466	0.7062116	1	1396
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	57	-0.927637	-1.141967	0.36635515	0.69736284	1	1498
KEGG_PROTEASOME	45	-0.965972	-1.140106	0.36555362	0.7064526	1	1498
REACTOME_AMYLOIDS	79	-0.861283	-1.139864	0.34541985	0.6993203	1	1272
REACTOME_TRNA_AMINOACYLATION	42	-0.972255	-1.1327	0.30601093	0.746862	1	1218
REACTOME_METABOLISM_OF_NON_CODING_RNA	48	-0.963298	-1.132623	0.41340783	0.7382546	1	1617
KEGG_HEMATOPOIETIC_CELL_LINEAGE	78	-0.868287	-1.131879	0.3463687	0.73699206	1	545
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	41	-0.964632	-1.131211	0.45403376	0.7329017	1	1036
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	246	-0.73071	-1.127931	0.25824177	0.75280493	1	1413
REACTOME_CELL_CELL_COMMUNICATION	109	-0.82682	-1.127834	0.30518234	0.7447584	1	1100
REACTOME_SIGNALLING_TO_ERKS	36	-0.983743	-1.125363	0.25252524	0.7576674	1	714
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	42	-0.964719	-1.124994	0.4342857	0.7517295	1	1553
REACTOME_GLYCOSPHINGOLIPID_METABOLISM	37	-0.983058	-1.122821	0.26713532	0.7657651	1	745
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	33	-0.984612	-1.122326	0.23498233	0.7610311	1	677
KEGG_GLYCEROLIPID_METABOLISM	41	-0.967145	-1.118327	0.42537314	0.78770375	1	715
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.972255	-1.117561	0.37275985	0.7854432	1	1218
KEGG_CELL_CYCLE	124	-0.799369	-1.116212	0.3001912	0.7875411	1	1509
KEGG_TRYPTOPHAN_METABOLISM	39	-0.962483	-1.115341	0.49816176	0.78837	1	1648
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	33	-0.984087	-1.113232	0.23304348	0.7983367	1	700
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	39	-0.966228	-1.111907	0.43327555	0.8009853	1	1482
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	36	-0.984086	-1.111842	0.26056337	0.7931834	1	700
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	42	-0.967162	-1.111176	0.41981983	0.7918292	1	1444
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	45	-0.961588	-1.107272	0.49371633	0.8221689	1	1690
REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	48	-0.938817	-1.106988	0.4954792	0.8160397	1	939
BIOCARTA_DEATH_PATHWAY	32	-0.992215	-1.106923	0.20274915	0.8084987	1	343
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	32	-0.986051	-1.105766	0.28	0.8106108	1	613
REACTOME_DEFENSINS	36	-0.968217	-1.104642	0.45251396	0.81109893	1	1396
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	122	-0.783547	-1.104452	0.33641404	0.8057548	1	858
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	250	-0.715721	-1.103731	0.2746615	0.80453926	1	1286

REACTOME_GLUCOSE_TRANSPORT	37	-0.965589	-1.103421	0.4731369	0.8001916	1	1256
KEGG_PRIMARY_IMMUNODEFICIENCY	34	-0.968903	-1.101413	0.45025295	0.81821275	1	1367
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	34	-0.964565	-1.100488	0.5365854	0.8195437	1	1558
REACTOME_S_PHASE	107	-0.805954	-1.096186	0.35897437	0.8623263	1	1498
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	174	-0.745644	-1.091785	0.33730158	0.9058555	1	1522
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	34	-0.970593	-1.09155	0.46785715	0.9008367	1	1292
REACTOME_RNA_POL_III_TRANSCRIPTION	33	-0.967763	-1.09044	0.5170068	0.90405005	1	1416
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	35	-0.967053	-1.090246	0.5218914	0.8977201	1	1452
REACTOME_SYNTHESIS_OF_DNA	91	-0.813556	-1.089626	0.35907337	0.89848727	1	1498
REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	32	-0.96943	-1.08782	0.48951048	0.91378504	1	1342
REACTOME_MRNA_3_END_PROCESSING	33	-0.967169	-1.086088	0.50359714	0.9292356	1	1444
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	113	-0.784283	-1.086046	0.3683206	0.922657	1	1542
KEGG_LINOLEIC_ACID_METABOLISM	24	-0.999976	-1.086037	0.001652893	0.91612875	1	1
REACTOME_SIGNAL_AMPLIFICATION	30	-0.986051	-1.08528	0.30533117	0.92117226	1	613
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	27	-0.984089	-1.083765	0.33275864	0.92992747	1	700
KEGG_PRION_DISEASES	35	-0.961286	-1.082933	0.6013986	0.9336537	1	78
REACTOME_GLUCONEOGENESIS	32	-0.972192	-1.081887	0.45172414	0.9412339	1	1222
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	26	-0.990801	-1.080974	0.3136289	0.9433922	1	405
KEGG_APOPTOSIS	81	-0.836968	-1.078628	0.43065694	0.9721876	1	449
BIOCARTA_PGC1A_PATHWAY	23	-0.999977	-1.078219	0	0.9726739	1	1
REACTOME_PURINE_METABOLISM	33	-0.965776	-1.076782	0.5490534	0.98427653	1	1505
REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULES	30	-0.978723	-1.076692	0.41237113	0.9773498	1	934
REACTOME_SIGNALLING_TO_RAS	27	-0.983746	-1.075618	0.36482084	0.9818135	1	714
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	31	-0.963289	-1.073815	0.61204016	1	1	1617
REACTOME_G_PROTEIN_ACTIVATION	27	-0.986052	-1.073664	0.33840948	0.9957269	1	613
