An Immune Gene Expression Signature Associated With Development of Human Hepatocellular Carcinoma Identifies Mice That Respond to Chemopreventive Agents

Short-title: Immune-mediated field cancerization as target for HCC prevention

Authors: Agrin Moeini¹, Sara Torrecilla¹, Victoria Tovar¹, Carla Montironi^{1,2}, Carmen Andreu-Oller¹, Judit Peix¹, Mónica Higuera^{1,3}, Dominik Pfister⁴, Pierluigi Ramadori⁴, Roser Pinyol¹, Manel Solé¹, Mathias Heikenwälder⁴, Scott L. Friedman², Daniela Sia^{2,*}, Josep M. Llovet^{1,2,5,*}.

Affiliations:

- Liver Cancer Translational Research Group, Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS)-Hospital Clínic, Liver Unit, Universitat de Barcelona, Barcelona, Catalonia, Spain.
- 2. Mount Sinai Liver Cancer Program, Department of Liver Diseases, Icahn School of Medicine at Mount Sinai, New York, USA.
- Liver diseases, Vall d'Hebron Institut de Recerca (VHIR), Hospital Universitari Vall d'Hebron, Barcelona, Spain
- 4. Division of Chronic Inflammation and Cancer, German Cancer Research Center Heidelberg (DKFZ), Heidelberg, Germany
- 5. Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Catalonia, Spain.

Grant Support:

JML is supported by the European Commission (EC)/Horizon 2020 Program (HEPCAR, Ref. 667273-2), U.S. Department of Defense (CA150272P3), an Accelerator Award *(CRUCK, AECC, AIRC)* (HUNTER, Ref. C9380/A26813), NCI Cancer Center Support Grant, National Cancer Institute, Tisch Cancer Institute (P30-CA196521), Samuel Waxman Cancer Research Foundation, Spanish National Health Institute (SAF2016-76390) and the Generalitat de Catalunya/AGAUR (SGR-1358). AM is supported by Spanish National Health Institute. ST and JP are funded by Centro de

Investigación Biomedica en Red de Enfermedades Hepáticas y Digestivas (Ciberehd-ISCIII). CM is a recipient of Josep Font grant. CAO is supported by "la Caixa" INPhINIT Fellowship Grant (LCF/BQ/IN17/11620024). RP is supported by HEPCAR and AECC. DS is supported by the Gilead Sciences Research Scholar Program in Liver Disease. SLF is supported by the National Institutes of Health Research project grant (R01, DK5662) and U.S. Department of Defense (CA150272P3). M.H. was supported by an ERC Consolidator grant (HepatoMetaboPath), the SFBTR 209, 1335 and SFBTR179. This project has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No 667273 and the Helmholtz future topic (Zukunftsthema) Immunology and Inflammation.

Abbreviations: ALT: alanine aminotransferase; α-SMA: α-smooth muscle actin; AKT: protein kinase B; Asp: aspirin; AST: aspartate aminotransferase; CCl4: carbon tetrachloride; CD-HFD (choline-deficient high-fat diet); Clo: clopidogrel; DEN: diethylnitrosamine; EMT: epithelial-mesenchymal transition, ERK: extracellular signal-regulated kinase; FC: Fold change, FDR: false discovery rate; FFPE: formalin-fixed paraffin-embedded; FGFR: fibroblast growth factor receptor; GSEA: gene set enrichment analysis; HCC: hepatocellular carcinoma; HCV: hepatitis C virus; HSC: hepatic stellate cell; ICF: immune-mediated cancer field; IPA: ingenuity pathway analysis; mo: months; NTP: nearest template prediction; PDGFR: platelet-derived growth factor receptor; SSGSEA: single sample gene set enrichment analysis; TKIs: tyrosine kinase inhibitors; Treg: regulatory T cells; qRT-PCR: quantitative real-time polymerase chain reaction; VEGFR: vascular endothelial growth factor receptor.

*Correspondence: Josep M. Llovet, MD, Liver Cancer Translational Research Laboratory, IDIBAPS-Hospital Clinic, Rosselló 153, 08039, Barcelona, Catalonia, Spain; Tel. 0034-932.279.155; Email address: jmllovet@clinic.cat; Daniela Sia, PhD, Mount Sinai Liver Cancer Program, Division of Liver Diseases, Tisch Cancer Institute, Icahn School of Medicine at Mount Sinai, Madison Ave 1425. 11F-70. Box 1123, New York, NY10029. USA. E-mail: daniela.sia@mssm.edu

Disclosures: Part of the study was supported with an investigator-initiated research grant by Boehringer Ingelheim. Prof. Josep M. Llovet has been a consultant, advisory board member and has received research funding from Boehringer Ingelheim; and is receiving research support from Bayer HealthCare Pharmaceuticals, Eisai Inc, Bristol-

Myers Squibb and Ipsen, and consulting fees from Bayer HealthCare Pharmaceuticals, Bristol-Myers Squibb, Eisai Inc, Celsion Corporation, Eli Lilly, Exelixis, Merck, Ipsen, Glycotest, Navigant, Leerink Swann LLC, Midatech Ltd, Fortress Biotech, Sprink Pharmaceuticals and Nucleix. Prof. Scott L Friedman has been a consultant for Abide Therapeutics, Allergan Pharmaceuticals, Angion Biomedica, Blade Therapeutics, Can-Fite Biopharma, Enanta Pharmaceuticals, Escient Therapeutics, Forbion, Galmed, Genfit, Glycotest, Glympse Bio, Metacrine Inc., Mistral Biosciences, Morphic Rock Therapeutics, North Sea Therapeutics, Novartis, Novo Nordisk, Pfizer Pharmaceuticals, Salix Pharmaceuticals, Scholar Rock, Seal Rock Therapeutics, Second Genome, Surrozen, Symic Bio, Viking Therapeutics and Kintai; has received research funding from Blade Therapeutics, Can-Fite Biopharma, Ferring Research Institute, Galmed; and has stock options from Intercept, Exalenz, Madrigal, Akarna Therapeutics, BirdRock Bio, Blade Therapeutics, Conatus, DeuteRx, Exalenz, Galectin, Galmed, Genfit, Glympse. The rest of the authors declare no conflict of interest relevant to the study reported.

Transcript profiling: Gene expression Omnibus accession number from previously deposited data from our group (GSE63898, GSE10143, GSE15654) and others (GSE84044). Newly profiled mice samples are in GEO under accession number (GSE125975 and GSE133969).

Author contribution: Study concept and design: AM, VT, DS, JML; acquisition of data: AM, ST, CM, JP, MH, MS; analysis and interpretation of data: AM, ST, VT, CM, CAO, MS; drafting of the manuscript: AM, DS, JML; critical revision of the manuscript for important intellectual content: RP, SF, DS, JML; obtained funding: JML; study supervision: JML, DS.

Acknowledgements: We thank Juan José Lozano for technical assistance in the normalization of transcriptomic array of the animal model. This study has been developed at the building of *Centre Esther Koplowitz* from IDIBAPS/CERCA Programme/Generalitat de Catalunya. We also acknowledge Angelo Sangiovanni and Massimo Colombo for providing the seminal cohort of cirrhotic patients in our previous studies^{12,14}.

ABSTRACT

Background & Aims: Cirrhosis and chronic inflammation precede development of hepatocellular carcinoma (HCC) in approximately 80% of cases. We investigated immune-related gene expression patterns in liver tissues surrounding early-stage HCCs and chemopreventive agents that might alter these patterns to prevent liver tumorigenesis.

Methods: We analyzed gene expression profiles of non-tumor liver tissues from 392 patients with early-stage HCC (training set, n=167 and validation set, n=225) and liver tissue from patients with cirrhosis without HCC (n=216, controls) to identify changes in expression of genes that regulate the immune response that could contribute to hepatocarcinogenesis. We defined 172 genes as markers for this deregulated immune response, which we called the immune-mediated cancer field (ICF). We analyzed the expression data of liver tissues from 216 patients with cirrhosis without HCC and investigated the association between this gene expression signature and development of HCC and outcomes of patients (median follow-up 10 years). Human liver tissues were also analyzed by histology. C57BL/6J mice were given a single injection of Diethylnitrosamine (DEN) followed by weekly doses of carbon tetrachloride to induce liver fibrosis and tumorigenesis. Mice were then given orally the multiple tyrosine inhibitor nintedanib or vehicle (controls); liver tissues were collected and histology, transcriptome, and protein analyses were performed. We also analyzed transcriptomes of liver tissues collected from mice on a choline-deficient high-fat diet, which developed chronic liver inflammation and tumors, given orally aspirin and clopidogrel or the anti-inflammatory agent sulindac vs mice on a chow (control) diet.

Results: We found the ICF gene expression pattern in 50% of liver tissues from patients with cirrhosis without HCC and in 60% of non-tumor liver tissues from patients with early-stage HCC. The liver tissues with the ICF gene expression pattern had 3 different features: increased numbers of effector T cells; increased expression of genes that suppress the immune response and activation of transforming growth factor beta signaling; or expression of genes that promote inflammation and activation of interferon gamma signaling. Patients with cirrhosis and liver tissues with the immunosuppressive profile (10% of cases) had a higher risk of HCC (hazard ratio, 2.41; 95% 1.21–4.80). Mice with chemically-induced fibrosis or diet-induced steatohepatitis given nintedanib or aspirin and clopidogrel downregulated the ICF gene expression pattern in liver and developed fewer and smaller tumors than mice given vehicle.

Conclusions: We identified an immune-related gene expression pattern in liver tissues of patients with early-stage HCC, called the ICF, that associates with risk of HCC development in patients with cirrhosis. Administration of nintedanib or aspirin and clopidogrel to mice with chronic liver inflammation caused loss of this gene expression pattern and developed fewer and smaller liver tumors. Agents that alter immune regulatory gene expression patterns associated with carcinogenesis might be tested as chemopreventive agents in patients with cirrhosis.

Keywords: cancer, microenvironment, cytokines, lymphocytes, immune exhaustion

INTRODUCTION

Liver cancer is the fourth leading cause of cancer-related mortality worldwide¹. Hepatocellular carcinoma (HCC) accounts for more than 90% of liver cancers and is the main cause of death in patients with cirrhosis^{2,3}. HCC arise from chronic liver inflammation, fibrosis and eventually cirrhosis in 70-80% of cases². In developed countries, curative treatments are feasible in 30-40% of cases, but recurrence is high and no effective adjuvant therapies are available^{2,4}. In addition, ~40-50% of patients are diagnosed at advanced stages when currently approved molecular therapies yield limited survival benefits (~1 year)³. Despite recent advances in the management and clearance of HCV infection, there is an unmet need for early detection and application of chemopreventive approaches in patients at high-risk of HCC development.

To date, there are no established preventive strategies for HCC in patients at risk beyond prevention with anti-viral therapies⁵. Once cirrhosis is established, anti-viral therapies reduce but do not eliminate the risk of HCC^{4,6,7}. Individual risk assessment is a key first step in the successful development of any chemopreventive strategy. In this regard, increasing evidence suggests the existence of the so-called "cancer field-effect" or field cancerization which consists of predisposing oncogenic and inflammatory signals occurring during chronic liver injury and ultimately leading to malignant transformation^{8–10}. Gene signatures derived from the cirrhotic tissue adjacent to HCC tumors have been designed to predict poor outcome, particularly in HCV-infected cirrhotic patients at higher risk of HCC development^{9,11–14}. Overall, these studies support the feasibility of using molecular scores of the carcinogenic roles of inflammation and immune response in the context of the field cancerization have been poorly explored. Understanding the immune features governing the unresolved cancer field-effect is crucial for identifying potential therapeutic targets in patients at high risk of HCC development.

In this study, the analysis of the inflammatory *milieu* that characterizes the underlying liver disease in which HCC tumors arise has led to the identification of an immunemediated cancer field (ICF) in 60% of early HCC patients and 50% of cirrhotic patients without HCC. This ICF comprises three distinct molecular subtypes including the *High Infiltrate ICF* subtype with increased infiltration of effector T cells, the *Immunosuppressive ICF* subtype with activation of stroma and TGF- β signaling, and the *Pro-inflammatory ICF* subtype with up-regulation of IFN- γ signaling. These immune profiles, particularly the *Immunosuppressive* cancer field, predict increased risk of HCC development in cirrhotic patients. Inhibition of this carcinogenic field significantly reduced HCC onset in two mouse models of chronic liver damage and hepatocarcinogenesis. Overall, our study provides the rationale to explore chemopreventive strategies in cirrhotic patients at high-risk of HCC development.

MATERIALS AND METHODS

Human cohort

Gene expression data from a cohort of 167 surgically resected fresh-frozen samples (Heptromic dataset, GSE63898) with matched tumor and adjacent non-tumor tissue were analyzed. Samples were previously collected (1998-2008) in the setting of the HCC Genomic Consortium upon institutional review board approval. Full description of the cohort and RNA profiling data are available in previous publications^{15,16}. **Supplementary Table 1** provides a summary of the clinical-pathological variables of the samples used in the current study (training cohort, n=167). Validation of the identified molecular profiles was then performed in an independent set of 225 adjacent non-tumor liver tissues previously characterized by our group (GSE10143)⁹. Finally, to identify those non-neoplastic patients at higher risk of HCC development and most likely to benefit from chemopreventive strategies, our findings were evaluated in a previously characterized cohort of patients with early cirrhosis (n=216, GSE15654)¹⁴ and a publicly available dataset of fibrotic liver tissues (n=124, GSE84044)¹⁷.

Modeling the immune-mediated cancer field

Enrichment scores of 4872 gene sets that represent cell states and perturbations of the immune system (Collection C7 of MSigDB, Broad Institute)¹⁸ were calculated by Single-sample Gene Set Enrichment Analysis (ssGSEA) in the non-tumor liver tissue of the training cohort. Next, unsupervised clustering analysis by non-negative matrix factorization (NMF consensus)¹⁹ method was performed to identify the presence of an immune-mediated cancer field. To characterize the samples presenting an ICF and to identify different immune-mediated field subtypes, a second unsupervised clustering was performed using ssGSEA scores obtained for a curated set of gene signatures representative of individual cell types^{20,21}, cancer immune-related signaling pathways²², and inflammation- or immune-specific biological processes (Hallmark collection of MSigDB, Broad Institute).

Generation of an immune-mediated field gene signature

An ICF field gene signature was generated using top differentially expressed genes in each molecular group (FDR<0.05; Fold-change \geq 2), which was then validated in an independent dataset using Nearest Template Prediction (NTP) analysis (p-value<0.05) (Gene Pattern modules)²³.

Molecular characterization of the ICF subtypes and identification of candidate therapies

To characterize the ICF subtypes, gene expression signatures [available in MSigDB (Broad Institute) or previously reported (**Supplementary Table 2**)] were assessed by GSEA, ssGSEA, NTP and Ingenuity Pathway Analyses (IPA). CIBERSORT²⁰ was used to estimate the relative fraction of 22 immune cell types within the leukocyte compartment of non-tumor liver tissues. The Immunophenoscore (IPS) algorithm²⁴ was used to analyze the major immunogenic determinants. An *in silico* analysis based on ssGSEA scores of ~1230 gene sets (DSigDB) recapitulating targets of approved therapies was also performed for the screening of candidate targeted therapies.

Histological evaluation of infiltrating inflammation

Histopathological analysis was performed in 98 out of 167 cases. Specifically, hematoxylin and eosin (H&E) staining of formalin-fixed paraffin embedded (FFPE) tissue section of HCCs and their matched adjacent non-tumor livers were evaluated by two expert pathologists (CM and MS). The presence of inflammation (portal/septal, interface, pericentral and lobular) as well as the lymphoid aggregates were assessed in the non-tumor liver tissue sections. More details on the histological evaluation of the samples have been included in **Supplementary material**.

Animal models

We generated a chemically-induced model of HCC and fibrosis in male C57BL/6J mice (Harlan Laboratories, n=55) by a single injection of Diethylnitrosamine (DEN) followed by weekly dosing with carbon tetrachloride (CCl₄), as previously described²⁵. Once fibrosis was established, mice were randomized to receive vehicle or nintedanib (50 mg/kg, Boehringer Ingelheim). Mice were sacrificed at different time-points and liver and tumor tissue samples were collected and processed for histological, transcriptomic and protein expression analyses (see **Supplementary material**). All experimental procedures were carried out following the approval of the institutional ethical committee of the University of Barcelona and Hospital Clinic of Barcelona. Additionally, liver samples of a choline-deficient high-fat diet (CD-HFD) fed mouse model reported in a recent study²⁶ were collected. A total of 25 samples were processed for transcriptomic profiling, including mice fed a chow diet (n=5) or CD-HFD for 12 months and given: vehicle (n=4); aspirin/clopidogrel (Asp/Clo) (n=6) or sulindac (n=10).

Statistical analysis

All analyses were performed using SPSS software version 23 (IBM) or GraphPad Prism version 5.00 (San Diego, CA). Correlations for categorical and continuous variables were analyzed by Fisher's exact test and Wilcoxon rank-sum test, respectively. The prognostic value of the signatures was assessed using Kaplan-Meier estimates, log-rank test, and Cox regression models. In *in vivo* studies, the Mann-Whitney U test was used to compare differences in body weights, liver function, tumor number, tumor size and CD4/CD8 stained area in human samples. Fisher exact test was performed for analysis of HCC incidence and pERK staining. Student T-Test was used to compare the differences in Sirius Red quantification, CD31 staining, CD4/CD8 staining proportion of immune cell infiltrate in mice and relative gene expression.

RESULTS

Identification of a novel immune-mediated cancer field effect in non-tumor liver tissue of patients with early HCC.

In order to characterize the immune features governing the unresolved cancer-field in which new cancers arise, transcriptome-based analysis of a compendium of ~5,000 annotated immunology-specific gene-sets¹⁸ was performed in the non-tumor liver tissue of patients with early stage HCC. This analysis revealed the presence of an immunemediated cancer field (ICF) in ~60% (98/167) of samples (Figure 1A and **Supplementary Figure 1**). Specifically, these samples were characterized by enrichment of several gene-sets recapitulating the presence of activated immune cells, up-regulation of core signaling pathways involved in immune response (both innate and adaptive) as well as those involved in the modulation of inflammatory response (i.e. IL2-STAT5, IL6-STAT3, IL17, IFN-y, CSF, TNF- α , and TGF- β signaling) (Figure 1A-B and Supplementary Figure 1). Moreover, histological evaluation confirmed that liver tissues with ICF contained a higher frequency of moderate to marked inflammatory infiltrate (74% in ICF vs. 52% in non ICF, p=0.034) and lymphoid aggregates (80% in ICF and vs. 55% in non ICF, p=0.009) (Figure 1C-1D and Supplementary Table 3). Immunostaining for CD4+ and CD8+ further confirmed significantly higher levels of T cell infiltrates in the adjacent livers of patients with the ICF (Supplementary Figure 2A). In contrast, histological evaluation of the tumor showed no significant correlation between the presence of the ICF and the detection of intratumoral or peritumoral infiltration (Supplementary Table 3). This is in accordance with our recent publication¹⁵, where the tumor immune-based profile did not correlate with presence or absence of immune gene signatures in the surrounding non-tumor tissue.

While characterizing the ICF we detected that, in addition to immunogenic features, several well-known carcinogenic signals such as epithelial-to-mesenchymal transition, KRAS, EGFR, and VEGF signaling were also significantly enriched in liver tissues containing the ICF (**Supplementary Table 4**). In line with these oncogenic signals, a significant enrichment of previously reported prognostic signatures derived from the adjacent non-tumoral liver were also detected. These signatures included the 186-gene cancer-field signature⁹, activated hepatic stellate cells (HSCs)¹¹, hepatic injury and regeneration (HIR)¹³, and multicentric occurrence of HCCs²⁷ (**Figure 1A**). The presence of the ICF significantly correlated with HCV infection, features indicative of liver dysfunction such as high bilirubin, low platelet count and albumin levels (**Supplementary Table 5**) and poor survival [median OS 43.4 mo in the ICF group vs 94.8 mo in non ICF; p=0.001], (**Supplementary Table 6** and **Supplementary Figure 1B**). Altogether, our

data highlight the presence of an immune-mediated cancer field in 60% of early HCC patients. This ICF is characterized by activation of immunomodulatory signaling cascades (i.e. IFN- γ , TNF- α , TGF- β , IL6) along with cancer promoting signaling pathways (i.e. EMT, EGFR and VEGFR), and is associated with HCV infection and poor prognosis.

The immune-mediated cancer field contains 3 distinct molecular subtypes.

Further dissection of the key immune-modulating signaling pathways and immune-cell infiltrates in those samples harboring the immune-mediated cancer field revealed the existence of three distinct molecular subtypes. The first molecular subtype, henceforth called the "High Infiltrate ICF" subtype (23% of the ICF), showed a significant enrichment of several previously established gene signatures mirroring the presence and/or activation of immune cell infiltrates such as lymphocytes (T and B cells)^{22,28} or macrophages²⁹ (Figure 2A-2B). Consistently, immunogenicity, herein captured either by the cytolytic activity score (Figure 2A)³⁰ or using the immunophenoscore algorithm²⁴ (Figure 2B), was also significantly higher in these samples (p<0.001). Specifically, nontumor liver samples belonging to the High Infiltrate ICF subtype showed significant infiltration of effector T cells (Figure 2B, p≤0.001), including increased levels of cytotoxic CD8+ T cells assessed both by transcriptomic (p=0.03) and immunohistochemistry (p=0.0002) (Figure 2C and Supplementary Figure 2B). This subtype also was characterized by enrichment of the previously reported ectopic lymphoid structures (ELS) signature³¹ (Figure 2A). In addition, the *High Infiltrate ICF* was significantly associated with poor survival in comparison to the rest of the patients (Supplementary Figure 1C), although there were no significant differences among the distinct ICF subtypes (Supplementary Figure 1D). The second subtype, the so-called "Immunosuppressive ICF" (36% of the ICF), was characterized primarily by activation of stroma and HSCs, increased TGF- β signaling and T cell exhaustion (Figure 2A). Moreover, several immune-checkpoints (i.e. CTLA-4, TIGIT, LAG3) were significantly over-expressed (IPS, p<0.01) in this class, along with higher levels of M2 macrophages (p=0.04) and CD4+ memory resting cells (p=0.005), which are among main mediators of immune tolerance and inhibition (Figure 2B-2C). The third subtype (41% of the ICF) showed a clear predominance of IFN-y signaling (p<0.001) and enrichment of the inflammatory M1 macrophages (p<0.0001), and was called the "Pro-inflammatory ICF" subtype (Figure 2A-2C). Interestingly, the High Infiltrate and Immunosuppressive subtypes shared several molecular features including the enrichment of key signaling pathways involved in modulating the immune response (i.e. IL2 and TNF signaling),

proliferation (i.e. KRAS signaling) and angiogenesis (Figure 2A, p<0.001).

In order to further confirm the presence and molecular traits of the identified ICF, we generated a transcriptome-based gene signature able to capture the three immunemediated cancer field subtypes. Interestingly, this signature only showed minimal overlap (0-5%) with previously reported gene signatures of field cancerization in HCC (Supplementary Figure 3)^{9,12,14,32}. The resulting 172-gene signature (Supplementary Table 7) was then validated in the adjacent non-tumor tissue of 225 patients with early HCC, previously characterized by our group^{9,33} (Supplementary Figure 4A). Similar to what was previously observed in the training cohort, 58% (130/225) of patients belonged to the ICF. Moreover, in this cohort, the presence of the ICF was an independent predictor of poor survival [HR=2.73; 95 CI: 1.1-6.8; p=0.03] (Supplementary Figure 4B, **Supplementary Table 8**). Within the ICF group, ~31% (40/130) presented the High Infiltrate ICF profile, ~27% (35/130) the Immunosuppressive ICF and ~42% (55/130) the Pro-inflammatory ICF subtype (Supplementary Figure 4A). Subsequent molecular characterization further confirmed the ability of the signature to capture the main molecular traits defining each subtype, such as increased infiltration of effector T cells in *High Infiltrate* subtype, activation of stroma and TGF- β signaling in *Immunosuppressive* subtype and up-regulation of IFN- γ signaling in *Pro-inflammatory* subtype (Supplementary Figure 4A). Overall, our results highlight the presence of a poor prognosis-related immune-mediated cancer field comprised of 3 molecular subtypes with a high degree of lymphocyte infiltration (overall 16% of HCC patients) or predominance of either immunosuppressive (overall 20% of HCC patients) or pro-inflammatory (24% of HCC patients) signaling cascades.

The immune cancer-field, particularly the immunosuppressive subtype, predicts a high risk of HCC development in cirrhotic patients

Following the identification of an immune-mediated cancer field in the livers of 60% of patients with early HCC, we next sought to assess its role in liver disease progression and HCC primary occurrence. To this end, the 172-gene signature was analyzed in a cohort of 216 non-malignant cirrhotic patients with a median follow-up of 10 years in the context of an HCC surveillance program¹⁴. Overall, 51% (110/216) of cirrhotic patients harbored the ICF, including the *High Infiltrate ICF* subtype in 28% (31/110), the *Immunosuppressive ICF* subtype in 19% (21/110), and the *Pro-inflammatory ICF* subtype in 53% (58/110) of cirrhotic patients harboring the ICF. Next, we tested the capacity of the ICF subtypes to predict the risk of HCC development in cirrhotic patients. Interestingly, the presence of the *Immunosuppressive ICF* subtype (10% of all cirrhotic

patients) was significantly associated with a higher risk of HCC development [median time to HCC development of 7.4 years (95% CI: 3.2-11.7) *vs* 17.1 years (95% CI: 10.6-23.7) in Rest, p<0.0001] and was found to be an independent predictor of HCC occurrence in cirrhotic patients in a multivariate analysis [HR 2.41 (95% CI: 1.2-4.8), p=0.012] (**Figure 3A** and **Table 1**). In addition, the *Immunosuppressive ICF* was also significantly associated with poor survival [median overall survival of 7.1 years (95% CI: 4.5-9.6) *vs* 16.3 years (95% CI: 9.1-23.5) in Rest, p<0.0001] and higher risk of hepatic decompensation [median time to hepatic decompensation of 6.5 years (95% CI: 4.3-8.6) *vs* >15 years in Rest, p<0.0001] (**Figure 3B-3C**). Cirrhotic patients harboring the other two ICF subtypes (*High Infiltrate* and *Pro-inflammatory* subtypes) also showed a non-significant trend towards a higher risk of HCC development compared to those patients lacking the ICF [mean time to HCC development of 12.8 years (95% CI:11.5-14.2) in Other ICF subtypes *vs* 16.3 years (95% CI: 14.2-18.5) in non ICF, p=0.06] (**Supplementary Figure 5A**).

Moreover, the analysis of an additional cohort of 124 non-neoplastic patients with liver fibrosis¹⁷ revealed that the immune-mediated cancer field may occur as a progressive event, as it significantly correlated with increasing levels of fibrosis stage and degree of inflammation (**Supplementary Figure 5B**). Particularly, the presence of the *Immunosuppressive ICF* significantly correlated with the presence of advanced liver fibrosis (Scheuer fibrosis S3-4 score¹⁷, p=0.034) (**Supplementary Figure 5B**).

In conclusion, the immune-mediated cancer field detected in patients with early HCC is also present in the livers of ~50% of cirrhotic patients and captures the presence of a damaging and continuous inflammatory response in the underlying liver disease. Furthermore, our results underscore the critical role of an *Immunosuppressive ICF* (overall, 10% of cirrhotic patients) in defining a 2.4 risk of HCC development, and to a smaller extent of the *High Infiltrate* and *Pro-inflammatory* subtypes.

The immune-mediated field as a target for chemoprevention in a mouse model recapitulating chronic liver inflammation and HCC development

Based on the compelling results described above, we hypothesized that the immunemediated cancer field, and particularly the *Immunosuppressive ICF* subtype, may represent an ideal target for chemopreventive strategies in cirrhotic patients at high risk of HCC development. To this purpose, an *in silico*-based analysis was performed using our training cohort to identify those candidate therapies most likely to modulate the identified ICF. This analysis was based on the enrichment of a compendium of ~1230 gene sets (DSigDB collections D1 and D2)³⁴ recapitulating the main targets of 1202 approved drugs. Among the top 10 most significantly enriched drugs (Supplementary Figure 6), nintedanib was the only FDA-approved therapy indicated for a non-cancer condition. Specifically, nintedanib is the first molecular targeted therapy with clinical efficacy in patients with idiopathic pulmonary fibrosis as both an anti-fibrogenic and antiinflammatory agent³⁵. Given these considerations, the efficacy of nintedanib in reverting the pro-tumorigenic immune-mediated cancer field was tested in a mouse model of HCC development in the setting of chronic inflammation and liver fibrosis (Supplementary Figure 7A). In this model, the macroscopic evaluation of explanted livers in DEN/CCl₄ mice sacrificed at the age of 15, 17 and 18 weeks confirmed the development of numerous hepatic tumors (Figure 4A). Tumor penetrance and number of tumors progressively increased, ultimately reaching a 100% incidence at 18 weeks of age (Figure 4A and 4B). At all-time points, histological evaluation of the liver sections showed that a portion of the tumors were pre-neoplastic (dysplastic) nodules (Figure 4C). In mice sacrificed at 15 weeks of age, Supplementary Figure 7A), nintedanib showed a clear trend towards reducing HCC incidence, number and size of tumors (Figure 4B, D and E). These differences reached significance at 17 weeks of age (Figure 4B), having a marked decrease in both overall tumor burden (30% in nintedanib vs 89% in vehicle group, p=0.019) and specifically in HCC incidence (7% vs 33%, p=0.04). Similarly, at 18 weeks of age, HCC incidence was significantly reduced in treated mice (Figure 4B, 22% vs 77%, p<0.001). In addition, nintedanib significantly reduced the overall tumor number and size both at 17 and 18 weeks of age (Figure 4D-E). Overall, nintedanib was well tolerated with no significant induction of body weight loss or hepatotoxicity measured by serum ALT and AST levels (Supplementary Figure 7B-**C**). Taken together, our data suggest that nintedanib is safe and efficacious in preventing HCC development in our experimental model.

Nintedanib treatment reverts the immune-mediated cancer field effect

Next, we sought to assess the impact of nintedanib treatment on the immune-mediated cancer field. For this purpose, we analyzed gene expression profiling of non-tumor liver samples from 17 weeks-old DEN/CCl₄ mice given nintedanib (n= 10) or vehicle (n=9), and 3 healthy control mice. First, the comparison between the healthy control group and vehicle group revealed a profile of activated pathways compatible with HCC development within a fibrotic and inflammatory background. In this regard, functional analysis of differentially expressed genes (**Supplementary Table 9**) highlighted the activation of hepatic stellate cells and fibrogenesis, as well as immune system activation

(inflammatory response, chemotaxis, binding of myeloid and leukocytes) in vehicle treated DEN/CCl₄ livers (Supplementary Table 10). Notably, our model presented a significant enrichment of the gene-set representing the ICF identified in humans (p=0.001) and faithfully recapitulated the human immune-mediated field subtypes described above (Figure 5A). The comparison of the gene expression profiles of adjacent non-tumor liver from mice treated with vehicle or nintedanib demonstrated that nintedanib significantly down-regulated the ICF subtypes and, more specifically the Pro-Inflammatory and the Immunosuppressive ICF phenotype, which predict risk of HCC development in cirrhotic patients (Figure 5A, p=0.02). A non-significant trend was also observed for the High Infiltration subtype (Figure 5A). Treatment with nintedanib led to a significant down-regulation of inflammatory cues (IL-6/STAT3, interferon- α , interferon- γ) and immune-related signaling (IL-2/STAT5 activation, allograft rejection) (Figure 5A). Among the infiltrating immune cells, nintedanib significantly reduced the presence of B and T cells, activated macrophages, helper T cells and Tregs along with associated immune modulators (i.e. IL1, CCL5 and PDL1) (Figure 5A). Despite exhibiting similar global levels of inflammatory infiltrates, quantification of CD4 and CD8 positive infiltrating lymphocytes by IHC revealed a significant decrease of CD4+ T cells in nintedanibtreated mice compared to controls (Figure 5B, p<0.05).

Next, in order to further characterize the chemopreventive effects of nintedanib we assessed the activation status of the main nintedanib targets (i.e. VEGFR2 and PDGFR- β). Western blot of non-tumor liver tissue confirmed that nintedanib blocked the activation of VEGFR2 (**Figure 5C**) and its downstream effectors AKT and ERK (**Supplementary Figure 8A**). Consistently, both liver parenchyma and liver tumors were pERK positive in vehicle-treated mice and pERK negative in nintedanib treated mice (**Supplementary Figure 8B**, p<0.05), indicating an anti-proliferative effect of nintedanib as well. Given the strong inhibition of VEGFR signaling observed, we next assessed the anti-angiogenic effect of nintedanib in DEN/CCl₄ mice. In this model, reduced CD31 staining was associated with diminished blood vessel area in both liver parenchyma and liver tumors of nintedanib-treated mice (**Figure 5D**). Altogether, these data suggest that nintedanib exhibits its chemopreventive effects in part by inducing vascular normalization and inhibiting hepatic proliferation. In contrast, no reduction of fibrosis degree, the profibrogenic signaling pathway PDGFR- β , or collagen markers were detected in the livers of nintedanib-treated mice (**Supplementary Figure 8C-E**).

Overall, our data confirm that therapeutic targeting of the immune-mediated cancer field, accompanied by liver vascular normalization and suppression of hepatic proliferation, can prevent the development of HCC associated with advanced chronic liver disease.

Immunomodulatory effects of Asp/Clo treatment revert the immune cancer field effect and prevent hepatocarcinogenesis in vivo

To further support the concept of an ICF in promoting HCC development and its therapeutic immunomodulation as candidate strategy for chemoprevention, we performed gene expression profiling in non-tumor liver derived from the recently described mouse model of choline-deficient high-fat diet (CD-HFD) treated either with the immunomodulatory combination aspirin/clopidogrel (Asp/Clo) or the antiinflammatory sulindac²⁶. Of particular interest, in this model, which presents nonalcoholic fatty liver-related liver inflammation with various degrees of fibrosis and HCC development after 12 months of diet regimen^{26,36,37}, HCC prevention was achieved only through the combination of the anti-inflammatory drug, aspirin, clopidrogel -an P2Y12 inhibitor-, (25% to 0% 12-mo HCC incidence control vs combo respectively, p=0.01)²⁶ and not sulindac alone (25% to 20%12-mo HCC incidence control vs sulindac, respectively, p=ns, data not shown). In the context of our study, comparative analysis between the non-tumor liver of healthy control and CD-HFD mice showed a significant enrichment of the ICF signature in CD-HFD mice (p=0.002, Figure 5E). Notably, all 3 ICF subtypes were significantly up-regulated in CD-HFD mice compared to healthy controls (Figure 5E) along with the enrichment of signaling pathways regulating inflammation (i.e. IL6-STAT3, TNFa), immune infiltration and activation^{22,28}, and epithelial-to-mesenchymal transition (i.e. TGFβ, p<0.05). These data were consistent with the high intrahepatic influx of metabolically activated CD8+ T cells and NK cells (CD3+NK1.1+) measured in CD-HFD fed mice by flow cytometry²⁶. Overall, these data confirm the existence of an ICF in an independent model of chronic liver disease further suggesting a role in hepatocarcinogenesis.

Next, we compared the expression profiles of liver samples from CD-HFD vehicle-treated mice with CD-HFD mice treated with the combination Asp/Clo (n=6) or sulindac alone (n=10). Interestingly, only Asp/Clo, but not sulindac alone, was able to prevent HCC and revert the ICF within the liver microenvironment (p=0.05), being the *Pro-inflammatory* ICF subtype the most significantly down-regulated upon treatment (**Figure 5B**). Particularly, based on previous molecular characterization²⁶, the inhibition of the ICF seemed to be accompanied by a significant reduction of the degree of liver damage, as well as a significantly reduced number of CD8+ and NKT cells in the liver.

Overall, these data support the role of the ICF in promoting carcinogenesis, and suggest that only those drugs able to simultaneously inhibit several components of the ICF by

targeting mitogenic, angiogenic and immunomodulatory kinases (i.e. nintedanib and Asp/Clo) present a more efficacious therapeutic index for HCC prevention.

DISCUSSION

This study represents an in-depth analysis of the *inflammatory milieu* associated with the "field cancerization" in the chronically injured liver, and investigates its clinical implications in the prediction and prevention of HCC occurrence in cirrhotic patients.

The role of the "cancer field effect" in promoting neoplastic transformation has gained much interest in recent years and currently an altered microenvironment is considered a promoter of cancer^{8,10}. Although, under physiological conditions, inflammation is an adaptive response to tissue injury, when the inflammatory stimuli persist, the nonresolved inflammation contributes to carcinogenesis^{38,39}. In this line, activation of HSC as well as certain pathways, such as nuclear factor-KB and TGF- β signaling, have been previously associated with liver fibrogenesis, eventually and neoplastic transformation^{9,12}. With this study, we move beyond the limits of current knowledge and provide a detailed description of the immune microenvironment underlying the field cancerization in the liver. To this end, we first characterized the immune profile of the non-tumor liver parenchyma of 392 early HCCs and then investigated its role in predicting HCC development in 216 cirrhotic patients with long-term surveillance for HCC (median of 10 years)¹⁴. The analysis revealed that up to 60% of HCCs and 50% of cirrhotic patients showed a deleterious immune-mediated response in the surrounding tissue, which was associated with impaired liver function, activation of specific oncogenic loops, angiogenesis and poor survival. Further characterization identified three distinct subtypes with different levels of lymphocyte infiltration and activation of either immunosuppressive or pro-inflammatory traits. In particular, the so-called Immunosuppressive ICF subtype (~10% of cirrhotic patients) was an independent predictor of HCC development, increasing 2.4 the risk of cancer development, whereas both the High-Infiltrate and the Pro-Inflammatory subtypes showed a trend towards higher risk of HCC occurrence in cirrhosis. The identification of distinct immune subtypes reflects the complex role of the immune system in hepatocarcinogenesis, with both an activated immune response and an exhausted immune-microenvironment contributing to create a pro-tumorigenic environment and increase the risk of HCC development⁴⁰.

