## SUPPLEMENTARY MATERIALS

## Supplemental Figure Legends

**Supplemental Figure 1.** *SF3B1* is frequently mutated in patients with RARS and RARS-T. We performed Sanger sequencing on exons 13, 14, 15, and 16 of *SF3B1* in 456 patients. Patients are divided in 4 groups: (A) MDS (n=93), (B) MDS/MPN (n=105), (C) AML (n=94), and (D) Others (n=164). Bar histograms show the frequency of *SF3B1* mutations. White bars and black bars indicate wild type and mutant patients, respectively. The frequency of *SF3B1* mutations is higher in patients with RARS (68%) and RARS-T (81%) compared to the other groups. (E) Schematic distribution of *SF3B1* mutations in different diseases according to 2008 World Health Organization criteria. Each color represents a specific mutation.

MDS, myelodysplastic syndromes; MPN, myeloproliferative neoplasms; AML, acute myeloid leukemia.

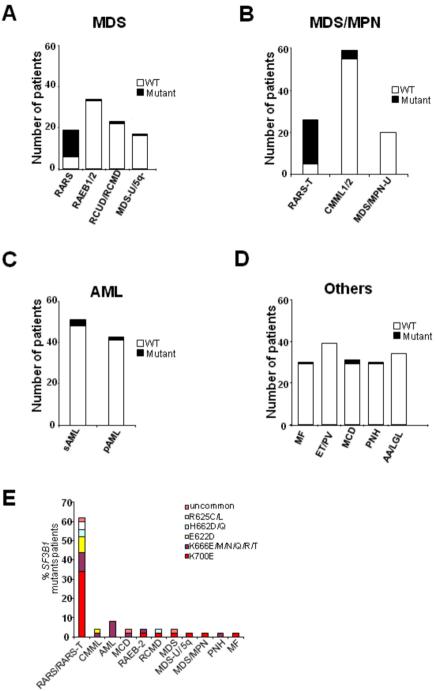
Supplemental Figure 2. Human Colony Forming-Units Cell Assay. Human clonogenic progenitor cells with and without different doses of meayamycin (2, 10, 50nM) were analyzed for the presence of ring sideroblasts (RS) after 2 weeks of culture. Bar histogram represents the percentage of RS calculated by scoring 200 erythroid cells per concentration of meayamycin in representative experiment.

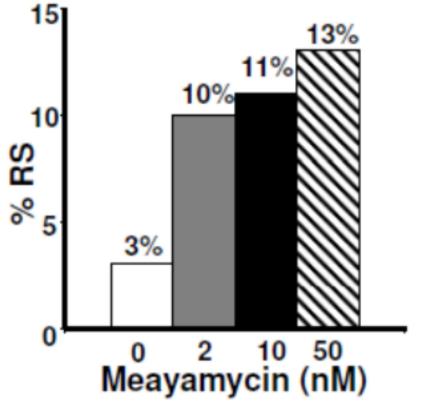
**Supplemental Figure 3.** *SF3B1* mutations predicts for better overall **survival.** Overall survival calculated by univariate analysis at time of sampling is presented for (A) MDS, (B) MDS/MPN, and (C) RARS/RARS-T groups. Blue and

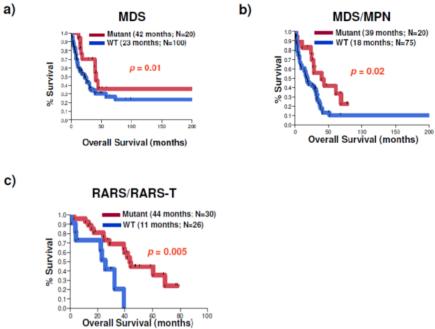
magenta lines represent wild type (WT) and mutant patients, respectively.  $P \le$  .05 is considered statistically significant.

**Supplemental Table 1. List of genes showing differential gene expression between** *SF3B1* **mutant and normal samples.** Differential gene expression was tested on 12,870 reference genes for differential expression. One hundred thirty genes were found to be differentially expressed using a False Discovery Rate (FDR) level of 0.05. Ninety-four % of these genes were under-expressed in *SF3B1* mutant compared to normal samples.

Supplemental Table 2. List of gene sets showing over and under representation of differential gene expression. MSigDB database version 3.0 (<a href="http://www.broadinstitute.org/gsea/msigdb/index.jsp">http://www.broadinstitute.org/gsea/msigdb/index.jsp</a>) was used to define gene set collections (c2-c5) of under and over represented genes. Adjusted P < 0.05 is considered significant for each gene set.