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	31	-0.963289	-1.071684	0.60267115	1	1	1617
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	26	-0.986052	-1.071183	0.3747927	1	1	613
REACTOME_CELL_CYCLE	394	-0.662591	-1.070904	0.32447818	1	1	1532
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN	28	-0.985801	-1.069572	0.36243823	1	1	625
REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_AND_AMINE_COMPOUNDS	88	-0.808334	-1.067033	0.4090909	1	1	959
REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE	25	-0.986053	-1.066994	0.37886178	1	1	613
KEGG_CITRATE_CYCLE_TCA_CYCLE	30	-0.966234	-1.066525	0.5711864	1	1	609
BIOCARTA_NKT_PATHWAY	29	-0.964364	-1.064254	0.61157024	1	1	1566
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS	31	-0.962079	-1.064028	0.6424682	1	1	1664
BIOCARTA_CASPASE_PATHWAY	22	-0.983474	-1.062878	0.49675325	1	1	727
KEGG_DORSO_VENTRAL_AXIS_FORMATION	23	-0.983748	-1.062527	0.44301766	1	1	714
KEGG_THYROID_CANCER	29	-0.966048	-1.062426	0.6026059	1	1	714
KEGG_ETHER_LIPID_METABOLISM	26	-0.975164	-1.060816	0.5135135	1	1	1090
REACTOME_BETA_DEFENSINS	28	-0.968223	-1.060689	0.59	1	1	1396
REACTOME_TRAF6_MEDIATED_NFKB_ACTIVATION	20	-0.992217	-1.060566	0.40552995	1	1	343
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	21	-0.999979	-1.059947	0	1	1	1
REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	21	-0.986054	-1.059938	0.4542536	1	1	613
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	23	-0.986053	-1.059349	0.43086818	1	1	613
REACTOME_MITOTIC_G2_G2_M_PHASES	78	-0.820858	-1.058504	0.44444445	1	1	1372
REACTOME_LIGAND_GATED_ION_CHANNEL_TRANSPORT	20	-0.998927	-1.057787	0.3494705	1	1	49
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	22	-0.986054	-1.057781	0.4667747	1	1	613
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	26	-0.967745	-1.057675	0.59126365	1	1	1416
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	24	-0.986053	-1.057481	0.45768026	1	1	613
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION	20	-0.99998	-1.056357	0	1	1	1
BIOCARTA_NFKB_PATHWAY	23	-0.980154	-1.056259	0.4511628	1	1	412
BIOCARTA_CERAMIDE_PATHWAY	22	-0.992217	-1.056101	0.40758294	1	1	343
REACTOME_ACYL_CHAIN_REMODELLING_OF_PC	18	-0.999982	-1.055476	0.001512859	1	1	1
BIOCARTA_G2_PATHWAY	24	-0.969869	-1.055357	0.59253246	1	1	1326
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	25	-0.966216	-1.055334	0.6337308	1	1	1482
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	19	-0.998605	-1.055137	0.3903577	1	1	47
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	30	-0.966943	-1.054513	0.6094771	1	1	1452
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	93	-0.797486	-1.053391	0.44212523	1	1	1498
REACTOME_RNA_POL_III_TRANSCRIPTION_TERMINATION	19	-0.999981	-1.052278	0	1	1	1
REACTOME_MITOTIC_G1_G1_S_PHASES	133	-0.731177	-1.051835	0.41016334	1	1	1509
REACTOME_ACYL_CHAIN_REMODELLING_OF_PE	17	-0.999983	-1.051024	0	1	1	1
REACTOME_CTLA4_INHIBITORY_SIGNALING	21	-0.984611	-1.050167	0.48387095	1	1	615
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	19	-0.999981	-1.050047	0	1	1	1
REACTOME_TIGHT_JUNCTION_INTERACTIONS	27	-0.948684	-1.047947	0.687389	1	1	178
REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	17	-0.999983	-1.047845	0	1	1	1
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	26	-0.965166	-1.047724	0.6672384	1	1	1256
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	26	-0.963271	-1.045913	0.7019231	1	1	1617
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA	20	-0.986054	-1.044326	0.45625	1	1	613
REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	19	-0.98375	-1.043765	0.51309705	1	1	714
KEGG_TYPE_I_DIABETES_MELLITUS	21	-0.977745	-1.043627	0.5496063	1	1	32
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRANE	17	-0.999983	-1.043517	0	1	1	1
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	-0.972243	-1.043431	0.60720134	1	1	1218
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	26	-0.964302	-1.043394	0.6834171	1	1	1256
BIOCARTA_MITOCHONDRIA_PATHWAY	20	-0.989638	-1.043326	0.43661973	1	1	456
BIOCARTA_P53HYPOXIA_PATHWAY	22	-0.983817	-1.043197	0.47351524	1	1	712
KEGG_ALZHEIMERS_DISEASE	140	-0.73382	-1.042833	0.41040462	1	1	1474
REACTOME_APOPTOSIS	142	-0.725695	-1.042557	0.4035433	1	1	1498
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	15	-0.999985	-1.042109	0	1	1	1
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	21	-0.979235	-1.042025	0.5489891	1	1	680
REACTOME_ENDOGENOUS_STEROLS	15	-0.999985	-1.041597	0	1	1	1
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_2_PROMOTER	23	-0.971673	-1.041541	0.6309148	1	1	1243
REACTOME_RNA_POL_III_CHAIN_ELONGATION	17	-0.999983	-1.04087	0	1	1	1
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_7ALPHA_HYDROXYCHOLESTEROL	15	-0.999985	-1.040817	0.001428571	1	1	1
KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	16	-0.999984	-1.039786	0	1	1	1