Reducing the incidence and mortality of HCC requires advances in chemopreventive approaches at pre-neoplastic stages, in addition to curative treatment options for early

lesions. Universal immunization against HBV and antiviral therapies against HBV and HCV have been associated with very reduced HCC risk^{2,41,42}. Once cirrhosis is established, the risk of HCC development remains despite achieving a sustained virologic response in HCV patients^{6,7}. In addition, the incidence of other risk factors, such as non-alcoholic steatohepatitis (NASH), is dramatically increasing². Thus, alternative HCC preventive strategies capable of interfering with molecular hepatocarcinogenesis are an unmet need. Furthermore, identifying those patients at high risk of HCC development should enable a cost-effective selection of patients most likely to benefit from chemopreventive approaches. In this scenario, our results are of clinical relevance since the ICF, and specifically the Immunosuppressive subtype, may provide a novel companion biomarker to enrich at-risk patients in chemoprevention clinical trials. Given these observations, we then sought to investigate if the molecular forces driving such cancer field could serve as target for chemopreventive strategies. Hence, we first verified that the molecular profiles observed in human cirrhosis were faithfully reproduced in two animal models of chronic liver injury. The DEN/CCl₄ chemically-induced mouse model as well as the recently described NASH-HCC model²⁶ reliably recapitulated the presence of a carcinogenic phenotype observed in liver tissues from patients belonging to the immune-mediated cancer field.

In order to identify the most promising candidate therapies for novel chemopreventive strategies, we conducted an *in silico* analysis using a large compendium of gene sets³⁴ recapitulating the main targets of 1202 approved drugs. Among the top ten most significantly enriched drugs, we selected nintedanib, the only FDA therapy approved for non-neoplastic conditions. In the DEN/CCl₄ animal model, oral administration of reduced the immune-mediated field, nintedanib cancer including the Immunosuppressive ICF subtype, ultimately reducing HCC incidence and growth. Reversion of the ICF induced by treatment with nintedanib was accompanied by reduction of CD4+ lymphocytes, which could be due to its mechanism of action inhibiting src family of kinases (i.e. LCK, FLT3 and SRC). These findings are in line with previous reports suggesting that CD4+ cells propagate immune-mediated liver injury in models of chronic liver inflammation or autoimmune liver disease^{43,44}. Pretreatment with T cellspecific Abs or immunosuppressive agents, such as anti-CD4 mAb, FK506 (Tacrolimus), or cyclosporine A, have shown to ameliorate hepatitis in these models, further supporting the role of CD4+ T cells in inducing liver damage⁴³. Results in a second animal model treated with the combination of the anti-inflammatory drug, aspirin, and clopidrogel -aP2Y12 inhibitor-, confirmed the therapeutic potential of immunomodulating the ICF and supported the pro-tumorigenic role exerted by the immune response. Indeed, only the

treatment able to modulate the ICF, as indicated by the reduction of immune cells (i.e. CD8⁺ and NKT cells) and the reversion of the ICF signature, successfully reduced liver damage and prevented HCC development. Overall, our study identifies a novel promising chemopreventive strategy for HCC and confirms the validity of using the reversion of the *ICF* as reliable read-out of efficacy. This is of great clinical importance since there is currently no effective method to monitor the short-term effects of chemopreventive drugs⁵. Nintedanib belongs to a new generation of TKIs that, in addition to exerting immune modulation blocks the activation of main angiogenic receptors⁴⁵. Many cytokines and growth factors are involved in modulating the formation of new vessels. Expression of VEGF and its receptors is elevated in HCC cell lines and tissues, as well as in the blood circulation of patients with HCC^{33,46–48}. In our model, nintedanib exerted its chemopreventive mechanisms in part through the inhibition of VEGF signaling, a major driver of angiogenesis⁴⁹. Thus far, independent studies had described that HCC prevention can be achieved in animal models by attenuating liver fibrosis through the inhibition of epidermal growth factor receptor (EGFR)^{50,51} or lysophosphatidic acid (LPA)³² signaling. With the current study, we demonstrate that modulation of the liver microenvironment by molecular targeted drugs, which simultaneously block liver inflammation and angiogenesis, might represent a powerful alternative strategy.

We recently defined the immune class of HCC¹⁵ and the Immune exclusion class (characterized by active Wnt/CTNNB1)^{3,15,52}, which might predict response and primary resistance to checkpoint inhibitors, respectively^{3,52}. We herein explore the immunomodulatory mechanisms underlying HCC occurrence by defining an immune-mediated field effect that conforms a cancer-permissive *milieu*, thus posing them at the highest risk of HCC development. In addition, our pre-clinical data with a drug approved in pulmonology and in non-small cell lung cancer treatment suggest that the permissive microenvironment can be reverted leading to a reduction in HCC occurrence. These data provide the rationale for testing this strategy in early chemoprevention trials targeting cirrhotic patients at high risk of HCC development. In addition, this strategy could also be further explored in the adjuvant setting considering that 60% of HCC undergoing resection also present this permissive *milieu* in the adjacent non-tumoral tissue.

FIGURE LEGEND

Figure 1. Identification of an ICF effect in non-tumoral liver tissue adjacent to early HCCs. A) Heatmap representation of the ICF present in 60% of HCC patients. High and low ssGSEA scores are represented in red and blue, respectively. B) Top predicted upstream cytokine and transcription factors activated in liver tissues of ICF patients. C) Representative images of degree of Portal/Septal infiltrating inflammation. D) Representative images depicting presence or absence of lymphoid aggregates.

Figure 2. The ICF contains 3 distinct molecular subtypes. A) Heatmap representation of the three ICF subtypes. Statistical significance is highlighted. B) Immunophenogram representing the enrichment of immunogenic determinants in the distinct ICF subtypes (MHC: Antigen presenting, EC: Effector cells, CP: Check-points, SC: Suppressor Cells). C) Comparison of estimated proportion of immune cells (CIBERSORT method) between the ICF subtypes, representing those immune populations with estimated average fraction >5% and significant differences between the ICF subtypes. Significant statistical differences observed among the different ICF subtypes are highlighted (High Infiltrate, *Purple*, Immunosuppressive, *Orange*; Pro-inflammatory, *Green*; and both High Infiltrate and Immunosuppressive, *Black*). *=p<0.05, **=p<0.01 and ***=p<0.001.

Figure 3. Association of the presence of the *Immunnosuppressive ICF* with HCC occurrence and prognostic variables in cirrhotic patients. (A) Kaplan-Meier estimates of HCC development, (B) overall survival, (C) hepatic decompensation, according to the presence of the *Immunosuppressive* ICF subtype (orange).

Figure 4. Nintedanib reduces HCC onset in mice. A) Representative pictures of macroscopic evaluation of hepatic tumors in mice given vehicle or nintedanib sacrificed at 15, 17 and 18 weeks of age. Arrows indicate macroscopically visible tumors. B) Evaluation of overall tumor burden and HCC incidence. ([#]) = statistical significance for overall tumor burden; (*) = statistical significance for HCC incidence. C) Microscopic evaluation of the number of tumors per mouse in each group. D) Number of macroscopic tumors per mouse given vehicle or nintedanib at the different time-points. E) Diameter size of the largest tumor per mouse given vehicle or nintedanib at the three different time-points. [#] or *=p<0.05, **=p<0.01 and ***=p<0.001.

Figure 5. Nintedanib and Asp/Clo reduce the *ICF* in animal models of chronic inflammation and HCC development. A) Heatmap representation of high and low

ssGSEA scores for the 172-gene signature and gene-sets recapitulating the ICF subtypes. B) Representative images and quantification of CD4+ and CD8+ infiltrating lymphocytes in the liver of 17 weeks old mice given vehicle (n=5) or nintedanib (n=5). C) Western-blot analysis of VEGFR2 activation in the non-tumor liver parenchyma of 17 weeks old mice given vehicle (n=6) or nintedanib (n=6). D) Morphometric quantification of blood vessel area by CD31 immunostaining in 5 randomly selected low magnification fields in mice given vehicle (n=5) or nintedanib (n=5). E) Single sample GSEA analysis of the ICF signature in the different treatment arms of the CD-HFD model. **=p<0.01 and ***=p<0.001.

TABLES

	Univariate analysis	Multivariate analysis (cox's regression)		
Variable	p-value	HR	CI(95% low-high limits)	p-values
Non-tumoral liver tissue-based transcriptomic profiles				
Immunosuppressive-ICF	0.03	2.41	1.21-4.80	0.01
186-gene Poor prognosis signature	<0.0001	1.56	0.89-2.7	0.12
<u>Clinicopathological variables</u>				
Age (>median)	0.87			
Gender	0.22			
Diabetes	0.48			
HCV genotype 1b	0.18			
Alcohol consumption (>80 g/day)	0.68			
HCVetiology plus alcohol consumption	0.68			
History of antiviral treatment (interferon-based)	0.65			
Varices	0.02	1.49	0.85-2.6	0.17
Spleen	0.13			
Ishaak score 6 vs 5	0.24			
Platelet count (<100,000/mm3)	0.02	1.51	0.91-2.64	0.15
Bilirubin (> 1 mg/dL)	0.00	1.85	1.07-3.2	0.03
AFP (> 10 ng/mL)	0.87			
Prothrombin time (international normalized ratio >1.2)	0.38			

Table 1. Uni- and Multivariate Analysis of risk of HCC development in cirrhotic patientsincluding gene signatures and clinico-pathological variables (n=216).

REFERENCES

- Bray F, Ferlay J, Soerjomataram I, et al. Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. CA Cancer J Clin 2018;68:394–424.
- 2. Llovet JM, Zucman-Rossi J, Pikarsky E, et al. Hepatocellular carcinoma. Nat Rev Dis Prim 2016;2:16018.
- 3. Llovet JM, Montal R, Sia D, et al. Molecular therapies and precision medicine for hepatocellular carcinoma. Nat Rev Clin Oncol 2018;15:599–616.
- 4. Galle PR, Forner A, Llovet JM, et al. EASL Clinical Practice Guidelines: Management of hepatocellular carcinoma. J Hepatol 2018.
- Fujiwara N, Friedman SL, Goossens N, et al. Risk factors and prevention of hepatocellular carcinoma in the era of precision medicine. J Hepatol 2018;68:526– 549.
- Calvaruso V, Cabibbo G, Cacciola I, et al. Incidence of Hepatocellular Carcinoma in Patients With HCV-Associated Cirrhosis Treated With Direct-Acting Antiviral Agents. Gastroenterology 2018;155:411–421.e4.
- Kanwal F, Kramer J, Asch SM, et al. Risk of Hepatocellular Cancer in HCV Patients Treated With Direct-Acting Antiviral Agents. Gastroenterology 2017;153:996–1005.e1.
- Lochhead P, Chan AT, Nishihara R, et al. Etiologic field effect: reappraisal of the field effect concept in cancer predisposition and progression. Mod Pathol 2015;28:14–29.
- 9. Hoshida Y, Villanueva A, Kobayashi M, et al. Gene expression in fixed tissues and outcome in hepatocellular carcinoma. N Engl J Med 2008;359:1995–2004.
- Hernandez-Gea V, Toffanin S, Friedman SL, et al. Role of the microenvironment in the pathogenesis and treatment of hepatocellular carcinoma. Gastroenterology 2013;144:512–27.
- Ji J, Eggert T, Budhu A, et al. Hepatic stellate cell and monocyte interaction contributes to poor prognosis in hepatocellular carcinoma. Hepatology 2015;62:481–95.
- Zhang DY, Goossens N, Guo J, et al. A hepatic stellate cell gene expression signature associated with outcomes in hepatitis C cirrhosis and hepatocellular carcinoma after curative resection. Gut 2016;65:1754–64.

- Kim JH, Sohn BH, Lee H-S, et al. Genomic predictors for recurrence patterns of hepatocellular carcinoma: model derivation and validation. Beck AH, ed. PLoS Med 2014;11:e1001770.
- Hoshida Y, Villanueva A, Sangiovanni A, et al. Prognostic gene expression signature for patients with hepatitis C-related early-stage cirrhosis. Gastroenterology 2013;144:1024–1030.
- Sia D, Jiao Y, Martinez-Quetglas I, et al. Identification of an Immune-specific Class of Hepatocellular Carcinoma, Based on Molecular Features. Gastroenterology 2017;153:812–826.
- 16. **Villanueva A, Portela A**, Sayols S, et al. DNA Methylation-based prognosis and epidrivers in hepatocellular carcinoma. Hepatology 2015.
- Wang M, Gong Q, Zhang J, et al. Characterization of gene expression profiles in HBV-related liver fibrosis patients and identification of ITGBL1 as a key regulator of fibrogenesis. Sci Rep 2017;7:43446.
- Godec J, Tan Y, Liberzon A, et al. Compendium of Immune Signatures Identifies Conserved and Species-Specific Biology in Response to Inflammation. Immunity 2016;44:194–206.
- 19. Brunet J-P, Tamayo P, Golub TR, et al. Metagenes and molecular pattern discovery using matrix factorization. Proc Natl Acad Sci U S A 2004;101:4164–9.
- 20. **Newman AM, Liu CL**, Green MR, et al. Robust enumeration of cell subsets from tissue expression profiles. Nat Methods 2015;12:453–7.
- 21. **Bindea G, Mlecnik B**, Tosolini M, et al. Spatiotemporal dynamics of intratumoral immune cells reveal the immune landscape in human cancer. Immunity 2013;39:782–95.
- 22. **Thorsson V, Gibbs DL**, Brown SD, et al. The Immune Landscape of Cancer. Immunity 2018;48:812–830.e14.
- 23. Reich M, Liefeld T, Gould J, et al. GenePattern 2.0. Nat Genet 2006;38:500–501.
- Charoentong P, Finotello F, Angelova M, et al. Pan-cancer Immunogenomic Analyses Reveal Genotype-Immunophenotype Relationships and Predictors of Response to Checkpoint Blockade. Cell Rep 2017;18:248–262.
- 25. **Dapito DH, Mencin A, Gwak G-Y**, et al. Promotion of hepatocellular carcinoma by the intestinal microbiota and TLR4. Cancer Cell 2012;21:504–16.
- 26. Malehmir M, Pfister D, Gallage S, et al. Platelet GPlbα is a mediator and

potential interventional target for NASH and subsequent liver cancer. Nat Med 2019;25:641–655.

- Okamoto M, Utsunomiya T, Wakiyama S, et al. Specific gene-expression profiles of noncancerous liver tissue predict the risk for multicentric occurrence of hepatocellular carcinoma in hepatitis C virus-positive patients. Ann Surg Oncol 2006;13:947–54.
- Wolf DM, Lenburg ME, Yau C, et al. Gene Co-Expression Modules as Clinically Relevant Hallmarks of Breast Cancer Diversity Haibe-Kains B, ed. PLoS One 2014;9:e88309.
- 29. Beck AH, Espinosa I, Edris B, et al. The macrophage colony-stimulating factor 1 response signature in breast carcinoma. Clin Cancer Res 2009;15:778–87.
- 30. Rooney MS, Shukla SA, Wu CJ, et al. Molecular and genetic properties of tumors associated with local immune cytolytic activity. Cell 2015;160:48–61.
- Finkin S, Yuan D, Stein I, et al. Ectopic lymphoid structures function as microniches for tumor progenitor cells in hepatocellular carcinoma. Nat Immunol 2015;16:1235–1244.
- Nakagawa S, Wei L, Song WM, et al. Molecular Liver Cancer Prevention in Cirrhosis by Organ Transcriptome Analysis and Lysophosphatidic Acid Pathway Inhibition. Cancer Cell 2016;30:879–890.
- 33. Chiang DY, Villanueva A, Hoshida Y, et al. Focal gains of VEGFA and molecular classification of hepatocellular carcinoma. Cancer Res 2008;68:6779–88.
- 34. **Yoo M, Shin J**, Kim J, et al. DSigDB: drug signatures database for gene set analysis: Fig. 1. Bioinformatics 2015;31:3069–3071.
- 35. Richeldi L, Bois RM du, Raghu G, et al. Efficacy and safety of nintedanib in idiopathic pulmonary fibrosis. N Engl J Med 2014;370:2071–82.
- Wolf MJ, Adili A, Piotrowitz K, et al. Metabolic Activation of Intrahepatic CD8+ T Cells and NKT Cells Causes Nonalcoholic Steatohepatitis and Liver Cancer via Cross-Talk with Hepatocytes. Cancer Cell 2014;26:549–564.
- Brown ZJ, Heinrich B, Greten TF. Mouse models of hepatocellular carcinoma: an overview and highlights for immunotherapy research. Nat Rev Gastroenterol Hepatol 2018;15:536–554.
- 38. Coussens LM, Werb Z. Inflammation and cancer. Nature 2002;420:860–7.
- 39. Hanahan D, Weinberg RA. Hallmarks of cancer: The next generation. Cell

2011;144:646-674.

- 40. Makarova-Rusher O V., Medina-Echeverz J, Duffy AG, et al. The yin and yang of evasion and immune activation in HCC. J Hepatol 2015;62:1420–1429.
- Papatheodoridis G V, Dalekos GN, Yurdaydin C, et al. Incidence and predictors of hepatocellular carcinoma in Caucasian chronic hepatitis B patients receiving entecavir or tenofovir. J Hepatol 2015;62:363–70.
- 42. Morgan RL, Baack B, Smith BD, et al. Eradication of hepatitis C virus infection and the development of hepatocellular carcinoma: a meta-analysis of observational studies. Ann Intern Med 2013;158:329–37.
- 43. Tiegs G, Hentschel J, Wendel A. A T cell-dependent experimental liver injury in mice inducible by concanavalin A. J Clin Invest 1992;90:196–203.
- Omenetti S, Brogi M, Goodman WA, et al. Dysregulated intrahepatic CD4+ T-cell activation drives liver inflammation in ileitis-prone SAMP1/YitFc mice. Cell Mol Gastroenterol Hepatol 2015;1:406–419.
- 45. Hilberg F, Roth GJ, Krssak M, et al. BIBF 1120: triple angiokinase inhibitor with sustained receptor blockade and good antitumor efficacy. Cancer Res 2008;68:4774–82.
- 46. Mas VR, Maluf DG, Archer KJ, et al. Angiogenesis soluble factors as hepatocellular carcinoma noninvasive markers for monitoring hepatitis C virus cirrhotic patients awaiting liver transplantation. Transplantation 2007;84:1262–71.
- 47. Poon RTP, Ho JWY, Tong CSW, et al. Prognostic significance of serum vascular endothelial growth factor and endostatin in patients with hepatocellular carcinoma. Br J Surg 2004;91:1354–60.
- Horwitz E, Stein I, Andreozzi M, et al. Human and mouse VEGFA-amplified hepatocellular carcinomas are highly sensitive to sorafenib treatment. Cancer Discov 2014;4(6):730–743.
- Carmeliet P. VEGF as a key mediator of angiogenesis in cancer. Oncology 2005;69 Suppl 3:4–10.
- 50. Schiffer E, Housset C, Cacheux W, et al. Gefitinib, an EGFR inhibitor, prevents hepatocellular carcinoma development in the rat liver with cirrhosis. Hepatology 2005;41:307–14.
- 51. Fuchs BC, **Hoshida Y, Fujii T**, et al. Epidermal growth factor receptor inhibition attenuates liver fibrosis and development of hepatocellular carcinoma. Hepatology

2014;59:1577–90.

52. Pinyol R, Sia D, Llovet JM. Immune exclusion-Wnt/CTNNB1 class predicts resistance to immunotherapies in HCC. Clin Cancer Res 2019.

Author names in bold designate shared co-first authorship.

Figure 1

Α













Α

Β

С





Α

Β

С





Figure 4





vehicle



Veh.

Nin.



С





nintedanib

p-VEGFR2 VEGFR2

Tubulin



D

SUPPLEMENTARY MATERIAL

SUPPLEMENTARY METHODS

Histological analysis of human samples

Histological evaluation was performed in 98 tissue samples obtained from patients with early HCC included in the study cohort. The Portal/septal, pericentral and lobular Inflammation were assessed as follows: 0=absent; 1= mild; 2= moderate; and 3= marked. The presence or absence (1 or 0, respectively) of interface inflammation, as well as lymphoid aggregates was also evaluated. The latter structures were mainly found in the periportal/periseptal areas. An inflammatory infiltrate score was created by summing the values given by the portal/septal, lobular and interface inflammation. Pericentral inflammation was not considered for the scoring system since 57% of patients were cirrhotic. According to the final score, we defined two inflammatory categories: the absent-mild category if the score was < 3, and the moderate-marked category if the score was \geq 3. The presence or absence of cirrhosis was defined according to METAVIR algorithm¹ (F0-1-2-3/F4). Ductular proliferation was also considered. Steatosis was assessed based on the size of the fat vesicles (macrovesicular or microvesicular) and the localization of the fat droplets in the liver parenchyma (periseptal/periportal, pericentral or lobular). The presence or absence of ballooning, apoptotic bodies and oncocytic change was also evaluated. Immunohistochemistry for CD4 and CD8 was performed in a subset of 70 patients of the training cohort. Staining was carried out on 3µm-thick FFPE tissue sections collected from an 40-44°C flotation bath containing deionized water and mounted on 25 X 75 mm positively (+) charged slides. The slides were dried at 60°C in convection oven for 30min. Deparaffinization was performed followed by standard cell conditioning 1 (ULTRA CC1 from Ventana Medical Systems, Inc.). Staining was performed using Ventana BenchMark ULTRA system with the primary antibody approximately 20min, 36°C. Signal was captured using ultraview universal diaminobenzidine (DAB) detection kit and blocked with antibody diluent (REF 251-018) for 8 min. Samples were counterstained with hematoxylin for 4 min and post counterstained with Bluing Reagent for 4 min. The primary antibodies used were anti-CD4 (Roche, clone SP35) and anti-CD8 (Roche, clone SP57). The quantification was done automatically (Image J) by calculating the positive areas (μm^2) -considering 5 random areas within lobular and portal/septal infiltrates of the non-tumor liver tissue- at 200X magnification and using the same threshold for all samples.

Generation of the DEN/CCl₄ animal Model

The chemically-induced (DEN/CCl₄) model was generated as previously described^{2,3}. HCC was induced by a single intraperitoneal (i.p.) injection of N-diethylnitrosamine (DEN; Sigma-Aldrich, MO; 25 mg/kg i.p. dissolved in 0.9% sodium chloride solution) given at day 15 postpartum followed by 11-14 weekly injections of carbon tetrachloride (CCl₄ 0.5 ml/kg i.p., dissolved in corn oil) starting at 4 weeks of age (Supplementary Figure 7A). Mice (n=55) were randomized at 12 weeks of age to receive 50 mg/kg/day of nintedanib (Boehringer Ingelheim) (n=29) or vehicle (n=26). The vehicle solution was formulated as follows: 1.8 % Hydroxypropyl Beta Cyclodextrin (HPB-CD), 5% acetic acid (10%) and Natrosol (0.5%). At 15, 17 and 18 weeks of age mice were sacrificed 48h after the last dose of CCl₄, having been treated with nintedanib for 3, 5 and 6 weeks, respectively (n=15-21 per time-point). Immediately after sacrifice, livers were explanted, digitally photographed and weighed. The evaluation of macroscopic malignant nodules was assessed by two independent investigators. Based on visual criteria, a hepatic lesion with a diameter >0.5 mm and with dysmorphic and/or dyschromic surface was considered a hepatic tumor. The diameter of tumors was measured with a hand caliper. The biological end-points for chemopreventive efficacy were a) incidence of hepatic tumors, b) number of tumors and c) size, considering the largest diameter of all counted tumors. The largest liver lobe was fixed in buffered 4% paraformaldehyde (PFA) for 24 hours for posterior histological and immunohistochemical analysis. In addition, samples of adjacent non-tumor liver were snap frozen at -80°C for subsequent RNA and protein analysis. Potential treatment-related toxicity was evaluated by monitoring body weight losses and quantitative determination of serum aspartate aminotransferase (AST) and alanine aminotransferase (ALT).

Histological and Immunohistochemical analysis of the mouse samples

Formalin-fixed paraffin-embedded (FFPE) mouse liver samples were cut in 4 μ m sections and stained with hematoxylin and eosin (H&E) for further histological examination. The samples were assessed taking into consideration non-tumor and tumor tissue by two expert liver pathologists (CM, MS) blinded to the treatments. In the non-tumor tissue, the number of lymphoid aggregates was determined. These were defined as polarized aggregates composed mainly of lymphocytes with scant plasma cells, neutrophils and macrophages localized in the periportal and pericentral areas with a measure no bigger than 0.1 mm. The presence of inflammatory infiltrates was also

determined for the periportal, pericentral and lobular area using a scoring system as follows: 0=absence or rare; 1=mild; 2=mild-moderate; 3=moderate; 4=moderatemarked; and 5=marked. Other variables such as the presence of microabscesses, ductular proliferation (0=absence; 1=<25% of portal tracts involved; 2=25-50% of portal tracts involved; 3=>50% of portal tracts involved), necrosis, steatosis, apoptotic bodies, were also determined. Ballooning was defined according to the following scale being 0= absence; 1= focal; 2= multiple foci; 3= diffuse. Hepatic fibrosis was assessed by Sirius Red staining. The METAVIR algorithm¹ was used to grade hepatic fibrosis from F0 (no scarring) to F4 (cirrhosis or severe fibrosis). Also, perisinusoidal fibrosis was evaluated as follows 1 = 0.5%; 2 = 5.33%; 3 = 33.66% and 4 = >60%. Histologically, hepatic tumors presented a high cellular density composed of small cells with altered nuclear/cytoplasmic ratio, and a clear cytoplasm. Among these hepatic tumors, those circular well-defined lesions with pushing margins were diagnosed as HCCs whereas a dysplastic nodule was considered when the lesion had an ill-defined shape within the liver parenchyma. The presence of vascular invasion was a characteristic attributed to HCC. The size of both lesions was not used to make a distinction between them, although HCC tend to be larger than dysplastic nodules. Finally, for the evaluation of the chemopreventive effects of a TKI in adjacent liver tissue, FFPE sections from mice sacrificed at 17 weeks of age were analyzed by immunohistochemistry (n=5 mice per treatment arm). Heat-induced antigen retrieval was performed with 10 mM sodium citrate buffer (pH 6.0) or 0.5 M Tris buffer (pH 10.0) for 15 minutes (5 minutes, 3 times), and the reaction was quenched using hydrogen peroxide 3%. After washing with PBS, samples were incubated with anti-pERK (phosphoThr202/Tyr204) (from Cell Signaling, Danvers, MA), anti-CD31 (Abcam plc, Cambridge, UK), and anti-CD4 and anti-CD8 (both from Cell Signaling, Danvers, MA). DAB (3,3'-diaminobenzidine) was used as detection system (EnVision+ System-HRP, Dako). Morphometric quantification of percentage area of liver vasculature (n=5 mice per treatment arm) was performed by evaluating the mean area of CD31 staining, in randomly selected low magnification fields (n=5, 10X fields for CD31 staining; n=10, 20x fields for collagen) using ImageJ software.

RNA extraction and gene expression profiling of mice livers

Total RNA from the two mouse models herein described was extracted from 20 mg freshfrozen non-tumoral liver tissue with Trizol reagent (Invitrogen) and purified with RNeasy
columns (Qiagen, Valencia, CA). RNA sample concentration and quality were assessed by NanoDrop ND-1000 spectrometer (NanoDrop, Wilmington, DE) and bioanalyzer (Agilent, Palo Alto, CA), respectively. Gene expression microarray studies were conducted using the Gene Chip HT MG-430 (Affymetrix). The raw .cel files were background corrected and normalized using the Robust Multiarray Averaging (RMA) procedure ⁴, with a custom chip definition file (.cdf) from the Custom CDF project (HTMG430PM_Mm_ENTREZG v18.0)⁵. To assess ICF-signature enrichment through ssGSEA (GenePattern), mice genes were humanized and intensity values were log transformed. For qRT-PCR analysis, cDNA was synthesized from 1 µg purified total RNA using SuperScript III reverse transcriptase (Invitrogen). Relative gene expression levels were measured by TaqMan Gene Expression Assays (Applied Biosystems, Foster City, CA) using specific probes for *Col1a1* (Mm00801666_g1), *Col1a2* (Mm00483888_m1), *Acta2* (Mm01546133_m1), and *Pdgfrb* (Mm00435546_m1). The housekeeping gene *GAPDH* (Mm99999915_g1) was used for normalization. Microarray data of these newly profiled samples are in GEO under accession number (GSE125975).

Western-blot analysis

Whole-cell extracts were collected in lysis buffer (50 mM Tris pH 7.4, 150 mM NaCl, 1% Triton X-100, 0.1% SDS, 0.25 mM EDTA, 1% Sodium deoxycholate) containing phosphatases and proteases inhibitors (Roche). 30-70 µg of total protein were resolved in polyacrylamide gels and transferred to nitrocellulose membranes (Pierce, Rockford, IL). Membranes were BSA-blocked and hybridized overnight at 4 °C with primary antibodies against VEGFR-2, phospho-VEGFR-2 (Tyr951), Akt, phospho-Akt (Ser473), ERK-1/2, phospho-ERK-1/2 (Thr202/Tyr204), Bcl-xL, PARP (all from Cell Signaling), and tubulin (Sigma). Appropriate HRP-conjugated secondary antibodies (Dako) were incubated for 1h at room temperature and immunoreactivity was detected with a LAS-3000 imaging system (Fujifilm, Tokyo, Japan) using Amersham[™] ECL[™] Prime western Blotting Detection Reagent (GE Healthcare, United Kingdom).

SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure 1. Identification of an immune-mediated cancer field in the non-tumor liver tissues and its association with overall survival in patients with early HCC. A) Consensus-clustered analysis of gene-sets recapitulating the different perturbation states of immune. The figure includes a subgroup of representative gene-sets among the ~5000 gene-sets evaluated (Collection C7 of MsigDB). B) Kaplan-Meier estimates of overall survival according to the presence of the immune-mediated cancer field, B) the presence of High-Infiltrate subtype, and C) the different ICF subtypes. ICF: immune-mediated cancer field. C)

Supplementary Figure 2. Immunohistochemistry assessment of CD4 and CD8 positivity in non-tumor liver tissues. Average stained area was automatically quantified and compared in **A**) samples from patients belonging to the ICF and non ICF subgroups, and **B**) between ICF subtypes. n= 15-19 samples per group. ***=p<0.001.

Supplementary Figure 3. Gene-overlapping between the 172 ICF gene-expression signature and other previously reported poor-prognosis expression signatures in non-tumor liver tissue. Signatures are denoted by the name of the first authors in each of the publications^{6–10}. Numbers in brackets indicate the total number of genes constitute each signature, whereas bold numbers represent the number of genes that overlap between each signature and the ICF signature (herein referred as *Moeini*).

Supplementary Figure 4. External validation of the molecular and clinical features of the immune-mediated cancer field and its subtypes. A) Main molecular characteristics of the immune-mediated cancer field and the 3 distinct molecular subtypes were validated in a previously reported cohort including 225 FFPE non-tumoral liver tissue from patients with early HCC profiled by DASL array. B) Kaplan-Meier estimates of overall survival according to the presence of the immune-mediated cancer field. ICF: immune-mediated cancer field.

Supplementary Figure 5. Association of the presence of immune-mediated cancer field subtypes with risk of HCC development and advanced liver disease in fibrotic patients. A) Kaplan-Meier analysis of the correlation of the immune-mediated cancer

field subtypes with risk of HCC development. **B)** Correlation of the prediction of immunemediated cancer field subtypes with fibrosis and inflammation degree. Fibrosis degree was classified as: none (S0), low (S1-S2) and high (S3-S4). Inflammation degree was classified as: none (G0), low (G1-G2) and high (G3-G4). other ICF: High Infiltrate and Pro-inflammatory ICFs. Non ICF: non ICF subtype and unclassified cases.

Supplementary Figure 6. In silico enrichment analysis of gene sets recapitulating the targets of approved molecular therapies in non-tumor liver of patients with early HCC. A) Heatmap representing the enrichment scores of gene sets recapitulating the molecular targets of top enriched therapies in non-tumor liver of HCC patients harboring the immune-mediated cancer field (ICF) in comparison to non ICF/other. B) Constellation map representation of enrichment of gene set of main targets of top scored therapies centered around the immune-mediated cancer field phenotype. The Blue lines denote presence of overlapping genes among the different gene sets. NMI: Normalized mutual information. AUC.pval: Area under the curve p-value. t.stat: t-statistic. t.pval: t-statistic p-value.

Supplementary Figure 7. Prolonged treatment with nintedanib does not induce significant toxicity in DEN/CCl₄ induced mouse models. A) Experimental design of the murine model of DEN/CCl4 induced hepatocarcinogenesis in the context of liver fibrosis. B) Monitoring of body weight in all mice from each experimental group during the administration of nintedanib or vehicle at the longest time-point, 18-weeks of age. C) Evaluation of the serum levels of alanine transaminase (ALT) and aspartate transaminase (AST) in each experimental group.

Supplementary Figure 8. Nintedanib inhibits downstream MAPK pathway but has no effect on reverting DEN/CCl4 induced PDGF signaling nor hepatic fibrosis. A) Western-blot analysis of downstream MAPK(AKT and ERK) signaling. B) Representative images and quantification of pERK staining in 17 weeks old mice treated with vehicle or nintedanib. In the vehicle arm the tumors and the adjacent non-tumor tissue are positive with patchy nuclear and cytoplasmic staining, while in the nintedanib arm both are negative. T: tumor. NT: non-tumor. C) Western-blot analysis of the pro-fibrogenic PDGFR signaling. D) Representative images of Sirius Red staining in mice treated with vehicle or nintedanib. Nintedanib did not exert any significant effect on liver fibrosis. E) Gene expression levels of pro-fibrogenic marker genes by quantitative RT-PCR in livers

of mice sacrificed at 15, 17 and 18 weeks of age treated with vehicle or nintedanib. The *GAPDH* gene was used as a housekeeper for normalization. Significant statistical differences are defined as follows: *<0.05 and ***=p<0.001.

SUPPLEMENTARY REFERENCES

- Bedossa P, Poynard T. An algorithm for the grading of activity in chronic hepatitis
 C. The METAVIR Cooperative Study Group. Hepatology 1996;24:289–93.
- 2. Uehara T, Ainslie GR, Kutanzi K, et al. Molecular Mechanisms of Fibrosis-Associated Promotion of Liver Carcinogenesis. Toxicol Sci 2013;132:53–63.
- 3. Dapito DH, Mencin A, Gwak G-Y, et al. Promotion of hepatocellular carcinoma by the intestinal microbiota and TLR4. Cancer Cell 2012;21:504–16.
- 4. Irizarry RA, Hobbs B, Collin F, et al. Exploration, normalization, and summaries of high density oligonucleotide array probe level data. Biostatistics 2003;4:249–64.
- 5. Dai M, Wang P, Boyd AD, et al. Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data. Nucleic Acids Res 2005;33:e175.
- Nakagawa S, Wei L, Song WM, et al. Molecular Liver Cancer Prevention in Cirrhosis by Organ Transcriptome Analysis and Lysophosphatidic Acid Pathway Inhibition. Cancer Cell 2016;30:879–890.
- 7. Hoshida Y, Villanueva A, Kobayashi M, et al. Gene expression in fixed tissues and outcome in hepatocellular carcinoma. N Engl J Med 2008;359:1995–2004.
- Kim JH, Sohn BH, Lee H-S, et al. Genomic predictors for recurrence patterns of hepatocellular carcinoma: model derivation and validation. Beck AH, ed. PLoS Med 2014;11:e1001770.
- Ji J, Eggert T, Budhu A, et al. Hepatic stellate cell and monocyte interaction contributes to poor prognosis in hepatocellular carcinoma. Hepatology 2015;62:481–95.
- Zhang DY, Goossens N, Guo J, et al. A hepatic stellate cell gene expression signature associated with outcomes in hepatitis C cirrhosis and hepatocellular carcinoma after curative resection. Gut 2016;65:1754–64.

Β

С









Α

В









Validation cohort (GSE10143, n=225 non-tumor liver tissues)





Β

Α

Α





Immunosuppressive ICF	21	13	3	1	Immunosuppressive ICF	21	13	3	1
High Infiltrate ICF	31	23	13	1	Other ICF	89	68	31	3
Pro-Inflammatory ICF	58	45	18	3	Non ICF	106	87	57	10
Non ICF	106	87	57	10					

В



Α

Β





Supplementary Figure 7





Nin.

Nin.

Nin

Variable	Value
Median age (years)	65.2
Gender, male (%n)	77
Etiology (%)	
Hepatitis C	46
Hepatitis B	25
Alcohol	14
Others	15
Child-Pugh score (%)	
A	99
В	1
Tumor size, cm (%)	
<2	11
2-3	28
>3	60
Multple Nodules (%)	
Absent	70
Present	30
Microvascular Invasion (%)	
Absent	69
Present	31
Satellites (%)	
Absent	70
Present	30
BCLC early stage, 0-A (%)	82
Degree of tumor differentiation (%)	
Well	16
Moderate	35
Poor	15
Bilirrubin, >1 mg/dL (%)	43
Albumin, <3.5 g/L (%)	12
Platelet Count, <100.000/mm3 (%)	22
AFP, >100 mg/dL (%)	24
Events (%)	
Recurrence	67
Death	59
Follow-up, median months (range)	67 (53-80)
Missing data, stillage (n=5) Child Durch	

Supplementary Table 1. Clinicopathological characteristics of study cohort (n=167).