Gene Name	Chr	Gene location	Adjust P-value	BaseM	BaseN	Log2fold(Mutant/Healthy Donor)	P-value
HBG1	11	5269502-5271087	3.49E-05	15068	121	6.77	1.11E-07
SLC7A5P1	16	29624424-29625038	1.35E-04	686	4	5.69	4.94E-07
PTTG3P	8	67679634-67680240	2.13E-03	181	0	5.17	1.08E-05
FAM57B	16	30035749-30042186	4.40E-03	6502	0	10.10	2.53E-05
LOC100271831	16	30125433-30125826	1.51E-02	1679	0	8.16	1.08E-04
RUNDC3A	17	42385927-42396037	2.31E-02	225	4	4.02	1.90E-04
FLJ42393	3	187896331-187898596	2.42E-02	448	0	6.32	2.03E-04
GDPD3	16	30116132-30124878	4.06E-02	94	0	4.27	3.79E-04
DEFA4	8	6793345-6795786	5.50E-19	6	24454	-10.56	4.28E-23
PRG3	11	57144243-57148623	6.33E-17	1	5799	-9.50	9.84E-21
EPX	17	56270089-56282534	2.14E-14	4	4592	-8.50	5.00E-18
RNASE3	14	21359562-21360506	1.09E-13	6	5527	-8.51	3.38E-17
CORO1A	16	30194926-30200396	9.20E-13	2	1986	-7.48	4.06E-16
PRG2	11	57154835-57158130	9.20E-13	97	43622	-9.31	4.29E-16
CEACAM6	19	42259398-42276113	1.02E-12	8	4279	-7.88	6.37E-16
ELANE	19	852291-856244	1.02E-12	167	71946	-9.65	5.89E-16
DEFA3	8	6873395-6875816	2.16E-12	4	2404	-7.57	1.51E-15
PPP4C	16	30087384-30096688	6.24E-12	2	1372	-7.31	4.85E-15
CAMP	3	48264862-48266975	2.29E-11	41	10636	-7.59	1.96E-14
LTF	3	46477497-46506395	6.03E-11	405	93610	-8.38	5.62E-14
CTSG	14	25042725-25045466	7.22E-11	37	9227	-7.86	7.29E-14
RNASE2	14	21423630-21424594	4.53E-10	62	10796	-7.22	4.93E-13
TCN1	11	59620281-59634041	6.73E-10	3	985	-6.37	7.85E-13
PRTN3	19	840985-848175	7.21E-10	247	41679	-8.62	8.97E-13
AZU1	19	827831-832017	9.44E-10	68	11331	-7.70	1.25E-12
BPI	20	36932552-36965905	1.75E-09	37	5356	-6.75	2.45E-12
OLR1	12	10310899-10324790	1.09E-08	3	724	-5.93	1.61E-11
CLC	19	40221896-40228668	1.12E-08	21	2835	-6.65	1.74E-11
SGK3	8	67624891-67774255	6.05E-08	0	335	-6.02	9.88E-11
SLPI	20	43880879-43883206	7.85E-08	3	670	-5.71	1.34E-10
MMP8	11	102582526-102595685	1.33E-07	67	5691	-6.64	2.38E-10
LCN2	9	130911732-130915734	1.82E-07	45	3174	-5.77	3.38E-10
MMP9	20	44637547-44645199	2.09E-07	27	2196	-5.79	4.06E-10
CEACAM8	19	43084395-43099082	2.12E-07	50	3734	-5.90	4.29E-10
MS4A3	11	59824101-59838587	6.24E-07	20	1717	-6.65	1.31E-09
CRISP3	6	49695092-49712056	1.11E-06	28	1944	-5.83	2.41E-09
C16orf54	16	29753786-29757340	1.46E-06	0	240	-5.56	3.29E-09
IL8	4	74606275-74609431	1.71E-06	385	19694	-5.80	3.98E-09
S100P	4	6695566-6698896	1.86E-06	14	941	-5.21	4.49E-09
MPO	17	56347217-56358296	3.12E-06	1607	81048	-7.58	7.76E-09
SRGN	10	70847828-70864565	6.54E-06	2673	92897	-5.17	1.68E-0
TMEM176B	7	150488378-150497621	8.17E-06	17	822	-5.06	2.16E-0

PGLYRP1	19	46522412-46526556	1.02E-05	6	489	-4.88	2.87E-08
SDC2	8	97505882-97624037	1.02E-05	1	230	-5.08	2.83E-08
ALOX15	17	4534221-4544960	1.47E-05	2	275	-5.06	4.24E-08