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	23	-0.967131	-1.039332	0.66169155	1	1	1444
BIOCARTA_CYTOKINE_PATHWAY	20	-0.976968	-1.038409	0.6	1	1	536
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	21	-0.978613	-1.0381	0.55254775	1	1	939
BIOCARTA_TNFR2_PATHWAY	17	-0.992217	-1.037875	0.48765433	1	1	343
REACTOME_METAL_ION_SLC_TRANSPORTERS	21	-0.978933	-1.037564	0.56414217	1	1	927
REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_DAI	17	-0.994865	-1.037467	0.45679012	1	1	227
REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	19	-0.983772	-1.037409	0.53015876	1	1	714
REACTOME_SULFUR_AMINO_ACID_METABOLISM	23	-0.964529	-1.036187	0.71770334	1	1	1558
REACTOME_RAP1_SIGNALLING	16	-0.999984	-1.035918	0	1	1	1
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	23	-0.965556	-1.035145	0.7069243	1	1	1512
KEGG_GRAFT_VERSUS_HOST_DISEASE	19	-0.976847	-1.034532	0.61001515	1	1	32
REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	21	-0.972405	-1.034424	0.6201923	1	1	1211
REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	19	-0.986055	-1.034201	0.51339287	1	1	613
REACTOME_ENOS_ACTIVATION_AND_REGULATION	20	-0.972474	-1.033679	0.6527778	1	1	1210
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	69	-0.812886	-1.032643	0.48653847	1	1	1611
BIOCARTA_PROTEASOME_PATHWAY	28	-0.937308	-1.032542	0.7016129	1	1	1346
KEGG_REGULATION_OF_AUTOPHAGY	33	-0.913516	-1.032481	0.64735943	1	1	1341
REACTOME_INSULIN_RECEPTOR_RECYCLING	22	-0.962247	-1.032336	0.7693548	1	1	1656
REACTOME_METABOLISM_OF_PROTEINS	442	-0.630142	-1.03086	0.37662336	1	1	1336
REACTOME_SHC_RELATED_EVENTS	16	-0.983751	-1.03072	0.5854015	1	1	714
REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	15	-0.998813	-1.030455	0.48579547	1	1	54
REACTOME_PYRUVATE_METABOLISM	18	-0.976469	-1.029666	0.6346749	1	1	1036
BIOCARTA_IL10_PATHWAY	17	-0.987567	-1.029613	0.5319813	1	1	23
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	-0.961538	-1.027937	0.7696	1	1	1687
REACTOME_ARMS_MEDIATED_ACTIVATION	17	-0.98375	-1.027245	0.5461422	1	1	714
REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI	16	-0.991328	-1.026855	0.5386819	1	1	382

REACTOME_ERK_MAPK_TARGETS	21	-0.96154	-1.02657	0.78971964	1	1	1687
BIOCARTA_CTLA4_PATHWAY	17	-0.98423	-1.026551	0.5762463	1	1	47
REACTOME_KINESINS	24	-0.963843	-1.026382	0.7447833	1	1	1591
REACTOME_FANCONI_ANEMIA_PATHWAY	20	-0.969803	-1.026107	0.70542634	1	1	1326
REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	31	-0.913424	-1.025802	0.6566164	1	1	453
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	22	-0.967497	-1.02556	0.7092308	1	1	1427
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	17	-0.98407	-1.025525	0.5802469	1	1	700
BIOCARTA_ATRBRCA_PATHWAY	20	-0.969872	-1.025331	0.70253164	1	1	1326
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	15	-0.984071	-1.024459	0.60795456	1	1	700
BIOCARTA_SPRY_PATHWAY	18	-0.973731	-1.023779	0.67261904	1	1	1153
REACTOME_SIGNALLING_TO_P38_VIA_RIT_AND_RIN	15	-0.983751	-1.023338	0.6172662	1	1	714
BIOCARTA_MCM_PATHWAY	18	-0.966929	-1.023303	0.74558824	1	1	1452
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	66	-0.806931	-1.022785	0.51459855	1	1	1644
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS	43	-0.876039	-1.020906	0.5934066	1	1	946
REACTOME_TELOMERE_MAINTENANCE	75	-0.802698	-1.020484	0.51498127	1	1	862
BIOCARTA_TALL1_PATHWAY	15	-0.984618	-1.020458	0.6091954	1	1	677
REACTOME_DEADENYLATION_OF_MRNA	17	-0.971746	-1.020093	0.7023644	1	1	1242
REACTOME_SHC_MEDIATED_SIGNALLING	15	-0.983751	-1.01933	0.62154293	1	1	714
BIOCARTA_LAIR_PATHWAY	16	-0.977898	-1.019262	0.67127496	1	1	23
REACTOME_INFLAMMASOMES	16	-0.978524	-1.019186	0.6622807	1	1	946
REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	18	-0.970079	-1.017264	0.73590505	1	1	1315
REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	15	-0.983751	-1.017121	0.615942	1	1	714
BIOCARTA_TH1TH2_PATHWAY	17	-0.964328	-1.015358	0.7966616	1	1	1566
REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	17	-0.967706	-1.014581	0.7695652	1	1	1418
KEGG_ASTHMA	16	-0.967798	-1.013773	0.77286136	1	1	1413
BIOCARTA_EIF_PATHWAY	16	-0.971746	-1.01372	0.729927	1	1	1242
REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION_INDEPENDENT_DOUBLE_STRAND_BREAKS	15	-0.979237	-1.013661	0.6897038	1	1	680
REACTOME_CGMP_EFFECTS	17	-0.964853	-1.013659	0.7886677	1	1	1542
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI	17	-0.969555	-1.013495	0.7394469	1	1	1336
BIOCARTA_CELLCYCLE_PATHWAY	23	-0.944974	-1.013446	0.7941176	1	1	1509
KEGG_ALLOGRAFT_REJECTION	17	-0.96782	-1.013414	0.7732733	1	1	1413
KEGG_OOCYTE_MEIOSIS	108	-0.739103	-1.01303	0.45383105	1	1	1299
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	162	-0.690757	-1.011808	0.44636014	1	1	1522