Missing data: etiology (n=5), Child Pugh score (n=3, tumo size (n=2), multiple nodules (n=2), microvascular invasion (n=4), degree of tumor differentiation (n=31), bilirrubin (n=5), albumin (n=5), platelet count (n=5), AFP (n=5), recurrence (n=9) death (n=3), follow-up (n=3).

Supplementary Table 2. Previously reported gene signatures used in this study.

Signature Name	Publication
Signatures used in non-tumor tissue	
Activated stroma	Moffitt RA, et al. Nat Genet 2015;47:1168-78
Activation of monocytes/macrophages	Beck AH, et al. Clin Cancer Res 2009;15:778–87
Activation of T and B cells	Wolf DM, et al. PLoS One 2014;9:e88309
Cholesterol-induced inflammatory response	Wunder C, et al. Nat Med 2006;12:1030-8
Cytolytic activity	Rooney MS, et al. Cell 2015;160:48-61
Ectopic lymphoid structures (ELS)	Finkin S, et al. Nat Immunol 2015;16(12):1235
Hepatic injury and regeneration (HIR) signature	Kim JH, et al. PloS Med 2014;11:e1001770
Hepatic Stellate Cell (HSC) signature	Zhang DY, et al. Gut 2016;65:1754-64
Immune enrichment score	Yoshihara K, et al. Nat Commun 2013;4:2612
Liver cancer multicentric occurrence	Okamoto M, et al Ann Surg Oncol 2006;13:947-54
Lymphocyte infiltration representative signature	Thorsson V, et al. Immunity 2018;48:812-30
PD-1 response signature	Quigley M, et al. Nat Med 2010;16:1147-51
Poor survival activated HSC signature	Ji J, et al. Hepatology 2015;62:481-95
Stromal enrichment score	Yoshihara K, et al. Nat Commun 2013;4:2612
Stromal wound repair and angiogenesis	Wolf DM, et al. PLoS One 2014;9:e88309
T cell exhaustion signature	Quigley M, et al. Nat Med 2010;16:1147-51
TGF-β response representative signature	Thorsson V, et al. Immunity 2018;48:812-30
Upregulated genes in exhausted T cells	Wherry EJ, et al. Immunity 2007;27:670–684
Wnt/TGF-β signature	Lachenmayer A, et al. Clin Cancer Res 2012;18:4997-5007
18-gene IFN-γ-related signature	Ayers M, et al. J Clin Invest 2017; 127:2930–40
186-gene Poor survival signature	Hoshida Y, et al. N Engl J Med 2008;359:1995-2004
Signatures of HCC molecular subclasses	
Boyault G3 class	Boyault S, et al. Hepatology 2007;45:42-52
Chiang HCC 5 classes	Chiang DY, et al. Cancer Res 2008;68:6779-88
Coulouarn late vs early TGF-β	Coulouarn C, et al. Hepatology. 2008;47:2059-67
Hoshida S1-S2-S3	Hoshida Y, et al. Cancer Res 2009;69:7385-92
Lee Cluster A	Lee JS, et al. Hepatology 2004;40:667–76
Minguez vascular invasion	Minguez B, et al. J Hepatol. 2011;55:1325-31
Sia HCC Immune class	Sia D, et al. Gastroenterology 2017;153:812-26
Villanueva CK19 positive	Villanueva A, et al. Gastroenterology 2011;140:1501-12.e2
Villanueva NOTCH	Villanueva A, et al. Gastroenterology 2012;143:1660-1669.e7
Woo early recurrence	Woo HG, et al. Clin Cancer Res 2008;14:2056–64
Yamashita EpCAM	Yamashita T, et al. Cancer Res 2008;68:1451–61

		ICF	non ICF		Fisher test	
Variable -	%	n patients	%	n patients	p-value	
Non-tumor tissue characteristics						
Fibrosis degree and cirrhosis						
F1-F2	11%	(7/71)	29%	(17/59)	0.01	
F3	17%	(12/71)	22%	(13/59)	0.37	
F4 (cirrhosis)	75%	(9/71)	49%	(29/59)	0.002	
Portal/Septal Inflammation						
Absent-mild	26%	(14/54)	50%	(22/44)		
Moderate-Marked	74%	(40/54)	50%	(22/44)	0.02	
Lobular Inflammation						
Absent-mild	94%	(51/54)	98%	(43/44)		
Moderate-Marked	6%	(3/54)	2%	(1/44)	0.63	
Interface Inflammation						
Present	37%	(20/54)	23%	(10/44)		
Absent	63%	(34/54)	77%	(34/44)	0.19	
Non-tumoral Inflammatory infiltrate score						
Absent-Mild	26%	(14/54)	48%	(21/44)		
Moderate-Marked	74%	(40/54)	52%	(23/44)	0.03	
Non-Tumoral lymphoid aggregates						
Absent	20%	(11/54)	45%	(20/44)		
Present	80%	(43/54)	55%	(24/44)	0.01	
Apoptotic bodies						
Absent	83%	(45/54)	77%	(34/44)	0.61	
Present	17%	(9/54)	23%	(10/44)		
Tumor tissue characteristics						
Number of lesions						
Single	63%	(62/98)	78%	(54/69)		
Multinodular	35%	(34/98)	22%	(15/69)	0.08	
Tumor size						
>3.5cm	58%	(56/97)	45%	(31/69)		
<3.5cm	42%	(41/97)	54%	(37/69)	0.15	
Tumor satellites						
Yes	34%	(33/97)	25%	(17/69)	0.23	
No	66%	(64/97)	75%	(52/69)		
Microscopic vascular invasion						
Yes	42%	(41/98)	30%	(21/69)	0.19	
No	56%	(55/98)	67%	(46/69)		
Histological grade						
Well	15%	(15/98)	10%	(7/69)	0.63	
Moderate	48%	(47/98)	46%	(32/69)	0.59	
Poor	22%	(22/98)	19%	(13/69)	1.00	
Intratumoral inflammatory infiltrate						
Mild	19%	(10/54)	21%	(9/42)	0.80	
Moderate	41%	(22/54)	55%	(23/42)	0.30	
Marked	37%	(20/54)	24%	(10/42)	0.18	
Intratumoral Neutrophilic infiltrate						
Absent-rare	78%	(42/54)	64%	(27/42)		
Present	22%	(12/54)	36%	(15/42)	0.17	
Peritumoral inflammatory infiltrate						
Mild	37%	(20/54)	24%	(10/42)	0.18	
Moderate	41%	(22/54)	55%	(23/42)	0.30	
Marked	19%	(10/54)	21%	(9/42)	0.80	
Tertiary Lymphoid Structures (TLS)		. /		. /		
Present	22%	(12/54)	8%	(8/42)		
Absent	77%	(42/54)	35%	(34/42)	0.80	

Supplementary Table 3. Correlation of the immune-mediated cancer field (ICF) with histological characteristics.

Supplementary Table 4. Pathways enriched by GSEA in immune-mediated cancer field.