HP	16	72088508-72094957	2.14E-05	26	1169	-4.98	6.31E-08
CCL7	17	32597240-32599255	2.90E-05	0	172	-5.11	9.02E-08
S100A8	1	153362509-153363549	2.90E-05	8552	243742	-4.85	8.80E-08
TXNIP	1	145438462-145442626	3.97E-05	192	6874	-6.79	1.29E-07
S100A12	1	153346184-153348075	5.51E-05	607	15905	-4.69	1.84E-07
LYZ	12	69742134-69748013	8.78E-05	36753	854523	-4.60	3.00E-07
LPP	3	187930721-188608459	1.20E-04	5	316	-4.45	4.20E-07
IL1R2	2	102608306-102644880	1.22E-04	10	525	-4.80	4.36E-07
B3GNT5	3	182971032-182991178	1.52E-04	69	1976	-4.65	5.67E-07
FCGR3B	1	161592990-161601158	1.66E-04	42	999	-4.74	6.30E-07
S100A9	1	153330330-153333502	1.79E-04	3901	79729	-4.43	6.96E-07
OLFM4	13	53602972-53626186	2.18E-04	12	519	-4.51	8.65E-07
CHI3L1	1	203148059-203155922	3.82E-04	24	812	-5.49	1.55E-06
FCAR	19	55385549-55401839	6.02E-04	116	2410	-4.21	2.48E-06
CD24	Y	21152526-21154705	7.14E-04	62	1409	-4.25	2.99E-06
PLAU	10	75670862-75677256	7.79E-04	11	399	-4.17	3.33E-06
ALPL	1	21835858-21904904	1.11E-03	2	178	-4.52	4.82E-06
CHIT1	1	203185207-203198860	1.29E-03	6	286	-4.34	5.73E-06
NCRNA00152	2	87754974-87821028	1.33E-03	0	108	-4.51	5.99E-06
MGAM	7	141695679-141806546	1.35E-03	18	466	-3.97	6.18E-06
ANXA3	4	79472742-79531602	1.37E-03	72	1463	-4.18	6.44E-06
GPR97	16	57702157-57723288	1.37E-03	46	1045	-4.39	6.49E-06
TNFRSF12A	16	3070313-3072381	1.43E-03	19	450	-3.96	6.90E-06
IL1RL1	2	102953717-102961180	1.77E-03	0	123	-4.33	8.67E-06
TMEM176A	7	150497854-150502208	1.82E-03	2	152	-4.26	9.06E-06
EMP1	12	13349602-13369707	2.22E-03	21	487	-3.89	1.14E-05
MAP3K8	10	30722866-30750761	2.33E-03	147	2166	-3.82	1.22E-05
CD177	19	43857825-43867479	2.53E-03	8	284	-4.12	1.34E-05
ALOX5AP	13	31309669-31338556	2.69E-03	345	5130	-3.83	1.44E-05
PLAUR	19	44152732-44174502	3.10E-03	688	9914	-3.83	1.69E-05
MME	3	154797436-154901518	3.35E-03	8	263	-3.87	1.85E-05
HDC	15	50534148-50557926	3.79E-03	4	199	-4.41	2.12E-05
CA4	17	58227302-58236904	4.40E-03	0	90	-4.28	2.53E-05
IFNGR1	6	137518621-137540567	4.54E-03	586	7212	-3.65	2.64E-05
NAMPT	7	105888734-105925638	5.11E-03	1321	15379	-3.64	3.02E-05
BCL2A1	15	80253233-80263643	5.60E-03	245	2727	-3.85	3.35E-05
HBEGF	5	139712429-139726188	6.04E-03	40	727	-3.90	3.66E-05
TREM1	6	41243712-41254457	6.12E-03	60	808	-3.67	3.76E-05
CHD1L	1	146714291-146767441	6.89E-03	32	493	-3.65	4.29E-05
SAMSN1	21	15857549-15918664	7.08E-03	289	3314	-3.55	4.46E-05
RETN	19	7733972-7735340	7.14E-03	19	403	-3.73	4.55E-05
ANPEP	15	90328127-90358072	7.51E-03	227	2963	-3.64	4.85E-05
7 11 11 ET	13	30020121-30000012	1.01L-03	221	2000	0.04	4.002-05

THBD	20	23026271-23030301	7.65E-03	10	273	-3.74	4.99E-05
MAPK3	16	30125427-30134630	8.36E-03	0	97	-4.03	5.52E-05
ANXA1	9	75766781-75785307	8.40E-03	2803	31070	-3.48	5.61E-05