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	15	-0.974988	-1.011419	0.73938507	1	1	1098
REACTOME_GLUCURONIDATION	18	-0.966222	-1.01107	0.809593	1	1	1482
REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE	15	-0.971633	-1.010759	0.7373737	1	1	1245
KEGG_RIBOFLAVIN_METABOLISM	15	-0.97056	-1.008219	0.75637394	1	1	1292
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES	91	-0.744322	-1.008175	0.4716312	1	1	1585
REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	15	-0.975878	-1.00785	0.7221418	1	1	1062
REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_TTP	17	-0.967706	-1.007474	0.78549385	1	1	1418
REACTOME_SYNTHESIS_OF_PC	18	-0.957618	-1.007428	0.851227	1	1	553
REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1	17	-0.967706	-1.007047	0.7912913	1	1	1418
REACTOME_G0_AND_EARLY_G1	24	-0.931521	-1.006398	0.78405315	1	1	1247
BIOCARTA_NO2IL12_PATHWAY	17	-0.964305	-1.006025	0.8192956	1	1	1566
REACTOME_PLATELET_SENSITIZATION_BY_LDL	16	-0.961545	-1.004381	0.8684211	1	1	1687
REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLP1	15	-0.970081	-1.00436	0.7710843	1	1	1315
KEGG_CHEMOKINE_SIGNALING_PATHWAY	176	-0.681206	-1.004237	0.44970414	1	1	1115
BIOCARTA_INFLAM_PATHWAY	25	-0.924975	-1.002439	0.7646104	1	1	545
BIOCARTA_HSP27_PATHWAY	15	-0.967844	-1.002184	0.81908834	1	1	1413
REACTOME_G1_S_TRANSITION	108	-0.731256	-1.001919	0.46561885	1	1	1498
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	16	-0.966657	-0.998224	0.8340307	1	1	1463
REACTOME_SIGNALING_BY_ILS	104	-0.733401	-0.996713	0.49704143	1	1	1153
KEGG_JAK_STAT_SIGNALING_PATHWAY	148	-0.688721	-0.995569	0.47398844	1	1	1566
BIOCARTA_DC_PATHWAY	22	-0.925203	-0.99157	0.7993827	1	1	158
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	23	-0.919102	-0.990112	0.7960725	1	1	966
KEGG_TIGHT_JUNCTION	127	-0.691458	-0.988864	0.4785047	1	1	714
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	-0.942827	-0.986318	0.8603269	1	1	153
REACTOME_REGULATION_OF_KIT_SIGNALING	16	-0.942894	-0.986035	0.8744461	1	1	1153
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	20	-0.923309	-0.982983	0.8390093	1	1	609
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	20	-0.924557	-0.982173	0.8273616	1	1	1173
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	94	-0.720912	-0.979127	0.5266055	1	1	1402
REACTOME_HIV_LIFE_CYCLE	109	-0.726722	-0.976693	0.5297398	1	1	1402
REACTOME_RECYCLING_PATHWAY_OF_L1	26	-0.899299	-0.972991	0.7862969	1	1	793
REACTOME_SIGNALING_BY_NODAL	18	-0.919385	-0.971562	0.8531685	1	1	698
REACTOME_CELL_CYCLE_MITOTIC	304	-0.615244	-0.966272	0.5248092	1	1	1532
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	31	-0.868793	-0.965328	0.74655175	1	1	619
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	20	-0.917541	-0.961237	0.87253416	1	1	88
BIOCARTA_IL1R_PATHWAY	33	-0.857958	-0.960012	0.73275864	1	1	449
BIOCARTA_MTOR_PATHWAY	23	-0.897312	-0.955363	0.8401254	1	1	1242
BIOCARTA_STATHMIN_PATHWAY	19	-0.895536	-0.950722	0.8489666	1	1	153
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	48	-0.783316	-0.945492	0.64737797	1	1	453
REACTOME_INTERFERON_SIGNALING	142	-0.656226	-0.943424	0.56037736	1	1	1286
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	99	-0.685872	-0.939534	0.58381504	1	1	412
REACTOME_SIGNALING_BY_CONSTITUTIVELY_ACTIVE_EGFR	18	-0.892476	-0.938794	0.8822606	1	1	1153
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	63	-0.751045	-0.936679	0.609901	1	1	1372
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	31	-0.835068	-0.932094	0.7599309	1	1	617
REACTOME_RNA_POL_II_TRANSCRIPTION	94	-0.693733	-0.927653	0.62030077	1	1	1444
KEGG_PYRUVATE_METABOLISM	39	-0.800767	-0.924855	0.7092593	1	1	667
CANCER-TESTIS-ANTIGEN	164	-0.635824	-0.924318	0.5864811	1	1	713
REACTOME_APOPTOTIC_EXECUTION_PHASE	50	-0.762226	-0.921834	0.67192984	1	1	765
REACTOME_BASIGIN_INTERACTIONS	25	-0.846071	-0.921287	0.81178397	1	1	784
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	18	-0.874473	-0.920062	0.8842593	1	1	927
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	22	-0.858184	-0.919186	0.84294873	1	1	1173
REACTOME_IL_2_SIGNALING	41	-0.78151	-0.909839	0.7209302	1	1	714
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	66	-0.712406	-0.905881	0.64480877	1	1	615
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	122	-0.638082	-0.904298	0.6184211	1	1	1464
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	25	-0.834523	-0.903397	0.83623695	1	1	656
REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS	26	-0.828922	-0.902554	0.8237288	1	1	1291
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	82	-0.687763	-0.900389	0.6397059	1	1	1115
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	122	-0.637679	-0.8979	0.6221374	1	1	1498
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	269	-0.568383	-0.897363	0.6360153	1	1	1522
REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	30	-0.814348	-0.897314	0.7958478	1	1	613
REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	15	-0.860186	-0.89209	0.9251412	1	1	675
KEGG_CELL_ADHESION_MOLECULES_CAMS	105	-0.647238	-0.890125	0.65346533	1	1	1464
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	22	-0.834524	-0.889284	0.87741935	1	1	656
REACTOME_SIGNALING_BY_SCF_KIT	74	-0.681661	-0.888998	0.649635	1	1	1153
REACTOME_PERK_REGULATED_GENE_EXPRESSION	27	-0.812484	-0.887594	0.8289703	1	1	106
KEGG_MTOR_SIGNALING_PATHWAY	48	-0.741086	-0.887141	0.69299823	1	1	1242
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	18	-0.843055	-0.885876	0.89209723	1	1	47
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	24	-0.812485	-0.880129	0.83686787	1	1	106
REACTOME_DNA_REPLICATION	182	-0.59802	-0.878126	0.67611337	1	1	1617
REACTOME_MITOTIC_M_M_G1_PHASES	162	-0.603085	-0.877434	0.68725866	1	1	1617
BIOCARTA_NTHI_PATHWAY	23	-0.80822	-0.872392	0.8519737	1	1	32
KEGG_MAPK_SIGNALING_PATHWAY	254	-0.56945	-0.871542	0.71146244	1	1	1213
KEGG_HOMOLOGOUS_RECOMBINATION	26	-0.805169	-0.870577	0.8471761	1	1	1128
REACTOME_TCR_SIGNALING	43	-0.753119	-0.870258	0.77459747	1	1	47
BIOCARTA_P38MAPK_PATHWAY	39	-0.744559	-0.868279	0.7513612	1	1	343
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	132	-0.61511	-0.86736	0.72038835	1	1	1238

REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS	24	-0.797906	-0.866489	0.8416	1	1	47
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	18	-0.814612	-0.860781	0.8913044	1	1	1173
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	26	-0.792611	-0.860273	0.8453427	1	1	1388
REACTOME_DNA_REPAIR	102	-0.624709	-0.857582	0.6990476	1	1	1326
KEGG_RNA_POLYMERASE	29	-0.787643	-0.857357	0.8496622	1	1	186
REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	57	-0.69469	-0.854874	0.7134935	1	1	966
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	187	-0.567174	-0.850018	0.7607843	1	1	1575
KEGG_LEISHMANIA_INFECTION	58	-0.691115	-0.844407	0.729927	1	1	482
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	122	-0.597836	-0.839414	0.7252337	1	1	1072
REACTOME_GLYCOLYSIS	27	-0.760125	-0.836177	0.8322259	1	1	1222
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	55	-0.691775	-0.831782	0.75189394	1	1	615
REACTOME_DOWNSTREAM_TCR_SIGNALING	27	-0.753329	-0.828799	0.8476821	1	1	47
KEGG_RETINOL_METABOLISM	57	-0.653935	-0.827264	0.7383721	1	1	1482
BIOCARTA_IL7_PATHWAY	16	-0.79	-0.822385	0.93519884	1	1	545
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	68	-0.648722	-0.821279	0.7485605	1	1	1498
KEGG_SPHINGOLIPID_METABOLISM	36	-0.714304	-0.81494	0.8128342	1	1	1291
BIOCARTA_EIF4_PATHWAY	24	-0.750293	-0.814439	0.8536978	1	1	1242
REACTOME_IL1_SIGNALING	38	-0.71261	-0.814341	0.8264015	1	1	449
REACTOME_METABOLISM_OF_CARBOHYDRATES	232	-0.522783	-0.811995	0.81764704	1	1	1287
KEGG_SPLICEOSOME	123	-0.574002	-0.804784	0.7868217	1	1	1553
KEGG_LONG_TERM_POTENTIATION	66	-0.63437	-0.804067	0.7509434	1	1	714
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	258	-0.516285	-0.803719	0.83514494	1	1	1116
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	43	-0.682335	-0.80081	0.7935606	1	1	1115
BIOCARTA_CSK_PATHWAY	20	-0.755	-0.797696	0.9296875	1	1	47
KEGG_CARDIAC_MUSCLE_CONTRACTION	70	-0.62462	-0.795503	0.78368795	1	1	1167
REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	27	-0.725356	-0.795246	0.85714287	1	1	553
REACTOME_SIGNALING_BY_FGFR_MUTANTS	40	-0.683709	-0.792318	0.8271605	1	1	1152
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	25	-0.725077	-0.783783	0.885274	1	1	981
BIOCARTA_NKCELLS_PATHWAY	19	-0.738868	-0.781884	0.9253049	1	1	812
REACTOME_CD28_CO_STIMULATION	31	-0.698117	-0.779156	0.86243385	1	1	615
REACTOME_UNFOLDED_PROTEIN_RESPONSE	75	-0.603975	-0.779149	0.8098859	1	1	1657
REACTOME_SIGNALING_BY_FGFR1_FUSION_MUTANTS	18	-0.742135	-0.778057	0.94356006	1	1	1152
REACTOME_ION_CHANNEL_TRANSPORT	53	-0.642717	-0.776743	0.796875	1	1	1249
KEGG_SMALL_CELL_LUNG_CANCER	81	-0.597632	-0.775841	0.798419	1	1	482
BIOCARTA_CARM_ER_PATHWAY	35	-0.681895	-0.771926	0.83652174	1	1	1247
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	47	-0.647934	-0.770553	0.81609195	1	1	1000
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	24	-0.712471	-0.767953	0.8955224	1	1	615
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	128	-0.539013	-0.766256	0.8593156	1	1	1503
REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING	35	-0.679331	-0.761979	0.879646	1	1	202
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	21	-0.716119	-0.761404	0.91935486	1	1	47
KEGG_PEROXISOME	78	-0.587109	-0.76089	0.8181818	1	1	1121
BIOCARTA_MAL_PATHWAY	18	-0.719274	-0.757287	0.9375	1	1	500
REACTOME_CHOLESTEROL_BIOSYNTHESIS	21	-0.715355	-0.753668	0.92987806	1	1	1264
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	40	-0.64671	-0.752129	0.83893806	1	1	784