NUMBER, LICOSAP, REFERENCI Non-on- transmission Non- energy No- energy Non- energy <th< th=""><th>INAME</th><th>MSigDB collection</th><th>SIZE</th><th>FS</th><th>NES</th></th<>	INAME	MSigDB collection	SIZE	FS	NES
NULLMAK Image <	HALLMARK ALLOGRAFT REJECTION	Hallmark	198	0,69	1.98
PALLMARK, DPL/AREPORT PRIVAT 200 PRIVAT 200 PRIVAT 200 PRIVAT 200 PRIVAT 200 PRIVAT PRIVAT<	HALLMARK IL2 STAT5 SIGNALING	Hallmark	196	0.56	1.86
NALLANDS (00.4 SUBMAR) LP NOTE Note of the standard o	HALLMARK INFLAMMATORY RESPONSE	Hallmark	200	0.61	1 85
NULLIMAR PARTIERS (SMALARG, UP Herman Yes		Hallmark	200	0.53	1.80
HALLMARK PERFERSIVE AGAMAN REPORTING Holman 200 0.78 HALLMARK PERFERSIVE Holman 0.00 0.04 1.78 HALLMARK PERFERSIVE Holman 0.00 0.04 1.78 HALLMARK PERFERSIVE Holman 0.00 0.01 1.78 HALLMARK PERFERSIVE HOLMAN PERFERSIVE HOLMAN PERFERSIVE 0.01 0.01 0.01 1.78 HALLMARK PERFERSIVE HOLMAN PERFERSIVE HOLMAN PERFERSIVE 0.01 0.01 1.78 0.01 1.78 0.01 1.78 0.01 1.78 0.01 1.78 0.01 1.78 0.01 1.78 0.01 1.78 0.01 1.78 0.01 1.78 0.01 0.01 0.01 0.01	HALLMARK KRAS SIGNALING UP	Hallmark	199	0.53	1.80
NALIMARY DETINES AND DESCRIPTION Heatman Page	HALLMARK INTERFERON GAMMA RESPONSE	Hallmark	200	0.33	1.00
NUMBER OF ERTS SOLVENS Helmest 54 0.61 17. NUMBER OF ERTS SOLVENS Holman 70 0.81 17. NUMBER OF ERTS SOLVENS C 40 0.81 18. NUMBER OF ERTS SOLVENS C 40 0.91 18. SOLVENS OF ERTS SOLVENS C 20 70 0.92 18. SOLVENS OF TRANS SOLVENS OF ERTS SOLVENS C 20 70 0.92 18. SOLVENS ALMER SOLVENS OF ERTS SOLVENS C 20 70	HALLMARK EPITHELIAL MESENCHYMAL TRANSITION	Hallmark	199	0.64	1.77
NULLINK, LG, ANY STATS SEGULAGY Helment 97 64.11 73 NULLINK, LG, ANY STATS SEGULAGY Helment 100 657 173 NULLINK, MARGORESS Helment 100 657 173 NULLINK, MARGORESS Helment 100 657 173 NULLINK, MARGORESS Helment 100 657 173 NULLINK, MARCHARD, MARGORESS HELMENT, MARGORESS 650 630 100 100 NULLINK, MARGORESS MARGORESS HELMENT, MARGORESS 650 63 100		Hallmark	54	0.61	1 74
HALLMARK APPORTS Hermon So OFF 171 HALLMARK APPORTS THAL HERMAN AD 0.00 0.	HALLMARK II 6. JAK STAT3 SIGNALING	Hallmark	87	0.61	1.74
HALMARK TAR SOUND VALUE HALMARK TAR SO		Hallmark	36	0.67	1.73
HUMMENT PERSONALING VALA PRIE HEIMENT 198 199 198 199 <t< td=""><td>HALLMARK APOPTOSIS</td><td>Hallmark</td><td>160</td><td>0.50</td><td>1.70</td></t<>	HALLMARK APOPTOSIS	Hallmark	160	0.50	1.70
JAM INST. PERMONSTRUCT STRUCTURE 100 200 200 0.00 150 SAM INST. PERMONSTRUCTURE CO CO 0.00 1.00<	HALLMARK THEA SIGNALING VIA NEKR	Hallmark	100	0.64	1.65
SECTOR (MARCHORSCHLATORY INTERACTIONS BETWEEN ALVMPHOD_AND AND ALVMPHOD_CE D2 07 07 07 150 SECTOR (MARCHARDER) SUP D2 07 07 07 150 DECK (MARCHARDER) SUP D2 07	IAATINEN HEMATOPOIETIC STEM CELL DN	C2	220	0.64	1.05
SIECTORQUARY TRUE Control Col	DEACTORE IMMUNOBECULATORY INTERACTIONS RETWEEN A LYMPHOLD AND A NON LYMPHOLD CE	02	60	0.60	1.00
TONES TRACET, OF KURK TRUST, FUSION, HER, ON TOP		C2	45	0.09	1.90
SHARE UNAL PARCE SIGNAL SIXE HEAL PREAM TO UP C2 171 C02 173 C02 174 C02 174 C02 175 C02		C2	182	0.79	1.90
SEGE 3F CAMMA EX MEDIATED FUNCTORS SOL 191 0.59 195 0.59 195 SEGE AF CAMMA EX MESTING C2 191 0.59 195 0.55 195 0.55 195 0.55 195 0.55 195 0.55 195 0.55 195 0.55 195 195 195 195 195 195 195 195 195 195 195 195 195 </td <td></td> <td>C2</td> <td>172</td> <td>0.67</td> <td>1.00</td>		C2	172	0.67	1.00
SAESUALDCT VARIATION PS OF START DATA C2 194 0.22 195 DROUGH IS ALONEY CARCEL CUBIEL AS C2 97 0.72 195 DROUGH IS ALONEY CARCEL CUBIEL AS C2 97 0.72 195 ROUGH IS ALONEY CARCEL CUBIEL AS C2 97 0.72 195 ROUGH IS ALONEY CARCEL AS C2 295 0.72 195 ROUGH IS ALONEY CARCEL AS C3 295 0.72 195 ROUGH IS ALONEY CARCEL AS C3 295 0.72 195 READER AS TORING ALL CARCEL AND ALONEY CONCENT CO		C2	01	0.50	1.00
DARSE CODE SERVICING UP COL COL CODE		C2	164	0.59	1.90
DAROBER BARDER CANCER SUP SALTARE C2 97 0.67 134 MARUBERT CANCER SUP SALTARE C2 24 0.67 134 WALAGHAL DENTAL CANED UP C2 24 0.67 134 WALAGHAL DENTAL CANED UP C2 24 0.66 133 MERGE WALAGHAL DENTAL CANED UP C2 46 0.62 135 MERGE WALAGHAL DENTAL CANED UP C2 46 0.62 135 MERGE WALAGHAL MACRATER C2 46 0.62 135 MERGE WALAGHAL MACRATER C2 46 0.64 135 MERGE WALAGHAL MACRATER C2 47 0.67 132 MERGE WALAGHAL MACRATER C1 0.67 132 0.77 134 152 MERGE WALAGHAL MACRATER C1 0.67 132 0.71 134 152 MERGE WALAGHAL MACRATER C1 0.67 132 134 152 135 135 MERGE WALAGHAL MACRATER C1 0.66 132 135		C2	00	0.02	1.95
FINAX BREAT CANCER SOP SOUNTING CO. CAL CAL <thcal< th=""> CAL <thcal< th=""> <thcal< td=""><td></td><td>C2</td><td>35</td><td>0.72</td><td>1.95</td></thcal<></thcal<></thcal<>		C2	35	0.72	1.95
NAX ADDRESS (UP C2 768 072 194 DEUBROA, AM, REVINATION, CLISTER 3, N C2 24 0.44 194 LUNDLOG T, TO MATURAL XILLER, UP C2 24 0.45 139 DEGO, MAN, MARCHARDON, CLISTER 3, N C2 24 0.45 139 DEGO, MARS, MARCHARD, COLL INFECTION C2 41 0.76 133 0.77 138 SEGO, FAND, MORD, ESK-BERCHAL COLL INFECTION C2 244 0.34 102 132 0.77 138 0.77 138 0.77 138 0.77 138 0.77 133 0.77 138 0.77 138 0.77 138 0.77 138 0.77 138 0.77 138 0.77 138 0.77 138 0.77 138 0.77 138 0.77 137 0.72 138 0.77 137 0.72 139 0.77 137 0.72 137 0.77 137 0.72 137 0.77 137 0.77 137<		C2	24	0.07	1.00
PROJERSON AM. NETTOCATION CLUSTER 5_DN C2 C2 C2 C4 194 DEGRED TO ANKUNGK, RULER UP C2 68 148 EGGS VARIAN KUNGK, RULER UP C2 68 148 EGGS VARIAN KUNGK, RULER UP C2 68 168 EGGS VARIAN KUNGK, RULER UP C2 68 163 REGS EXTROSON, RULER UP C2 163 152 REGS EXTROSON, RULER UP, RULER UP, OK UP C2 63 152 REGS EXTROSON, RULER UP, RULER UP, OK UP C2 64 152 REGNER RULES VARIANCES VARIANTS UP C2 64 164 RULES RULES VARIANTS VARIANTS VARIANTS UP C2 64 164 RULES RULES RUNAL AFTER EXAMPLE VARIANTS UP C2 64 164 RULES RULES RUNAL AFTER EXAMPLE VARIANTS UP C2 74 75 181 RULES RULES RUNAL ATTER EXAMPLE VARIANTS UP C2 74 77 181 RULES RUSSTANCE CONCERNAL CARIANTS UP C2 74 64 191 RULES RUSSTANCAL UP C2 75<		C2	236	0.02	1.54
DNARDDOEDT TO TANUDAX ACLER UP DOI DOI <thdoi< th=""> DOI <thdoi< th=""> <thdoi<< td=""><td></td><td>02</td><td>230</td><td>0.72</td><td>1.94</td></thdoi<<></thdoi<></thdoi<>		02	230	0.72	1.94
Code UNIX, INFOCATION STATUS Code Name Code Nam Code Name Code Na		02	42	0.54	1.94
DRINDBORDS SUBJECX TARGETS ON 02 48 0.02 133 REGG PATICOGNE (SCHERECH, CL), IMPECTON C2 131 0.57 133 REGG PATICOGNE (SCHERECH, CL), MEGTON C2 131 0.57 133 REGG PATICOGNE (SCHERECH, CL), MEGTON C2 131 0.57 133 REGG PATICOGNE (SCHERECH, CL), MEGTON C2 132 0.56 132 NUMBER TARGETS DN C2 332 0.56 132 DUNNE TARGETS DN C2 363 0.56 132 DUNNE TARGETS DN C2 48 0.56 131 DUNNE TARGETS DN C2 78 0.56 131 DUNNE TARGETS DN C2 78 0.56 131 DUNNE TARGETS DN C2 78 0.56 131 DUNNESON TARG		02	297	0.55	1.93
BEGG PARTOGENC ESTREPRICIAL COLL INFECTION C2 37 0.70 133 BEGG LENCOTT EARSENDTO-LELA, MORATION C2 248 0.51 152 BOYLAM MALTIPLE (MENDAN C.D. DN C2 248 0.51 152 LECONTER TARSENDTO-LELA, MORATION C2 157 0.51 152 LECONTER TARSEND TO LELA, MORATION C2 157 0.51 152 DUNE TARGETS DATA TELECTURY DALLA MEDICAL MOLTANE ADDITION C2 157 0.56 152 MUNE TARGETS DATA MELLITICS CAMAL MEDICAL MOLTANE ADDITION ADDITION C2 158 0.56 152 MUNE TARGETS DATA MELLITICS CAMAL MEDICAL MOLTANE ADDITION ADDITION C2 151 152 MUNE TARGETS LIPUAL MEDICAL MEDICAL ADDITION ADDITION C2 151 151 MUNE TARGETS SUPPLANE ADDITION ADDITION C2 151 152 152 MUNE TARGETS SUPPLANE ADDITION C2 151 153 151 MUNE TARGETS SUPPLANE ADDITION C2 150 154 151 MUNE TARGETS SUPPLANE ADDITION C2 150 156		02	49	0.62	1.93
Description Description <thdescription< th=""> <thdescription< th=""></thdescription<></thdescription<>		02	40	0.02	1.93
Description Description <thdescription< th=""> <thdescription< th=""></thdescription<></thdescription<>		02	110 110	0.70	1.93
D'ALCHARE JUNION TRAVELOTED VS OK UP C2 47 0.31 1.02 DERME GRAFY VENSUS HÖDT JUNION (JUNION PARCENTE) C2 1.02 1.02 1.02 PASIN BJZ12 TARGETS DN C2 302 0.66 1.92 DANNE TARGETS ON C2 302 0.66 1.92 MAUNGSON POOR SURVIVUL AFTER GAMAR RADATION 20 C2 403 0.69 1.92 MAUNGSON POOR SURVIVUL AFTER GAMAR RADATION 20 C2 40 0.69 1.92 MAUNGSON POOR SURVIVUL AFTER GAMAR RADATION 20 C2 43 0.70 1.91 MAUNGSON POOR SURVIVUL AFTER GAMAR RADATION 20 C2 43 0.72 1.91 MAUNGSON POOR SURVIVUL AFTER GAMAR RADATION 20 C2 73 0.72 1.91 MAUNGSON POOR SURVIVUL AFTER GAMAR RADATION 20 C2 70 0.90 1.91 MAUNGSON POOR SURVIX AFTER STRONG MISK UP C2 70 0.90 1.90 MAUNGSON POOR SURVIX AFTER STRONG MISK UN C2 2.90 0.97 1.90 SULVIVIANS MAUNGSON POOR SURVIX AFTER STRONG MISK UN C2		02	246	0.07	1.93
LANDBACK LADDATES C2 07 07 102 SAND SUP2 TARGETS OF AUX MODE SOUND UP C2 112 072 112 SUPAR SUP2 TARGETS OF AUX MODE FUSION UP C2 112 072 112 072 112 072 112 072 112 072 112 073 072 072 073 072 073 072 073 072 073 072 073 072 073 072 073 072 073 073 073 073 073 073 073 103 074 073 103 074 073 103		02	240 07	0.04	1.92
OVERAL DURY: A PLOOP AND UNDER SUBJURG 100		02	0/	0.01	1.92
CONTRUCTORY DEFINITION C2 105 105 105 MANNOSON FORS SUMMULA TERE CAMBAR RADATION 26 C2 105 0.55 132 BOYLAN MULTIPLE MYELOWA D. DN C2 46 0.55 132 BOYLAN MULTIPLE MYELOWA D. DN C2 46 0.80 131 WALLAGE RAGER RACE UP C2 46 0.80 131 WALLAGE RAGER RACE UP C2 73 0.77 131 HUNG GLANZ, TARGETS UP C2 73 0.77 131 HUNG GLANZ, TARGETS UP C2 76 0.88 130 MASON FORS' TARGETS UP C2 76 0.88 130 SU THMUS C2 77 0.88 130 SU THMUS C2 70 0.89 130 MASON FORS'STASTIC STORPOM RISK DN C2 20 0.77 130 SU THMUS C2 70 0.89 130 MUNDSON FORS SURS'CONSTASTIC STORPOM RISK DN C2 24 0.77 130 SURTHMU	ויטווטא_טואר ו_עברסטס_חטס ו_טוסבאסב_סטע_טא האפואון פו וזיז דארמבדק האו	02	120	0.72	1.92
NUMBER U.G. 1000 0.0 <t< td=""><td></td><td>02</td><td>312</td><td>0.62</td><td>1.92</td></t<>		02	312	0.62	1.92
CONCUMPONE_ADVICE_ADVICE_ADVICE_ADVICE_ADV C2 163 1.03 CENT_ECL_WITH WEREARGAND_RELENTS UP C2 27.4 0.70 1.91 WALLAGE ROSTATE CANCER RACE UP C2 27.3 0.72 1.91 WALLAGE ROSTATE CANCER RACE UP C2 1.47 0.00 1.91 WALLAGE ROSTATE CANCER RACE UP C2 1.47 0.00 1.91 WALLAGE ROSTATE CANCER RACE UP C2 1.47 0.00 1.91 WALLAGE ROSTATE CANCER RACE UP C2 1.5 0.84 1.91 WALLAGE ROSTATE CANCER RACE UP C2 1.91 0.84 1.91 WALLAGE ROSTATE CANCER RACE UP C2 1.90 1.90 1.90 WALL CANCER RACE UP C2 1.90 1.90 1.90 SUTHYMAIS C2 2.0 0.66 1.90 SUTHYMAIS C2 2.45 0.71 1.90 MANNER PROL TARGETS C2 3.66 1.90 1.90 MANNER PROL TARGETS C2 3.66 1.90 1.90<		02	50	0.66	1.92
DUILDTS MALINES DECOMPOSIDE C2 7.2 0.82 1.82 DAULAGE REGISTE CANCER AND LOW DELTS UP C2 4.4 0.87 1.91 INSIND LIVER CANCER ASSERVAL UP C2 1.91 0.80 1.91 INSIND LIVER CANCER SURVIAL UP C2 1.91 0.82 1.91 INSIND LIVER CANCER SURVIAL UP C2 1.91 0.82 1.91 INAGE CANCER SURVIAL UP C2 6.5 0.88 1.91 INAGE CANCER SURVIAL UP C2 6.5 0.88 1.91 INAGE CANCER STARCE UP C2 7.8 0.89 1.80 ORDINAND MELODISTARCE UP AND MELON C2 2.6 0.89 1.80 SAURINE PSING LIVER CONCLASSED C2 2.6 0.87 1.80 SCHUETZ BREAST CANCER DUCTAL, INVASING UP C2 3.45 0.73 1.80 SCHUETZ BREAST CANCER UP POORE DUP C2 3.45 0.87 1.80 VERNANA, MERCISTARSE MARCE ALUP POORE DUP C2 3.45 1.80 CANCER SURVAL ASTRE CAMARE RADUATION 80	ANUNDOUN_FUUK_SUKVIVAL_AFTEK_GANNNA_KADIATIUN_2G	02	108	0.56	1.92
Incl. J. ac. J. m. P. T. ROMONEUE (J. D. 1997) C2 46 0.80 1.91 INCL. J. C. ALL, M. R. C. LUE, M. A. D. L. LUE, M. A. D. L. LUE, M. A. D. L. LUE, M. A. D. LUE, M. D.		02	/5	0.62	1.92
MONSTRUCT TWEE CALLEDERS SIGNATE C2 263 0.77 161 MARSEN FORM STARCETS UP C2 175 0.64 191 DIAZ CHRONIC MENDOSINUS LEULEMA DN C2 656 0.68 191 MARSEN FORM STARCETS UP C2 656 0.68 191 HUANG SATATINE RESISTANCE UP C2 656 0.68 130 HUANG SATATINE RESISTANCE UP C2 278 0.69 130 MARSON FORM STARCETS MORE UP C2 278 0.69 130 SCHUETZ BREAST CANCER DUCTAL INVASIVE UP C2 365 0.67 130 SCHUETZ BREAST CANCER DUCTAL INVASIVE UP C2 426 0.66 138 SCHUETZ BREAST CANCER DUCTAL INVASIVE UP C2 426 0.66 138 SCHUETZ BREAST CANCER DUCTAL INVASIVE UP C2 426 0.66 138 SCHUETZ BREAST CANCER DUCTAL INVASIVE UP C2 426 0.66 138 VERIVARA ATTER DIN C2 426 0.66 138 UNCTANDAR SON POORD STASTS	FAELI_B_CLL_WITH_VH_KEAKKANGEMENTS_UP	62	46	0.60	1.91
PULSHIDAL UTSEL VARGETS DURY VALUE C2 7.4 0.6 1.81 MARSDA LIVES, VARGETS DURY VALUE C2 7.6 0.60 1.91 MARSDA FOXP3 TARGETS UP C2 7.6 0.69 1.90 MARSDA FOXP3 TARGETS UP C2 7.6 0.69 1.90 MORDAN MELODYSPLASTIC, SYNDROM, FISK, DN C2 2.0 0.75 1.80 GAURINER PRIMA TARGETS C2 7.0 0.68 1.90 GAURINER PRIMA TARGETS C2 7.0 0.68 1.90 GAURINER PRIMA TARGETS C2 7.0 0.68 1.90 MARINGSON POOR SURVING, AFRE GAMAR ADATION 86 C2 2.40 0.57 1.80 MARINGSON POOR SURVING, AFRE GAMAR ADATION 86 C2 2.40 0.57 1.80 MARINGSON POOR SURVING, AFRE GAMAR ADATION 86 C2 2.40 0.57 1.80 MARINGSON POOR SURVING, MARKE PAR UP C2 5.66 0.66 1.89 MARINGSON POOR SURVING, MARKE PARUNP C2 7.67 0.57 1.89 MARAMAR,	WALLACE_PROSTATE_CANCER_RACE_UP	C2	281	0.70	1.91
Index.goAlac_lawGaisgUong C2 147 0.80 191 INDEXEGON_CONSTRUCTS C2 78 0.69 190 HARMSON_CONSTRUCTS C2 78 0.69 190 HUMMS_CONSTRUCTS C2 78 0.69 190 HOPMANN, MARCONSPELASTIC, SYNDROM, RISK DN C2 22 0.69 190 NEGG, INTESTINAL, LIMAURE, NETWORK, FOR, IGA, PRODUCTION C2 45 0.69 130 KEGG, INTESTINAL, MANURE, NETWORK, FOR, IGA, PRODUCTION C2 455 0.73 180 GUELLIZZ, REASCA CANCER DUCTION C2 455 0.73 180 VERGO, INTESTINAL, MANURE, NETWORK, FOR, IGA, PRODUCTION C2 455 0.73 180 VERGO, INTESTINAL, MANURE, NETWORK, FOR, IGA, PRODUCTION C2 456 0.66 180 GUELLIZZ, MARCON, INTESTINATION C2 456 0.66 180 GUELLIMORATION C2 78 0.66 189 GUELLIMORATION C2 78 0.66 180 MARAYA	HOSHIDA_LIVER_CANCER_SURVIVAL_UP	C2	73	0.72	1.91
DAL_CHRONIC METLOGENOUS LEUKEMIN UN C2 115 0.44 1191 MARCON FOOZ TARGETS UN C2 26 0.66 1191 HOFMANN MICOORDEDING: SYNGROM RISK DN C2 27 0.68 1190 SUP TYMOS C2 20 0.69 190 SCALERIER PSMOA_TARGETS C2 20 0.69 190 SCALEXTZ, BREAST CANCER DUCTAL, INVASIVE UP C2 345 0.73 130 SCALEXTZ, BREAST CANCER DUCTAL, INVASIVE UP C2 346 160 190 VERHARK AML, WITH NETWORK, FOR IGA PRODUCTION C2 442 0.46 180 VERHARK AML, WITH NETWORK, FOR IGA PRODUCTION C2 346 160 160 VERHARK AML, WITH NETWORK, FOR IGA PRODUCTION C2 442 0.46 180 VERHARK AML, WITH NETWORK, FOR IGA PRODUCTION C2 442 0.46 180 VERHARK AML, WITH NETWORK, FOR IGA PRODUCTION C2 460 160 161 159 VERLOW, CARLER AND, NE PROGENTOR DN C2 76 164 <td>HUANG_GATAZ_TARGETS_UP</td> <td>62</td> <td>147</td> <td>0.60</td> <td>1.91</td>	HUANG_GATAZ_TARGETS_UP	62	147	0.60	1.91
MANGO LANS LANGE 19 UP C2 65 0.88 1.91 MANG DASTINE RESISTANCE, UP C2 78 0.68 1.80 MOMENTAL MALER RESISTANCE, UP C2 78 0.68 1.80 AURINEE, FRANK TARGETS C2 70 0.68 1.80 REGG INTESTINAL IMMURE NETWORK FOR IGA PRODUCTION C2 445 0.69 1.90 VERANK ALL MAUNDSON POOR SURVIVAL AFTER CAMMA RADATION 8G C2 345 0.73 1.90 VERNAK ALL VERNAK ALL VERNAK ALL 0.66 1.89 1.90 VERNAK ALL VERNAK ALL 0.66 1.89 1.90 1.90 VERNAK ALL VERNAK ALL 0.66 1.89 1.90 1.91 1.90 1.91 1.90 1.91 1.91 1.91 1.91 1.		C2	115	0.64	1.91
HLANG DASAI INB, BESIS LANCE, QP C2 78 0.88 1.80 POPAMAN, MERCONSPERSITS, SWINROM, RISK, DN C2 70 0.68 1.80 GAURINER, PSINDA TARGETS C2 70 0.68 1.80 GG, INTESTINIL, MAILINE, INETWORK, FOR IGA PRODUCTION C2 45 0.73 1.90 SCHUETZ, BREAT CANCER, DUCTAL, INVASIVE, UP C2 456 0.73 1.90 MAUNDSON FOOD SURVIXA, ALTRE CAMMA RADATION 86 C2 240 0.57 1.90 VERNAXA, ALL, WITH, MPH MUTATED, DN C2 442 0.46 1.80 JOHANSSON GLOMACERAIC, CANCER UP C2 66 0.66 1.89 GURLTZMANN, PANCEARIC, CANCER UP C2 52 0.61 1.89 VOCELL, MARGETS MARCAMA, SOPT TISSON GLOMACERATIC, MARCARIT, CANCER UP C2 1.64 1.80 VOCELL, MARGETS MARCAMA, SOPT TISSON GLOMACERATIC, MARCARIT, CANCER UP C2 1.64 1.81 MARCAMA, SOPT TISSON GLOMACERATIC, MARCARIT, CANCER UP C2 1.64 1.80 MARCATARACETS, OF NUPROE TINN C2	MARSON_FOXP3_TARGETS_UP	C2	65	0.68	1.91
HOPHANN MPELODYSPLASIIC_SYNDROM RISK DN C2 22 0.06 1.00 REGG_INTESTINAL_IMAINE_NETWORK FOR (GA PRODUCTION C2 40 0.07 1.00 REGG_INTESTINAL_IMAINE_NETWORK FOR (GA PRODUCTION C2 40 0.07 1.00 REGG_INTESTINAL_IMAINE_NETWORK FOR (GA PRODUCTION C2 435 0.07 1.00 VERIAGK_MAL_UNTH_NEM_INTREE DN C2 430 0.07 1.00 AMUNDSON FOOR SURVIAL ATTER GAMMA RADIATION &G C2 442 0.46 1.90 REACTORME_HEMOSTASIS C2 442 0.46 1.90 OLDANASCON GLUCAMAGENESS BY POGFB_UP C2 42 0.46 1.89 GRUETZMANN_PANCREATUC_GANCER UP C2 35 0.61 1.89 VALK AML_CLUSTER 11 WC LEL MARATION C2 86 0.64 1.89 VALCAUL CLUSTER 11 WC LEL MARATION C2 1.62 1.86 1.89 MACDEL LAWRENCESSING, AND PRESENTATION C2 1.62 0.64 1.89 1.80 MACLEL LAWRENCESSING, AND PRESENTATION	HUANG_DASATINIB_RESISTANCE_UP	C2	78	0.69	1.90
SU_HIMUS C2 20 0.79 1.30 AGUNNER_PARCETS C2 70 0.88 1.30 REGISTERST C2 70 0.88 1.30 REGISTERST C2 70 0.88 1.30 REGISTERST C2 240 0.57 1.50 VERHAR ARL WITH NEW MUTATED DN C2 240 0.57 1.50 VERHAR ARL WITH NEW MUTATED DN C2 240 0.66 1.99 JOHANSSON GLOMAGENESIS BY PORTE OF UP C2 36 0.66 1.99 JOHANSSON FORMULATER 11 C2 36 0.66 1.89 NAKAYMAN SOFT TISSUE TUMORS PCALUP C2 73 0.75 1.89 NAKAYMAN SOFT TISSUE TUMORS PCALUP C2 100 0.61 1.89 NAKAYMAN SOFT TISSUE TUMORS PCALUP C2 100 0.61 1.89 NUL CALL MORATION C2 100 0.61 1.89 NUL CALL MORATION C2 10 0.61 1.89 NUL CALL MORAT	HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_DN	C2	22	0.66	1.90
GAUSRIEL PSM04_IAKGETS C2 70 0.88 1.30 GAUSRIEL PSM04_IAKGETS C2 45 0.69 1.30 SCHUETZ BREAST CANCER DUCTAL INVASIVE UP C2 45 0.73 1.80 SCHUETZ BREAST CANCER DUCTAL INVASIVE UP C2 45 0.73 1.80 VERNAMA CALL WITH WARK DUP C2 46 0.75 1.80 VERNAMA CALL WITH WARK DUP C2 46 0.66 1.80 VERNAMA CALL WITH WARK DUP C2 46 0.66 1.80 VERNAMA CALL WITH WARK DUP C2 36 0.66 1.80 GRUETZMANN PARCERATIC CANCER UP C2 36 0.66 1.89 VALK AML, CLUSTER 11 C2 36 0.61 1.89 MACYAMA SCH PROCESSING AND PRESENTATION C2 62 0.64 1.89 PID LUZ ZPATHWAY C2 62 0.65 1.89 DUCCKER PATHWAY C2 162 0.64 1.89 DID CXCRE PATHWAY C2 16 0.74 1.8		C2	20	0.79	1.90
REGG INTESTINAL IMMUNE NETWORK POR IGA PRODUCTION C2 45 0.69 1.90 ABUINDSON POOR SURVINAL AFTER GAMMA RADIATION 86 C2 33 0.57 1.90 ABUINDSON POOR SURVINAL AFTER GAMMA RADIATION 86 C2 245 0.73 1.90 ABUINDSON POOR SURVINAL AFTER GAMMA RADIATION 86 C2 246 0.66 1.90 CECTOME FUNCTION C2 56 0.66 1.90 DIAMASSON GULOMAGENESIS BY POOFE UP C2 352 0.61 1.91 NAKAYAMA SOFT TISSUE TUMORS PCAJ UP C2 160 0.61 1.99 VAK AME, CUBURTER, 11 C2 160 0.61 1.99 VAK AME, CUBURTER, 11 C2 160 0.61 1.89 VAK AME, CUBURTER, 11 C2 160 0.61 1.89 DALK AME, CUBURTER, 11 C2 160 0.61 1.89 DE L1, 2PARTHWAY C2 62 0.66 1.89 DE L1, 2PARTHWAY C2 62 0.66 1.89 DO CART FARTHWAY C2	GAURNIER_PSMD4_1ARGE1S	C2	70	0.68	1.90
SchUe T2 SHEAST CANCER DUCTAL INVASIVE UP C2 345 0.73 1.93 VERNAXA AML WITH NMAIT MED DN C2 93 0.57 1.90 VERNAXA AML WITH NMAIT MED DN C2 240 0.57 1.90 VERNAXA AML WITH NMAIT MED DN C2 242 0.657 1.90 VERNAXA AML WITH NMAIT MED DN C2 442 0.46 1.89 URLEXAND C2 363 0.67 1.90 URLEXAND C2 363 0.61 1.99 VALK AML CLUSTER 11 C2 36 0.61 1.99 VALK AML CLUSTER 11 C2 36 0.61 1.99 VALK AML CLUSTER 11 C2 160 0.61 1.99 VOLEL MEGG ANTICEN PROCESSING AND PRESENTATION C2 167 0.64 1.99 PID LT2 ZPATHWAY C2 162 0.66 1.89 DID CXCR PAPHWAY C2 160 0.76 1.88 CARGETS ON NUPRES HOADS PUSION 16D UP C2 160 0.76 1.88	REGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	C2	45	0.69	1.90
AMUMBSON POOR SURVAL AFTER GAMMA FADIATION BG C2 93 0.57 190 REACTOME (FEMOSTABIS C2 240 0.57 190 REACTOME (FEMOSTABIS C2 442 0.46 190 OLTAMASEN (GLIMAGENESIS BY PDGFB UP C2 362 0.61 1.89 GRUETZMANN PARCREATIC CANCER UP C2 362 0.61 1.89 GRUETZMANN PARCREATIC CANCER UP C2 73 0.75 1.89 VALUAL CLUBATION C2 160 0.64 1.89 MUMODAT TYNOR PCALUP C2 170 0.64 1.99 MODAT TYNOR C2 170 0.64 1.99 MUMODAT TYNWY C2 102 0.66 1.89 PID CXCR4 PATHWAY C2 102 0.68 1.89 PID CXCR4 PATHWAY C2 160 1.68 1.89 PID CXCR4 PATHWAY C2 26 0.74 1.88 PID CXCR4 PATHWAY C2 26 0.74 1.88 PID CAPS TAR	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	C2	345	0.73	1.90
VB-BR4WA, XML, WITH, NMT, MUTATED, N C2 240 0.57 130 REACTOME, FUNCKSTASIS C2 442 0.46 1.89 JDHANSSON, GLUDMAGENESIS, BY PDGFB, UP C2 352 0.66 1.89 MURCHAMA, SOFT, TISSUE, TUMORS, FCAL, UP C2 362 0.661 1.89 NAKAYAMA, SOFT, TISSUE, TUMORS, FCAL, UP C2 36 0.661 1.89 WILZLAM, MAL, SUBJER, 11 C2 36 0.661 1.89 WILZLAM, MARTION C2 62 0.64 1.89 WILZLAM, MALTHOCYTE, AND NK PROGENITOR, DN C2 62 0.661 1.89 PID L12, ZPATHWAY C2 62 0.661 1.89 PID L12, ZPATHWAY C2 62 0.661 1.89 PID L12, ZPATHWAY C2 62 0.66 1.88 PID L12, ZPATHWAY C2 162 1.66 1.88 PID L12, ZPATHWAY C2 160 1.88 1.88 ROTOR INFATHWAY C2 160 1.88 1	AMUNDSON POOR SURVIVAL AFTER GAMMA_RADIATION_8G	C2	93	0.57	1.90
NEBACI DME, HEMOSI RASIS C2 442 0.46 1.90 JOHANSSON (GLIOMAGENES) BY PDGFB UP C2 56 0.66 1.89 GRUETZMANN PANCREATIC CANCER UP C2 73 0.75 1.89 VALK AML, CLUSTER, 11 C2 36 0.61 1.89 VALK AML, CLUSTER, 11 C2 36 0.61 1.89 VALK AML, CLUSTER, 11 C2 100 0.61 1.89 VALK AML, CLUSTER, 11 C2 100 0.61 1.89 VALK AML, CLUSTER, 11 C2 100 0.61 1.89 PLODE, TURPHOCYTE, AND NK, PROGENITOR DN C2 100 0.61 1.89 PID CLYCR4 PATHWAY C2 102 0.60 1.88 CONC FOXPT ATRGETS ON C2 42 0.68 1.88 REACTOME, INFLAMMASOMES C2 167 1.58 1.88 C12/CIPICAN, IPATHWAY C2 24 0.65 1.88 RUTELLA, RESPONSE, TO HGF DN C2 24 0.63 1.88 <td>VERHAAR_AML_WIIH_NPM1_MUTATED_DN</td> <td>C2</td> <td>240</td> <td>0.57</td> <td>1.90</td>	VERHAAR_AML_WIIH_NPM1_MUTATED_DN	C2	240	0.57	1.90
JJPARASSON GLOMAGENESIS BY POOFB UP C2 36 0.66 1.89 MAKAYAMA, SOFT TISSUE TUMORS PCALUP C2 73 0.75 1.89 VAR. AM, CUSTER, 11 C2 36 0.61 1.89 WARAYAMA, SOFT TISSUE TUMORS PCALUP C2 180 0.61 1.89 WARAYAMA, SOFT TISSUE, TUMORS PCALUP C2 180 0.61 1.89 WILZLAL MIGRATION C2 62 0.64 1.89 WILZLAL MIGRATION C2 62 0.64 1.89 PIDAZE TTYMWAY C2 62 0.66 1.88 PIDAZE TATIWAY C2 16 0.76 1.88 REACTOME INFLAMMASOMS C2 16 0.76 1.88 REACTOME INFLAMMASOMS C2 46 0.76 1.88 REACTOME INFLAMENTANING C2 26 0.77 1.88 RUTELLARESTON C2 26 0.77 1.88 RUTELLARESTON C2 26 0.77 1.88 RUTELAR ESTONO	REACTOME_HEMOSTASIS	C2	442	0.46	1.90
GRUET IZMAIN C2 362 0.61 1.89 MAKVAMA, SOT TISSUE TUNCRS, PCALUP C2 73 0.75 1.89 VALK AML, CLUSTER, 11 C2 36 0.61 1.89 WOLCELL (MERATION C2 62 0.64 1.89 WALK AML, CLUSTER, 11 C2 62 0.64 1.89 WALK AML, CLUSTER, 11 C2 62 0.64 1.89 VALK AML, CLUSTER, 11 C2 62 0.64 1.89 PID_LIZZ PATHWAY C2 62 0.65 1.89 PID_CXCR4 PATHWAY C2 107 0.54 1.88 CNOF FORAT TARGETS OF, NUPBB, HOXA9 FUSION 16D UP C2 16 0.76 1.88 REACTOME_INFLAMMASOMES C2 16 0.76 1.88 1.88 ROLESTARGETS OF, NUPBB, HOXA9 FUSION 16D UP C2 24 0.65 1.88 RITELLA, RESPONSE TO HGF VS, CSP2RB, AND LL4, DN C2 26 0.74 1.88 NOL MILT, TRAGETS DN C2 41	JOHANSSON_GEIOMAGENESIS_BY_PDGFB_0P	C2	56	0.66	1.89
NARAYAMA SUF1_IISSUE_IUMORS PCAT_UP C2 73 0.75 1.89 VALK AME_CUSTER_11 C2 36 0.61 1.89 WUL CELL MIGRATION C2 180 0.61 1.89 WIL CELL MIGRATION C2 180 0.61 1.89 KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION C2 62 0.64 1.89 PID_LIZ_2PATHWAY C2 102 0.66 1.89 PID_CXDR1_PATHWAY C2 102 0.66 1.89 PID_CXDR1_PATHWAY C2 102 0.66 1.88 OND_FOXP3_TARGETS_ON C2 160 .76 1.88 RUTELLA_RESPONSE TO HGF VS CSP2RB AND_LLA DN C2 240 0.55 1.88 RUTELLA_RESPONSE TO HGF ON C2 241 0.64 1.88 RUTELLA_RESPONSE TO HGF ON C2 241 0.64 1.88 VID GLYPICAN_IPATHWAY C2 53 0.68 1.87 VID GLYPICAN C2 41 0.64 1.88	GRUETZMANN_PANCREATIC_CANCER_UP	C2	352	0.61	1.89
VALE AMIL CLUS FERSION C2 36 0.61 1.89 WALE AMIL CLUS FERSION C2 160 0.61 1.89 HADGAD T, LYMPHOCYTE AND NK PROGENITOR DN C2 62 0.64 1.89 HADGAD T, LYMPHOCYTE AND NK PROGENITOR DN C2 62 0.64 1.89 PID LIZ ZPATHWAY C2 62 0.65 1.89 PID LXCR4 PATHWAY C2 160 0.64 1.89 DID CXCR4 PATHWAY C2 160 0.66 1.88 TAKEDA TARGETS ON C2 167 0.54 1.88 REACTOME INFLAMMASOMES C2 16 0.76 1.88 REACTOME INFLAMMASOMES C2 26 0.74 1.88 REACTOME INFLAMMASOMES C2 26 0.74 1.88 INTELLA RESPONSE TO HGF VS CSF2RB AND LL4 DN C2 240 0.55 1.88 RITELLA RESPONSE TO HGF ON C2 241 0.64 1.88 REACTOME INTERPERONS SIGNALUP C2 110 0.53 1.87<	NARATAMI SOFI_ISSUE_IUMORS_PCAT_UP	62	73	0.75	1.89
WILDELL MIGRATION C2 180 0.61 1.89 HADDAD T_UMPHOCYTE AND NK PROGENITOR DN C2 62 0.64 1.89 KEGG ANTIGEN PROCESSING AND PRESENTATION C2 62 0.64 1.89 PID LIZ 2RTHWAY C2 62 0.65 1.89 PID CXCR4 PATHWAY C2 167 0.64 1.89 PID CXCR4 PATHWAY C2 167 0.64 1.89 PID CXCR4 PATHWAY C2 167 0.54 1.88 ONO FOXP3 TARGETS OF NUP98 HOXA9 FUSION_16D_UP C2 160 0.76 1.88 RACTOME INFLAMMASOMES C2 16 0.76 1.88 RUTELLA RESPONSE TO HOF VS CSP2RB AND_LL4 DN C2 280 0.71 1.88 RUTELLA RESPONSE TO HOF SONGMALLY DN C2 284 0.74 1.88 RUTELLA RESPONSE TO HOF SONGMAL UP C2 53 0.68 1.87 VIM MC TARGETS DN C2 451 0.63 1.87 VIM MC TARGETS DN C2 451 0.63 </td <td>VALK_AME_CLUSTER_11</td> <td>62</td> <td>36</td> <td>0.61</td> <td>1.89</td>	VALK_AME_CLUSTER_11	62	36	0.61	1.89
InduDal_LtmitPicCrite_AND_NERVOSENTOR_UN C2 b2 0.04 1.89 REGG ANTIGEN PROCESSING AND PRESENTATION C2 62 0.65 1.89 PID_LIZ2_ZPATHWAY C2 62 0.65 1.89 PID_LIZ2_ZPATHWAY C2 162 0.60 1.88 TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP C2 167 0.54 1.88 ONO_FOXP3_TARGETS_DN C2 16 0.76 1.88 REACTOME_INFLAMMASOMES C2 16 0.76 1.88 RUTELLA_RESPONSE_TO_HOF VS_CSPER_AND_IL4_DN C2 260 0.74 1.88 RUTELLA_RESPONSE_TO_HOF DN C2 240 0.55 1.88 RON_AMI_TARGETS_UP C2 241 0.64 1.88 REACTOME_INTERFERON SIGNALING C2 151 0.63 1.88 VI_MYC_TARGETS_DN C2 441 0.64 1.87 VI_MYC_TARGETS_DN C2 451 0.63 1.87 VI_MYC_TARGETS_DN C2 451 0.63		62	180	0.61	1.89
NEGG ANTIGEN, PROJESSING AND PRESENTATION C2 77 0.04 1.89 PID LIZZ ZRATHWAY C2 62 0.65 1.89 PID CXCR4, PATHWAY C2 102 0.60 1.88 PID CXCR4, PATHWAY C2 102 0.60 1.88 OND FOXP3, TARGETS, DN C2 42 0.68 1.88 RACTOME, INFLAMMASOMES C2 16 0.76 1.88 RUTELLA, RESPONSE TO HOF, VS CSF2RB, AND_LL4 DN C2 26 0.74 1.88 RUTELLA, RESPONSE TO HOF, VS CSF2RB, AND_LL4 DN C2 22 0.57 1.88 RUTELLA, RESPONSE TO HOF, DN C2 24 0.74 1.88 RUTELLA, RESPONSE TO HOF, DN C2 41 0.64 1.88 RUTELLA, RESPONSE TO HOF, DN C2 44 0.64 1.88 RUTELLA, RESPONSE TO, HOF, DN C2 41 0.64 1.88 RUTELA, RESPONSE UP C2 161 0.63 1.87 VI MCY TARGETS DN C2 451 0.64 <td></td> <td>02</td> <td>62</td> <td>0.64</td> <td>1.89</td>		02	62	0.64	1.89
PID_LIC2_PARTHWAY C2 62 62 6.085 1.89 PID_CXCR4 PATHWAY C2 167 0.54 1.88 TAKEDA_TARGETS_DN C2 167 0.54 1.88 REACTOME_INFLAMMASOMES C2 42 0.68 1.88 REACTOME_INFLAMMASOMES C2 42 0.68 1.88 RUTELLA_RESPONSE_TO_HOF_VS_CSPRB_AND_IL4_DN C2 26 0.74 1.88 PID_GLYPICAN_IPATHWAY C2 26 0.74 1.88 RUTELLA_RESPONSE_TO_HOF_VS_CSPRB_AND_IL4_DN C2 24 0.66 1.88 RUTELLA_RESPONSE_TO_HOF_DN C2 24 0.66 1.88 REACTOME_INTERFERON_SIGNALING C2 41 0.64 1.88 VI_MYC_TARGETS_DN C2 451 0.68 1.87 UARCATARGETS_DNALING C2 451 0.64 1.87 UARCATARGETS_DN C2 451 0.63 1.87 CHARAFE_BREAST_CANCER_UMATION D C2 67 0.64 1.87	REGG_ANTIGEN_PROCESSING_AND_PRESENTATION	62	11	0.64	1.89
PID_USACR4_PRINTNAT C2 102 0.60 1.86 TAKEDA_TARGETS OF_NUP98_HOXA9_FUSION_16D_UP C2 167 0.54 1.88 CAND_FOXP3_TARGETS ON C2 16 0.76 1.88 REACTOME_INFLAMMASOMES C2 16 0.76 1.88 RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN C2 26 0.74 1.88 RUTELLA_RESPONSE_TO_HGF_DN C2 26 0.74 1.88 RUTELLA_RESPONSE_TO_HGF_DN C2 244 0.74 1.88 ONO_AMLI_TARGETS ON C2 44 0.64 1.88 REACTOME_INTERFERON_SIGNALING C2 151 0.63 1.88 VJ_MC_TARGETS DN C2 63 0.66 1.87 WANG_ESOPHAGUS_CANCER_VS NORMALUP C2 63 0.66 1.87 WANG_ESOPHAGUS_CANCER_VS NORMALUP C2 67 0.64 1.87 WANG ESOPHAGUS_CANCER_VS NORMALUP C2 67 0.64 1.87 ULIA_SIGNALING C2 67 0.64		02	62	0.65	1.69
Instance Transform C2 167 0.54 1.88 REACTOME_INFLAMMASOMES C2 16 0.76 1.88 REACTOME_INFLAMMASOMES C2 16 0.76 1.88 REACTOME_INFLAMMASOMES C2 26 0.74 1.88 PID_GLYPICAN_IPATHWAY C2 26 0.74 1.88 RUTELLA RESPONSE TO HGF VS_CSF2RB_AND_IL4_DN C2 284 0.74 1.88 RUTELLA RESPONSE TO HGF VS_CSF2RB_AND_IL4_DN C2 24 0.63 1.88 RUTELLA RESPONSE TO HGF NS_CSF2RB_AND_IL4_DN C2 41 0.64 1.88 RMICLISZ_TARGETS DN C2 41 0.64 1.88 VU MYC_TARGETS CNACER_VS_NORMAL_UP C2 117 0.58 1.87 CHARAFE_BREAST_CANCER_UNINAL_VS_MESENCHYMAL_DN C2 451 0.63 1.88 VU MYC_TARGETS_DN C2 451 0.63 1.87 CBADAASCL_TARGETS_DN C2 451 0.63 1.87 CHARAFE_BREAST_CANCER_UNALIVARY C2 18		02	102	0.00	1.00
DNU TOARS INNOUSS UN C2 42 0.06 1.86 REACTOME INFLAMMASOMES C2 146 0.76 1.88 RUTELLA RESPONSE TO HGF VS CSF2RB AND L4 DN C2 240 0.55 1.88 RUTELLA RESPONSE TO HGF DN C2 220 0.57 1.88 RUTELLA RESPONSE TO HGF DN C2 229 0.57 1.88 RUTELLA RESPONSE TO HGF DN C2 41 0.64 1.88 ONO AMLI TARGETS DN C2 41 0.64 1.88 REACTOME INTERFERON SIGNALING C2 151 0.63 1.87 WANG CARGETS DN C2 151 0.63 1.87 WANG CARGETS DN C2 67 0.64 1.87 UNC TARGETS DN C2 67 0.64 1.87 UNAR SEGNEANT CALL MATURATION D C2 67 0.64 1.87 UNLLA SIGNALING C2 24 0.75 1.87 REACTOME INTERFECT DN C2 67 0.64 1.87 D		02	107	0.04	1.00
Numerical Data L2 10 0.76 1.88 NUTELLA RESONSE TO HGF VS CSPRB AND IL4 DN C2 240 0.55 1.88 PID GLYPICAN. 1PATHWAY C2 26 0.74 1.88 RUTELLA RESPONSE TO HGF DN C2 26 0.74 1.88 KIM GLISZ TARGETS UP C2 84 0.74 1.88 REACTOME INTERFERION C2 84 0.74 1.88 REACTOME INTERFERION SIGNALING C2 151 0.63 1.88 WU MYC TARGETS DN C2 151 0.63 1.87 CHARAFE BREAST CANCER LUMINAL VS MESENCHYMAL DN C2 451 0.63 1.87 CHARAFE BREAST CANCER LUMINAL VS MESENCHYMAL DN C2 451 0.63 1.87 UNSTEDT DENDRITIC CELL MATURATION D C2 451 0.63 1.87 CARAFE BREAST CANCER LUMINAL VS MESENCHYMAL DN C2 461 1.87 LU JLA SIGNALING C2 451 0.63 1.87 DER JEN GAMMA RESPONSE UP C2 28		02	42	0.00	1.00
INVESTIGATION CZ 240 0.53 1.88 PID_GLYPICAL FORMAT C2 26 0.74 1.88 RUTELLA RESPONSE TO HOF DN C2 28 0.77 1.88 RUTELLA RESPONSE TO HOF DN C2 84 0.74 1.88 ONO ANLI TARGETS DN C2 41 0.64 1.88 REACTOME_INTERFERION_SIGNALING C2 151 0.63 1.88 VU MYC_TARGETS DN C2 43 0.68 1.87 WANG ESOPHAGUS CANCER VS NORMAL_UP C2 451 0.63 1.87 UI MC_TARGETS DN C2 451 0.63 1.87 UI AL SIGNALING C2 451 0.63 1.87 UI AL SIGNALING C2 451 0.63 1.87 INSALASIC CARGETS DN C2 451 1.87 REACTOME_INTERFERION MOLECULES CAMS C2 24 0.75 1.87 REACTOME_SEMAMA RESPONSE UP C2 181 1.87 1.87 REACTOME_SEMAP		02	01	0.70	1.00
Ind_duting C2 20 0.1/4 1.88 RUTELLA_RESPONSE_TO_HGE_DN C2 229 0.57 1.88 KIM_GLISZ_TARGETS_UP C2 84 0.74 1.88 ONO AMLI TARGETS DN C2 41 0.64 1.88 REACTOME_INTERFERON_SIGNALING C2 151 0.63 1.88 REACTOME_INTERFERON_SIGNALING C2 151 0.63 1.88 WANG ESOPHAGUS_CANCER_VS_NORMAL_UP C2 177 0.88 1.87 CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN C2 451 0.63 1.87 LINDSTEDT DENDRITIC CELL MATURATION D C2 67 0.64 1.87 CSADA_ASCL_TARGETS DN C2 24 0.75 1.87 KEGG CELL ADHESION MOLECULES CAMS C2 100 0.53 1.87 PERAFT_CARGETS DN C2 100 0.53 1.87 ULIAYA SPROSTONE UP C2 100 0.53 1.87 REACTOME_PLATELET ACTIVATION SIGNALING AND AGGREGATION C2 269		02	240	0.00	1.00
INDITED_INCIDENT C2 223 0.57 1.88 INDIGED_INCENTING C2 84 0.74 1.88 ONO ANLI_TARGETS DN C2 41 0.64 1.88 REACTOME_INTERFEREND SIGNALING C2 151 0.63 1.88 YU MYC_TARGETS DN C2 53 0.68 1.87 WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP C2 451 0.63 1.87 CHARAFE BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN C2 451 0.63 1.87 LINDSTEDT_DENDRTIC_CELL_MATURATION_D C2 67 0.64 1.87 CSADA_ASCL1_TARGETS_DN C2 80 0.61 1.87 CSADA_ASCL1_TARGETS_DN C2 71 0.75 1.87 KEGG_CELL_ADHESION MOLECULES_CAMS C2 71 0.72 1.87 REACTOME_SEMANDAR_RESPONSE_UP C2 71 0.72 1.87 REACTOME_SEMANDAR C2 63 0.64 1.87 LU_VAY3_PROSTATE_CARCINOGENESIS_UP C2 63 0.64 1.87 LU_VAY3_PROSTATE_CARCINGOENESIS_UP C2 23 <t< td=""><td></td><td>02</td><td>20</td><td>0.74</td><td>1.00</td></t<>		02	20	0.74	1.00
Num. Disc. Latoc. 19 or 0.2 04 0.74 1.88 NON OMLITARGETS DN C2 41 0.64 1.88 REACTOME_INTERFERON SIGNALING C2 151 0.63 1.88 WIMYG ESOPHAGUS_CANCER_VS NORMAL UP C2 117 0.58 1.87 CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN C2 451 0.63 1.87 LUDISTED DENDRTIC CELL_MATURATION D C2 67 0.64 1.87 CSADA_ASCL1_TARGETS_DN C2 67 0.64 1.87 LU_LIA_SIGNALING C2 67 0.64 1.87 CSADA_ASCL_TARGETS_DN C2 62 130 0.53 1.87 CSADA_ASCL_TARGETS_DN C2 130 0.53 1.87 DER_IFN_GAMMA_RESPONSE_UP P C2 130 0.53 1.87 REACTOME_ENAMPORIN_INTERACTION S C2 269 0.52 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 268 0.63 1.87 UL_VAV3 PROSTATE_CARCINOGENESIS_UP		02	229	0.07	1.00
Disconte Lange 1 D2 41 0.64 1.88 REACTOME INTERFERONS SIGNALING C2 151 0.63 1.88 YU_MYC_TARGETS DN C2 53 0.68 1.87 CHARAFE BREAST_GANCER LUMINAL VS_MESENCHYMAL_DN C2 451 0.63 1.87 LINDSTEDT_DENDRTIC_CELL MATURATION_D C2 467 0.64 1.87 CHARAFE BREAST_GANCER LUMINAL VS_MESENCHYMAL_DN C2 67 0.64 1.87 LINDSTEDT_DENDRTIC_CELL MATURATION_D C2 67 0.64 1.87 OSADA_ASCL1_TARGETS_DN C2 24 0.75 1.87 KEGG_CELL_ADHESION_MOLECULES_CAMS C2 71 0.72 1.87 REACTOME_PLATELT_ACTIVION UP C2 269 0.52 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 106 0.53 1.87 REACTOME_PLATELT_ACTIVION_SIGNALING_AND_AGGREGATION C2 160 0.53 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 88 0.63 1.87 ULU_VAS_PROSTATE_		02	/1	0.74	1.00
Instruction C2 101 0.63 1.86 WU MYC_TARGETS DN C2 53 0.68 1.87 CHARAFE BREAST_CANCER LUMINAL VS_MESENCHYMAL DN C2 451 0.63 1.87 LIDDSTEDT DENDRITIC CELL MATURATION D C2 451 0.63 1.87 LUNSTEDT DENDRITIC CELL MATURATION D C2 67 0.64 1.87 CSADA_ASCL1_TARGETS DN C2 24 0.75 1.87 KEGG CELL_ADHESION_MOLECULES_CAMS C2 130 0.53 1.87 REACTOME_PLATELET_ACTIVATION_UP C2 269 0.52 1.87 REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION C2 196 0.53 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 88 0.63 1.87 LIU_VAV3_PROSTATE_CARCINGENESIS_UP C2 88 0.63 1.87 LIU_VAV3_PROSTATE_CARCINGENESIS_UP C2 30 0.65 1.87 ULVAV3_PROSTATE_CARCINGENESIS_UP C2 30 0.65 1.87 ULVAV3_PROSTATE_CARCINGE	REACTOME INTEREERON SIGNALING	C2	41	0.04	1.00
Industry C2 C3 0.08 1.67 WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP C2 117 0.58 1.87 CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN C2 451 0.63 1.87 LINDSTEDT_DENDRITIC_CELL_MATURATION_D C2 67 0.64 1.87 LINDSTEDT_DENDRITIC_CELL_MATURATION_D C2 89 0.61 1.87 CSADA_ASCL_TARGETS_DN C2 24 0.75 1.87 KEGG_CELL_DHESION_MOLECULES_CAMS C2 71 0.72 1.87 REACTOME_PLATELT_ACTIVATION_UP C2 71 0.72 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 63 0.64 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 63 0.64 1.87 ULU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 63 0.64 1.87 ULU_VAV3_PROSTATE_CARCINGENESIS_UP C2 30 0.65 1.87 UAVAG_SILENCED BY_METHYLATION_UP C2 30 0.65 1.87 UAVAG_SILENCED BY_METHYLATION_UP		C2	53	0.03	1.00
Instruction OZ III 0.35 1.87 CHARAFE BREAST <cancer_luminal_vs_mesenchymal_dn< td=""> C2 451 0.63 1.87 LUNDSTEDT DENORITIC_CELL_MATURATION_D C2 67 0.64 1.87 LU_IL4_SIGNALING C2 89 0.61 1.87 C2 24 0.75 1.87 KEGG_CELL_ADHESION_MOLECULES_CAMS C2 130 0.53 1.87 DER_IFN_GAMMA_RESPONSE_UP C2 71 0.72 1.87 REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION C2 269 0.52 1.87 REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION C2 63 0.64 1.87 UL VAX3_PROSTATE_CARCINGENESIS_UP C2 88 0.63 1.87 PID_L12_STAT4_PATHWAY C2 88 0.63 1.87 UL VAX3_PROSTATE_CARCINCGENESIS_UP C2 30 0.65 1.87 PID_L12_STAT4_PATHWAY C2 30 0.65 1.87 UL VAX3_PROSTATE_CARCINCGENESS_DN</cancer_luminal_vs_mesenchymal_dn<>	WANG ESOPHAGUS CANCER VS NORMAL UP	C2	117	0.58	1.07
CLID STED TENDENT CELL MATURATION D C2 431 0.03 1.07 LID DENDRITIC CELL MATURATION D C2 67 0.64 1.87 LU LIA SIGNALING C2 89 0.61 1.87 UL LIA SIGNALING C2 24 0.75 1.87 REG CELL ADHESION MOLECULES CAMS C2 71 0.72 1.87 DER_IFN_GAMMA_RESPONSE_UP C2 71 0.72 1.87 REACTOME_PLATELET_ACTIVATION UP C2 269 0.52 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 63 0.64 1.87 ULV 3/9 PROSTATE CARCINOGENESIS UP C2 63 0.64 1.87 ULV 3/9 PROSTATE CARCINOGENESIS UP C2 88 0.63 1.87 VILLANG SILENCED BY METHYLATION UP C2 30 0.65 1.87 VILLANG SILENCED BY METHYLATION UP C2 30 0.65 1.87 VILLANG SILENCED BY METHYLATION UP C2 30 0.65 1.87 VILANG SILENCED BY METHYLATION UP C2	CHARAFE BREAST CANCER LUMINAL VS MESENCHYMAL DN	C.2	451	0.63	1.87
ILITILATION CL 07 0.64 1.87 OSADA_ASCL1_TARGETS_DN C2 89 0.61 1.87 CSADA_ASCL1_TARGETS_DN C2 24 0.75 1.87 KEGG_CELL_ADHESION_MOLECULES_CAMS C2 130 0.53 1.87 DER_IFN_GAMMA_RESPONSE_UP C2 71 0.72 1.87 HELLER_SILENCED_BY_METHYLATION_UP C2 269 0.52 1.87 REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION C2 196 0.53 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 63 0.64 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 30 0.65 1.87 URAGESIENCED_BY_METHYLATION_UP C2 30 0.65 1.87 URAGESIENCED_BY_METHYLATION_UP C2 202 0.52 1.87 URAGESIENCED_BY_METHYLATION_UP C2 30 0.66 1.86 ZHAN_EARCHORED C2 20		C.2	67	0.00	1.07
Image: Construction OL OD OL OD OL Instruction OSADA ASCL1_TARGETS_DN C2 24 0.75 1.87 KEGG_CELL_ADHESION_MOLECULES_CAMS C2 130 0.53 1.87 DER_IFN_GAMMA_RESPONSE_UP C2 71 0.72 1.87 HELLER_SILENCED_BY_METHYLATION_UP C2 269 0.52 1.87 REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION C2 196 0.53 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 63 0.64 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 30 0.65 1.87 ULANG_SILENCED_BY_METHYLATION_UP C2 30 0.65 1.87 UANG_SILENCED_BY_METHYLATION_UP C2 30 0.65 1.87 UANG_SILENCED_BY_METHYLATION_UP C2 30 0.65 1.87 UANG_SILENCED_BY_METHYLATION_UP C2 30 0.65 1.87		C2	89	0.61	1.07
International control Original control Original control International control KEGG_CELL_ADHESION_MOLECULES_CAMS C2 130 0.53 1.87 DER_IFN_GAMMA_RESPONSE_UP C2 71 0.72 1.87 HELLER_SILENCED_BY_METHYLATION_UP C2 269 0.52 1.87 REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION C2 169 0.53 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 63 0.64 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 UAVG_SILENCED_BY_METHYLATION_UP C2 33 0.71 1.87 UANG_SILENCED_BY_METHYLATION_UP C2 33 0.71 1.87 UANG_SILENCED_BY_METHYLATION_UP C2 30 0.65 1.87 WIERENGA_STATE_CARCINGENES_DN C2 20 0.52 1.87 UANG_SILENCED_BY_METHYLATION_GENES_DN C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 42 0.63 1.86 SWEET_KRAS_	OSADA ASCLI TARGETS DN	C2	24	0.75	1.87
Intervention OZ 100 0.33 1.07 DER_IFN_GAMMA_RESPONSE_UP C2 71 0.72 1.87 HELLER_SILENCED_BY_METHYLATION_UP C2 269 0.52 1.87 REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION C2 196 0.53 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 63 0.64 1.87 IUL VAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 PID_IL12_STAT4_PATHWAY C2 33 0.71 1.87 ULANG_SILENCED_BY_METHYLATION_UP C2 30 0.65 1.87 WIEREINGA_STAT5A_TARGETS_DN C2 202 0.52 1.87 DEMAGALHAES_AGING_UP C2 53 0.68 1.86 ZHAN_EARLY_DIFFERENTIATION_GENES_DN C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 45 0.71 1.86 SWEET_KRAS_TARGETS_UP C2 45 0.71 1.86 SRATINKO_PLATELET_SIGNATURE C2 45	KEGG CELL ADHESION MOLECULES CAMS	C2	130	0.53	1.87
Initial Initial <t< td=""><td>DER IFN GAMMA RESPONSE UP</td><td>C.2</td><td>71</td><td>0.72</td><td>1.87</td></t<>	DER IFN GAMMA RESPONSE UP	C.2	71	0.72	1.87
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION G2 100 REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION G2 100 0.32 1.87 REACTOME_SEMAPHORIN_INTERACTIONS C2 63 0.64 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 LIU_XAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 LIANG_SILENCED_BY_METHYLATION_UP C2 30 0.65 1.87 UARGSILENCED_BY_METHYLATION_UP C2 202 0.52 1.87 DEMAGALHAES_AGING_UP C2 202 0.52 1.87 ZHAN EARLY_DIFFERENTIATION_GENES_DN C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 45 0.71 1.86 GNATENKO_PLATELET_SIGNATURE C2 162 0.56 1.86 RASHI_RESPONSE_TO_IONIZING_RADIATION_6 C2	HELLER SILENCED BY METHYLATION UP	C.2	269	0.52	1.87
REACTOME_SEMAPHORIN_INTERACTIONS C2 63 0.64 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 LIU_VAV3_PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 PID_LI12_STAT4_PATHWAY C2 33 0.71 1.87 LIANG_SILENCED_BY_METHYLATION_UP C2 30 0.65 1.87 WERENGA_STATSA_TARGETS_DN C2 202 0.52 1.87 DEMAGALHAES_AGING_UP C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 42 0.63 1.86 SERVITJA_ISLET_HNF1A_TARGETS_UP C2 45 0.71 1.86 SERVITJA_ISLET_HNF1A_TARGETS_UP C2 162 0.56 1.86 RASHI_RESPONSE_TO_IONZING_RADIATION_6 C2 77 0.63 1.86 RAGHAVACHARI_PLATELET_SPECIFIC_GENES C2 <	REACTOME PLATELET ACTIVATION SIGNALING AND AGGREGATION	C2	196	0.53	1.87
ILL VAV3 PROSTATE_CARCINOGENESIS_UP C2 88 0.63 1.87 PID_IL12_STAT4_PATHWAY C2 33 0.71 1.87 LIANG_SILENCED_BY_METHYLATION_UP C2 33 0.71 1.87 WIEREINGA_STAT5A_TARGETS_DN C2 202 0.55 1.87 DEMAGALHAES_AGING_UP C2 202 0.52 1.87 ZHAN_EARLY_DIFFERENTIATION_GENES_DN C2 42 0.63 1.86 ZHAN_EARLY_DIFFERENTIATION_GENES_DN C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 45 0.71 1.86 SWEET_KRAS_TARGETS_UP C2 45 0.71 1.86 SERVITJA_ISLET_HNF1A_TARGETS_UP C2 45 0.71 1.86 SERVITJA_ISLET_HNF1A_TRGETS_UP C2 162 0.56 1.86 RASHI_RESPONSE_TO_IONIZING_RADIATION_6 C2 70 0.66 1.86 RAGHAVACHAR_PLATELET_SPECIFIC_GENES C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 7	REACTOME SEMAPHORIN INTERACTIONS	C2	63	0.64	1.87
DELINITY DELINITY DELINITY DID_L12_STAT4_PATHWAY C2 33 0.71 1.87 LIANG_SILENCED_BY_METHYLATION_UP C2 30 0.65 1.87 WIERENGA_STATSA_TARGETS_DN C2 202 0.52 1.87 DEMAGALHAES_AGING_UP C2 202 0.52 1.87 ZHAN_EARLY_DIFFERENTIATION_GENES_DN C2 53 0.68 1.86 ZHAN_EARLY_DIFFERENTIATION_GENES_DN C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 45 0.71 1.86 SERVITJA_ISLET_HNF1A_TARGETS_UP C2 45 0.71 1.86 RASHI_RESPONSE_TO_IONIZING_RADIATION_6 C2 81 0.59 1.86 RASHI_RESPONSE_TO_ONIZING_RADIATION_6 C2 77 0.63 1.86 JACKSON_DNMT1_TARGETS_UP C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 1.20.57 1.86	LIU VAV3 PROSTATE CARCINOGENESIS UP	C2	88	0.63	1.87
LIANG_SILENCED_BY_METHYLATION_UP C2 C3 0.11 1.07 WIERENGA_STAT5A_TARGETS_DN C2 202 0.52 1.87 DEMAGALHAES_AGING_UP C2 202 0.52 1.87 DEMAGALHAES_AGING_UP C2 53 0.68 1.86 ZHAN_EARLY_DIFFERENTIATION_GENES_DN C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 82 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 45 0.71 1.86 SWEET_KRAS_TARGETS_UP C2 45 0.71 1.86 SRATTJA_ISLET_HNF1A_TARGETS_UP C2 81 0.59 1.86 RASHI_RESPONSE_TO_IONIZING_RADIATION_6 C2 70 0.66 1.86 RASHI_RESPONSE_TO_IONIZING_RADIATION_6 C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 77 0.63 1.86 CHEOK_RESPONSE_TO_HD_MTX_UP C2 22 0.76 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71	PID IL12 STAT4 PATHWAY	C2	33	0.71	1.87
WIERENGA_STATSA_TARGETS_DN 0.00 1.00 DEMAGALHAES_AGING_UP C2 0.02 0.52 1.87 DEMAGALHAES_AGING_UP C2 53 0.68 1.86 ZHAN_EARLY_DIFFERENTIATION_GENES_DN C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 42 0.63 1.86 GNATENKO_PLATELET_SIGNATURE C2 42 0.63 1.86 SERVITJA_ISLET_HNF1A_TARGETS_UP C2 45 0.71 1.86 SERVITJA_ISLET_HNF1A_TARGETS_UP C2 162 0.56 1.86 RAGHAVACHARI_PLATELET_SECIFIC_GENES C2 70 0.66 1.86 JACKSON_DNMT1_TARGETS_UP C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 77 0.63 1.86 CHEOK_RESPONSE_TO_HD_MTX_UP C2 112 0.57 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86	LIANG SILENCED BY METHYLATION UP	C2	30	0.65	1.87
DEMAGALHAES_AGING_UP C2 53 0.62 1.07 ZHAN_EARLY_DIFFERENTIATION_GENES_DN C2 53 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 42 0.63 1.86 GNATERKO_PLATELET_SIGNATURE C2 42 0.63 1.86 SWEET_KRAS_TARGETS_UP C2 45 0.71 1.86 SERVITJA_ISLET_HNF1A_TARGETS_UP C2 162 0.56 1.86 RASH_RESPONSE_TO_IONIZING_RADIATION_6 C2 81 0.59 1.86 RAGHAVACHARI_PLATELET_SPECIFIC_GENES C2 70 0.66 1.86 DACKSON_DIMTI_TARGETS_UP C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 77 0.63 1.86 CHEOK_RESPONSE_TO_HD_MTX_UP C2 12 0.57 1.86 CHEOK_RESPONSE_UP C2 12 0.71 1.86	WIERENGA STAT5A TARGETS DN	C2	202	0.52	1.87
ZHAN_EARLY_DIFFERENTIATION_GENES_DN C2 32 0.00 1.00 SWEET_KRAS_TARGETS_UP C2 42 0.63 1.86 GNATENKO_PLATELET_SIGNATURE C2 42 0.63 1.86 SERVITJA_ISLET_INF13_TARGETS_UP C2 45 0.71 1.86 RASHI_RESPONSE_TO_IONIZING_RADIATION_6 C2 162 0.56 1.86 RAGHAVACHAR_PLATELET_SPECIFIC_GENES C2 81 0.59 1.86 JACKSON_DNMT1_TARGETS_UP C2 70 0.66 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 112 0.57 1.86 CHEOK_RESPONSE_TO_ID_MIX_UP C2 22 0.76 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86	DEMAGALHAES AGING UP	C2	53	0.68	1.86
SWEET_KRAS_TARGETS_UP C2 42 0.03 1.00 GNATENKO_PLATELET_SIGNATURE C2 82 0.63 1.86 GNATENKO_PLATELET_SIGNATURE C2 45 0.71 1.86 SERVITJA_ISLET_HNF1A_TARGETS_UP C2 162 0.56 1.86 RASHI_RESPONSE_TO_IONIZING_RADIATION_6 C2 81 0.59 1.86 RAGHAVACHARI_PLATELET_SPECIFIC_GENES C2 70 0.66 1.86 JACKSON_DNMT1_TARGETS_UP C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 77 0.63 1.86 CHEOK_RESPONSE_TO_HD_MTX_UP C2 112 0.57 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86 DER_IEN_ESIGNALUG_PATHWAY C2 102 0.71 1.86	ZHAN EARLY DIFFERENTIATION GENES DN	C.2	42	0.63	1.86
CRATEIRKO_PLATELET_SIGNATURE C2 02 0.03 1.80 GNATEIRKO_PLATELET_SIGNATURE C2 45 0.71 1.86 SERVITJA_ISLET_HNF1A_TARGETS_UP C2 162 0.56 1.86 RASHI_RESPONSE_TO_IONIZING_RADIATION_6 C2 81 0.59 1.86 RAGHAVACHARI_PLATELET_SPECIFIC_GENES C2 70 0.66 1.86 JOCKSON_DNMT1_TARGETS_UP C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 77 0.63 1.86 DER_IFN_BETA_RESPONSE_TO_HD_MTX_UP C2 112 0.57 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86	ISWEET KRAS TARGETS UP	C.2	82	0.63	1.86
SERVITA_ISLET_INF1A_TARGETS_UP C2 10 1.00 RASHI_RESPONSE_TO_ONIZING_RADIATION_6 C2 162 0.56 1.86 RASHI_RESPONSE_TO_ONIZING_RADIATION_6 C2 81 0.59 1.86 RAGHAVACHAR_PLATELET_SPECIFIC_GENES C2 70 0.66 1.86 JACKSON_DNMT1_TARGETS_UP C2 77 0.63 1.86 BOSCO_TH1_CVTOTOXIC_MODULE C2 112 0.57 1.86 CHEOK_RESPONSE_TO_HD_MTX_UP C2 22 0.76 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86	GNATENKO PLATELET SIGNATURE	C2	45	0.00	1.86
RASHI_RESPONSE_TO_IONIZING_RADIATION_6 C2 81 0.59 1.86 RASH_RESPONSE_TO_IONIZING_RADIATION_6 C2 81 0.59 1.86 RAGHAVACHARI_PLATELET_SPECIFIC_GENES C2 70 0.66 1.86 JACKSON_DNMT1_TARGETS_UP C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 112 0.57 1.86 CHEOK_RESPONSE_TO_HD_MTX_UP C2 22 0.76 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86	SERVITJA ISLET HNF1A TARGETS UP	C2	162	0.56	1.86
AGHAVACHARI_PLATELET_SPECIFIC_GENES C2 70 0.66 1.86 JACKSON_DNMT1_TARGETS_UP C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 112 0.57 1.86 CHEOK_RESPONSE_TO_HD_MTX_UP C2 22 0.76 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86 VEGG_CHEMOKING_PATHWAY C2 102 0.71 1.86	RASHI RESPONSE TO IONIZING RADIATION 6	C2	81	0.59	1.86
DACKSON_DNMT1_TARGETS_UP C2 77 0.63 1.86 BOSCO_TH1_CYTOTOXIC_MODULE C2 112 0.57 1.86 CHEOK_RESPONSE_TO_HD_MTX_UP C2 22 0.76 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86 CEG_CHEMOKING_SIGNALING_PATHWAY C2 102 0.71 1.86	RAGHAVACHARI PLATELET SPECIFIC GENES	C2	70	0.66	1.86
BOSCO_TH1_CYTOTOXIC_MODULE C2 11 0.63 1.66 BOSCO_TH1_CYTOTOXIC_MODULE C2 112 0.57 1.86 CHEOK_RESPONSE_TO_HD_MTX_UP C2 22 0.76 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86 KEGG_CHEMOKING_SIGNALING_PATHWAY C2 102 0.71 1.86	JACKSON DNMT1 TARGETS UP	C.2	77	0.63	1.86
CHEOK_RESPONSE_TO_HD_MTX_UP C2 112 0.07 1.00 CHEOK_RESPONSE_TO_HD_MTX_UP C2 22 0.76 1.86 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86 KEGG_CHEMOKING_PATHWAY C2 179 0.55 1.86	BOSCO THI CYTOTOXIC MODULE	C2	112	0.57	1.86
DER_IFN_BETA_RESPONSE_UP C2 100 1.00 DER_IFN_BETA_RESPONSE_UP C2 102 0.71 1.86 KEGG_CHEMOKING_PATHWAY C2 102 0.75 1.86	CHEOK RESPONSE TO HD MTX UP	C2	22	0.76	1.86
CE C2 C1 L00 VEGG CHEMOKINE SIGNALING PATHWAY C2 172 0.55 1.86	DER IFN BETA RESPONSE UP	C2	102	0.71	1.86
	KEGG CHEMOKINE SIGNALING PATHWAY	C.2	179	0.55	1.86