PCOLCE2	3	142536712-142607934	9.57E-03	0	79	-4.12	6.47E-05
LRG1	19	4537228-4540036	1.04E-02	24	413	-3.52	7.14E-05
IL1RAP	3	190231840-190348071	1.16E-02	19	341	-3.49	8.02E-05
SPN	16	29674580-29681821	1.24E-02	40	612	-3.58	8.70E-05
OSM	22	30658821-30662840	1.29E-02	80	1134	-3.85	9.11E-05
C19orf59	19	7741943-7744719	1.61E-02	123	1360	-3.33	1.17E-04
SERPINE1	7	100770379-100782546	1.61E-02	21	308	-3.57	1.18E-04
ALDOA	16	30077044-30081734	1.64E-02	1002	10163	-3.32	1.24E-04
CXCR1	2	219027570-219031716	1.64E-02	25	362	-3.41	1.25E-04
FCN1	9	137801436-137809806	1.64E-02	5124	47277	-3.32	1.23E-04
ORM1	9	117085303-117088757	1.64E-02	3	134	-3.57	1.25E-04
FPR2	19	52264453-52273777	1.70E-02	80	945	-3.33	1.31E-04
QPCT	2	37571753-37600464	1.72E-02	225	2119	-3.37	1.33E-04
IL1RN	2	113885138-113891592	1.74E-02	91	919	-3.42	1.37E-04
HIF1A	14	62162119-62214977	1.94E-02	901	8757	-3.26	1.54E-04
TMCC3	12	94960900-95044324	2.04E-02	35	419	-3.45	1.63E-04
ACSL1	4	185676749-185747215	2.04E-02	307	2990	-3.24	1.65E-04
CLEC5A	7	141627157-141646783	2.09E-02	20	321	-3.36	1.70E-04
SLC2A5	1	9097007-9129887	2.38E-02	3	140	-3.99	1.98E-04
SLC2A3	12	8071825-8088892	2.49E-02	1612	15486	-3.26	2.11E-04
ANGPTL4	19	8429011-8439257	2.69E-02	0	66	-3.90	2.30E-04
MXD1	2	70142203-70170074	2.93E-02	523	4746	-3.15	2.54E-04
NLRP3	1	247581351-247612404	2.93E-02	203	1914	-3.15	2.58E-04
RBM8A	1	145507638-145511444	2.93E-02	84	1055	-4.26	2.60E-04
SAT1	×	23801275-23804325	2.93E-02	3346	26184	-3.24	2.56E-04
DNTT	10	98064085-98098319	3.44E-02	7	178	-4.04	3.09E-04
NUCB2	11	17298286-17353069	3.44E-02	474	4708	-3.44	3.10E-04
VSTM1	19	54544085-54567207	3.68E-02	12	233	-3.53	3.35E-04
PHACTR1	6	12717833-13287528	4.00E-02	3	107	-3.34	3.67E-04
PADI4	1	17634690-17690495	4.02E-02	267	2601	-3.34	3.72E-04
NR4A1	12	52445191-52453285	4.22E-02	85	820	-3.07	3.97E-04
SERPINB10	18	61582745-61602474	4.23E-02	34	448	-3.50	4.01E-04
COL17A1	10	105791048-105845638	4.35E-02	5	154	-3.94	4.16E-04
CCL2	17	32582296-32584218	4.36E-02	6	141	-3.26	4.23E-04
CD93	20	23059994-23066977	4.36E-02	179	1456	-3.05	4.27E-04
CXCL16	17	4636830-4643223	4.36E-02	289	2143	-3.20	4.28E-04
DEFA5	8	6912829-6914259	4.36E-02	0	60	-3.78	4.26E-04 4.31E-04
RILPL2	12		4.36E-02 4.36E-02	281	2174		4.33E-04 4.33E-04
ARG1		123899936-123921264			1060	-3.06	
F-1277025-136-136-1	6	131894365-131905468	4.67E-02	113		-3.08	4.68E-04
CXCL12	10	44865607-44880545	4.72E-02	6	161	-3.54	4.77E-04