REACTOME_FRS2_MEDIATED_CASCADE	33	-0.672004	-0.751719	0.8687392	1	1	714
REACTOME_INNATE_IMMUNE_SYSTEM	253	-0.494692	-0.748954	0.93495935	1	1	946
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	67	-0.591615	-0.748113	0.8509804	1	1	1136
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	56	-0.599289	-0.746851	0.84826326	1	1	1372
KEGG_PYRIMIDINE_METABOLISM	95	-0.548067	-0.739831	0.8593156	1	1	1427
BIOCARTA_TNFR1_PATHWAY	29	-0.669891	-0.735232	0.9134126	1	1	1413
REACTOME_GABA_RECEPTOR_ACTIVATION	50	-0.602281	-0.73204	0.8374291	1	1	1115
REACTOME_SHC_MEDIATED_CASCADE	25	-0.672007	-0.730005	0.9081803	1	1	714
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_SYNTHESIS	24	-0.671256	-0.729514	0.9104	1	1	1287
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	38	-0.639115	-0.7293	0.8813869	1	1	1066
KEGG_BLADDER_CANCER	39	-0.632899	-0.729065	0.88	1	1	822
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	61	-0.579318	-0.719777	0.90185183	1	1	966
REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPORTERS	17	-0.683894	-0.713518	0.9519651	1	1	453
REACTOME_PKB_MEDIATED_EVENTS	27	-0.648649	-0.71316	0.90084034	1	1	1242
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	83	-0.537481	-0.708504	0.91698843	1	1	784
REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDATION_IN_MUSCLE	17	-0.675806	-0.707584	0.95224315	1	1	660
REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BETA_PATHWAYS	71	-0.559646	-0.706134	0.8897196	1	1	617
REACTOME_IL_3_5_AND_GM_CSF_SIGNALING	42	-0.60709	-0.705159	0.8863233	1	1	1153
REACTOME_SIGNALING_BY_ROBO_RECEPTOR	27	-0.645036	-0.702923	0.91137123	1	1	98
BIOCARTA_GSK3_PATHWAY	27	-0.642029	-0.699752	0.91797554	1	1	412
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	36	-0.588616	-0.6801	0.88729876	1	1	727
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	32	-0.607457	-0.677008	0.92413795	1	1	1115
KEGG_INSULIN_SIGNALING_PATHWAY	133	-0.476293	-0.670337	0.994	1	1	1242
KEGG_VIRAL_MYOCARDITIS	50	-0.548646	-0.666183	0.9259259	1	1	1464
REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	21	-0.627814	-0.66405	0.9512579	1	1	714
REACTOME_SIGNAL_TRANSDUCTION_BY_L1	34	-0.580904	-0.661444	0.91296625	1	1	63
KEGG_GNRH_SIGNALING_PATHWAY	96	-0.488497	-0.659222	0.97096187	1	1	1115
BIOCARTA_FAS_PATHWAY	30	-0.598021	-0.656909	0.95238096	1	1	1195
REACTOME_SIGNALING_BY_FGFR1_MUTANTS	28	-0.597628	-0.656559	0.93634844	1	1	1152
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	-0.60471	-0.6533	0.9424	1	1	124
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	16	-0.629027	-0.650434	0.9790732	1	1	1173
REACTOME_NOD1_2_SIGNALING_PATHWAY	28	-0.585904	-0.643093	0.93771046	1	1	412
REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS	75	-0.496106	-0.642965	0.9609375	1	1	1136
REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	18	-0.612985	-0.641004	0.96390975	1	1	1121
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	26	-0.582123	-0.637641	0.9479866	1	1	1247
REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKS_COMPLEX	22	-0.585905	-0.636503	0.9328969	1	1	412
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	46	-0.534614	-0.634052	0.9508772	1	1	124
REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	16	-0.602106	-0.628349	0.97771174	1	1	660
KEGG_PANCREATIC_CANCER	67	-0.496027	-0.627305	0.9834559	1	1	1096
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	56	-0.517754	-0.6201	0.964486	1	1	915
REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	17	-0.585907	-0.615338	0.97337276	1	1	412
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS	26	-0.561153	-0.612545	0.95408165	1	1	981
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	26	-0.559318	-0.61194	0.9629005	1	1	693
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TAK1	16	-0.585907	-0.611676	0.9775112	1	1	412
BIOCARTA_NFAT_PATHWAY	51	-0.500462	-0.611049	0.9810964	1	1	675
REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	47	-0.50743	-0.610144	0.96045196	1	1	776
REACTOME_LIPOPROTEIN_METABOLISM	24	-0.559792	-0.603461	0.965625	1	1	429
BIOCARTA_GCR_PATHWAY	19	-0.568246	-0.60326	0.969651	1	1	1393
KEGG_TYROSINE_METABOLISM	34	-0.527049	-0.596639	0.96466434	1	1	1399
REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	26	-0.547978	-0.596261	0.9650582	1	1	971
REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	18	-0.563401	-0.589287	0.98275864	1	1	776
REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	36	-0.520543	-0.587878	0.9678571	1	1	202
KEGG_BASE_EXCISION_REPAIR	34	-0.523273	-0.585933	0.98109967	1	1	215
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	34	-0.518298	-0.585327	0.97861844	1	1	1125
REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	18	-0.55427	-0.583039	0.97720367	1	1	74
KEGG_BASAL_TRANSCRIPTION_FACTORS	34	-0.511515	-0.58245	0.9711375	1	1	1039