IGLESIAS E2E TARGETS UP	C2	149	0.66	1.86
	C2	253	0.54	1.86
	02	233	0.04	1.00
KEGG_ASTHMA	C2	28	0.69	1.86
REACTOME INTEGRIN CELL SURFACE INTERACTIONS	C2	79	0.63	1.86
MUNSHI MULTIPLE MYELOMA UP	C2	81	0.57	1.86
	C2	28	0.69	1.86
	02	20	0.00	1.00
CROONQUIST_NRAS_SIGNALING_UP	C2	39	0.72	1.86
MORI_SMALL_PRE_BII_LYMPHOCYTE_UP	C2	85	0.55	1.85
PID CD8 TCR PATHWAY	C2	52	0.69	1.85
ICHIBA GRAFT VERSUS HOST DISEASE DZ LIP	C2	107	0.72	1.85
	02	00	0.07	1.00
KEGG_LEISHMANIA_INFECTION	C2	68	0.67	1.85
YAN_ESCAPE_FROM_ANOIKIS	C2	24	0.74	1.85
PID BAC1 PATHWAY	C2	51	0.58	1.85
DEACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	C2	260	0.56	1.95
	02	200	0.00	1.65
BORLAK_LIVER_CANCER_EGF_UP	C2	55	0.65	1.85
REACTOME_TCR_SIGNALING	C2	49	0.69	1.85
BASSO HAIRY CELL LEUKEMIA UP	C2	80	0.63	1 85
	C2	22	0.66	1.05
	02		0.00	1.05
GOLDRATH_ANTIGEN_RESPONSE	C2	337	0.54	1.85
WIELAND UP BY HBV INFECTION	C2	98	0.80	1.85
REACTOME GPVI MEDIATED ACTIVATION CASCADE	C2	30	0.73	1 85
	C2	69	0.60	1.05
	62	00	0.00	1.65
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP	C2	180	0.57	1.85
GUENTHER GROWTH SPHERICAL VS ADHERENT DN	C2	25	0.71	1.84
	C2	65	0.66	1 84
	C2	07	0.60	1.01
	62	67	0.02	1.04
REGG_SMALL_CELL_LUNG_CANCER	C2	84	0.54	1.84
CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN	C2	441	0.57	1.84
RADMACHER AMI PROGNOSIS	C:2	77	0.60	1 8/
	02	400	0.00	1.0+
	62	400	10.0	1.04
KEGG_AUTOIMMUNE_THYROID_DISEASE	C2	48	0.61	1.84
LEE DIFFERENTIATING T LYMPHOCYTE	C2	187	0.68	1.84
HELLER HDAC TARGETS DN	C2	284	0.51	1.8/
	02	204	0.01	1.04
	02	59	0.67	1.84
DIRMEIER_LMP1_RESPONSE_LATE_UP	C2	56	0.70	1.84
PID ILK PATHWAY	C2	45	0.65	1.84
	<u> </u>	100	0.64	1.07
CHAOHAN_RESPONSE_TO_METHOXYESTRADIOL_DN	62	100	0.64	1.64
HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENESIS	C2	80	0.59	1.84
DER IFN ALPHA RESPONSE UP	C2	74	0.74	1.84
WOO LIVER CANCER RECURRENCE UP	C2	105	0.77	1 84
	62	001	0.70	1.04
PEIROVA_PROXI_TARGETS_DN	62	04	0.72	1.64
PID_PI3KCI_PATHWAY	C2	48	0.63	1.84
MA MYELOID DIFFERENTIATION UP	C2	39	0.65	1.84
VANASSE BCL2 TARGETS DN	C2	72	0.51	1 84
	62	50	0.01	1.04
BARIS_IHYROID_CANCER_DN	62	58	0.59	1.84
HE_PTEN_TARGETS_UP	C2	16	0.74	1.84
MORI LARGE PRE BII LYMPHOCYTE DN	C2	57	0.71	1.84
ROSS ACLITE MYELOID LEUKEMIA CBE	C2	70	0.55	1.8/
	62	50	0.00	1.04
IRUSS AME WITH CBEB MITHIL FUSION		201	1100	1 4 /1
	02	00	0.00	1.04
PID_NFAT_3PATHWAY	C2	53	0.60	1.83
PID_NFAT_3PATHWAY KEGG NATURAL KILLER CELL MEDIATED CYTOTOXICITY	C2 C2	53 127	0.60	1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_BESPONSE_TO_CONDOTPODEINS_DN	C2 C2 C2	53 127 87	0.60	1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN ECRONANG_T_AVL_DELTAVL_EDUCATION	C2 C2 C2 C2 C2	53 127 87	0.60 0.60 0.51 0.62	1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP	C2 C2 C2 C2 C2 C2	53 127 87 85	0.60 0.60 0.51 0.62 0.56	1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP	C2 C2 C2 C2 C2 C2 C2 C2	53 127 87 85 132	0.60 0.60 0.51 0.62 0.56 0.54	1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FL11_EUSION_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2	53 127 87 85 132 30	0.60 0.60 0.51 0.62 0.56 0.54 0.64	1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEOPEONTAGE_HSO_MAPKEPS	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2	53 127 87 85 132 30	0.60 0.60 0.51 0.62 0.56 0.54 0.64	1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2	53 127 87 85 132 30 66	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60	1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_EWSRT_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2	53 127 87 85 132 30 66 30	0.60 0.61 0.51 0.62 0.56 0.54 0.64 0.60 0.63	1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TÄRGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79	1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126	0.60 0.61 0.62 0.56 0.54 0.64 0.63 0.79 0.56	1.84 1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASPESTOS_UING_CANCER_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.64 0.60 0.63 0.79 0.56 0.56	1.84 1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN PODUCEL_DATABLESSION_BUCCONCENTER_2	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 28	0.00 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67	1.84 1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.64 0.60 0.63 0.79 0.56 0.67 0.62	$\begin{array}{c} 1.83\\$
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TÄRGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 28 211 17	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.67 0.62 0.77	1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSRT_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.63 0.79 0.56 0.67 0.62 0.77 0.65	1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_CML_RESPONSE_NOT_VIA_P38	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337	$\begin{array}{c} 0.60\\ 0.60\\ 0.51\\ 0.62\\ 0.56\\ 0.54\\ 0.64\\ 0.60\\ 0.63\\ 0.79\\ 0.56\\ 0.67\\ 0.62\\ 0.77\\ 0.62\\ 0.77\\ 0.65\\ 0.51\\ \end{array}$	1.04 1.83 1.82 1.83 1
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JCARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 25	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.64 0.63 0.79 0.56 0.67 0.62 0.67 0.62 0.77	1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405	$\begin{array}{c} 0.60\\ 0.60\\ 0.51\\ 0.62\\ 0.56\\ 0.54\\ 0.64\\ 0.60\\ 0.63\\ 0.79\\ 0.56\\ 0.67\\ 0.62\\ 0.77\\ 0.65\\ 0.51\\ 0.58\\ \end{array}$	$\begin{array}{c} 1.64\\ 1.83\\ 1.82\\$
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TÄRGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER 2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307	$\begin{array}{c} 0.60\\ 0.60\\ 0.51\\ 0.62\\ 0.56\\ 0.54\\ 0.64\\ 0.60\\ 0.63\\ 0.79\\ 0.56\\ 0.67\\ 0.62\\ 0.77\\ 0.65\\ 0.51\\ 0.58\\ 0.61\\ \end{array}$	1.04 1.83 1.82 1.82 1.82 1.82 1.82 1.82
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1F_USION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILÜRE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU RESPONSE_TO_TRETINOIN AND NSC682994_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17	$\begin{array}{c} 0.60\\ 0.60\\ 0.51\\ 0.62\\ 0.56\\ 0.54\\ 0.64\\ 0.60\\ 0.63\\ 0.79\\ 0.56\\ 0.67\\ 0.62\\ 0.77\\ 0.66\\ 0.51\\ 0.58\\ 0.61\\ 0.79\\ \end{array}$	1.04 1.83 1.82
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_1OT_TRETINOIN_AND_NSC682994_UP VAIK AML_CLUSTER_4	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.65 0.67 0.65 0.51 0.58 0.51 0.58 0.61 0.79	1.04 1.83 1.82 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 PEACTOME	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 50	$\begin{array}{c} 0.60\\ 0.60\\ 0.51\\ 0.62\\ 0.56\\ 0.54\\ 0.64\\ 0.60\\ 0.63\\ 0.79\\ 0.56\\ 0.67\\ 0.62\\ 0.77\\ 0.65\\ 0.51\\ 0.58\\ 0.61\\ 0.79\\ 0.69\\$	1.83 1.82 1.83 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCEN_DN PHONG_TIF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING HEONWRENT_DN_ADD_NSC68204_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 59	$\begin{array}{c} 0.60\\ 0.60\\ 0.51\\ 0.62\\ 0.56\\ 0.54\\ 0.64\\ 0.60\\ 0.63\\ 0.79\\ 0.56\\ 0.67\\ 0.62\\ 0.77\\ 0.65\\ 0.67\\ 0.62\\ 0.51\\ 0.58\\ 0.61\\ 0.79\\ 0.69\\$	$\begin{array}{c} 1.64\\ 1.83\\ 1.82\\$
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JJ_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEAT_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 FRACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61	$\begin{array}{c} 0.60\\ 0.60\\ 0.51\\ 0.62\\ 0.56\\ 0.54\\ 0.64\\ 0.60\\ 0.63\\ 0.79\\ 0.56\\ 0.67\\ 0.65\\ 0.67\\ 0.65\\ 0.51\\ 0.58\\ 0.61\\ 0.79\\ 0.68\\ 0.68\\ 0.68\\ 0.65\\ \end{array}$	$\begin{array}{c} 1.64\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.82\\$
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TIF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILÜRE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROLE_CORRELATED_WITH_LS_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.63 0.67 0.62 0.77 0.62 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.61 0.79 0.68 0.61 0.79 0.68 0.62 0.51 0.55 0.51 0.55 0.51 0.55 0.51 0.55 0.51 0.55 0.62 0.51 0.55 0.55 0.51 0.62 0.55 0.55 0.55 0.55 0.65 0.62 0.55 0.55 0.55 0.65 0.65 0.65 0.65 0.68 0.65 0.59	1.83 1.82 1.82
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IL5_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.65 0.51 0.51 0.58 0.61 0.79 0.68 0.69 0.68 0.69 0.68 0.69 0.69 0.59 0.59 0.58 0.51 0.51 0.54 0.54 0.54 0.54 0.54 0.54 0.54 0.54 0.54 0.55 0.54 0.55 0	1.04 1.83 1.82 1
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRËSSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_EWSRT_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IL5_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.69 0.69 0.69 0.69 0.69 0.69 0.77 0.69 0.69 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.77 0.69 0.69 0.77 0.69 0.77 0.69 0.69 0.77 0.69 0.77 0.69 0.69 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.69 0.77 0.69 0.69 0.69 0.77 0.69 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.77 0.69 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0	1.83 1.82 1.82
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_ILS_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.69 0.77 0.77 0.77 0.77 0.77 0.77	1.04 1.83 1.82 1.83
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINION_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_ILS_UP NIELSEN_LEIOMINOS_ARCOMA_CNIN_DN GILDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.65 0.67 0.65 0.51 0.51 0.58 0.61 0.79 0.69 0.68	1.04 1.83 1.82
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WKMAN_ASBESTOS_UNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TIF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_LS_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN GRUDAM_NS_NOCRASC_DUP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.63 0.69 0.68 0.65 0.59 0.77 0.66 0.69 0.63	$\begin{array}{c} 1.64\\ 1.83\\ 1.82\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.81\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.83\\ 1.82\\$
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IL5_UP NIELSEN_LEIOMYOSARCOMA_CNI1_DN GILDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSPCRMATION_KRAS_CDC25_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.66 0.67 0.67 0.65 0.51 0.51 0.58 0.61 0.79 0.68 0.69 0.68 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.63 0.77 0.63 0.77 0.63 0.77 0.63 0.77 0.63 0.77 0.63 0.77 0.77 0.63 0.77 0.77 0.63 0.77 0.77 0.77 0.77 0.63 0.77 0	1.04 1.83 1.82 1.81 1.81
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILÜRE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINION_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROLEC_CORRELATED_WITH_LS_UP NIELSEN_LEIOMYOSARCOMA_CNIN_DN GILDEA_METASAISIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.63 0.67 0.62 0.77 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.67 0.69 0.77 0.65 0.51 0.79 0.62 0.77 0.65 0.51 0.79 0.62 0.77 0.65 0.51 0.79 0.65 0.61 0.77 0.62 0.79 0.65 0.51 0.79 0.62 0.77 0.65 0.51 0.62 0.61 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.64 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.63 0.76 0.69 0.68 0.69 0.69 0.68 0.69 0.69 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.68 0.69 0.68 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68 0.69 0.68	1.04 1.83 1.82 1.84 1
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IL5_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN GILDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEC = AMPLOTY_T_TANSPLANT_MEDICE_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 57	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.68 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.77 0.63 0.77 0.69 0.77 0.69 0.77 0.63 0.77 0.69 0.77 0.69 0.77 0.63 0.79 0.66 0.69 0.79 0.66 0.67 0.62 0.79 0.66 0.67 0.62 0.77 0.65 0.51 0.51 0.67 0.62 0.77 0.65 0.51 0.51 0.67 0.62 0.77 0.65 0.51 0.51 0.51 0.55 0.51 0.55 0.51 0.55 0.51 0.55 0.67 0.65 0.55 0.51 0.66 0.66 0.67 0.62 0.77 0.65 0.65 0.67 0.66 0.66 0.67 0.65 0.55 0.55 0.55 0.67 0.66 0.66 0.67 0.66 0.67 0.65 0.55 0.55 0.67 0.66 0.67 0.66 0.66 0.66 0.66 0.66 0.66 0.67 0.66 0.66 0.67 0.66 0.66 0.67 0.66 0.67 0.66 0.66 0.67 0.66 0.67 0.66 0.67 0.67 0.66 0.66 0.67 0.67 0.67 0.66 0.67 0.67 0.67 0.69 0.67 0.66 0.66 0.76 0.77 0.66 0.77 0.66 0.77 0.66 0.77 0.66 0.77 0.67 0.77 0.77 0.67 0.77 0.77 0.67 0.77 0.77 0.67 0.77 0.77 0.67 0.77 0.77 0.67 0.77 0.67 0.77	1.04 1.83 1.82 1.81
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_EWSRT_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_ILS_UP NIELSEN_LEIOMYOSARCOMA_CN1_DN GILDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SK1_TARGETS_UP SNIJDERS_UP_LSTANSFORMATION_KRAS_CDC25_UP LE_EARLETS_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.65 0.67 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.68 0.69 0.63 0.77 0.69 0.63 0.77 0.69 0.63 0.77 0.69 0.63 0.77 0.69 0.63 0.77 0.69 0.63 0.77 0.69 0.63 0.77 0.69 0.68 0.59 0.77 0.69 0.69 0.63 0.77 0.69 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.77 0.69 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.69 0.77 0.77 0.77 0.69 0.77 0.69 0.77 0.77 0.77 0.77 0.69 0.77 0.77 0.69 0.63 0.77 0.77 0.69 0.66 0.77 0.77 0.69 0.66 0.77 0.77 0.69 0.66 0.77 0.77 0.69 0.66 0.77 0.77 0.69 0.66 0.77 0.77 0.69 0.66 0.77 0.77 0.66 0.77 0.66 0.77 0.76 0.66 0.77 0.76 0.76 0.77 0.76 0.77 0.76 0.76 0.77 0.76 0.77 0.76 0.77 0.76 0.76 0.77 0.76 0.77 0.76 0.76 0.77 0.76 0.77 0.76 0.77 0.76 0.77 0.77 0.76 0.77 0.77 0.76 0.77 0.77 0.76 0.77 0.77 0.76 0.77 0.77 0.77 0.76 0.77 0.77 0.77 0.76 0.76 0.77 0.77 0.77 0.76 0.77 0.77 0.77 0.77 0.76 0.77 0	1.04 1.83 1.82 1.81 1.81 1.81
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_LS_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN GILDEA_METASISS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NCOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEF_EARLY_T_LYMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE	$\begin{array}{c} 0.2 \\$	53 127 87 85 132 30 66 30 15 126 211 17 90 337 405 307 17 28 59 61 49 20 37 37 57 17 37 54 141	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.62 0.77 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.69 0.69 0.69 0.67 0.69 0.69 0.67 0.69 0.67 0.69 0.69 0.77 0.65 0.77 0.65 0.54 0.65 0.54 0.67 0.62 0.77 0.65 0.67 0.62 0.77 0.65 0.65 0.54 0.67 0.62 0.77 0.65 0.65 0.51 0.65 0.51 0.65 0.55 0.67 0.65 0.55 0.67 0.65 0.65 0.55 0.65 0.55 0.65 0.65 0.55 0.65 0.77 0.65 0.65 0.65 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.77 0.77 0.65 0.77 0.77 0.77 0.77 0.65 0.77 0.77 0.77 0.77 0.63 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.77 0.65 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.77 0.77 0.65 0.77 0.77 0.77 0.65 0.77 0.77 0.77 0.77 0.65 0.77 0.77 0.77 0.77 0.77 0.77 0.77 0.77 0.57 0.57	1.83 1.82 1.81 1.81 1.81 1.81 1.81 1.81
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IL5_UP NIELESEN_LEIOMINOS_ARCOMA_CON1_DN GILDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSPCRMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_LYMPHOCD_TTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID FCERL PATHWAY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54 141 60	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.65 0.51 0.51 0.51 0.58 0.61 0.79 0.68 0.69 0.68 0.69 0.68 0.69 0.63 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.77 0.77 0.65 0.59 0.77 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.77 0.77 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.57 0.77 0.77 0.65 0.57 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.57 0.57 0.65 0.57 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0	1.04 1.83 1.82 1.81 1.81 1.81 1.81 1.81 1.81
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILÜRE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINON_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROLECM_CORRELATED_WITH_LS_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN GILDEA_METASISS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKL_TARGETS_UP BOCABTA_MEST	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54 141 60 18	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.69 0.68 0.65 0.59 0.77 0.77 0.66 0.65 0.59 0.77 0.77 0.66 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.77 0.65 0.59 0.77 0.69 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.77 0.69 0.69 0.65 0.77 0.69 0.69 0.65 0.77 0.69 0.69 0.66 0.77 0.69 0.69 0.66 0.77 0.69 0.69 0.66 0.77 0.69 0.66 0.77 0.69 0.66 0.77 0.69 0.66 0.77 0.69 0.66 0.77 0.69 0.66 0.77 0.69 0.77 0.69 0.66 0.77 0.77 0.69 0.66 0.77 0.69 0.77 0.69 0.77 0.77 0.69 0.77	1.04 1.83 1.82 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IL5_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN GILDA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNJIDERS_AMPLFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLYT_LYMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FORET_PATHWAY BIOCARTA_MECTER_DATHWAY BIOCARTA_MECTER_DATHWAY BIOCARTA_MECTER_DATHWAY BIOCARTA_MECTER_DATHWAY BIOCARTA_MECTER_DATHWAY BIOCARTA_MEFERON_GAMMA_SIGNALING FLECEN_PARL_KIDNEY_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLYT_LYMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCER_PATHWAY BIOCARTA_MEFERON_FCENTER	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54 141 60 18	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.68 0.69 0.69 0.69 0.69 0.69 0.69 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.66 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.57 0.65 0.57 0.55 0.51 0.55 0.51 0.55 0.51 0.55 0.55 0.55 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.55 0.57 0.55 0.57 0.65 0.57 0.55 0.57 0.55 0.57 0.65 0.57 0.55 0.57 0.55 0.57 0.55 0.57 0.55 0.57 0.55 0.57 0.55 0.57 0.57 0.55 0.57 0.66 0.72 0.65 0.72 0.65 0.72 0.65 0.72 0.57 0.57 0.65 0.72 0.57 0.65 0.72 0.57 0	1.04 1.83 1.82 1.81
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_ILS_UP NIELSEN_LEIOMYOSARCOMA_CNIN_DN GILDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCERT_NATASIS	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 30 20 57 17 37 54 141 60 18 59	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.66 0.51 0.51 0.58 0.61 0.79 0.68 0.65 0.59 0.77 0.69 0.63 0.77 0.69 0.63 0.77 0.69 0.59 0.77 0.69 0.63 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.72 0.72 0.55 0.75 0.55 0.75 0.55 0.75 0.55 0.75 0.55 0.75 0.55 0.75 0.55 0.75 0.55 0.75 0.55 0	1.034 1.83 1.82 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_POGFB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_LS_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN GRIDER_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSPCRMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCER1_PATHWAY BIOCARTA_METASTASIS CROONQUIST_L6_DEPRIVATION_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SALTARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SALTARGETS_HANYA	$\begin{array}{c} 0.2 \\$	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54 141 60 18 59 35	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.69 0.77 0.69 0.69 0.77 0.65 0.77 0.69 0.69 0.77 0.65 0.77 0.69 0.69 0.77 0.65 0.77 0.65 0.51 0.51 0.54 0.54 0.67 0.62 0.77 0.65 0.51 0.55 0.51 0.55 0.51 0.55 0.51 0.55 0.51 0.55 0.51 0.55	1.83 1.82 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81
PID_INFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP J_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEAT_FALLURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINON_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_ILS_UP NIELSEN_LEIOMYOSARCOMA_CINIT_DN GILDEA_METASISS GROONQUIST_ILG_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_LWMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCR_1_PATHWAY SISAEVA_MLL2_TARGETS SNIJNERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_FARLY_T_LWMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCR1_PATHWAY SISAEVA_MLL2_TARGETS HAN_JNK_SINGALING_UP OSMAN BLADDER_CANCER DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 54 141 60 18 59 35 376	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.66 0.51 0.58 0.61 0.79 0.68 0.61 0.79 0.68 0.65 0.59 0.77 0.77 0.69 0.63 0.77 0.66 0.77 0.79 0.66 0.77 0.65 0.51 0.51 0.51 0.51 0.51 0.51 0.56 0.57 0.62 0.57 0.62 0.57 0.65 0.51 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.58 0.67 0.79 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.57 0.59 0.66 0.57 0.59 0.77 0.66 0.59 0.77 0.65 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.59 0.77 0.66 0.57 0.57 0.69 0.66 0.57 0.57 0.69 0.66 0.57 0.66 0.57 0.59 0.66 0.57 0.66 0.59 0.66 0.57 0.69 0.66 0.57 0.69 0.66 0.59 0.66 0.57 0.69 0.66 0.57 0.69 0.66 0.57 0.69 0.66 0.57 0.69 0.66 0.57 0.66 0.65 0.57 0.66 0.65 0.57 0.66 0.66 0.72 0.66 0.65 0.72 0.66 0.72 0.65 0.72 0.65 0.72 0.59 0.65 0.72 0.59 0.65 0.72 0.59 0.68 0.65 0.72 0.59 0.65 0.72 0.59 0.68 0.65 0.72 0.59 0.68 0.65 0.59 0.72 0.59 0.68 0.65 0.72 0.59 0.68 0.65 0.59 0.72 0.59 0.68 0.59 0.68 0.59 0.72 0.59 0.68 0.68 0.59 0.59 0.66 0.59 0.59 0.59 0.59 0.68 0.59 0.59 0.59 0.68 0.59 0.59 0.68 0.59 0.59 0.68 0.59 0.59 0.68 0.59 0.59 0.68 0.55 0.55	1.83 1.82 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81 1.81
PID_NFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_EN_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP J_CARCINOGENESIS_BY_KRAS_ND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_ILS_UP NIELSEN_LEOMYOSARCOMA_CNN1_DN GILDEA_METASTASIS CROONQUIST_IL6_DERRIVATION_UP CHIARADONNA_NEEDPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LES_SKI_TARGETS_UP SNUDERS_MPLIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_MPLIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_LYMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCER1_PATHWAY BIOCARTA_MEEDPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LES_SKI_TARGETS_UP SNUDERS_MPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_MPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_MPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_MMELIZERSEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCER1_PATHWAY BIOCARTA_MEEZD_PATHWAY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54 141 60 18 59 35 376	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.66 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.69 0.69 0.63 0.77 0.65 0.77 0.77 0.65 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.77 0.65 0.77 0.77 0.77 0.65 0.77 0.77 0.77 0.65 0.77 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.77 0.65 0.77 0.65 0.77 0.77 0.65 0.77 0.65 0.77 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.59 0.57 0.57 0.65 0.57 0.57 0.65 0.57 0.57 0.65 0.57 0.57 0.65 0.55 0.55 0.77 0.65 0.55 0.55 0.72 0.55 0.55 0.55 0.55 0.72 0.55 0.55 0.55 0.55 0.72 0.55 0.55 0.55 0.55 0.55 0.55 0.66 0.55 0.55 0.55 0.66 0.55 0.55 0.55 0.66 0.55 0.55 0.66 0.55 0.55 0.66 0.55 0.55 0.66 0.55 0	1.04 1.83 1.82 1.81
PID_INFAT_3PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_EN_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP J_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINON_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IDS_UP NIELSEN_LEIOMYOSARCOMA_CIN1_DN GILDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNJIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_LYMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCERT_NARSEN_SUP BIOCARTA_MEED_LATARGETS HAN_JNK_SINGALING_UP DISCRASE_NOPTIANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNJIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_LYMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCERT_PATHWAY BIOCARTA_MEEP2D_PATHWAY BIOCARTA_MEEP2D_PATHWAY BIOCARTA_MEEP2D_PATHWAY BIOCARTA_MEEP2D_PATHWAY BIOCARTA_MEEP2D_FATHWAY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 30 20 30 20 30 20 30 20 30 20 30 20 30 20 30 20 30 20 30 377 54 18 59 35 376 33 33	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.65 0.51 0.51 0.51 0.51 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.63 0.77 0.65 0.54 0.79 0.65 0.51 0.54 0.57 0.65 0.57 0.65 0.54 0.57 0.65 0.51 0.58 0.67 0.65 0.51 0.58 0.54 0.55 0.65 0.55 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.66 0.55 0.65 0.55 0.66 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0	1.04 1.83 1.82 1.81
PID INFAT_SPATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_EVENT_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JJ_CARCINOGENESIS BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINON_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IL5_UP NIELSEN_EIOMYOSARCOMA_CNN1_DN GILDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSPLANT_RAS_CDC25_UP LE_SKI_TARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SALT_TYMPHOCYTE_DN BOSCO_ALLERGEN_NOCUTAL_AND_NECK_TUMORS LEE_SALT_PATHWAY BIOCARTA_METAD_NECK_TUMORS LEE_SALT_PATHWAY BIOCARTA_METAD_NAVA SINGALING_UP OSMAN_BLADDER_CANCER_DN EXACUTATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LESNLET_DN SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SALT_PATHWAY BIOCARTA_METAD_NAVA SINGALING_UP OSMAN_BLADDER_CANCER_DN EXACUTATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LESNLE_TARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SALT_TYMPHOCYTE_DN BOSCO_ALLEGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCER1_PATHWAY BIOCARTA_METAD_PATHWAY BIOCARTA_METAD_PATHWAY BIOCARTA_METAD_PATHWAY BIOCARTA_METAD_PATHWAY BIOCARTA_NERS_CDC2E_UP CANTATION_UP CHIARADONNA_NECK_TUMORS LEE_SALT_TYMPHOCYTE_DN BOSCO_ALLEGENS_NAMA_NECK_TUMORS LEE_SALT_TYMPHOCYTE_DN BOSCO_ALLEGENS_NAMA_NECK_TUMORS LEE_SALT_TYMPHOCYTE_DN BIOCARTA_METAD_TARS_DADA_NE_NECHTUMATS BIOCARTA_METAD_PATHWAY BIOCARTA_NERS_DADA_NE_NECHTUMANANANANANANANANANANANANANANANANANANAN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 30 20 57 17 30 20 57 17 37 54 141 60 18 59 35 376 33 76	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.77 0.65 0.51 0.58 0.61 0.77 0.69 0.63 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.59 0.63 0.77 0.65 0.55 0.55 0.77 0.65 0.55 0.55 0.55 0.55 0.65 0.77 0.65 0.55 0.55 0.55 0.55 0.65 0.77 0.65 0.55 0.55 0.55 0.55 0.55 0.55 0.55 0.65 0.77 0.65 0.55 0.66 0.55 0.55 0.66 0.55 0.55 0.66 0.55 0.66 0.55 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.66 0.66 0.55 0.66 0.55 0.66 0.66 0.66 0.55 0.66 0.66 0.66 0.55 0.66 0.66 0.66 0.66 0.66 0.66 0.55 0.66 0	1.83 1.82 1.81 1.81
PID INFAT_\$PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP J_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIONEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WTH_LIS_UP NIELSEN_LEIOMYOSARCOMA_CNIN_DN GILDEA_METASTASIS CROONQUST_ILG_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSPCANTION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTALON_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTALON_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTALON_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTALON_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTALON_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTALON_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTALON_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSPCANTION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDBERS_MOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS HAN_JNK_SINGALING_UP OSMAN BLADDER_CANCER_DN REACTOME_OMISTREAM_TCR_SIGNALING FRIDMAN_SLADDER_CANCER_DN REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	$\begin{array}{c} 0.2 \\$	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 30 20 30 20 30 20 30 20 30 20 30 20 30 20 30 20 30 20 30 30 4141 60 18 59 3376 337 31	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.69 0.63 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.59 0.72 0.56 0.63 0.79 0.66 0.69 0.77 0.65 0.55 0.65 0.55 0.55 0.65 0.55 0.55 0.55 0.55 0.65 0.55 0.55 0.65 0.55 0.65 0.55 0.66 0.66 0.55 0.66 0.66 0.55 0.66 0.66 0.66 0.55 0.66 0.66 0.66 0.66 0.55 0.66 0.66 0.66 0.66 0.66 0.55 0.66 0.56 0	1.83 1.82 1.81 1.81
PID INFAT_SPATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_EVENT_FL11_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JJ_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINON_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IL5_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN GILDEA_MERTSATSIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SK	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 30 20 57 17 30 20 57 17 37 54 141 60 18 59 35 376 33 76 51 170	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.66 0.67 0.62 0.77 0.66 0.67 0.65 0.51 0.58 0.61 0.79 0.68 0.65 0.51 0.79 0.66 0.65 0.51 0.79 0.66 0.65 0.51 0.77 0.65 0.51 0.79 0.66 0.65 0.51 0.77 0.65 0.65 0.51 0.77 0.65 0.65 0.51 0.77 0.65 0.65 0.51 0.77 0.65 0.65 0.51 0.77 0.65 0.65 0.51 0.77 0.65 0.55 0.51 0.77 0.65 0.59 0.77 0.65 0.65 0.77 0.65 0.59 0.72 0.55 0.55 0.72 0.65 0.72 0.55 0.66 0.72 0.68 0.72 0.68 0.72 0.68 0.72 0.68 0.72 0.68 0.72 0.68 0.72 0.68 0.72 0.68 0.72 0.66 0.72 0.66 0.66 0.72 0.66 0.66 0.72 0.66 0.66 0.72 0.66 0.66 0.77 0.65 0.66 0.72 0.68 0.66 0.67 0.68 0.72 0.68 0.66 0.67 0.66 0.72 0.68 0.66 0.66 0.66 0.66 0.67 0.66 0.66 0.66 0.66 0.66 0.66 0.66 0.66 0.66 0.66 0.66 0.66 0.66 0.66 0.67 0.66 0.65 0.66 0.66 0.66 0.66 0.66 0.67 0.66 0.66 0.66 0.66 0.66 0.66 0.67 0.66 0.66 0.66 0.67 0.66 0.67 0.66 0.66 0.66 0.67 0.67 0.66 0.66 0.66 0.66 0.67 0.67 0.66 0.66 0.66 0.67 0.67 0.66 0.66 0.67 0.67 0.66 0.66 0.67 0.74 0.67 0.66 0.66 0.67 0.77 0.65 0.66 0.66 0.67 0.77 0.65 0.66 0.67 0.77 0.65 0.66 0.67 0.77 0.65 0.66 0.67 0.77 0.65 0.66 0.67 0.77 0.65 0.66 0.67 0.77 0.65 0.67 0.77 0.65 0.67 0.77 0.65 0.67 0.77 0.65 0.67 0.77 0.65 0.67 0.77 0.77 0.55 0.66 0.77 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55	1.83 1.82 1.81 1.81
PID INFAT_SPATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS_OF_PUSNST_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER_2 RAY_TARGETS_OF_PUID_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JJ_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_L5_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN GILDEA_METASISS CROONQUIST_IL6_DEPRIVATION_UP CHARADONAN_NEOPLASTIC_TRANSPCRMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLYT_TY_WMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCER_1PATHWAY BSAEVA_MLL2_TARGETS HAN_JNK_SINGALING_END_NECK_TUMORS LEE_FARLYT_Y_WMPHORYTE	C2	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54 141 60 18 59 35 376 33 76 51 170	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.63 0.79 0.65 0.51 0.58 0.61 0.79 0.68 0.65 0.51 0.58 0.64 0.77 0.65 0.51 0.58 0.67 0.62 0.77 0.65 0.51 0.58 0.67 0.62 0.77 0.65 0.51 0.51 0.55 0.67 0.62 0.77 0.65 0.51 0.55 0.51 0.55 0.51 0.55 0.51 0.55 0.55 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.57 0.65 0.59 0.77 0.66 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.66 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.66 0.77 0.65 0.77 0.69 0.77 0.69 0.77 0.66 0.77 0.65 0.77 0.69 0.77 0.66 0.77 0.66 0.77 0.65 0.77 0.66 0.77 0.66 0.77 0.66 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.75 0.66 0.75 0.66 0.55 0.66 0.66 0.55 0.66 0.66 0.66 0.55 0.66 0.66 0.66 0.66 0.55 0.66 0.66 0.66 0.65 0.55 0.66 0.66 0.65 0.66 0.66 0.65 0.55 0.66 0.66 0.66 0.65 0.66 0.66 0.66 0.65 0.65 0.66 0.65 0.65 0.66 0.65 0.66 0.65 0.65 0.66 0.65 0.65 0.65 0.66 0.65 0.65 0.65 0.66 0.65 0.65 0.65 0.66 0.65 0.65 0.65 0.65 0.65 0.66 0.65 0.66 0.66 0.65 0.55 0.66 0.65 0.55 0.66 0.65 0.55 0.66 0.65 0.55 0.66 0.65 0.55 0.55 0.66 0.66 0.65 0.55 0.55 0.66 0.65 0.55 0.55 0.66 0.65 0.55 0.55 0.55 0.55 0.66 0.65 0.55	1.83 1.82 1.81 1.84 1
PID_NFAT_3PATHWAY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 54 141 60 18 59 33 76 51 170 111 20	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.66 0.67 0.51 0.58 0.61 0.77 0.65 0.51 0.79 0.68 0.65 0.67 0.79 0.68 0.67 0.79 0.68 0.69 0.69 0.63 0.77 0.69 0.69 0.69 0.69 0.65 0.69 0.65 0.65 0.65 0.65 0.59 0.77 0.66 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.66 0.65 0.57 0.65 0.59 0.77 0.65 0.59 0.77 0.66 0.59 0.77 0.65 0.59 0.77 0.65 0.57 0.65 0.59 0.77 0.66 0.65 0.57 0.65 0.59 0.77 0.66 0.59 0.77 0.69 0.66 0.57 0.66 0.57 0.66 0.59 0.77 0.69 0.66 0.57 0.66 0.66 0.65 0.59 0.77 0.69 0.66 0.65 0.59 0.77 0.69 0.66 0.59 0.65 0.77 0.69 0.66 0.72 0.59 0.66 0.72 0.59 0.68 0.65 0.72 0.59 0.68 0.65 0.72 0.69 0.68 0.66 0.72 0.69 0.68 0.66 0.65 0.72 0.69 0.66 0.66 0.66 0.66 0.66 0.66 0.65 0.66 0.67 0.65 0.66 0.66 0.66 0.66 0.67 0.66	1.83 1.82 1.81 1.81
PID_NFAT_3PATHWAY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54 141 60 18 59 35 376 33 76 51 170 111 89	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.69 0.69 0.69 0.69 0.63 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.54 0.51 0.77 0.65 0.51 0.77 0.65 0.51 0.77 0.65 0.51 0.77 0.65 0.55 0.65 0.77 0.65 0.55 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.55 0.72 0.55 0.66 0.55 0.55 0.66 0.55 0.66 0.55 0.55 0.66 0.55 0.55 0.66 0.55 0.66 0.55 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.55 0.66 0.66 0.55 0.55 0.66 0.55 0.66 0.55 0.66 0.55 0.55 0.66 0.55 0.66 0.55 0.55 0.66 0.55 0.55 0.66 0.55 0.55 0.66 0.55 0.55 0.66 0.55 0.55 0.55 0.66 0.55 0.55 0.55 0.55 0.66 0.55 0.55 0.55 0.66 0.55 0.55 0.55 0.55 0.66 0.55	1.83 1.82 1.81 1.81
PID_NFAT_\$PATHWAY PID_VEAT_\$PATHWAY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MIL_ENL_FUSION_UP RORE_TARGETS_OF_EVENT_FLIT_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA_CLUSTER 2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP J_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DVIDING_VS_NORMAL_QUIESCENT_DN PHOMG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FAILURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINON_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WTH_LIS_UP NIELSEN_LEIOMYOSARCOMA_CNIN_DN GILDEA_METASTASIS CORONQUIS_IL6_DEPRIVATION_UP CHARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SAN_TARGETS_UP SNIDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_LYMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCERT_PATHWAY BIOCARTA_ATEGTS HAN_NIK_SINGALING FRICHMENT	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 337 405 307 17 28 59 61 49 20 30 20 57 17 33 66 49 20 30 20 57 17 54 141 60 18 59 35 376 33 76 51 170 111 89 85	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.51 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.69 0.69 0.69 0.67 0.69 0.69 0.69 0.77 0.65 0.59 0.67 0.69 0.69 0.67 0.69 0.69 0.67 0.69 0.69 0.69 0.77 0.65 0.59 0.67 0.65 0.51 0.55 0.51 0.55 0.51 0.55 0.67 0.65 0.55 0.55 0.55 0.55 0.55 0.55 0.66 0.77 0.65 0.59 0.67 0.65 0.77 0.65 0.55 0.55 0.55 0.59 0.67 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.69 0.63 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.69 0.77 0.65 0.77 0.69 0.77 0.65 0.77 0.69 0.77 0.65 0.77 0.69 0.77 0.65 0.77 0.69 0.72 0.65 0.72 0.65 0.72 0.66 0.72 0.66 0.66 0.72 0.66 0.66 0.72 0.66 0.66 0.66 0.72 0.66 0.66 0.66 0.66 0.66 0.72 0.66 0.65	1.034 1.83 1.82 1.81
PID_NFAT_\$PATHWAY KEGG NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMADT_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLIT_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN_B_CELL_LYMPHOMA CLUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JJ_CARCINOGENESIS_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FALLURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC882994_UP VALK_AML_CUISTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_LS_UP NIELSEN_LEIOMYOSARCOMA_CN11_DN GLDEA_METSTASIS CROONQUIST_L6_DEPRIVATION_UP CHURARDONNA_NOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_UP SNUDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_SKI_TARGETS_Z_DIN_ SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_DN SNAN_BLADER_CANCER_SUNTYAL_DN SNAN_BLADER_CANCER_SUNTYAL_DN SNAN_BLADER_	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 30 20 57 17 33 76 33 76 51 170 111 89 85 16	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.77 0.65 0.51 0.58 0.61 0.77 0.65 0.59 0.66 0.65 0.77 0.65 0.59 0.67 0.65 0.59 0.66 0.65 0.77 0.65 0.59 0.66 0.65 0.77 0.65 0.59 0.65 0.77 0.65 0.65 0.77 0.65 0.55 0.77 0.65 0.55 0.55 0.65 0.77 0.65 0.65 0.77 0.65 0.55 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.66 0.65 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.55 0.77 0.65 0.77 0.65 0.55 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.75 0.65 0.75 0.55 0.55 0.55 0.55 0.55 0.55 0.66 0.55 0.66 0.55 0.55 0.66 0.65 0.65 0.65 0.65 0.77	1.83 1.82 1.81 1.81
PID_NFAT_3PATHWAY KEGG NATURAL KILLER CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PARGAS_TUMORS_SUPPESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN B_CELL_IYMPHOMA CLUSTER 2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TINF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FALURE_UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_IL5_UP NIELSEN_LEIOMYOSARCOMA_CN11_DN GILDEA_METASTASIS CROONQUIST_LG_DEPRIVATION_UP CHIARADONIA_NED_NECK_TUMORS LEE_SKI_TARGETS_UP SNILDERS_DATE_TC_TRANSPLANT_REJECTED_VS_OK_UP BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCET_DEPRIVATION_UP CHIARADONIA_NEDPLASTIC_TRANSPLANT_REJECTED_VS_OK_UP BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCET_TARSTASIS CROONQUIST_LG_DEPRIVATION_UP CHIARADONIA_NEDPLASTIC_TRANSPLANT_REJECTED_VS_OK_UP BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCET_TARMSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNILDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_UMPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCET_PATHWAY BIOCARTA_MEF2D_PATHWA	C2	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 300 20 57 17 37 54 141 60 18 59 3376 337 76 51 170 111 89 85 16 362	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.69 0.69 0.69 0.69 0.69 0.69 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.66 0.77 0.65 0.59 0.77 0.66 0.77 0.65 0.51 0.55 0.64 0.55 0.51 0.55 0.66 0.77 0.65 0.55 0.51 0.55 0.55 0.66 0.77 0.65 0.55 0.66 0.72 0.65 0.72 0.66 0.72 0.65 0.72 0.65 0.72 0.66 0.74 0.55 0.66 0.72 0.65 0.66 0.74 0.55 0.66 0.65 0.72 0.65 0.66 0.74 0.55 0.66 0.66 0.65 0.74 0.55 0.66 0.66 0.65 0.74 0.55 0.66 0.65 0.74 0.55 0.66 0.65 0.74 0.55 0.66 0.62 0.74 0.56 0.62 0.77 0.62 0.77 0.62 0.62 0.77 0.77 0.77 0.66 0.66 0.66 0.74 0.55 0.66 0.62 0.77 0.77 0.77 0.77 0.77 0.65 0.66 0.62 0.77 0.77 0.77 0.77 0.62 0.77 0.77 0.77 0.65 0.66 0.62 0.77 0.77 0.77 0.77 0.77 0.65 0.62 0.77 0.77 0.77 0.77 0.77 0.77 0.77 0.62 0.62 0.77	1.04 1.83 1.82 1.81
PID_NFAT_SPATHWAY PID_NFAT_SPATHWAY PID_NFAT_SPATHWAY KEGG NATURAL KILLER CELL MEDIATED_CYTOTOXICITY SASSON RESPONSE TO G ONADOTROPHINS_DN FERRANDO_T_ALL WITH MLL_ENL_FUSION_UP PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORE_TARGETS OF_EWSR1FLI1_FUSION_UP GEORGANTAS HSC_MARKERS SHIN B_CELL_IYMPHOMA CLUSTER 2 RAY_TARGETS OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER DN RODWELL AGING KIDNEY_NO_BLOOD_UP J] CARCINOGENESIS BY KRAS_AND_STK11_DN GRAHAM_CML_DIVDING_VS_NORMAL_QUESCENT_DN PHONG_TNF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART FAILURE UP DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CULSTER 4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WTH_ILG_UP NIELSEN_LEIOMYOSARCOMA_CINI_DN GIDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WTH_ILG_UP NIELSEN_LEIOMYOSARCOMA_CINI_DN GIDEA_METASTASIS CROONQUIST_IL6_DEPRIVATION_UP CHIARADONNA_NEOPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WTH_ILG_UP SNUDERS_ATMPLOYTE_DN GOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCER_TPATHWAY BIGOCARTA_MEDIOLE_TH2_ASSOCIATED_MODULE PID_FCER_TPATHWAY BIGOCARTA_MEDIOLE_TH2_ASSOCIATED_MODULE PID_FCER_TPATHWAY BIGOCARTA_MALDEN_CANCEN_COMP BIGORART_ADDEN_CANCEN_DN MORI_MALL2_TARGETS EMINOUCED_TH2_ASSOCIATED_MODULE PID_FCER_TPATHWAY BIGOCARTA_MEDIOLE_TH2_ASSOCIATED_MODULE PID_FCER_TPATHWAY BIGOCARTA_MEDIOLE_TPATHWAY B	C2	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 30 20 57 17 33 76 51 170 111 89 85 16 362	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.66 0.67 0.62 0.77 0.66 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.68 0.65 0.59 0.77 0.69 0.63 0.77 0.69 0.63 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.69 0.72 0.65 0.72 0.65 0.72 0.65 0.77 0.65 0.72 0.65 0.72 0.65 0.77 0.65 0.72 0.65 0.77 0.65 0.72 0.65 0.77 0.65 0.72 0.65 0.77 0.65 0.77 0.65 0.72 0.65 0.65 0.77 0.65 0.72 0.65 0.66 0.74 0.55 0.66 0.62 0.71 0.55 0.66 0.77 0.65 0.62 0.62 0.77 0.65 0.62 0.62 0.77 0.65 0.62 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.77 0.77 0.77 0.77 0.65 0.77 0.65 0.77	1.04 1.83 1.82 1.81
PID_NFAT_3PATHWAY KEGG NATURAL KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG NATURAL KILLER_CELL_MEDIATED_CYTOTOXICITY KEGG NATURAL KILLER_CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PANGAS_TUMOR SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLIT_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN B_CELL_IYMPHOMA CLUSTER 2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_PDGFRB_PATHWAY WIKMAN_ASBESTOS_LUNG_CANCER_DN RODWELL_AGING_KIDNEY_NO_BLOOD_UP JI_CARCINOGENESIS BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TINF_RESPONSE_NOT_VIA_P38 THUM_SYSTOLIC_HEART_FALURE_UP DEURIG T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_ILS_UP NIELSEN_LEIOMYOSARCOMA_CNN1_DN GRIDEA_METASTASIS CROONQUIST_LG_DEPRINT_CANSPCMMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_LWIPHOCYTE_DN BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE PID_FCET_PATHWAY BIOCARTA_MEEJD_PATHWA	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54 141 60 18 59 35 376 33 76 51 170 111 89 85 16 362 46	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.66 0.51 0.77 0.65 0.51 0.77 0.66 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.77 0.65 0.65 0.77 0.65 0.55 0.66 0.77 0.55 0.66 0.55 0.66 0.55 0.66 0.77 0.56 0.66 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.65 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.65 0.66 0.66 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.65 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.65 0.66 0.77 0.47 0.47 0.47 0.63 0.63 0.63 0.77 0.47 0.47 0.63 0.63 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.77 0.47 0.47 0.63 0.65 0.65 0.65 0.65 0.65 0.77 0.47 0.47 0.63 0.63 0.65 0.65 0.65 0.65 0.65 0.65 0.77 0.47 0.47 0.63 0.65 0.65 0.65 0.65 0.77 0.47 0.65 0.65 0.65 0.77 0.47 0.65 0.65 0.65 0.65 0.77 0.47 0.47 0.65 0.65 0.65 0.65 0.65 0.77 0.47 0.65 0.55	1.83 1.82 1.81 1.81
PID_NFAT_3PATHWAY KEGG NATURAL KILLER CELL_MEDIATED_CYTOTOXICITY SASSON_RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PARGAS_TUMOR SUPPRESSION_BY_SMAD1_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN B_CELL_IYMPHOMAC_LUSTER_2 RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN PID_POGRES DF_P210_BCR_ABL_FUSION_DN PID_POGRES DF_P210_BCR_ABL_FUSION_DN PID_POGRESSION_BY_KRAS_AND_STK11_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_INF_RESPONSET_OT_REITINOIN_AND_SKC882994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_ILS_UP NUESEN_LEIDMYDSAMA_SIGNALING GRADANN_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP CROONQUIST_IL6_DEPRIVATION_UP CRIARGETS_UP SNIDERS_MTUFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_IYMPHOCYTE_DN BOSCO_ALLERGEN JANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNIDERS_MTUFIED_IN_HEAD_AND_NECK_TUMORS LEE_EARLY_T_IYMPHOCYTE_DN BOSCO_ALLERGEN INDUCED_TH2_ASSOCIATED_MODULE PID_FORT_PATHWAY BIOCARTA_MEDED_AND_NECK_TUMORS LEE_EARLY_T_IYMPHOCYTE_DN BOSCO_ALLERGEN INDUCED_TH2_ASSOCIATED_MODULE PID_FORT_PATHWAY BIOCARTA_MERCED_PATHWAY BIOCARTA_L_TARGETS_DN ANAMURA_METAST	$\begin{array}{c} 0.2 \\$	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 54 141 60 18 59 35 376 33 76 51 170 111 89 85 16 362 46 36	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.66 0.67 0.51 0.58 0.61 0.77 0.65 0.61 0.79 0.68 0.65 0.59 0.77 0.69 0.63 0.77 0.69 0.63 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.66 0.65 0.57 0.65 0.59 0.77 0.66 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.65 0.57 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.66 0.65 0.77 0.65 0.59 0.77 0.66 0.65 0.59 0.77 0.66 0.65 0.59 0.77 0.66 0.65 0.77 0.66 0.65 0.77 0.66 0.65 0.77 0.65 0.57 0.65 0.59 0.77 0.66 0.65 0.77 0.65 0.59 0.77 0.66 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.59 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.59 0.77 0.66 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.72 0.65 0.66 0.66 0.66 0.66 0.72 0.66	1.83 1.82 1.81 1.81
PID NFAT 3PATHWAY KEGG NATURAL KILER CELL MEDIATED CYTOTOXICITY SASSON RESPONSE TO GONADOTROPHINS DN FERRANDO T ALL WITH MLL ENL FUSION UP PARGAS TUMOR SUPPRESSION BY SMADT AND SMAD5 UP RORIE TARGETS OF EWSRT FLI1 FUSION UP GEORGANTAS HSC MARKERS SHIN B CELL LYMPHOMA CLUSTER 2 RAY TARGETS OF P210 BCR ABL FUSION DN PID POGFRB PATHWAY WIKMAN ASBESTOS LUNG CANCER DN RODWELL AGING KÜDNEY NO BLOOD UP JI CARCINOGENESIS BY KRAS AND STK11 DN GRAHAM CML DIVIDING VS NORMAL QUIESCENT_DN PHONG TNF RESPONSE TO TVA P38 THUM SYSTOLIC, HEART FAILURE UP DEURIG T CELL PROLYMPHOCYTIC LEUKEMIA DN XU RESPONSE TO TRETINOIN AND NSC882994 UP VALK AML CLUSTER 4 REACTOME, INTERFERON GAMMA SIGNALING FLECHNER PBL KIDNEY TRANSPLANT, REJECTED_VS_OK_UP BYSTROEM CORRELATED WITH ILS UP NIELSEN LEIOMYOSARCOMA CINIT_DN GILDEA METASTASIS GRONQUIST LLG DEPRIVATION_UP CHURADDONNA NEOPLASTIC, TRANSPORMATION KRAS_CDC25_UP LE SKI TARGETS UP SNIJDERS AMPLIFIED IN HEAD AND_NECK_TUMORS LEE SKI ARGETS UP SNIJDERS AMPLIFIED IN HEAD AND_NECK_TUMORS LEE SKI ARGETS UP SNIJDERS AMPLIFIED IN HEAD AND_NECK_TUMORS LEE SKI TARGETS UP SNIJDERS AMPLIFIED IN HEAD AND_NECK_TUMORS LEE LIVER CANCER SURVIYAL DN SMAN BLADER CANCER DN MORI MATURE B_ LYMPHOCYTE UP BUCARTA MEF2D PATHWAY ISSAEVA MLL2 TARGETS HAN JINK SINGALING UP CHURADONNA NEESCENCE UP REACTOME CHEMOKINE RECEPTORS BIND_CHEMOKINES LEE LIVER CANCER SURVIYAL DN SMIRNOV RESPONSE TO IR 6HR_DN MORI MATURE B_ LYMPHOCYTE UP BURTON ADDERC CANCER SURVIYAL DN SMIRNOV RESPONSE TO IR 6HR_DN MORI MATURE B_ LYMPHOCYTE UP BURTON ADDERC S 2 DN YAGI AML WITH T 8.21 TRANSLOCATION NACAMURA METASTASIS	$\begin{array}{c} 0.2 \\$	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 30 20 57 17 37 54 141 60 18 59 35 376 333 76 51 170 111 89 85 36 36 19	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.79 0.69 0.68 0.69 0.69 0.69 0.69 0.69 0.63 0.77 0.65 0.72 0.55 0.66 0.66 0.66 0.77 0.66 0.63 0.77 0.47 0.63 0.63 0.77 0.47 0.63 0.72	1.83 1.82 1.81 1.81
PID_NFAT_3PATHWAY KEGG NATURAL KILLER_CELL MEDIATED_CYTOTOXICITY SASSON RESPONSE_TO_GONADOTROPHINS_DN FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP PARGAS_TUMOR_SUPPRESSION BY_SMADT_AND_SMAD5_UP RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP GEORGANTAS_HSC_MARKERS SHIN B_CELL_LYMPHOMACLUSTER_2 RAY TARGETS_OF_P210_BCR_ABL_FUSION_DN PD_POGERBERS_BY_KARS_AND_STK1_DN GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN PHONG_TNF_RESPONSE_TO_TRAINAGUUESCENT_DN PHONG_TNF_RESPONSE_TO_TRAINAGUUESCENT_DN PHONG_TNF_RESPONSE_TO_TRAINAGUUESCENT_DN PHONG_TNF_RESPONSE_TO_TRAINAGUUESCENT_DN PHONG_TNF_RESPONSE_TO_TRAINAGUUESCENT_DN PHONG_TNF_RESPONSE_TO_TRAINAGUUESCENT_DN PEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN XU_RESPONSE_TO_TRAINON_AND_NSC882994_UP VALK_AML_CLUSTER_4 REACTOME_INTERFERON_GAMMA_SIGNALING FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP BYSTROEM_CORRELATED_WITH_L5_UP NIELSEN_LEGNMOSARCOMA_CNN_T_ND GILDEA_METASTASIS GROONQUIST_LIG_DEPRIVATION_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP LE_SKI_TARGETS_UP SNIDERS_AMFLIFED_IN_HEAD_AND_NSC&CAUSE DEURIGEN_INDUCED_TH2_ASSOCIATED_MODULE PD_FCER_PATHWAY BIOCARTA_MEP2D_PATHWAY SINROV_RESPONSE_TO_IR_GHR_DN MORI_MATURE B_LYMPHOCYTE_UP BURTON_ADIPOGENESIS_8 BUCARTA_THTHZ_PATHWAY SINROV_RESPONSE_TO_IR_GHR_DN MAKAMURA_METASTASIS BIOCARTA_THTHZ_PATHWAY SINN SCHARGES DN SINN SCHARGES DN SINN SCHARGES DN SINN SCHARGES DN SINN SCHARGES DN SINN SCHARGES DN SINN S	C2	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 300 20 57 17 37 54 141 60 18 59 3376 337 76 51 170 111 89 85 16 362 46 36 19 102	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.51 0.58 0.61 0.79 0.68 0.69 0.65 0.77 0.65 0.59 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.59 0.77 0.65 0.77 0.65 0.59 0.77 0.65 0.77 0.69 0.69 0.77 0.69 0.63 0.77 0.65 0.72 0.59 0.66 0.72 0.59 0.66 0.72 0.59 0.66 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.77 0.69 0.63 0.77 0.65 0.77 0.65 0.77 0.69 0.63 0.77 0.65 0.77 0.66 0.77 0.65 0.77 0.69 0.63 0.77 0.65 0.72 0.59 0.66 0.72 0.59 0.68 0.65 0.77 0.66 0.72 0.59 0.66 0.72 0.59 0.66 0.72 0.59 0.66 0.72 0.59 0.66 0.72 0.66 0.72 0.66 0.72 0.59 0.66 0.77 0.66 0.72 0.59 0.66 0.72 0.59 0.66 0.77 0.66 0.72 0.66 0.66 0.77 0.66 0.72 0.59 0.66 0.66 0.77 0.66 0.72 0.59 0.66 0.77 0.66 0.66 0.72 0.65 0.66 0.66 0.66 0.62 0.65 0.77 0.55 0.66 0.62 0.77 0.55 0.66 0.62 0.77 0.55 0.65 0.77 0.55 0.66 0.77 0.55 0.66 0.77 0.55 0.66 0.77 0.55 0.66 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55	1.83 1.82 1.81 1.81
PID NFAT 3PATHWAY KEGG NATURAL KILLER CELL MEDIATED CYTOTXICITY SASSON RESPONSE TO GONADOTROPHINS DN FERRANDO T ALL WITH MLL ENL FUSION UP PARGAS TUMOR SUPPRESSION BY SNAD1 AND SMAD5 UP RORIE TARGETS OF EWSR1 FLI1 FUSION UP GEORGANTAS HSC MARKERS SHIN B CELL LYWFHOMA CLUSTER 2 RAY TARGETS OF P210 BCR ABL FUSION DN PID POGREN PATHWAY WIKMAN ASBESTOS LUNG CANCER DN RODWELL AGING KIDNEY NO BLOOD UP JI CARCINOCENESIS BY KRAS AND STK11 DN GRAHAM_CML DIVIDING_VS NORMAL QUESCENT_DN PHONG TINF RESPONSE TOT VIA P38 THUM SYSTOLIC HEART FAILURE UP DEURIG T CELL PROLYMPHOCYTIC LEUKEMIA DN XU RESPONSE TO TRETINOIN AND INSC682994 UP VALK AML CLUSTER 4 REACTOME INTERFERON GAMMA SIGNALING FLECHNER, PBL KIDNEY TRANSPLANT REJECTED_VS OK UP BYSTROEM CORRELATED WITH ILS UP NIELSEN LEIOMYOSARCOMA_CNN1_DN GILDEA METASTASIS GRONAUSI ILG DEPRIVATION_UP CHIARADONNA NEOPLASTIC, TRANSFORMATION KRAS_CDC25_UP LE SKI TARGETS UP SNIJDERS AMPLIFIED IN HEAD AND NECK TUMORS LEE SKI TARGETS UP SNIJDERS AMPLIFIED IN HEAD AND NECK TUMORS LEE SKI TARGETS UP SNIJDERS AMPLIFIED IN HEAD AND NECK TUMORS LEE SKI TARGETS UP SNIJDERS AMPLIFIED IN HEAD AND NECK TUMORS LEE SKI TARGETS UP SNIJDERS AMPLIFIED IN HEAD AND NECK TUMORS LEE SKI TARGETS UP SNIJDERS AMPLIFIED IN HEAD AND NECK TUMORS LEE SKI TARGETS UP SNIJDERS AMPLIFIED IN HEAD AND NECK TUMORS LEE SKI TARGETS UP SNIJDERS AMPLIFIED IN SIGNALING REACTOME UPD THAY SIGOARTIA MERCERD NEDY TRANSFORMATION_KRAS_CDC25_UP LE SKI TARGETS UP SNIJDERS AMPLIFIED IN SIGNALING FROCANTA NEOPLASTIC, TRANSFORMATION_KRAS_CDC25_UP LE SKI TARGETS UP SNIJDERS AMPLIFIED IN SIGNALING FROMAN SENDERS CENCE UP SNIJDERS AMPLIFIED IN READ AND NECK TUMORS LEE LEVER CANCER DN SIGNAU RESPONSE TO IR GALL ASSOCIATED_MODULE PID FOCERT SPATHWAY SIGNAU RESPONSE TO IR GALL ASSOCIATED_MODULE PID FOCERT SPATHWAY SIGNAU RESPONSE TO IR GALL ASSOCIATED_MODULE PID FOCERT SPATHWAY SIGNAU RESPONSE TO IR GALL ASSOCIATED MODULE FID MAN SIGNAU RESPONSE TO IR GALL ASSOCIATED MODULE SIGNAU R	$\begin{array}{c} 0.2 \\$	53 127 87 85 132 30 66 30 15 126 28 211 17 90 337 405 307 17 28 59 61 49 20 307 17 28 59 61 49 20 307 177 337 54 141 60 18 59 35 376 33 76 51 170 111 89 85 16 362 46 36 19	0.60 0.60 0.51 0.62 0.56 0.54 0.64 0.60 0.63 0.79 0.56 0.67 0.62 0.77 0.65 0.51 0.58 0.61 0.77 0.65 0.51 0.58 0.61 0.77 0.65 0.65 0.51 0.58 0.61 0.77 0.65 0.65 0.51 0.58 0.65 0.51 0.58 0.65 0.51 0.58 0.65 0.51 0.58 0.65 0.55 0.65 0.65 0.65 0.65 0.59 0.65 0.65 0.65 0.59 0.65 0.65 0.65 0.65 0.77 0.65 0.59 0.65 0.59 0.65 0.65 0.65 0.77 0.65 0.59 0.65 0.65 0.59 0.65 0.65 0.77 0.65 0.65 0.59 0.65 0.65 0.77 0.65 0.65 0.59 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.59 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.65 0.77 0.65 0.59 0.66 0.65 0.77 0.65 0.77 0.65 0.77 0.65 0.65 0.77 0.65 0.66 0.77 0.66 0.77 0.66 0.77 0.66 0.77 0.66 0.77 0.66 0.66 0.77 0.66 0.66 0.77 0.66 0.66 0.77 0.66 0.66 0.66 0.77 0.66 0.66 0.66 0.66 0.62 0.66 0.62 0.65 0.66 0.66 0.62 0.65 0.65 0.65 0.66 0.65 0.65 0.66 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.77 0.55 0.66 0.65 0.77 0.47 0.56 0.65 0.77 0.57 0.65 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.55 0.65 0.77 0.58 0.65 0.77 0.58 0.63 0.77 0.58 0.63 0.72 0.58 0.58 0.58 0.55 0.58 0.58 0.55 0.58 0	1.83 1.82 1.81 1.81