Supplemental Table 2. List of gene sets showing signific:  Gene set  SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP  MCLACHLAN_DENTAL_CARIES_UP  MCLACHLAN_DENTAL_CARIES_UP  MCLACHLAN_DENTAL_CARIES_DN  DUNNE_TARGETS_OF_AML1_MTGS_FUSION_UP  TAKEDA_TARGETS_OF_AML1_MTGS_FUSION_UP  TAKEDA_TARGETS_OF_NUPSB_HOXAS_FUSION_SD_DN  BOYLAN_MULTIPLE_MYELOMA_C_D_DN  BOYLAN_MULTIPLE_MYELOMA_C_D_DN  BOYLAN_MULTIPLE_MYELOMA_C_D_DN  ONDER_COH1_TARGETS_2_DN  VERHAAK_AML_WITH_NPM1_MUTATED_UP  CAIRO_LIVER_DEVELOPMENT_DN  HAHTOLA_MYCOSIS_FUNGOIDES_CO4_UP  JAATINEN_HEMATOPOIETIC_STEM_CELL_DN  RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP  LENAOUR_DENDRITIC_CELL_DN  RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP  LENAOUR_DENDRITIC_CELL_MATURATION_DN  RHEIN_ALL_GLUCOCOGRTICOID_THERAPY_UP  DELYS_THYROID_CANCER_UP  RUTELLA_RESPONSE_TO_GSF2RB_AND_IL4_DN  LINGGREN_BLADDER_CANCER_CLUSTER_28  TARTE_PLASM_CELL_VS_PLASMABLAST_UP  HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN  NAGASHIMA_GEF_SIGNALING_UP  ZHANG_RESPONSE_TO_KK_INHIBITOR_AND_TINF_UP  SMID_BREAST_CANCER_LUMINAL_B_DN  REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS  VERHAAK_AML_WITH_NPM1_MUTATED_DN  ICHIBA_GRAFT_VERSUS_HOST_DISEASE_3SD_UP  MARTINELLI_IMMATURE_NEUTROPHIL_UP  BILD_HASS_ONCOGENIC_SIGNATURE  NAGASHIMA_NRG1_SIGNALING_UP  CHECK_RESPONSE_TO_HEMTALED_IND  RICKMAN_HEAD_AND_NECK_CANCER_C  REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS  HARRIS_HYPOXIA_  ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP  LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT  TONKS_TARGETS_OF_RUNX1_RUNXITI_FUSION_ERYTHROCYTE_ KEGG_CYTOKINE_CYTOKINE_RECEPTORS_BIND_CHEMOKINES  DIAGET_METASTASIS_DN  MISSIAGLIA_REGULATED_BY_METHALATION_UP  TONKS_TARGETS_OF_RUNX1_RUNXITI_FUSION_HSC_DN  REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	collecti		ion of differential lue Direction over over over over over over over over	#sig ger 33 36 36 36 27 18 26 29 31 20 33 25 23 16 27 26 35 19 16 30 30 28 27 14 12 21 30 13 22 17 6 20 17 8 18 8 19 9 9 14 12 23 11 16 17 16 13 18 9		P-value  2.44E-26 3.20E-24 5.12E-23 4.09E-22 1.87E-19 1.93E-19 7.20E-19 5.57E-18 8.34E-17 5.15E-16 1.86E-15 3.21E-14 3.85E-14 7.58E-14 1.24E-13 1.19E-13 1.19E-13 1.52E-13 2.93E-13 4.67E-13 6.14E-13 5.46E-12 9.56E-12 1.19E-11 3.24E-11 4.90E-11 6.37E-11 8.47E-11 3.42E-10 9.18E-10 9.80E-10 1.04E-09 1.34E-09 2.60E-09 3.03E-09 3.03E-09 3.06E-09 3.48E-09 5.24E-09 5.24E-09 5.24E-09 5.24E-09 5.24E-09 9.72E-09 1.21E-08 1.37E-08 1.37E-08 1.56E-08 1.83E-08 2.73E-08	
DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN SMID_BREAST_CANCER_BASAL_UP SWEET_LUNG_CANCER_KRAS_UP PARK_APL_PATHOGENESIS_DN NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_D WU_CELL_MIGRATION GRAHAM_CMILESCENT_VS_CML_DIVIDING_DN GRAHAM_CML_OUIESCENT_VS_CML_DIVIDING_DN GRUETZMANN_PANCREATIC_CANCER_UP REACTOME_GPCR_LIGAND_BINDING LEE_LUVER_CANCER_DENA_UP AMIT_EGF_RESPONSE_TO_HELA RUTELLA_RESPONSE_TO_HELA RUTELLA_RESPONSE_TO_HELA RUTELLA_RESPONSE_TO_HOS_DN SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LIMP1_DN KUMAR_TARGETS_OF_MIL_AF9_FUSION HOSHIDA_LIVER_CANCER_SUBCLASS_S1 SENESE_HOACT_AND_HOAC2_TARGETS_UP THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UF REACTOME_G_ALPHA_I_SIGNALLING_EVENTS GERY_CEBP_TARGETS LEE_LIVER_CANCER_E2F1_UP GESERICK_TERT_TARGETS_DN SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP SEKI_INFLAMMATORY_RESPONSE_LPS_UP MARTINELLI_IMMATURE_NEUTROPHIL_DN VART_KSHY_INFECTION_ANGIOGENIC_MARKERS_DN SABATES_COLORECTAL_ADENOMA_UP CHIANG_LIVER_CANCER_ESTE_UP GOVYER_TATI_TARGETS_UP AMIT_SERUM_RESPONSE_TISM_CELL_IN_COLLAGEN_GEL_DN OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP MARTINELT_PSS_TARGETS_UP GOUYER_TATI_TARGETS_UP AMIT_SERUM_RESPONSE_TO_TOSEDOSTAT_24HR_UP CROMER_TUMORIGENESIS_UP ZHOU_INFLAMMATORY_RESPONSE_LPS_UP MARTINEL_PSS_TARGETS_UP MURATA_VIRULENCE_OF_H_PILORI SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN CROMER_TUMORIGENESIS_ON WONG_ENDMETRIUM_CANCER_UP VALK_AMIL_WITH_CEBPA	83 83 83 83 83 83 83 83 83 83 83 83 83 8	2.39E-06 2.55E-06 2.72E-06 2.90E-06 3.15E-06 3.35E-06 4.36E-06 4.83E-06 6.42E-06 7.95E-06 9.02E-06 9.02E-06 9.02E-06 9.02E-06 9.02E-06 9.02E-05 1.31E-05 1.31E-05 1.71E-05 1.73E-05 2.57E-05 2.57E-05 2.57E-05 2.57E-05 3.39E-05 3.27E-05 5.44E-05 5.44E-05 5.44E-05 5.44E-05 5.44E-05 6.03E-05 6.03E-05 6.04E-05 7.13E-05 7.13E-05 7.13E-05 7.13E-05 9.08E-05 9.08E-05 9.08E-05 9.08E-05 9.08E-05 9.08E-05 9.08E-05 9.08E-05 9.08E-05 9.08E-05	over over over over over over over over	14 27 27 9 5 22 9 15 6 11 23 14 9 10 19 11 12 11 12 9 6 19 10 5 10 9 12 16 16 16 16 16 25 5 8 5 7 15 8 7 7 15 8 7 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8	101 376 369 35 6 270 39 123 12 64 304 106 40 53 223 69 303 211 166 71 84 68 87 42 15 233 59 65 47 92 183 183 411 10 42 11 336 123 267 29 159 657 20 218 409 12 159 657 20 218 409 12 159 657 20 21 21 21 21 21 21 21 21 21 21 21 21 21	3.59E-08 3.91E-08 4.25E-08 4.63E-08 5.12E-08 5.55E-08 7.35E-08 8.28E-08 1.03E-07 1.14E-07 1.44E-07 1.44E-07 1.77E-07 1.77E-07 1.77E-07 1.85E-07 2.18E-07 2.13E-07 3.00E-07 3.66E-07 3.77E-07 4.03E-07 5.90E-07 5.89E-07 6.58E-07 7.73E-07 8.10E-07 8.15E-06 1.35E-06 1.55E-06 1.55E-06 1.55E-06 1.90E-06 2.42E-06 2.50E-06 2.60E-06 2.91E-06 4.90E-06 5.28E-06 5.25E-06	
ZHAN_MULTIPLE_MYELOMA_DN LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP KIM_WT1_TARGETS_8HR_UP LIAN_LIPA_TARGETS_3M  XU_HGF_TARGETS_TEPRESSED_BY_AKT1_UP HSIAO_LIVER_SPECIFIC_GENES  TAKEDA_TARGETS_OF_NUP9B_HOXA9_FUSION_3D_DN POOLA_INVASIVE_BREAST_CANCER_UP MUELLER_METHYLATED_IN_GLIOBLASTOMA WALLACE_PROSTATE_CANCER_RACE_UP DAUER_STAT3_TARGETS_UP SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1 GU_PDEF_TARGETS_UP MARKEY_RB1_ACUTE_LOF_UP FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN MCBRYAN_PUBERTAL_BREAST_3_4WK_UP KEGG_RENIN_ANGIOTENSIN_SYSTEM CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_DN LIAN_LIPA_TARGETS_6M YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_1 TURASHYILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAI WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP LEE_LIVER_CANCER_CIPROFIBRATE_UP JIANG_HYPOXIA_NORMAL ONDER_CDH1_TARGETS_1_DN WATTEL_AUTONOMOUS_THYROID_ADENOMA_DN KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2	T_DN	1.97E-04 2.15E-04 2.22E-04 2.50E-04 2.72E-04 3.15E-04 3.23E-04 3.27E-04 3.55E-04 3.99E-04 4.00E-04 4.14E-04 4.46E-04 4.52E-04 5.70E-04 6.49E-04 6.49E-04 6.49E-04 6.84E-04 7.13E-04 7.26E-04 7.30E-04 8.55E-04 8.55E-04 9.10E-04 1.08E-03	over over over over over over over over	6 8 12 8 4 12 6 17 6 17 7 15 26 5 24 11 4 5 8 7 10 10 7 14 11 5 34 6	22 47 124 48 7 114 24 227 23 232 27 236 42 182 476 15 453 113 9 18 56 45 93 88 41 176 123 18 803 30 10	6.05E-06 6.65E-06 6.93E-06 7.90E-06 8.68E-06 1.01E-05 1.05E-05 1.07E-05 1.13E-05 1.13E-05 1.35E-05 1.37E-05 1.43E-05 1.56E-05 1.56E-05 2.04E-05 2.28E-05 2.39E-05 2.39E-05 2.41E-05 2.56E-05 2.69E-05 2.69E-05 2.80E-05 2.96E-05 3.33E-05 3.51E-05 3.60E-05 4.31E-05	
FOSTER_INFLAMMATORY_RESPONSE_LPS_UP XU_HGF_SIGNALING_NOT_VIA_AKT1_6HR ENK_UV_RESPONSE_EPIDERMIS_DN AMIT_EGF_RESPONSE_60_HELA LIU_VAV3_PROSTATE_CARCINOGENESIS_UP PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP SENESE_HDAC1_TARGETS_UP GAURNIER_PSMD4_TARGETS PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN HUPER_BREAST_BASAL_VS_LUMINAL_UP REACTOME_HEMOSTASIS HELLER_SILENCED_BY_METHYLATION_UP IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN DELYS_THYROID_CANCER_DN RUTELLA_RESPONSE_TO_HGF_UP FOSTER_INFLAMMATORY_RESPONSE_LPS_DN KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY MULLIGHAN_MLL_SIGNATURE_2_UP KHETCHOUMIAN_TRIM24_TARGETS_UP	63 63 63 63 63 63 63 63 63 63 63 63 63 6	1.11E-03 1.15E-03 1.32E-03 1.43E-03 1.44E-03 2.01E-03 2.16E-03 2.43E-03 2.43E-03 2.58E-03 2.84E-03 2.84E-03 2.84E-03 3.88E-03 3.08E-03	over over over over over over over over	11 5 22 6 8 7 19 7 10 5 14 13 11 14 10 20 18 7 20 6	117 20 417 35 64 48 360 45 117 22 208 174 124 214 112 370 329 54 371 37	4.47E-05 4.64E-05 5.37E-05 5.89E-05 5.90E-05 6.01E-05 8.44E-05 9.13E-05 9.26E-05 1.05E-04 1.05E-04 1.13E-04 1.20E-04 1.26E-04 1.27E-04 1.33E-04 1.33E-04 1.36E-04 1.42E-04	