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	47	-0.489516	-0.576699	0.991119	1	1	1498
REACTOME_EXTENSION_OF_TELOMERES	27	-0.529226	-0.576037	0.9821718	1	1	862
REACTOME_IL_RECEPTOR_SHC_SIGNALING	27	-0.521274	-0.574516	0.97875816	1	1	158
REACTOME_GAP_JUNCTION_TRAFFICKING	26	-0.498066	-0.544151	0.9897084	1	1	1364
BIOCARTA_NO1_PATHWAY	30	-0.481325	-0.537516	0.9982456	1	1	784
BIOCARTA_IL2_PATHWAY	22	-0.50354	-0.536006	0.9968799	1	1	47
REACTOME_G1_PHASE	36	-0.468886	-0.535083	1	1	1	1687
KEGG_STEROID_BIOSYNTHESIS	16	-0.506189	-0.527849	0.9941349	1	1	1264
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	26	-0.478185	-0.518583	1	1	1	1238
BIOCARTA_TID_PATHWAY	19	-0.485499	-0.512902	0.9984375	0.99940956	1	1413

Table S23

GSEA Analysis (Hallmark gene sets) on TCGA HNSC comparing tumors with or without 9p loss, Pathways Depleted

NAME	SIZE	ES	NES	NOM p-value	FDR q-value	FWER p-value	RANK AT MAX
HALLMARK_INTERFERON_GAMMA_RESPONSE	190	-0.855109	-2.744375	0	0	0	1317
HALLMARK_ALLOGRAFT_REJECTION	183	-0.829341	-2.623169	0	0	0	1005
HALLMARK_INTERFERON_ALPHA_RESPONSE	91	-0.885347	-2.578858	0	0	0	1809
HALLMARK_COMPLEMENT	195	-0.728917	-2.34002	0	0	0	1959
HALLMARK_INFLAMMATORY_RESPONSE	197	-0.730056	-2.338272	0	0	0	2367
HALLMARK_IL6_JAK_STAT3_SIGNALING	87	-0.731323	-2.160054	0	0	0	2179
HALLMARK_IL2_STAT5_SIGNALING	194	-0.637947	-2.066072	0	0	0	2951
HALLMARK_KRAS_SIGNALING_UP	193	-0.614807	-1.950687	0	0	0	2401
HALLMARK_TNFA_SIGNALING_VIA_NFKB	197	-0.606805	-1.941103	0	0	0	2922
HALLMARK_APOPTOSIS	158	-0.534577	-1.670234	0	0.002546372	0.025	1413
HALLMARK_MYOGENESIS	198	-0.487981	-1.572575	0.001265823	0.011794602	0.118	4426
HALLMARK_COAGULATION	136	-0.498312	-1.516129	0.001408451	0.019545117	0.212	2535
HALLMARK_APICAL_SURFACE	43	-0.554415	-1.448977	0.03301887	0.038945436	0.405	2694
HALLMARK_PI3K_AKT_MTOR_SIGNALING	103	-0.485388	-1.440448	0.015625	0.040478278	0.438	3797
HALLMARK_APICAL_JUNCTION	194	-0.415006	-1.332427	0.030612245	0.11372461	0.825	4265
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	194	-0.39935	-1.285401	0.04935065	0.16172253	0.934	4265
HALLMARK_P53_PATHWAY	190	-0.402605	-1.283451	0.037958115	0.15477194	0.94	2794
HALLMARK_TGF_BETA_SIGNALING	54	-0.436768	-1.188955	0.19809826	0.31416717	1	3796
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	45	-0.437367	-1.164183	0.2257525	0.35447887	1	3287
HALLMARK_ANDROGEN_RESPONSE	95	-0.393577	-1.158838	0.18785311	0.3485101	1	3475
HALLMARK_UV_RESPONSE_DN	137	-0.363454	-1.124269	0.26287264	0.41170365	1	3416
HALLMARK_XENOBIOTIC_METABOLISM	197	-0.334834	-1.068999	0.33462533	0.5457384	1	2441
HALLMARK_KRAS_SIGNALING_DN	183	-0.337534	-1.067487	0.3126649	0.5262501	1	2808
HALLMARK_HEME_METABOLISM	188	-0.316462	-1.016585	0.44530246	0.6528651	1	2828
HALLMARK_UV_RESPONSE_UP	150	-0.327607	-1.01619	0.4238683	0.62860024	1	3125
HALLMARK_ESTROGEN_RESPONSE_EARLY	191	-0.307421	-0.98401	0.47556144	0.70073336	1	2680
HALLMARK_HYPOXIA	190	-0.293301	-0.93711	0.6111111	0.8168293	1	4039
HALLMARK_ANGIOGENESIS	36	-0.36884	-0.933068	0.5620915	0.79852504	1	4928
HALLMARK_NOTCH_SIGNALING	32	-0.368209	-0.924665	0.56053066	0.7947106	1	3159
HALLMARK_BILE_ACID_METABOLISM	112	-0.293459	-0.882431	0.7089136	0.88307863	1	3156
HALLMARK_CHOLESTEROL_HOMEOSTASIS	72	-0.29527	-0.85229	0.72534144	0.9309138	1	2694
HALLMARK_PROTEIN_SECRETION	95	-0.281959	-0.834622	0.7866473	0.9438062	1	1561
HALLMARK_HEDGEHOG_SIGNALING	34	-0.320207	-0.817857	0.75166667	0.9504564	1	1814
HALLMARK_FATTY_ACID_METABOLISM	154	-0.259991	-0.81369	0.87109905	0.93067247	1	2202
HALLMARK_PEROXISOME	101	-0.265368	-0.792086	0.8718704	0.9426724	1	2725
HALLMARK_ESTROGEN_RESPONSE_LATE	195	-0.237139	-0.759483	0.9711286	0.9605489	1	3811
HALLMARK_MITOTIC_SPINDLE	196	-0.206286	-0.651896	0.9987097	0.99241215	1	3740

Table S24

GSEA Analysis (Hallmark gene sets) on HNSC cancer cell lines comparing cell lines with or without 9p loss, Pathways Depleted

NAME	SIZE	ES	NES	NOM p-value	FDR q-value	FWER p-value	RANK AT MAX	LEADING EDGE
HALLMARK_TNFA_SIGNALING_VIA_NFKB	198	-0.619899	-2.170048	0	0	0	4069	tags=42%, list=15%, sig
HALLMARK_COAGULATION	124	-0.590234	-1.9757	0	0	0	4463	tags=34%, list=17%, sig
HALLMARK_INFLAMMATORY_RESPONSE	193	-0.571366	-1.974279	0	0	0	3097	tags=30%, list=12%, sig
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	198	-0.534657	-1.860491	0	2.16E-04	0.001	1844	tags=17%, list=7%, sign
HALLMARK_KRAS_SIGNALING_UP	187	-0.519257	-1.795184	0	9.94E-04	0.005	3604	tags=28%, list=14%, sig
HALLMARK_ANGIOGENESIS	33	-0.656333	-1.75946	0.00501672	0.0023008	0.014	2975	tags=33%, list=11%, sig
HALLMARK_IL6_JAK_STAT3_SIGNALING	84	-0.544827	-1.711052	0.00150602	0.00354771	0.026	3605	tags=38%, list=14%, sig
HALLMARK_UV_RESPONSE_DN	142	-0.510999	-1.710883	0	0.00310424	0.026	7022	tags=43%, list=27%, sig