MORI_IMMATURE_B_LYMPHOCYTE_UP	C2	52	0.71	1.81
DANG_REGULATED_BY_MYC_DN	C2	250	0.51	1.81
TING_SILENCED_BY_DICER	C2	30	0.63	1.81
BURTON_ADIPOGENESIS_9	C2	90	0.61	1.81
ZHU CMV ALL UP	C2	119	0.61	1.81
HUMMERICH_SKIN_CANCER_PROGRESSION_UP	C2	86	0.60	1.81
	62	46	0.61	1.81
	C2	51	0.38	1.01
	C2	15	0.83	1.01
VERRECCHIA FARLY RESPONSE TO IGERI	C2	55	0.65	1.80
	C2	112	0.53	1.80
	C2	37	0.74	1.80
	C2	23	0.69	1.80
REACTOME NUCLEOTIDE BINDING DOMAIN LEUCINE RICH REPEAT CONTAINING RECEPTOR NLR SIG	C2	44	0.60	1.80
ALONSO METASTASIS EMT UP	C2	36	0.67	1.80
REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS	C2	15	0.85	1.80
DELYS_THYROID_CANCER_UP	C2	434	0.52	1.80
PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_DN	C2	162	0.61	1.80
VANTVEER_BREAST_CANCER_ESR1_DN	C2	234	0.53	1.80
REACTOME_METABOLISM_OF_MRNA	C2	206	0.65	1.80
SYED_ESTRADIOL_RESPONSE	C2	18	0.72	1.80
BOYAULT_LIVER_CANCER_SUBCLASS_G5_DN	C2	27	0.82	1.80
ZHANG_PROLIFERATING_VS_QUIESCENT	C2	49	0.62	1.80
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP	C2	204	0.63	1.80
KUNINGER_IGF1_VS_PDGFB_TARGETS_DN	C2	45	0.59	1.80
HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN	C2	272	0.50	1.80
GRANDVAUX_IRF3_TARGETS_DN	C2	19	0.67	1.80
	C2	222	0.57	1.80
	C2	30	0.59	1.80
	C2	31	0.63	1.80
	C2	88	0.64	1.80
	C2	39	0.60	1.80
	C2	15	0.72	1.80
	C2	71	0.61	1.80
	C2	33	0.65	1.80
	C2	45	0.62	1.80
	C2	46	0.63	1.80
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP	C2	155	0.54	1.80
HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN	C2	76	0.63	1.79
WINTER_HYPOXIA_DN	C2	49	0.75	1.79
NAKAMURA_METASTASIS_MODEL_UP	C2	43	0.60	1.79
WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLESTEROL_UP	C2	55	0.65	1.79
LEE_AGING_CEREBELLOM_UP	C2	83	0.54	1.79
MORI_PLASMA_CELL_DN	C2	32	0.69	1.79
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	C2	84	0.53	1.79
HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_UP	C2	176	0.62	1.79
POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_DN	C2	59	0.64	1.79
BRUECKNER_TARGETS_OF_MIRLET7A3_DN	C2	76	0.60	1.79
REACTOME_METABOLISM_OF_RNA	C2	250	0.65	1.79
BIOCARTA_MCALPAIN_PATHWAY	C2	25	0.61	1.79
REGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	C2	44	0.58	1.79
DELPUECH_FOXO3_TARGETS_UP	C2	68	0.57	1.79
GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_UP	C2	38	0.65	1.79
BOQUESI SIEM_CELL_DN	C2	215	0.57	1.79
SHID_B_CELL_LYMPHOMA_CLUSTER_3	C2	27	0.71	1.79
LI_WILMS_TUMOR_VS_FETAL_KIDNEY_Z_DN	C2	51	0.64	1.79
WORSCHECH TUMOR REJECTION UP	C2	54	0.61	1.79
WATTEL_AUTONOMOUS_THYROID_ADENOMA_DN	62	55	0.63	1.79
BIOCARTA_KHO_PATHWAY	62	31	0.62	1.79
	62	101 70	0.50	1.79
	62	170	0.52	1.79
	C2	140 50	0.40	1.79
	C2		0.00	1.70
	C2	70 54	0.09	1.70
	C2	230	0.00	1.70
KEEN RESPONSE TO ROSIGI ITAZONE DN	C.2	104	0.40	1.70
KEGG NOD LIKE RECEPTOR SIGNALING PATHWAY	C2	62	0.04	1.70
MA PITUITARY FETAL VS ADULT DN	C2	19	0.00	1 78
PID AVB3 OPN PATHWAY	C.2	31	0.69	1 78
KANG AR TARGETS UP	C.2	17	0.73	1 78
BIOCARTA TCR PATHWAY	C2	43	0.65	1.78
KAPOSI LIVER CANCER MET UP	C2	17	0.75	1.78
DAVIES MULTIPLE MYELOMA VS MGUS DN	C2	27	0.76	1.78
HSIAO HOUSEKEEPING GENES	C2	384	0.66	1.78
TORCHIA TARGETS OF EWSR1 FLI1 FUSION DN	C2	309	0.47	1.78
PID CD8 TCR DOWNSTREAM PATHWAY	C2	64	0.55	1.78
AKL_HTLV1_INFECTION_DN	C2	65	0.60	1.77
DORSEY GAB2 TARGETS	C2	31	0.66	1.77
HERNANDEZ MITOTIC ARREST BY DOCETAXEL 1 UP	C2	34	0.61	1.77
KEGG_HEMATOPOIETIC_CELL_LINEAGE	C2	85	0.52	1.77
GERHOLD_ADIPOGENESIS_DN	C2	63	0.68	1.77
MORI_SMALL_PRE_BII_LYMPHOCYTE_DN	C2	74	0.57	1.77
WATANABE_RECTAL_CANCER_RADIOTHERAPY_RESPONSIVE_DN	C2	91	0.61	1.77
ZHENG_BOUND_BY_FOXP3	C2	479	0.54	1.77
BURTON_ADIPOGENESIS_7	C2	50	0.63	1.77
TOMLINS_PROSTATE_CANCER_DN	C2	40	0.67	1.77
KEGG_FOCAL_ADHESION	C2	196	0.54	1.77
HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_UP	C2	60	0.51	1.77
WIERENGA_STAT5A_TARGETS_GROUP2	C2	56	0.60	1.77
RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP	C2	332	0.50	1.77
LIM_MAMMARY_LUMINAL_MATURE_DN	C2	97	0.60	1.77
BILANGES_SERUM_RESPONSE_TRANSLATION	C2	36	0.69	1.77
CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY	C2	28	0.61	1.77
LIU_SMARCA4_TARGETS	C2	59	0.56	1.77
JISON_SICKLE_CELL_DISEASE_DN	C2	174	0.60	1.77
BASSO CD40 SIGNALING DN	C2	66	0.54	1.77