HALLMARK_APOPTOSIS	158	-0.48388	-1.654786	0	0.00628327	0.057	5767	tags=36%, list=22%, sig
HALLMARK_INTERFERON_GAMMA_RESPONSE	188	-0.471526	-1.63304	0	0.00712844	0.073	2406	tags=19%, list=9%, sign
HALLMARK_ALLOGRAFT_REJECTION	162	-0.464622	-1.580121	0.00282087	0.01053302	0.116	3066	tags=21%, list=12%, sig
HALLMARK_IL2_STAT5_SIGNALING	192	-0.445174	-1.541696	0.002849	0.0151668	0.168	3882	tags=24%, list=15%, sig
HALLMARK_COMPLEMENT	188	-0.420759	-1.447641	0.00278164	0.03660318	0.388	5168	tags=30%, list=20%, sig
HALLMARK_P53_PATHWAY	196	-0.397632	-1.380204	0.01081081	0.06433246	0.621	3456	tags=20%, list=13%, sig
HALLMARK_MYOGENESIS	183	-0.394919	-1.36761	0.01969058	0.06886461	0.662	2498	tags=16%, list=9%, sign
HALLMARK_CHOLESTEROL_HOMEOSTASIS	72	-0.44087	-1.346827	0.06026059	0.07996611	0.733	2866	tags=18%, list=11%, sig
HALLMARK_APICAL_SURFACE	43	-0.465589	-1.286086	0.11575563	0.13013865	0.901	4443	tags=30%, list=17%, sig
HALLMARK_HYPOXIA	193	-0.366242	-1.275969	0.0455192	0.13387458	0.923	3468	tags=18%, list=13%, sig
HALLMARK_INTERFERON_ALPHA_RESPONSE	95	-0.39273	-1.244748	0.11620795	0.16426632	0.967	4418	tags=20%, list=17%, sig
HALLMARK_ANDROGEN_RESPONSE	97	-0.380451	-1.212907	0.14285715	0.19757609	0.985	5264	tags=21%, list=20%, sig
HALLMARK_PROTEIN_SECRETION	96	-0.371022	-1.187122	0.17204301	0.23100984	0.994	4307	tags=22%, list=16%, sig
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	110	-0.355734	-1.149209	0.2185129	0.28581247	0.997	2230	tags=10%, list=8%, sign
HALLMARK_HEME_METABOLISM	180	-0.328723	-1.130226	0.2168331	0.31082824	0.999	5916	tags=29%, list=22%, sig
HALLMARK_XENOBIOTIC_METABOLISM	190	-0.321674	-1.124744	0.19855073	0.30841008	0.999	3941	tags=17%, list=15%, sig
HALLMARK_KRAS_SIGNALING_DN	170	-0.322385	-1.096166	0.25637394	0.35064724	1	4137	tags=24%, list=16%, sig
HALLMARK_ESTROGEN_RESPONSE_EARLY	197	-0.298795	-1.049508	0.35021707	0.4385567	1	5627	tags=23%, list=21%, sig
HALLMARK_GLYCOLYSIS	196	-0.2988	-1.036344	0.36219338	0.45062795	1	3275	tags=16%, list=12%, sig
HALLMARK_APICAL_JUNCTION	197	-0.298921	-1.03401	0.392022	0.43924826	1	5734	tags=27%, list=22%, sig
HALLMARK_BILE_ACID_METABOLISM	103	-0.31583	-1.022427	0.41097924	0.45043015	1	5617	tags=24%, list=21%, sig
HALLMARK_TGF_BETA_SIGNALING	53	-0.296927	-0.855525	0.6930693	0.83178765	1	6869	tags=25%, list=26%, sig
HALLMARK_HEDGEHOG_SIGNALING	35	-0.305406	-0.823129	0.74429965	0.8723356	1	7394	tags=43%, list=28%, sig
HALLMARK_PI3K_AKT_MTOR_SIGNALING	102	-0.250278	-0.808546	0.8445122	0.8709158	1	3406	tags=13%, list=13%, sig

Table S25
Cox proportional hazards model for OCFS of the indicated parameters in Real-World Evidence Cohort

Plot_Title	HR	HR_95CI_LowerBound	HR_95CI_UpperBound	p-value	arm2_name	arm1_name	arm2_n	arm1_n	arm2_median_weeks	arm1_median_weeks
3p - IO	0.781	0.410	1.489	0.449	Loss	No Loss	35	87	43	79
3p - non-IO	0.506	0.239	1.070	0.069	Loss	No Loss	15	59	67	86
17p - IO	1.074	0.426	2.712	0.881	Loss	No Loss	11	111	48	79
17p - non-IO*					Loss	No Loss	2	72	6	72
9p - IO	0.468	0.232	0.944	0.030	Loss	No Loss	19	103	43	79
9p - non-IO	0.988	0.397	2.457	0.980	Loss	No Loss	12	62	83	67
9p13 - IO	0.636	0.342	1.183	0.150	Loss	No Loss	29	93	79	53
9p13 - non-IO	1.020	0.468	2.224	0.960	Loss	No Loss	19	55	174	67
9p21.3 - IO	0.907	0.514	1.603	0.738	Loss	No Loss	45	77	50	80
9p21.3 - non-IO	1.168	0.558	2.444	0.681	Loss	No Loss	26	48	83	49
9p24.1 - IO	0.482	0.249	0.934	0.028	Loss	No Loss	24	98	43	79
9p24.1 - non-IO	0.986	0.439	2.218	0.973	Loss	No Loss	17	57	83	67
PDL1 - IO	0.594	0.336	1.050	0.071	Deletion	No Deletion	37	85	43	79
PDL1 - non-IO	0.752	0.361	1.568	0.446	Deletion	No Deletion	21	53	83	67
PDL2 - IO	0.582	0.321	1.055	0.072	Deletion	No Deletion	32	90	43	79
PDL2 - non-IO	0.649	0.311	1.353	0.245	Deletion	No Deletion	20	54	72	69
JAK2 - IO	0.580	0.313	1.074	0.081	Deletion	No Deletion	33	89	43	79
JAK2 - non-IO	0.715	0.348	1.466	0.358	Deletion	No Deletion	24	50	72	69
PDL1, JAK2 - IO	0.436	0.235	0.810	0.007	Co-Deletion	No Co-Deletion	29	93	27	80
PDL1, JAK2 - non-IO	0.979	0.450	2.133	0.958	Co-Deletion	No Co-Deletion	19	55	83	67
PDL2, JAK2 - IO	0.473	0.252	0.888	0.018	Co-Deletion	No Co-Deletion	28	94	43	79
PDL2, JAK2 - non-IO	0.843	0.387	1.838	0.667	Co-Deletion	No Co-Deletion	18	56	83	67
PDL1, PDL2 - IO	0.554	0.306	1.006	0.050	Co-Deletion	No Co-Deletion	31	91	43	79
PDL1, PDL2 - non-IO	0.649	0.311	1.353	0.245	Co-Deletion	No Co-Deletion	20	54	72	69
PDL1, PDL2, JAK2 - IO**	0.473	0.252	0.888	0.018	Co-Deletion	No Co-Deletion	28	94	43	79
PDL1, PDL2, JAK2 - non-IO**	0.843	0.387	1.838	0.667	Co-Deletion	No Co-Deletion	18	56	83	67

*Insufficient n in the No Loss arm to perform hazard ratio calculations
**For the 32 PDL2 deletions, PDL1 was always co-deleted resulting in identical numbers in the PDL2, JAK2 and the PDL2, PDL2, JAK2 cohorts. PDL1 was deleted 5 times without PDL2 being co-deleted.