BIOCARTA_FCER1_PATHWAY	C2	38	0.64	1.77
BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP	C2	200	0.54	1.77
MATSUDA_NATURAL_KILLER_DIFFERENTIATION	C2	471	0.44	1.77
BIOCARTA_ILZRE_PATHWAY	C2	38	0.62	1.77
REACTOME SIGNALING BY ILS	C2	105	0.56	1.//
RASHI RESPONSE TO IONIZING RADIATION 2	C2	126	0.58	1.77
BOYAULT LIVER CANCER SUBCLASS G3 UP	C2	120	0.65	1.76
WIEDERSCHAIN TARGETS OF BMI1 AND PCGF2	C2	57	0.62	1.76
KYNG_RESPONSE_TO_H2O2	C2	69	0.60	1.76
ST_INTEGRIN_SIGNALING_PATHWAY	C2	81	0.54	1.76
ZUCCHI_METASTASIS_DN	C2	44	0.70	1.76
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	C2	61	0.56	1.76
WESTON_VEGFA_TARGETS	C2	106	0.56	1.76
	C2	120	0.56	1.76
ALONGO METAGTAGIO MEDIOLOGI INTO K VS DONOR UP	C2	151	0.53	1.76
	C2	290	0.51	1.76
LENAOUR DENDRITIC CELL MATURATION DN	C2	127	0.58	1.76
CHYLA_CBFA2T3_TARGETS_UP	C2	374	0.43	1.76
SANA_TNF_SIGNALING_DN	C2	88	0.62	1.76
CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP	C2	170	0.51	1.76
	C2	34	0.58	1.76
	62	50	0.65	1.76
ZHORI TNE SIGNI ING 4HR	C2	54	0.65	1.70
RUTELLA RESPONSE TO CSE2RB AND IL4 DN	C2	309	0.53	1.76
LINDVALL IMMORTALIZED BY TERT UP	C2	74	0.58	1.76
PID_TXA2PATHWAY	C2	57	0.59	1.76
MISSIAGLIA_REGULATED_BY_METHYLATION_UP	C2	118	0.58	1.76
REACTOME_INFLUENZA_LIFE_CYCLE	C2	134	0.71	1.76
	C2	202	0.57	1.75
PARK_TIGU_AND_MULTPUTENT_PROGENITORS	C2	48	0.59 0.4F	1.75
KEGG ALLOGRAFT REJECTION	C2	230	0.45	1.75
ROZANOV MMP14 TARGETS SUBSET	C2	33	0.69	1.75
KEGG T CELL RECEPTOR SIGNALING PATHWAY	C2	107	0.52	1.75
JECHLINGER EPITHELIAL TO MESENCHYMAL TRANSITION UP	C2	70	0.62	1.75
SWEET_LUNG_CANCER_KRAS_DN	C2	426	0.50	1.75
RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP	C2	74	0.66	1.75
PID_INTEGRIN_A4B1_PATHWAY	C2	33	0.65	1.75
HINATA_NFKB_TARGETS_KERATINOCYTE_UP	C2	91	0.62	1.75
TIEN INTESTINE PROBIOTICS 6HR UP	C2	55	0.69	1.75
	C2		0.68	1.75
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION GRANULOCYTE DN	C2	150	0.30	1.75
	C2	24	0.68	1.75
APRELIKOVA BRCA1 TARGETS	C2	47	0.65	1.75
SHIPP_DLBCT_VS_FOLLICULAR_LYMPHOMA_DN	C2	45	0.66	1.75
BIOCARTA_CTLA4_PATHWAY	C2	19	0.73	1.75
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	C2	25	0.76	1.75
HASLINGER_B_CLL_WITH_CHROMOSOME_12_TRISOMY	C2	24	0.66	1.75
SANA_INF_SIGNALING_UP	C2	82	0.61	1.75
	C2	403	0.53	1.75
KEGG EPITHELAL CELL SIGNALING IN HELICOBACTER PYLORI INFECTION	C2	68	0.53	1.75
XU RESPONSE TO TRETINOIN UP	C2	15	0.69	1.75
THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN	C2	225	0.53	1.75
ZHAN_MULTIPLE_MYELOMA_DN	C2	40	0.61	1.75
MARKEY_RB1_CHRONIC_LOF_DN	C2	117	0.53	1.75
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP	C2	185	0.52	1.75
GHU_ATF5_TARGETS_DN	C2	16	0.69	1.75
BROWNE HCMV INFECTION 8HR DN	C.2	45	0.58	1.74
KLEIN TARGETS OF BCR ABL1 FUSION	C2	45	0.65	1.74
YAGI AML FAB MARKERS	C2	187	0.49	1.74
CHIBA_RESPONSE_TO_TSA_UP	C2	51	0.64	1.74
FUJII_YBX1_TARGETS_UP	C2	41	0.57	1.74
	C2	141	0.61	1.74
	C2	21/	0.56	1.74
BOYLAN MULTIPLE MYELOMA D. CLUSTER DN	C2		0.73	1.74
SIG REGULATION OF THE ACTIN CYTOSKELETON BY RHO GTPASES	C2	35	0.57	1.74
YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP	C2	51	0.63	1.74
ROSS_LEUKEMIA_WITH_MLL_FUSIONS	C2	76	0.55	1.74
ZHAN_MULTIPLE_MYELOMA_LB_DN	C2	39	0.68	1.74
WILENSKY_RESPONSE_TO_DARAPLADIB	C2	28	0.75	1.74
MARSON_FOXP3_CORE_DIRECT_TARGETS	C2	19	0.78	1.74
	C2	01	0.03	1.74
PLASARI TGEB1 SIGNALING VIA NEIC 1HR LIP	C.2	33	0.00	1.74
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 8D DN	C2	199	0.52	1.73
LEE_LIVER_CANCER_E2F1_UP	C2	60	0.60	1.73
ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP	C2	26	0.61	1.73
LINDVALL_IMMORTALIZED_BY_TERT_DN	C2	79	0.56	1.73
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	C2	64	0.66	1.73
ALIEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION	C2	125	0.60	1.73
	C2	16	0.74	1.73
REACTOME IL 3.5 AND GM CSE SIGNALING	C2	43	0.04	1.73
REACTOME FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND PLATELET PRODUCTION	C2	120	0.40	1.73
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	C2	75	0.55	1.73
PID_GMCSF_PATHWAY	C2	37	0.60	1.73
WANG_SMARCE1_TARGETS_UP	C2	274	0.53	1.73
	C2	19	0.67	1.73
	C2 C2	19 98	0.67	1.73
KEGG_TOLL_LIKE_RECEPTING_SIGNALING_PATHWAY STEARMAN_LUNG_CANCER_EARLY_VS_LATE_DN	C2 C2 C2 C2	19 98 59	0.67 0.50 0.58	1.73 1.73 1.73 1.73

REACTOME SEMA4D INDUCED CELL MIGRATION AND GROWTH CONE COLLAPSE	C2	24	0.64	1.73
	C2	03	0.60	1.73
	02	75	0.00	1.70
	62	/5	0.49	1.73
WANG_TARGETS_OF_MLL_CBP_FUSION_UP	C2	42	0.53	1.73
YAMAZAKI_TCEB3_TARGETS_UP	C2	173	0.51	1.73
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM3	C2	68	0.53	1.72
PATTERSON DOCETAXEL RESISTANCE	C2	28	0.64	1.72
HOLLEMAN ASPARAGINASE RESISTANCE ALL DN	C2	24	0.74	1 72
	62	20	0.62	1.72
BIOCARTA FAS FATHWAY	62	30	0.63	1.72
FRIDMAN_IMMORTALIZATION_DN	C2	33	0.62	1.72
JEON_SMAD6_TARGETS_UP	C2	23	0.67	1.72
PID IL2 PI3K PATHWAY	C2	34	0.56	1.72
WESTON VEGEA TARGETS 12HR	C:2	33	0.64	1 72
	62	10	0.00	1.72
	62	10	0.68	1.72
RIGGI_EWING_SARCOMA_PROGENITOR_UP	C2	414	0.43	1.72
WU_HBX_TARGETS_3_UP	C2	18	0.70	1.72
BAELDE DIABETIC NEPHROPATHY DN	C2	427	0.52	1.72
HOLLEMAN ASPARAGINASE RESISTANCE ALL UP	C2	22	0.59	1 72
	62	46	0.00	1.72
	62	40	0.00	1.72
	62	30	0.67	1.72
PARK_APL_PATHOGENESIS_DN	C2	49	0.60	1.72
DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN	C2	66	0.51	1.72
REACTOME MHC CLASS II ANTIGEN PRESENTATION	C2	89	0.54	1.72
SASAL RESISTANCE TO NEOPLASTIC TRANSFROMATION	C2	49	0.67	1 72
	62	251	0.07	1.72
	62	201	0.44	1.72
JISON_SICKLE_CELL_DISEASE_UP	C2	180	0.54	1.72
	C2	46	0.64	1.72
TAVOR_CEBPA_TARGETS_DN	C2	30	0.58	1.72
WAMUNYOKOLI OVARIAN CANCER GRADES 1.2 DN	C2	65	0.62	1.72
WOTTON RUNX TARGETS UP	C2	21	0.57	1 72
	02	20	0.07	1.72
	62	29	C0.U	1.72
ZEMBUTSU_SENSITIVITY_TO_VINCRISTINE	C2	17	0.64	1.72
PODAR_RESPONSE_TO_ADAPHOSTIN_UP	C2	143	0.56	1.72
REACTOME IL 2 SIGNALING	C2	41	0.60	1.72
VISALA AGING LYMPHOCYTE DN	(.2	19	0.67	1 72
DEACTOME NONSERVE MEDIATED DECAY ENLIANCED BY THE EVAN UNACTON CONDERY	02	102	0.07	1.72
	62	103	0.74	1.72
BIUGARTA_BCR_PATHWAY	C2	34	0.60	1.71
HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_UP	C2	80	0.51	1.71
REACTOME G ALPHA Z SIGNALLING EVENTS	C2	43	0.54	1.71
DORN ADENOVIRUS INFECTION 48HB DN	C2	40	0.64	1.71
	C2	103	0.01	1.71
	02	103	0.49	1.71
MCBRYAN_PUBERIAL_BREASI_4_5WK_UP	62	269	0.48	1.71
HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_DN	C2	72	0.51	1.71
KEGG_SPLICEOSOME	C2	124	0.61	1.71
TSAI RESPONSE TO RADIATION THERAPY	C2	32	0.67	1.71
MARSON FOXP3 TARGETS STIMULATED UP	C2	29	0.70	1.71
	C2	1/19	0.51	1.71
	02	F7	0.01	1.71
CROUNQUISI_STRUMAL_STIMULATION_UP	62	57	0.68	1.71
PID_FAK_PATHWAY	C2	58	0.55	1.71
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN	C2	73	0.65	1.71
LAIHO COLORECTAL CANCER SERRATED UP	C2	112	0.68	1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP	C2 C2	112 166	0.68	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP	C2 C2 C2	112 166 21	0.68 0.53 0.58	1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_VELOD_CEL_DEVELOPMENT_UP	C2 C2 C2 C2	112 166 21	0.68 0.53 0.58	1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP	C2 C2 C2 C2 C2	112 166 21 161	0.68 0.53 0.58 0.51	1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN	C2 C2 C2 C2 C2 C2 C2 C2	112 166 21 161 438	0.68 0.53 0.58 0.51 0.51	1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE	C2 C2 C2 C2 C2 C2 C2 C2 C2	112 166 21 161 438 36	0.68 0.53 0.58 0.51 0.51 0.70	1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2	112 166 21 161 438 36 153	0.68 0.53 0.58 0.51 0.51 0.70 0.46	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMUNODEFICIENCY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2	112 166 21 161 438 36 153 35	0.68 0.53 0.58 0.51 0.51 0.70 0.46 0.68	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY DODNNELL_TARGETS_OF_MYC_AND_TERC_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2	112 166 21 161 438 36 153 35 81	0.68 0.53 0.58 0.51 0.51 0.70 0.46 0.68 0.55	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17	0.68 0.53 0.58 0.51 0.70 0.46 0.68 0.55 0.74	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_NOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANC_DEVEST_TARGETS_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 17	0.68 0.53 0.58 0.51 0.51 0.70 0.46 0.68 0.55 0.74	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 438 36 153 35 81 17 15	0.68 0.53 0.58 0.51 0.51 0.70 0.46 0.68 0.55 0.74 0.70	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393	0.68 0.53 0.58 0.51 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_NOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_P01_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52	0.68 0.53 0.58 0.51 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42 0.52	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49	0.68 0.53 0.58 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42 0.52 0.59	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68	0.68 0.53 0.51 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42 0.52 0.59 0.54	1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_GRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15	0.68 0.53 0.58 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42 0.52 0.59 0.54 0.74	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOD_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_FFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MCL_AP9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIEFDENGA_STAT6A_TARGETS_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 200	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.70\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOYB_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WERENGA_STATSA_TARGETS_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 22	0.68 0.53 0.51 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42 0.52 0.52 0.59 0.54 0.74	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 55	0.68 0.53 0.58 0.51 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42 0.55 0.74 0.70 0.52 0.59 0.54 0.74 0.74 0.74 0.46	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OLWSTER_CAND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MIL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPR_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.52\\ 0.54\\ 0.74\\ 0.74\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.67\\ \end{array}$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOYR5_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_TCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZIMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WEERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.74\\ 0.72\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.74\\ 0.46\\ 0.59\\ 0.67\\ 0.43\\ \end{array}$	$\begin{array}{c} 1.71 \\ 1.71 \end{array}$
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_OPRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORCAG_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.67\\ 0.43\\ 0.59\end{array}$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STAT5A_TARGETS_UP ST_ERK1_ENK2_MAPR_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_WELOMAC_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.52\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.59\\ 0.54\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ \end{array}$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_OPRIMARY IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_MCL_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EVSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.55\\ 0.74\\ 0.55\\ 0.55\\ 0.55\\ 0.59\\ 0.54\\ 0.74\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.55\\ 0.54\\ 0.55\\ 0.54\\ 0.55\\ 0.54\\ 0.55\\ 0.54\\ 0.57\\ 0.55\\$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORCOLA_TERATOMA_UP WEERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGËR_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLA_DAMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 42	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.57\\ 0.56\\ 0.56\\ 0.56\\ 0.57\\ 0.56\\$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 43 43 43	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.54\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.57\\ 0.65\\ 0.57\\ 0.61\\ 0.57\\ 0.61\\ 0.57\\ 0.61\\ 0.57\\ 0.61\\ 0.57\\ 0.61\\ 0.57\\ 0.61\\ 0.57\\ 0.57\\ 0.61\\ 0.57\\ 0.61\\ 0.57\\$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_OPRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.74\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ \end{array}$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STAT5A_TARGETS_UP ST_ERK1_ENK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_KIT_PATHWAY BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 43 52 44	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.57\\ 0.63\\ \end{array}$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CARD_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_GRMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLA_F9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EVERS1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CTYDTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_KIT_PATHWAY BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 43 52 44 87	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.63\\ 0.54\end{array}$	1.71 1.71
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_OPRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLA_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_KIT_PATHWAY BOYAULT_LIVER_CANCERS_UPAUSA	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 54 43 52 44 87 36	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.52\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.54\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ \end{array}$	1.71 1.70 1.70 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STAT5A_TARGETS_UP ST_ERK1_ENK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_KIT_PATHWAY PID_K	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 43 43 52 44 87 36 94	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.52\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.54\\ 0.55\\ 0.55\\ 0.51\\ 0.55\\ 0.51\\ 0.55\\$	1.71 1.70 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUB_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_ORIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_IKIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 43 52 43 52 43 52 43 52 52 43 52 52 52 52 52 52 52 52 52 52	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.74\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.55\\$	1.71 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WEERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGËR_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLA_AMDLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP LEE_TAGIN_NEDETAL_BREAST_3_4WK_DN KAYO_CALORIE_RESTRICTION_MUSCLE_UP ZHANG_NOUTIPLE_MYELOMA_CD_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 43 52 44 87 36 94 43 36 94 43	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_GRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WTH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EVSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN EOTXMIN_PATHWAY PID_INTEGRIN3_PATHWAY PID_INTEGRIN3_PATHWAY PID_INTEGRIN3_PATHWAY PID_KIT_PATHWAY BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCORTEX_UP MCBRYAN_PUBERTAL_BREAST_3_4WK_DN KAYO_CALORIE_RESTICION_MUSCLE_UP ZHANM_ULTIPLE_MYELOMA_CD_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 43 52 44 87 36 94 43 272	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.54\\ 0.67\\ 0.61\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.46\\ 0.46\\ 0.46\\ 0.58\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.46\\ 0.46\\ 0.58\\ 0.54\\ 0.46\\ 0.58\\ 0.54\\ 0.46\\ 0.58\\ 0.54\\ 0.46\\ 0.46\\ 0.58\\ 0.54\\ 0.46\\ 0.58\\ 0.54\\ 0.46\\ 0.58\\ 0.54\\ 0.46\\ 0.58\\ 0.54\\ 0.46\\ 0.58\\ 0.54\\ 0.46\\ 0.58\\ 0.54\\ 0.46\\ 0.58\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.55\\$	1.71 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_OPRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_P01_SIGNALING CHANG_P0U5F1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_INTEGRIN3_PATHWAY PID_INTEGRIN3_PATHWAY PID_INTEGRIN3_PATHWAY PID_KIT_PATHWAY PID	$\begin{array}{c} C2 \\ C2 $	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 272 180	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.74\\ 0.74\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.54\\ 0.46\\ 0.46\\ 0.46\\ 0.46\\ 0.46\\ 0.46\\ 0.46\\ 0.58\\ 0.58\\ 0.58\\ 0.54\\ 0.46\\ 0.46\\ 0.46\\ 0.46\\ 0.58\\ 0.58\\ 0.58\\ 0.58\\ 0.54\\ 0.46\\ 0.46\\ 0.46\\ 0.58\\$	1.71 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPR_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLA_AMULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INT_PATHWAY BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCORTEX_UP STAULT_LIVER_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCORTEX_UP MCBRYAN_DUBERTAL_BREAST_3_4WK_DN KAYO_CALORIE_RESTRICTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_CD_UP ZHANG_NOLATERCANCER_SUBCLASS_G123_UP LEE_AGING_NEOCORTEX_UP MCBRYAN_PUBERTAL_BREAST_3_4WK_DN KAYO_CALORIE_RESTRICTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_CD_N OKUMURA_INFLAMMATORY_RESPONSE_LPS LEE_GRAZ_TARGETS_UP	$\begin{array}{c} C2 \\ C2 $	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 47 36 94 43 272 180 107	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.54\\ 0.55\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_OPRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_MLL_AF9_FUSION COMMENDERTINELA_FOMDUSEDUP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EVSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_REATOMA_CD2_UP MCBRYAN_PUBERTAL_BREAST_3_4WK_DN KAYO_CALORER_ESTRICTION_MUSCLE_UP ZHAN MULTIPLE_MYELOMA_CD2_UP MULLIGHAN_MLL_SIGNATURE_2_DN OKUMURA_INFLAMMATORY_RESPONSE_LPS LE_EGR2_TARGETS_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 272 180 107 16	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.55\\ 0.55\\ 0.59\\ 0.54\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.46\\ 0.51\\ 0.72\\ \end{array}$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_CPRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UF KUMAR_TARGETS_OF_MIL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_KIT_PATHWAY PID_KIT_PATHWAY BOYAUN_ULTIPLE_MYELOMA_C_DN CHUNG_RUSCORTEX_UP MCERRIAD_AMPLICON_12P11_12_UP BOYAUN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY BOYAUN_ULTIPLE_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCORTEX_UP MCEBRYAN_PUBERTAL_BREAST_3_4WK_DN KAYO_CALORIE_RESTRICTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_CD2_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 54 43 52 44 87 36 94 43 272 180 107 16 85	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.52\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.55\\ 0.51\\ 0.56\\ 0.72\\ 0.56\\$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXO6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSU_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_GRIMARY_IMMUNODEFICIENCY DODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLC_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_KT_PATHWAY PID_KT_PATHWAY PID_KT_PATHWAY PID_KT_PATHWAY PID_KT_PATHWAY PID_KT_PATHWAY PID_KT_PATHWAY PID_KT_RESTING_DEUCLASS_G123_UP LEE_AGING_NECOCRTEX_UP MCREYAN_PUBERTAL_BREAST_3_4WK_DN KAYO_CALORIE_RESTING_IDU MULTIPLE_MYELOMA_CD_UP MULTIPLE_STRCTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_KT_PATHWAY PID_K	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 45 44 87 36 94 43 272 180 107 16 85	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\$	1.71 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXO6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_ML_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INT_PATHWAY BOYAUN_ULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INT_PATHWAY BOYAUN_ULTIPLE_MYELOMA_CD_N KAYO_CALORIER_RESRICTION_MUSCLE_UP ZHANM_ATURGETS_OF_EWSR1_ETS_400 KAYO_CALORIER_RESRICTION_MUSCLE_UP ZHANM_MULTIPLE_MYELOMA_CD_UP MULLIGHAN_MUL_SIGNATURE_2_DN OKUMUMA_INFLAMMATORY_RESPONSE_LPS LE_EGR2_TARGETS_UP REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY BOYLAN_MULTIPLE_MYELOMA_CD_UP MULLIGHAN_MATORY RESPONSE_LPS LE_EGR2_TARGETS_UP REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY BOYLAN_MULTIPLE_MYELOMA_CD_UP MULLIGHAN_MATORY_RESPONSE_LPS LE_EGR2_TARGETS_UP REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY BOYLAN_MULTIPLE_MYELOMA_CD_UP MULLIGHAN_MATORY_RESPONSE_LPS LE_EGR2_TARGETS_UP REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY BOYLAN_MULTIPLE_MYELOMA_CD_UP MULLIGHAN_MATORY_RESPONSE_LPS LE_EGR2_TARGETS_UP REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY BHATTACHARYA_EMBRYONIC_STEM_CELL JUBAN_TARGETS_OF_SPI1_AND_LUPOD	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 52 44 87 36 94 43 52 180 107 16 85 86 85	$\begin{array}{c} 0.68\\ 0.53\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.46\\ 0.51\\ 0.72\\ 0.56\\ 0.55\\$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_P01_SIGNALING CHANG_POU5F1_TARGETS_UP KUMAR_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTUVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13014_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLA_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KIT_PATHWAY PID_KAT_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCORTEX_UP MCBRYAN_PUBERTAL_BREAST_3_4WK_DN KAYO_CALORIE_RESTRICTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_C_DN CHUNG_REST_OF_EWSPI_SE_SONSE_LPS LEE_AGING_NEOCORTEX_UP MCBRYAN_PUBERTAL_BREAST_3_4WK_DN KAYO_CALORIE_RESTRICTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_C_DN MULLIGHAN_MIL_SIGNATURE_2_DN OKUMURA_INFLAMMATORY_RESPONSE_LPS LEE_AGING_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY BHATTACHARYA_EMBRYONIC_STEM_CELL JUBAN_TARGETS_OF_SPI_AND_FLID_DN WEIGEL_OXIDATIVE_STRESSE_NY_TBH_AND_H2O2 HORDENTALMENTE	$\begin{array}{c} C2 \\ C2 $	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 272 180 107 16 85 86 35	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.55\\$	1.71 1.70 1
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_RAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_RRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTURIAR_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWÄY HASLINGER_B_CLL_WTH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EVSRIF_TS_FUSIONS_UP HEIDENBLAD_AMPLICON_12PI1_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRINS_PATHWAY PID_KIT_PATHWAY PD_KIT_PATHWAY PD_KIT_PATHWAY DOYAUN_INER_RESPAST_3_4WK_DN KARYO_CALORIE_RESTRICTION_MUSCLE_UP ZHANG_ANTURER_RESPAST_3_4WK_DN KARYO_CALORIE_RESTRICTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_CD2_UP MULLIGHAN_MLL_SIGNATURE_2_DN OCUMUM_A_IRFLAMMATORY_RESPONSE_LOS_G123_UP LEE_AGING_NEOCORTEX_UP MCBRYAN_PUBERTAL_BREAST_3_4WK_DN KKAYO_CALORIE_RESTRICTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_CD2_UP MULLIGHAN_MLL_SIGNATURE_2_DN OCUMUMA_INFLAMMATORY_RESPONSE_LPS LEE_GR2_TARGETS_OF_SNS_LPS LEE_GR2_TARGETS_OF_SNS_LPS LEE_GR2_TARGETS_OF_SNS_LPS_LEMAND_H2O2 MONDTIVE_TRESS_OF_SNS_LPS_LEMAND_H2O2 MONDTIVE_STRESS_OF_SNS_TEM_AND_H2O2 MONDTIVE_STRESS_OF_SNTEMS_DATHWAY BHATTACHARYA_EMBRYONIC_STEM_CELL JUBAN_TARGETS_OF_SNTEMS_DNS_LPS LEE_GR2_TARGETS_OF_SNTEMS_DNS_LPS LEE_GR2_TARGETS_OF_SNTEMS_DNS_LPS LEE_GR2_TARGETS_OF_SNTEMS_LPS LEE_GR2_TARGETS_OF_SNTEMS_LPS LEE_GR2_TARGETS_OF_SNTEMS_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS LEEGR2_TARGETS_OF_SNTEMS_DNS_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_LPS MEGEL_ONDATIVE_STRESS_ONSE_	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 272 180 107 16 85 86 35 41	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.46\\ 0.59\\ 0.67\\ 0.61\\ 0.59\\ 0.67\\ 0.61\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.55\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.55\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.55\\$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNDDEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WEIEREIGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_KIT_PATHWAY PID_K	$\begin{array}{c} C2 \\ C2 $	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 272 180 107 16 85 86 35 41 56	$\begin{array}{c} 0.68\\ 0.53\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.54\\ 0.74\\ 0.74\\ 0.46\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.67\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.46\\ 0.55\\ 0.55\\ 0.55\\ 0.55\\ 0.55\\ 0.55\\ 0.55\\ 0.55\\ 0.55\\ 0.55\\ 0.65\\ 0.67\\ 0.55\\$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MTELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_RAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_RRIMARY_IMMUNDEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13014_DELETION MIYAGAWA_TARGETS_OF_EVSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN COLON_SISTER_CYTOTOXICITY_DN PID_INTEGRINS_PATHWAY BOYAUL_LIVER_CANCER_SUBCLASS_G123_UP LEE_AGING_NECORTEX_UP MCBRYAD_VERKENS_G12_SUBCLASS_G123_UP LEE_AGING_NECORTEX_UP MCBRYAD_VERKENS_G12_SUBCLASS_G123_UP LEE_AGING_NECORTEX_UP MCBRYAD_VERKENS_G12_SUBCLASS_G123_UP LEE_AGING_NECORTEX_UP MCBRYAD_NULER_RESTRICTION_MUSCLE_UP ZHAN MULTIPLE_MYELOMA_CD_N CAULIGH_RESTRICTION_MUSCLE_UP ZHAN MULTIPLE_MYELOMA_CD_UP MULLIGHAN_MLL_SIGNATURE_2_DN OKUMULRA_INFLAMMATORY_RESPONSE_LPS LEE_GR2_TARGETS_OF_SUBCLASS_G123_UP BEGEL_CONTEX_UP MULLIGHAN_MLL_SIGNATURE_2_DN OKUMULRA_INFLAMMATORY_RESPONSE_LPS LEE_GR2_TARGETS_OF_SH_AND_FLIT_DN WEIGEL_OXIDATIVE_STEM_STEM_ST_MAND_H2O2 MOND_HIPPOCAMPUS_PRENATL_AND_H2O2 MOND_HIPPOCAMPUS_PRENATL_AND_H2O2 MOND_HIPPOCAMPUS_PRENATLA_ AMIT_SERUM_RESPONSE_240_MCF10A GENTLES_LEVKEMIC_STEM_CELL_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 272 180 107 16 85 86 35 41 56 28	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.55\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.55\\ 0.66\\ 0.55\\ 0.65\\$	1.71 1.70 1.70
LAHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_OLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MVC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_OF_MUL_AP9_FUSION LEE_TARGETS_OF_MLL_AP9_FUSION LEE_TARGETS_OF_MLL_AP9_FUSION LEE_TARGETS_OF_MLL_AP9_FUSION CHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CL_L_WIH_13014_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_2_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PD_INTEGRNIN3_PATHWAY PD_INTEGRNIN3_P	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 52 44 87 36 94 43 52 44 87 36 94 43 272 180 107 16 85 86 35 41 56 28 40 <td>$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.74\\ 0.74\\ 0.74\\ 0.59\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.55\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.55\\ 0.65\\ 0.55\\ 0.65\\$</td> <td>1.71 1.70 1.70</td>	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.74\\ 0.74\\ 0.74\\ 0.59\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.55\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.55\\ 0.65\\ 0.55\\ 0.65\\$	1.71 1.70 1.70
LAHO_COLORECTAL_CANCER_SERRATED_UP CARD_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_RRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MLL_AP9_FUSION LEE_TARGETS_OF_MLL_AP9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PD_INTEGRIN3_PATHWAY BOYAUN_MULTIPLE_MEEADMA_UP MCBRYAN_WDEERTAL_BERAST_3_4WK_DN KARYO_CALORE_RESTRICTION_MUSCLE_UP ZHANU_MULTIPLE_MEEADMA_UP MULGIGH_RESTRICTION_MUSCLE_UP ZHANU_MULTIPLE_MEEADMA_UP MULGIGH_MULLSTER_OF_SONSE_LPS LE_EGGR_TARGETS_UP MULLIPLAM_MATORY_RESPONSE_LPS LE_EGGT_TARGETS_UP MEDIAT_DATHWAY BOYAUN_MULTIPLE_MEEATS	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 54 43 52 44 87 36 94 43 272 180 107 16 85 86 355 41 56 28 40 96	$\begin{array}{c} 0.68\\ 0.53\\ 0.53\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.52\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.55\\ 0.55\\ 0.65\\ 0.56\\$	1.71 1.70 1.70
LAHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_GRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MVC_AND_TFRC_UP REACTOME_P01_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MUC_AND_TFRC_UP REACTOME_P01_SIGNALING CHANG_POUSF1_TARGETS_UP UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TÄRGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGETS_OF_MUT_13Q14_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_2_UP BOYLAN_MULTIPLE_MVELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRINS_PATHWAY PID_KIT_	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 272 180 107 16 85 86 35 41 56 28 40 96 275	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.59\\ 0.54\\ 0.74\\ 0.46\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.55\\ 0.61\\ 0.54\\ 0.55\\ 0.55\\ 0.51\\ 0.54\\ 0.56\\ 0.55\\ 0.65\\ 0.65\\ 0.65\\ 0.65\\ 0.65\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.65\\$	1.71 1.70 1.70
LAHO_COLORECTAL_CANCER_SERRATED_UP CARO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_OLUSTER_P3 KEGG_RIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TRC_UP REACTOME_P01_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MYC_AND_TRC_UP REACTOME_TON_SOFTUNED_UP CHANG_POUSF1_TARGETS_UP STRANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERX2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13014_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_K1T_PATHWAY PD_K1T_PATHWAY DEGYAULT_UKER_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCORTEX_UP MCRERVAN_PUBERTAL BREAST_3_4WK DN KAYO_CALORIER_ESTICTION_MUSCLE_UP ZHANKA_TARGETS_UP STAN_WULTIPLE_MYELOMA_CD_UP MCRERVAN_PUBERTAL BREAST_3_4WK DN KAYO_CALORIER_ESTATION_UP MCRERVAN_PUBERTAL BREAST_3_4WK DN KKYO_CALORIER_ESTERCTON_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_CD_UP MCLIGHAN_MULSIGNATURE_2_DN OULUIGHAN_MIL_SIGNATURE_2_DN OULUIGHAN_MIL_SIGNATURE_2_DN OULUIGHAN_TARGETS_UP STATURE_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCORTEX_UP MCLIGHAN_MULTIPLE_MYELOMA_CD_UP MCLARGYNA_PUBERTAL BREAST_3_4WK DN MCKAYO_CALORIE_RESTRCTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_CD_UP MULLIGHAN_MIL_SIGNATURE_2_DN OULUIGHAN_MIL_SIGNATURE_2_DN OULUIGHAN_MIL_SIGNATURE_2_DN OULUIGHAN_MIL_SIGNATURE_2_DN OULUIGHAN_TARGETS_UP REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY BHATTACHARYA_EMBRYONIC_STEM_CELL JUBAN_TARGETS_UP_REMATAL AMIT_SERUM_RESPONSE_240_MCF10A GENTLES_LEUKEMIC_STEM_CELL_UP KEGG_TYPE_I_DIABETES_MELITUS HANTOLA_SEZARY_SYNDROM_UP OKMANOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_UP	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 52 44 87 36 94 43 52 44 87 36 94 43 52 41 56 28 40 96 25	$\begin{array}{c} 0.68\\ 0.53\\ 0.53\\ 0.58\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.59\\ 0.54\\ 0.74\\ 0.74\\ 0.74\\ 0.74\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.55\\ 0.55\\ 0.65\\ 0.65\\ 0.65\\ 0.65\\ 0.63\\ 0.55\\ 0.63\\ 0.56\\ 0.56\\$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CARRO_LIVER_DEVELOPMENT_UP MCCABE_HOXGE TARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_P1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MIL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTURAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_PITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13014_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CALVING_RESTRICTONSCIPUEN MURENGA_STATSA_TARGETS_UP DI_NITEGRIN3_PATHWAY PD_INTEGRIN3_PATHWAY PD_INTEGRIN3_PATHWAY DOYAULT_UVER_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCONTEX_UP KARYO_ALORIE_STRUCTONSCIPUEN MKARYO_ALORIE_STRUCTONSCIPUEN MERENGA_STATAGETS_OF_PINE MULLIGHAN_MALTON_E2_DN MCRERVAN_MERENAN_MAY DOYAULT_LIVER_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCONTEX_UP MCRERVAN_WERTAL_RESTRUCTON_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_C_DN KAYO_CALORIE_RESTRUCTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_CD_UP MULLIGHAN_MIL_SIGNATURE_2_DN OKUMURA_INFLAMMATORY_RESPONSE_LPS LEE_GONT_CANCER_SUBCLASS_G123_UP LEE_AGING_NEOCONTEX_UP MULLIGHAN_MIL_SIGNATURE_2_DN OKUMURA_INFLAMMATORY_RESPONSE_LPS LEE_GONT_CHAPERONIN_TUBULIN_FOLDING_PATHWAY BIATTACHARYA_MERSPONSE_LPS LEE_GONT_CHAPERONIN_TUBULIN_FOLDING_PATHWAY BIATTACHARYA_MERSPONSE_240_MCF10A GENTAL_VER_SONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SELWARESPONSE_240_MCF10A GENTAL_SEL	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 54 43 52 44 87 36 94 43 272 180 107 16 85 86 35 41 56 28 40 96 25 56	$\begin{array}{c} 0.68\\ 0.53\\ 0.58\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.52\\ 0.59\\ 0.54\\ 0.74\\ 0.70\\ 0.42\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.59\\ 0.54\\ 0.55\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.51\\ 0.55\\ 0.66\\ 0.69\\ 0.53\\ 0.55\\ 0.65\\ 0.69\\ 0.53\\ 0.55\\ 0.65\\ 0.69\\ 0.53\\ 0.55\\$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER_DEVELOPMENT_UP MCCABE_HOXC6_TARGETS_DN BROWN_INYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_GRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MCC_AND_TRC_UP REACTOME_P01_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MCC_AND_TRC_UP REACTOME_P01_SIGNALING CHANG_POUSF1_TARGETS_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MARK_PATHWAY HASLINGER_B_CL_WITH_13014_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PID_INTEGRIN3_PATHWAY PID_KT_PATHWAY BOYAULT_UVERC_CANCER_SUBCLASS_G123_UP LEE_ARGINS_NELERSUBCLASS_G123_UP LEE_ARGINS_RESPONSE_LPS LEE_ARGINS_NELERSUBCLASS_G123_UP LEE_ARGINS_NELERSUBCLASS_G123_UP LEE_ARGINS_NELERSUBCLASS_G123_UP LEE_ARGINS_NELERSUBCLASS_G123_UP LEE_ARGINS_NELERSUBCLASS_G123_UP LEE_ARGINS_NELERSUBCLASS_G123_UP LEE_ARGINS_N	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 36 94 43 52 44 36 94 43 272 180 107 16 85 86 35 41 56 28 40 96 25 56 33	0.68 0.53 0.55 0.51 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42 0.55 0.59 0.54 0.74 0.46 0.59 0.54 0.59 0.54 0.59 0.54 0.59 0.54 0.59 0.54 0.55 0.67 0.55 0.61 0.54 0.55 0.54 0.55 0.54 0.55 0.55 0.55 0.63 0.55 0.66 0.66 0.55 0.65 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.65 0.55 0.55 0.55 0.65 0.55 0.55 0.65 0.55 0.65 0.55	1.71 1.70 1.70
LAHD_COLORECTAL_CANCER_SERATED_UP CARD_LIVER_DEVELOPMENT_UP MCABE_HOXGETARGETS_DN BROWN_MYELOID_CELL_DEVELOPMENT_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CLUSTER_P3 KEGG_PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_P01_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_MIL_AF9_FUSION LEE_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_PTHTHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WIERENGA_STATSA_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13014_DELETION MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CORNOLT_TERATOMA_UP MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_MYELOMA_C_DN CONCORTEX_UP DI_NIT_PATHWAY PID_INTEGRIN3_PATHWAY PID_INTEGRIN_TESEV_NECELL_UP KEACTOME_DOST_PATHWAY PID_INTEGRIN_TESEV_NECELL_UP KEACTOME_DIABETES_MELLITUS HATACHARY_ENDUNCESTEM_CELL_UP	$\begin{array}{c} C2 \\ C2 $	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 272 180 107 16 85 86 35 41 56 28 40 96 25 56 33 32	$\begin{array}{c} 0.68\\ 0.53\\ 0.53\\ 0.51\\ 0.51\\ 0.70\\ 0.46\\ 0.68\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.74\\ 0.70\\ 0.42\\ 0.55\\ 0.54\\ 0.74\\ 0.74\\ 0.46\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.67\\ 0.43\\ 0.59\\ 0.54\\ 0.57\\ 0.61\\ 0.54\\ 0.55\\ 0.51\\ 0.54\\ 0.55\\ 0.55\\ 0.55\\ 0.55\\ 0.65\\ 0.65\\ 0.65\\ 0.65\\ 0.65\\ 0.65\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.56\\ 0.63\\ 0.58\\ 0.61\\ 0.58\\ 0.58\\ 0.61\\ 0.58\\ 0.61\\ 0.58\\ 0.61\\ 0.58\\ 0.61\\ 0.58\\ 0.61\\ 0.58\\ 0.61\\ 0.58\\ 0.61\\ 0.58\\ 0.58\\ 0.61\\ 0.58\\ 0.58\\ 0.61\\ 0.58\\ 0.58\\ 0.61\\ 0.58\\ 0.58\\ 0.61\\ 0.58\\$	1.71 1.70 1.70
LAIHO_COLORECTAL_CANCER_SERRATED_UP CAIRO_LIVER DEVELOPMENT_UP MCCABE_HOXC6 TARGETS DN BROWN, MYELOID_CELL_DEVELOPMENT_UP EILCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN KEGG_GRAFT_VERSUS_HOST_DISEASE GAVIN_FOXP3_TARGETS_CULSTER_P3 KEGG PRIMARY_IMMUNODEFICIENCY ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KKUMAR_TARGETS_OF_MYC_AND_TFRC_UP REACTOME_PD1_SIGNALING CHANG_POUSF1_TARGETS_UP KUMAR_TARGETS_OF_PTCH1_AND_SUFU_UP ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN GOTZMANN_PPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP KORKOLA_TERATOMA_UP WERENGA_STAT5A_TARGETS_UP ST_ERK1_ERK2_MAPK_PATHWAY HASLINGER_B_CLL_WITH_13O14_DELETION MYAGAWA_TARGETS_OF_EWSRT_ETS_FUSIONS_UP HEIDENBLAD_AMPLICON_12P11_12_UP BOYLAN_MULTIPLE_WFELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PD_INTEGRIN3_PATHWAY DD_INTEGRIN3_PATHWAY BOYALUT_ULTIPLE_WFELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PD_INTEGRIN3_PATHWAY BOYALUT_ULTIPLE_WFELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PD_INTEGRIN3_PATHWAY BOYALUT_ULTIPLE_WFELOMA_C_DN CHUNG_BLISTER_CYTOTOXICITY_DN PD_INTEGRIN3_PATHWAY BOYALUT_ULTIPLE_WFELOMA_C_DN CHUNG_RUSTER_SUBCLASS_G123_UP LEE_AGING_NECONTEX_UP MCRERYAN_PUBERTAL_BREAST_3_4WK_DN KAYO_CALORIE_RESTRICTION_MUSCLE_UP ZHAN_MULTIPLE_MYELOMA_CD2_UP MULLIGHAN_ML_SIGNATURE_2_DN OKUMUNGA_INFLAMMATORY_RESPONSE_LPS LE_EAGING_NOTX_RESPONSE_LPS LE_EAGING_NOTX_RESPONSE_LPS LE_EAGING_NTW_RESPONSE_LPS LE_EAGING_NTW_RESPONSE_LPS LE_EAGING_NTW_RESPONSE_LPS LE_EAGING_NTW_RESPONSE_LPS LE_EAGING_SONSTURE_2_DN OKUMUNGA_INFLAMMATORY_RESPONSE_LPS LE_EAGING_TARGETS_OF_SNILAND_FUL_DN VEGEL_OXIAN_WERSPONSE_S_DT_SNILAND_SUB_ MODY_HIPPCCAMPUS_PRENATAL AMIT_SERUM_RESPONSE_20_OCCURRENCE_UP DELASERNA_MYOD_TARGETS_DN BIOCARTA_MPR_PATHWAY VALK_AM_CLUSTER_10 UL_UTUMOK_NENCONCES_UP	$\begin{array}{c} C2 \\ C2 $	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 272 180 107 16 85 86 35 41 56 28 40 96 25 56 33 32 25 56 33 32 25	0.68 0.53 0.55 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42 0.52 0.59 0.54 0.74 0.70 0.42 0.52 0.59 0.54 0.74 0.74 0.70 0.43 0.59 0.54 0.59 0.54 0.57 0.54 0.57 0.54 0.55 0.54 0.55 0.54 0.55 0.54 0.55 0.55	1.71 1.70 1.70
LAHEQ COLORECTAL CANCER SERRATED UP CARE LIVER DEVELOPMENT UP MCCABE HOXO6 TARGETS DN BROWN, MYELOID CELL DEVELOPMENT UP FULCHER INFLAMMATORY RESPONSE LECTIN VS LPS DN KEGG GRAFT VERSUS HOST DISEASE GAVIN FORY TARGETS OF MYC AND TFRC UP REACTOME PD1 SIGNALING CHANG POUSF1 TARGETS OF MYC AND TFRC UP REACTOME PD1 SIGNALING CHANG POUSF1 TARGETS OF MYC AND TFRC UP REACTOME PD1 SIGNALING CHANG POUSF1 TARGETS OF MYC AND TRACUP REACTOME PD1 SIGNALING CHANG POUSF1 TARGETS OF MYC AND TRACUP REACTOME PD1 SIGNALING CHANG POUSF1 TARGETS OF MIL AF9 FUSION LEE TARGETS OF FUCH AND SUFU UP ZHANG ANTURAL RESPONSE TO RIBAVRIN DN GOTZMANN EPITHELIAL TO MESENCHYMAL TRANSITION_UP KORKOLA TERATOMA_UP WIRERNGA STATSA TARGETS UP ST_ERK1 ERK2 MAPK PATHWAY HASLINGER B CLL WITH 13014 DELETION MYAGAWA TARGETS OF EWSRI ETS FUSIONS_UP HEIDENBLAD AMPLICON 12P1 12 UP DOYAULT LIVER CANCER SUBCLASS G123 UP LEE AGING NEOCORTEX UP MCBRIAN PUERTHAU BAY AWAY PID INTEGRNS PATHWAY PID INTEGRNS PATHWAY PID INTEGRNS PATHWAY PID LIVER CANCER SUBCLASS G123 UP LEE AGING NEOCORTEX UP MCBRIAN PUERTAL BREAST 3.4WK DN KKAYO CALORE RESTRICTION MUSCLE UP ZHAN MULTIPLE MYELOMA CD UP MCBRIAN PUERTAL BREAST 3.4WK DN KKAYO CALORE RESTRICTION MUSCLE UP ZHAN MULTIPLE MELOMA CD UP MCBRIAN PUERTAL BREAST 3.4WK DN KKAYO CALORE RESTRICTION MUSCLE UP ZHAN MULTIPLE MELOMA CD UP MCBRIAN PUERTAL BREAST 3.4WK DN KKAYO CALORE RESTRICTION MUSCLE UP ZHAN MULTIPLE MELOMA CD2 UP MULGHAN MULTIPLE MELOMA CD2 UP MULGHAN MULTIPLE MELOMA CD2 UP MULGHAN MULTIPLE MELOMA CD2 UP MULGHAN FILAMBATORY RESPONSE LPS LE EGR2 TARGETS UP RESPONSE LPS LE EGR2 TARGETS UP REATAL AMIT SERUM RESPONSE 240 MCF10A GENTLES LEUKEMIC STEM CELL JUBAN TARGETS OF SPIT BAI AND H202 MODY HIPDOCAMPUS PREATAL AMIT SERUM RESPONSE 240 MCF10A GENTLES LEUKEMIC STEM CELL JUBAN TARGETS OF SPIT BAI AND H202 MODY HIPDOCAMPUS PREATAL AMIT SERUM RESPONSE 240 MCF10A GENTLES LEUKEMIC STEM CELL UP KEAGG TYPE J DABETES MELLTUS HAHTACHARYA EMBRYONIC STEM CELL JUBAN TARGETS OF SPIT AND H202 MODY HIPDOLAMEST SOF SPIT AND H202 MODY	C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C	112 166 21 161 438 36 153 35 81 17 15 393 52 49 68 15 209 32 23 249 33 54 43 52 44 87 36 94 43 52 44 87 36 94 43 52 44 87 36 94 43 272 180 107 16 85 86 35 41 56 28 40 <	0.68 0.53 0.55 0.51 0.51 0.70 0.46 0.68 0.55 0.74 0.70 0.42 0.55 0.59 0.54 0.74 0.74 0.74 0.74 0.70 0.59 0.59 0.54 0.59 0.54 0.59 0.54 0.59 0.54 0.57 0.63 0.55 0.54 0.55 0.54 0.55 0.54 0.55 0.55	1.71 1.70 1.70

TENEDINI_MEGAKARYOCYTE_MARKERS	C2	66	0.53	1.70
FARMER_BREAST_CANCER_CLUSTER_4	C2	19	0.81	1.70
GENTILE_UV_RESPONSE_CLUSTER_D6	C2	35	0.64	1.70
GAVIN FOXP3 TARGETS CLUSTER P4	C2	98	0.49	1.70
CAIRO PML TARGETS BOUND BY MYC UP	C2	23	0.67	1.70
GAJATE_RESPONSE_TO_TRABECTEDIN_UP	C2	65	0.57	1.70
SIG_CHEMOTAXIS	C2	45	0.52	1.70
BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN	C2	40	0.55	1.70
LINDSTEDT_DENDRITIC_CELL_MATURATION_A	C2	65	0.66	1.70
ROY_WOUND_BLOOD_VESSEL_UP	C2	49	0.65	1.70
HINATA_NFKB_TARGETS_FIBROBLAST_UP	C2	84	0.59	1.70
YANG_BREAST_CANCER_ESR1_DN	C2	25	0.67	1.70
PID INTEGRIN CS PATHWAY	C2	26	0.65	1.69
PAPASPYRIDONOS UNSTABLE ATEROSCLEROTIC PLAQUE UP	C2	52	0.65	1.69
PID_ALK1_PATHWAY	C2	26	0.61	1.69
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	C2	81	0.54	1.69
DAVICIONI_MOLECULAR_ARMS_VS_ERMS_DN	C2	177	0.48	1.69
SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES	C2	36	0.62	1.69
REACTOME_PROTEIN_FOLDING	C2	49	0.63	1.69
GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN	C2	44	0.61	1.69
SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_DN	C2	45	0.59	1.69
VERRECCHIA_RESPONSE_TO_TGFB1_C1	C2	17	0.71	1.69
GAVIN_FOXP3_TARGETS_CLUSTER_T4	C2	90	0.58	1.69
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP	C2	67	0.66	1.69
MCDOWELL_ACUTE_LUNG_INJURY_UP	C2	45	0.65	1.69
ONO_AML1_TARGETS_UP	C2	24	0.65	1.69
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_UP	C2	44	0.64	1.69
HOLLMANN_APOPTOSIS_VIA_CD40_UP	C2	194	0.50	1.69
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	C2	125	0.46	1.69
LEI_MYB_TARGETS	C2	312	0.50	1.69
POS_HISTAMINE_RESPONSE_NETWORK	C2	32	0.60	1.69
JIANG_AGING_CEREBRAL_CORTEX_DN	C2	52	0.57	1.69
PID TNF PATHWAY	C2	46	0.57	1.69
REACTOME 1CAM INTERACTIONS	C2	83	0.46	1 69

Variable	ICF		no	on ICF	Fisher test	
variable	%	n# patients	%	n# patients	p-value	
General Clinicopathological variables						
Age						
≥65 years	53%	(52/98)	47%	(46/98)		
<65 years	46%	(45/98)	23%	(23/98)	0.11	
Gender						
Female	29%	(28/97)	14%	(10/69)	0.04	
Male	71%	(69/97)	86%	(59/69)		
Etiology						
HCV	58%	(57/98)	26%	(18/69)	<0.0001	
HBV	16%	(16/98)	36%	(25/69)	0.01	
Alcohol	9%	(9/98)	19%	(13/69)	0.10	
Others	13%	(13/98)	16%	(11/69)	0.66	
BCLC stage						
BCLC 0 or A	76%	(74/98)	91%	(63/69)		
BCLC B or C	22%	(22/98)	7%	(5/69)	0.01	
Blood tests						
AFP levels (>100 mg/dL)	24%	(23/96)	24%	(16/67)	1.00	
Albumin levels (<3.5 gr/L)	18%	(17/95)	4%	(3/68)	0.01	
Bilirubin (>1 mg/dL)	53%	(50/94)	28%	(19/68)	0.00	
Platelet count (<100,000/mm3)	29%	(28/96)	12%	(8/68)	0.01	

Supplementary Table 5. Correlation of the immune-mediated cancer field with clinicopathological characteristics.

Supplementary Table 6. Uni- and Multivariate Analysis of Survival in HCC Patients (Heptromic cohort, n=167)

	Univariate analysis		Multivariate analysis (cox's regression)			
Variable	p-value		CI (95% low-high limits)	p-values		
Clinicopathological variables						
Vascular invasion	<0.001	1.79	1.11-2.92	0.018		
Multinodularity	<0.001	2.67	1.56-4.58	<0.001		
BCLC stage B or C	0.006					
HCV etiology	0.009					
Platelet count (<100,000/mm3)	0.012	2.23	1.32-3.78	0.003		
Satellites	0.016					
Gender	0.024					
Albumin levels (<3.5 gr/L)	0.029					
Tumor size (>3.5cm)	0.039					
Prognostic liver tissue-based transcriptomic profiles						
Immune-mediated cancer-field (ICF, current manuscript)	0.001					

Supplementary Table 7. 172-gene signatures of immune-mediated cancer field.			
Gene name	Immune-mediated field	Immune-mediated field subtype	
PTX3	ICF	Immunosuppressive	
IL6	ICF	Immunosuppressive	
MMP7	ICF	Immunosuppressive	
IL8	ICF	Immunosuppressive	
S100A9	ICF	Immunosuppressive	
CXCL3	ICF	Immunosuppressive	
SPP1	ICF	Immunosuppressive	
IL1B	ICF	Immunosuppressive	
FNDC1	ICF	Immunosuppressive	
PTGS2	ICF	Immunosuppressive	
CFTR	ICF	Immunosuppressive	
AREG	ICF	Immunosuppressive	
THBS2	ICF	Immunosuppressive	
FABP4	ICF	Immunosuppressive	
LOH3CR2A	ICF	Immunosuppressive	
COL15A1	ICF	Immunosuppressive	
HBG1	ICF	Immunosuppressive	
EMP1	ICF	Immunosuppressive	
VCAN	ICF	Immunosuppressive	
S100A8	ICF	Immunosuppressive	
COL1A2	ICF	Immunosuppressive	
FHL2	ICF	Immunosuppressive	
CD93	ICF	Immunosuppressive	
CLIC6	ICF	Immunosuppressive	
TAC1	ICF	Immunosuppressive	
NTS	ICF	Immunosuppressive	
AKR1B10	ICF	Immunosuppressive	
DEFA1	ICF	Immunosuppressive	
HSPA6	ICF	Immunosuppressive	
STMN2	ICF	Immunosuppressive	
EFEMP1	ICF	Immunosuppressive	
HSPA7	ICF	Immunosuppressive	
GREM1	ICF	Immunosuppressive	
CH25H	ICF	Immunosuppressive	
SERPINB2	ICF	Immunosuppressive	
CCDC80	ICF	Immunosuppressive	
PMEPA1	ICF	Immunosuppressive	
CCL2	ICF	Immunosuppressive	
FCGR3B	ICF	Immunosuppressive	
IFI6	ICF	Proinflammatory	
CXCL10	ICF	Proinflammatory	
OASL	ICF	Proinflammatory	
IF127	ICF	Proinflammatory	
IFIT3	ICF	Proinflammatory	
EPSTI1	ICF	Proinflammatory	
ISG15	ICF	Proinflammatory	
MX1	ICF	Proinflammatory	
DDX60	ICF	Proinflammatory	
RSAD2	ICF	Proinflammatory	
OAS1	ICF	Proinflammatory	
	1	· · · · · · · · · · · · · · · · · · ·	

IFIT1	ICF	Proinflammatory
OAS2	ICF	Proinflammatory
HERC5	ICF	Proinflammatory
IFIT2	ICF	Proinflammatory
STAT1	ICF	Proinflammatory
OAS3	ICF	Proinflammatory
CXCL9	ICF	Proinflammatory
IF144	ICF	Proinflammatory
CXCL11	ICF	Proinflammatory
RTP4	ICF	Proinflammatory
GABBR1	ICF	Proinflammatory
UBD	ICF	Proinflammatory
GBP4	ICF	Proinflammatory
LAMP3	ICF	Proinflammatory
B2M	ICF	Proinflammatory
PSME1	ICF	Proinflammatory
UBE2L6	ICF	Proinflammatory
PSMB9	ICF	Proinflammatory
HLA-B	ICF	Proinflammatory
HLA-A	ICF	Proinflammatory
IFITM1	ICF	Proinflammatory
RARRES3	ICF	Proinflammatory
TAP1	ICF	Proinflammatory
GBP1		Proinflammatory
CYP3A7	ICF	Proinflammatory
HIA-F		Proinflammatory
BST2	ICF	Proinflammatory
TDRD7	ICF	Proinflammatory
IFI35		Proinflammatory
CXCI 13		High Infiltrate
MS4A1	ICF	High Infiltrate
CR2	ICE	High Infiltrate
BANK1	ICE	High Infiltrate
FCRL3	ICE	High Infiltrate
C4orf7	ICE	High Infiltrate
IGKV3D-11	ICE	High Infiltrate
AIM2	ICE	High Infiltrate
POLI2AF1		High Infiltrate
CCR7		High Infiltrate
MMP9	ICE	High Infiltrate
CD52		High Infiltrate
TRBC1		High Infiltrate
ТК		High Infiltrate
CCI 21		High Infiltrate
		High Infiltrate
GZMK		High Infiltrate
BCI 11B		High Infiltrate
1 \ 75		High Infiltrate
EVB		High Infiltrate
PRKCH		High Infiltrate
		High Infiltrate
TPBC2		High Infiltrato
		I IIGH IIIIIII ale

RGS10	ICF	High Infiltrate
TRAC	ICF	High Infiltrate
TRAJ17	ICF	High Infiltrate
TRAV20	ICF	High Infiltrate
TRAF5	ICF	High Infiltrate
DOCK10	ICF	High Infiltrate
NLRC5	ICF	High Infiltrate
RHOH	ICF	High Infiltrate
PVRIG	ICF	High Infiltrate
STAG3	ICF	High Infiltrate
CD8A	ICF	High Infiltrate
GPR18	ICF	High Infiltrate
RAC2	ICF	High Infiltrate
LAPTM5	ICF	High Infiltrate
WDFY4	ICF	High Infiltrate
CD48	ICF	High Infiltrate
CD2	ICF	High Infiltrate
LTB	ICF	High Infiltrate
IRF4	ICF	High Infiltrate
GIMAP7	ICF	High Infiltrate
EMB	ICF	High Infiltrate
EMBP1	ICF	High Infiltrate
DOCK11	ICF	High Infiltrate
LCK	ICF	High Infiltrate
CST7	ICF	High Infiltrate
CCL5	ICF	High Infiltrate
CD53	ICF	High Infiltrate
PRKCB	ICF	High Infiltrate
PTPRC	ICF	High Infiltrate
GZMA	ICF	High Infiltrate
UGT2B17	non-ICF	Non-immune-mediated
SLC16A12	non-ICF	Non-immune-mediated
ALPK2	non-ICF	Non-immune-mediated
CYP2C19	non-ICF	Non-immune-mediated
FAM151A	non-ICF	Non-immune-mediated
LOC646982	non-ICF	Non-immune-mediated
DHRS2	non-ICF	Non-immune-mediated
TRIM55	non-ICF	Non-immune-mediated
CYP4A22	non-ICF	Non-immune-mediated
CYP26A1	non-ICF	Non-immune-mediated
ADCY1	non-ICF	Non-immune-mediated
PPP1R3G	non-ICF	Non-immune-mediated
C5orf27	non-ICF	Non-immune-mediated
MOGAT1	non-ICF	Non-immune-mediated
FITM1	non-ICF	Non-immune-mediated
USH2A	non-ICF	Non-immune-mediated
CYP1A1	non-ICF	Non-immune-mediated
CPS1-IT	non-ICF	Non-immune-mediated
RAPH1	non-ICF	Non-immune-mediated
CNDP1	non-ICF	Non-immune-mediated
SULT1E1	non-ICF	Non-immune-mediated
ABCC6P1	non-ICF	Non-immune-mediated

KCNN2	non-ICF	Non-immune-mediated
PCOLCE2	non-ICF	Non-immune-mediated
BCHE	non-ICF	Non-immune-mediated
HEPACAM	non-ICF	Non-immune-mediated
LPAL2	non-ICF	Non-immune-mediated
ADAMTS17	non-ICF	Non-immune-mediated
MME	non-ICF	Non-immune-mediated
SLC22A25	non-ICF	Non-immune-mediated
LPA	non-ICF	Non-immune-mediated
IDO2	non-ICF	Non-immune-mediated
BBOX1	non-ICF	Non-immune-mediated
CUX2	non-ICF	Non-immune-mediated
AKR1D1	non-ICF	Non-immune-mediated
PPP1R1A	non-ICF	Non-immune-mediated
SNORA59A	non-ICF	Non-immune-mediated
SNORA59B	non-ICF	Non-immune-mediated
GPR125	non-ICF	Non-immune-mediated
CYP1A2	non-ICF	Non-immune-mediated

Supplementary Table 8. Uni- and Multivariate Analysis of Survival in HCC Patients (Validation cohort, n=225)

	Univariate analysis		Multivariate analysis		
			(cox's regression)		
Variable	p-value	HR	CI (95% Iow-high limits)	p-values	
Clinicopathological variables					
Vascular invasion	0.02				
Multinodularity	0.13				
Satellites	<0.001	2.22	0.87-5.67	0.096	
Albumin levels (<3.5 gr/L)	0.016	2.6	0.89-7.58	0.08	
Tumor size (>3.5cm)	0.003	2.66	1.13-6.25	0.025	
AFP (>100mg/dL)	0.059	2.28	0.96-5.56	0.064	
Prognostic liver tissue-based transcriptomic profiles					
Immune-mediated cancer-field (ICF, current manuscript)	0.001	2.73	1.09-6.83	0.032	

Supplementary Table 9. List of 300 differentially expressed genes in non-tumor liver parenchyma of DEN/CCl4 mice, treated with vehicle vs liver of healthy control mice (FC \geq 1.5, FDR q<0.05).

Symbol	Fold change	p value	FDR q value
Up-regulated			-
Gpnmb	5.01	0.00	0.00
Apoa4	4.86	0.00	0.00
Mmp12	4.05	0.00	0.00
Col1a2	3.9	0.00	0.00
Ly6d	3.88	0.00	0.00
S100a8	3.82	0.00	0.00
Ccl5	3.7	0.00	0.01
Mt2	3.61	0.00	0.03
Dpt	3.61	0.00	0.00
2010003K11Rik	3.57	0.00	0.00
Gstm3	3.45	0.00	0.00
Mt1	3.14	0.00	0.02
Ms4a7	3.11	0.00	0.01
Cpe	3 11	0.00	0.00
Ubd	3.1	0.00	0.00
Hamp2	3.07	0.00	0.00
Tuba8	3.06	0.00	0.00
Mtmr11	3.01	0.00	0.00
Mfsd2a	2.94	0.00	0.00
Tinag	2.01	0.00	0.01
lum	2.02	0.00	0.00
Cond1	2.91	0.00	0.00
Akr1c18	2.87	0.00	0.04
Crtan	2 78	0.00	0.01
Cdkn2c	2 71	0.00	0.00
lfi27l2b	2.69	0.00	0.00
Mmp2	2.67	0.00	0.00
Abcd2	2.67	0.00	0.00
Cvp7a1	2.62	0.00	0.02
Emp1	2.59	0.00	0.01
Cd24a	2.58	0.00	0.00
Col3a1	2.58	0.00	0.00
lgha	2.57	0.00	0.01
Prom1	2.56	0.00	0.01
S100a9	2.56	0.00	0.00
Lepr	2.53	0.00	0.00
Nek2	2.48	0.00	0.04
Ccdc80	2.44	0.00	0.00
Cdk1	2.39	0.00	0.00
2210013O21Rik	2.39	0.00	0.00
Ms4a6b	2.37	0.00	0.00
Tmem86a	2.36	0.00	0.01
Sparcl1	2.34	0.00	0.01
Rnf145	2.3	0.00	0.01
Hsd17b6	2.3	0.00	0.01
Cenpa	2.23	0.00	0.00
•			

Clec7a	2.2	0.00	0.00
Blnk	2.17	0.00	0.04
Cyp39a1	2.17	0.00	0.00
Slco1a4	2.15	0.00	0.04
lgkc	2.12	0.00	0.03
Sftpd	2.11	0.00	0.04
Olfml3	2.1	0.00	0.04
Lgals3	2.1	0.00	0.00
Jchain	2.1	0.00	0.03
Lgals4	2.08	0.00	0.00
Ttc39aos1	2.08	0.00	0.01
Col5a2	2.08	0.00	0.00
S100a6	2.08	0.00	0.02
Sace	2.07	0.00	0.00
Klf4	2.06	0.00	0.03
Gpc1	2.04	0.00	0.02
Tceal8	2.02	0.00	0.00
Fstl1	2.01	0.00	0.00
Slc39a4	2.01	0.00	0.01
Pvab	1.98	0.00	0.04
Cbr3	1.98	0.00	0.01
Golm1	1.98	0.00	0.00
Lipo1	1.98	0.00	0.04
Coro1a	1.97	0.00	0.01
l vve1	1.96	0.00	0.02
Sulf2	1.96	0.00	0.01
Spink1	1.96	0.00	0.05
Cbr1	1.95	0.00	0.00
Col6a3	1.95	0.00	0.01
Abcc4	1.95	0.00	0.00
Cvp4a31	1.93	0.00	0.02
Pf4	1.92	0.00	0.00
ll2ra	1.91	0.00	0.02
Vim	1.91	0.00	0.01
Serpina3g	1.9	0.00	0.01
Plat	1 89	0.00	0.01
Rhhdf1	1 89	0.00	0.01
Uan111	1.87	0.00	0.01
Ptorc	1.87	0.00	0.03
Hvcn1	1.86	0.00	0.02
I thn2	1.85	0.00	0.02
Etop2 Fbn1	1.85	0.00	0.02
Defh1	1.80	0.00	0.04
Tom1	1.84	0.00	0.00
Nina1	1.84	0.00	0.00
Man	1.83	0.00	0.00
ltaa8	1.00	0.00	0.03
Ληχο1	1.83	0.00	0.02
Pdzk1in1	1.00	0.00	0.00
Cona?	1.02	0.00	0.04
Snha1	1.02	0.00	0.00
Col1a1	1.02	0.00	0.04
Contan	1.01	0.00	0.02

H2-Eb1	1.8	0.00	0.00
Spc25	1.79	0.00	0.01
Klrd1	1.79	0.00	0.04
Cdt1	1.79	0.00	0.01
Armcx4	1.78	0.00	0.01
Map4k4	1.77	0.00	0.01
Abcb1a	1.77	0.00	0.05
Ect2	1.77	0.00	0.02
Cst2rb2	1.76	0.00	0.03
ltih5	1.76	0.00	0.01
Col6a2	1.75	0.00	0.01
Ms4a4b	1.75	0.00	0.04
Steap2	1.74	0.00	0.00
Nid1	1.74	0.00	0.01
Rnaseh2b	1.74	0.00	0.01
lcam1	1.74	0.00	0.04
Col4a2	1.74	0.00	0.01
Ctla2a	1.74	0.00	0.01
Mad2l1	1.73	0.00	0.01
Pecam1	1.73	0.00	0.02
H2-Ab1	1.73	0.00	0.03
Cyp3a44	1.73	0.00	0.05
Aim1	1.72	0.00	0.03
Csrp1	1.72	0.00	0.01
Glipr1	1.71	0.00	0.01
Plcg2	1.7	0.00	0.01
Cd52	1.7	0.00	0.02
Sh3bgrl3	1.7	0.00	0.01
Bicc1	1.7	0.00	0.02
Postn	1.7	0.00	0.01
Gdf10	1.7	0.00	0.00
Tmtc2	1.7	0.00	0.05
Psat1	1.69	0.00	0.01
Arl2bp	1.69	0.00	0.04
Acot9	1.69	0.00	0.05
Npdc1	1.69	0.00	0.03
Cmtm7	1.68	0.00	0.03
Cybb	1.68	0.00	0.04
Tmem164	1.67	0.00	0.01
Rdh9	1.67	0.00	0.00
Trim24	1.67	0.00	0.03
Sparc	1.67	0.00	0.00
Bax	1.66	0.00	0.00
Sirpa	1.66	0.00	0.03
Gm32031	1.66	0.00	0.00
Fmo4	1.65	0.00	0.02
Col4a5	1.65	0.00	0.02
Itpripl2	1.64	0.00	0.00
Tmem178	1.64	0.00	0.03
Hpse	1.64	0.00	0.02
Ppic	1.64	0.00	0.03

Laptm5	1.64	0.00	0.02
Myof	1.63	0.00	0.04
Gja1	1.63	0.00	0.01
Rab3d	1.62	0.00	0.02
St3gal5	1.62	0.00	0.02
Col4a1	1.62	0.00	0.00
Fam84b	1.62	0.00	0.01
Cdca3	1.62	0.00	0.04
H2-Aa	1.62	0.00	0.03
Cers6	1.61	0.00	0.04
Ptgr1	1.61	0.00	0.04
Plekho1	1.61	0.00	0.03
Fam46a	1.6	0.00	0.03
Zfp53	1.6	0.00	0.03
Chtf8	1.6	0.00	0.02
Mfge8	1.6	0.00	0.03
Pam	1.6	0.00	0.01
Cd9	1.6	0.00	0.04
Rhoc	1.59	0.00	0.00
Adcy7	1.59	0.00	0.00
Soat1	1.59	0.00	0.01
Cd74	1.59	0.00	0.03
Slc6a8	1.58	0.00	0.02
lsyna1	1.58	0.00	0.03
Cxcl16	1.57	0.00	0.04
Ppap2c	1.57	0.00	0.02
Arhgap11a	1.57	0.00	0.03
Cygb	1.57	0.00	0.04
Mapkapk3	1.56	0.00	0.03
Setd7	1.56	0.00	0.01
Ctss	1.56	0.00	0.01
Tubb6	1.55	0.00	0.02
Phlda3	1.55	0.00	0.03
Lxn	1.55	0.00	0.02
Ptprcap	1.55	0.00	0.02
Tagln2	1.54	0.00	0.02
Pou2af1	1.53	0.00	0.02
Fam102b	1.52	0.00	0.01
Mndal	1.52	0.00	0.01
Mxra8	1.52	0.00	0.02
Ptpre	1.52	0.00	0.03
NhIrc2	1.52	0.00	0.05
Wbp5	1.52	0.00	0.01
lqgap1	1.51	0.00	0.04
lgsf8	1.51	0.00	0.04
Tbc1d10b	1.51	0.00	0.02
Slamf7	1.5	0.00	0.05
Down-regulated			
Hsd3b5	-14.54	0.00	0.01
Fitm1	-11.68	0.00	0.00
Susd4	-11.17	0.00	0.00

Lect1	-6.72	0.00	0.00
Cyp7b1	-5.62	0.00	0.00
Olig1	-5	0.00	0.00
Serpina4-ps1	-4.27	0.00	0.02
Serpine2	-3.82	0.00	0.00
Adh6-ps1	-3.76	0.00	0.00
Tenm3	-3.72	0.00	0.00
Serpina12	-3.56	0.00	0.04
Lhpp	-3.49	0.00	0.01
Nxpe2	-3.46	0.00	0.00
Avpr1a	-3.25	0.00	0.01
Oat	-3.11	0.00	0.00
Sucnr1	-2.81	0.00	0.00
Cela1	-2.7	0.00	0.00
1500017E21Rik	-2.56	0.00	0.01
Slc1a2	-2.49	0.00	0.00
Cyp2u1	-2.42	0.00	0.00
Cyp2c37	-2.38	0.00	0.00
Rarres1	-2.37	0.00	0.00
Npr2	-2.34	0.00	0.00
Cml5	-2.28	0.00	0.01
Tex12	-2.26	0.00	0.01
Clstn3	-2.23	0.00	0.00
Wdr89	-2.18	0.00	0.01
Slc22a7	-2.17	0.00	0.05
Cyp4a12a	-2.14	0.00	0.04
Pnldc1	-2.14	0.00	0.01
Dct	-2.12	0.00	0.02
Nat1	-2.12	0.00	0.01
Tmem19	-2.09	0.00	0.00
Dpy19l3	-2.04	0.00	0.00
Fgf1	-2.04	0.00	0.00
Slco1a1	-2	0.00	0.04
Gna14	-1.98	0.00	0.00
Acad12	-1.97	0.00	0.00
Cyp2c54	-1.96	0.00	0.02
Slc17a3	-1.92	0.00	0.01
Pmm1	-1.92	0.00	0.00
Mogat1	-1.89	0.00	0.01
Cd163	-1.84	0.00	0.04
5033404E19Rik	-1.83	0.00	0.01
Glul	-1.83	0.00	0.04
Hdhd3	-1.82	0.00	0.02
Plbd1	-1.82	0.00	0.02
Eme2	-1.8	0.00	0.03
Tspyl4	-1.77	0.00	0.02
Rbm20	-1.76	0.00	0.04
Tsc22d1	-1.74	0.00	0.01
Gabrr1	-1.74	0.00	0.02
Pdilt	-1.74	0.00	0.00
Cyp2j6	-1.74	0.00	0.02
Tuba4a	-1.74	0.00	0.01

Gmppb	-1.74	0.00	0.04
Rmdn2	-1.72	0.00	0.00
Pfkfb1	-1.71	0.00	0.04
Hrc	-1.7	0.00	0.01
Zbtb21	-1.7	0.00	0.01
Zmat1	-1.67	0.00	0.03
Cav1	-1.66	0.00	0.02
Bmp4	-1.66	0.00	0.02
Slc22a3	-1.65	0.00	0.01
Nat8	-1.65	0.00	0.02
Capn8	-1.65	0.00	0.01
Inhba	-1.64	0.00	0.04
Ldhd	-1.63	0.00	0.00
Aatk	-1.62	0.00	0.04
Srsf3	-1.62	0.00	0.02
Adrb3	-1.61	0.00	0.04
Hes6	-1.61	0.00	0.03
2610305D13Rik	-1.6	0.00	0.05
3110070M22Rik	-1.6	0.00	0.04
Mup5	-1.6	0.00	0.02
Tada3	-1.6	0.00	0.03
Fam228a	-1.6	0.00	0.01
Ppapdc1a	-1.59	0.00	0.04
Fzd7	-1.59	0.00	0.01
Mal2	-1.59	0.00	0.02
Ufl1	-1.59	0.00	0.02
Hyal1	-1.59	0.00	0.01
Slc6a7	-1.59	0.00	0.04
Khdrbs3	-1.58	0.00	0.01
Ces1e	-1.57	0.00	0.01
Ces4a	-1.57	0.00	0.04
Them7	-1.57	0.00	0.02
ld3	-1.56	0.00	0.05
Dusp1	-1.55	0.00	0.03
Angptl6	-1.55	0.00	0.02
Trpv4	-1.54	0.00	0.03
C1qtnf4	-1.53	0.00	0.05
Mapk1ip1	-1.53	0.00	0.02
Mfsd8	-1.53	0.00	0.01
Zfhx4	-1.52	0.00	0.02
C6	-1.52	0.00	0.05
Csrp3	-1.52	0.00	0.01
Pole4	-1.52	0.00	0.01
Poc1b	-1.52	0.00	0.00
Snhg11	-1.52	0.00	0.00
1700001C02Rik	-1.52	0.00	0.01
Chic1	-1.52	0.00	0.04
Sdr42e1	-1.51	0.00	0.02
Moxd1	-1.5	0.00	0.02
Ccdc185	-1.5	0.00	0.01
Nars2	-1.5	0.00	0.01

Supplementary Table 9. IPA analysis of genes upregulated (FC > 1.5, FDR < 0.05) in livers of DEN/CCl4 treated with vehicle (compared with healthy control group).

p value
2,54E-11
1,90E-06
7,23E-06
1,04E-05
1,10E-05
p-value
2,88E-04 - 1,04E-29
2,88E-04 - 1,04E-29
2,09E-04 - 8,99E-22
2,65E-04 - 5,10E-20
2,52E-04 - 2,18E-18
p-value
1,22E-03 - 1,22E-03
8,43E-02 - 3,38E-02
1,74E-01 - 7,08E-02