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP REACTOME_DOWNSTREAM_EVENTS_IN_GPCR_SIGNALING MIZUKAMI_HYPOXIA_DN RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN HINATA_NFKB_TARGETS_KERATINOCYTE_UP WANG_SMARCE1_TARGETS_UP HAHTOLA_SEZARY_SYNDROM_UP MOHANKUMAR_TLX1_TARGETS_DN MARTINEZ_RB1_TARGETS_UP SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP TAVOR_CEBPA_TARGETS_UP CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_UP SEMENZA_HIF1_TARGETS VART_KSHY_INFECTION_ANGIOGENIC_MARKERS_UP MCBRYAN_PUBERTAL_BREAST_4_5WK_UP CHEN_LVAD_SUPPORT_OF_FAILING_HEART_DN BROCKE_APOPTOSIS_REVERSED_BY_IL6 CHEN_HOXAS_TARGETS_6HR_UP MATSUDA_NATURAL_KILLER_DIFFERENTIATION SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN KORKOLA_CHORIOCARCINOMA_UP LI_AMPLIFIED_IN_LUNG_CANCER WANG_ESOPHAGUS_CANCER_PROGRESSION_UP AMIT_SERUM_RESPONSE_240_MCF10A SHEN_SMARCA2_TARGETS_DN SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP DOANE_BREAST_CANCER_EST1_DN DANG_REGULATED_BY_MYC_DN BUDHU_LIVER_CANCER_BETASTASIS_UP PRAMOONJAGO_SOX4_TARGETS_UP SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN SABATES_COLORECTAL_ADENOMA_DN ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN FERRANDO_TAL1_NEIGHBORS FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN HAHTOLA_MYCOSIS_FUNGOIDES_UP	23 23 23 23 23 23 23 23 23 23 23 23 23 2	3.19E-03 3.27E-03 3.31E-03 3.39E-03 3.58E-03 3.68E-03 3.80E-03 3.80E-03 4.02E-03 4.02E-03 4.02E-03 4.17E-03 4.57E-03 4.57E-03 4.57E-03 4.57E-03 5.15E-03 5.15E-03 5.15E-03 5.15E-03 5.16E-03	over over over over over over over over	11 13 3 16 7 9 8 22 6 6 8 5 9 11 5 10 3 11 3 6 10 4 4 13 3 6 12 9 12 9 12 9 14 9 14 9 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18	141 184 6 268 53 99 93 74 460 40 39 78 25 95 136 26 123 6 123 6 123 6 123 6 123 6 125 127 6 129 15 15 15 15 197 6 44 158 100 169 179 189 189 189 189 189 189 189 189 189 18	1.48E-04 1.52E-04 1.55E-04 1.60E-04 1.70E-04 1.76E-04 1.79E-04 1.84E-04 1.88E-04 1.93E-04 2.00E-04 2.01E-04 2.21E-04 2.11E-04 2.14E-04 2.34E-04 2.38E-04 2.38E-04 2.38E-04 2.54E-04 2.60E-04 2.60E-04 2.73E-04 2.78E-04 2.78E-04 2.78E-04 2.80E-04 2.80E-04 2.87E-04 3.10E-04 3.12E-04 3.12E-04 3.27E-04 3.23E-04 3.27E-04 3.23E-04	
NUYTTEN_EZH2_TARGETS_UP  TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_DN  NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP  STEARMAN_TUMOR_FIELD_EFFECT_UP  SESTO_RESPONSE_TO_UV_C3  YAO_HOXA10_TARGETS_VIA_PROGESTERONE_UP  AMIT_EGF_RESPONSE_240_MCF10A  DODD_NASOPHARYNGEAL_CARCINOMA_UP  KIM_LRRC3B_TARGETS  BROWNE_HCMV_INFECTION_6HR_UP  SMID_BREAST_CANCER_ERBB2_UP  SMID_BREAST_CANCER_NORMAL_LIKE_UP  RICKMAN_HEAD_AND_NECK_CANCER_D  BROWNE_HCMV_INFECTION_4HR_UP  MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP	23 CS	5.70E-03 5.78E-03 5.78E-03 6.01E-03 6.21E-03 6.29E-03 6.45E-03 6.62E-03 7.26E-03 7.47E-03 7.62E-03	over over over over over over over over	30 5 7 5 4 6 4 36 5 6 8 18 4 5 13	743 30 60 29 16 44 17 922 28 46 85 343 16 34 204	3.25E-04 3.24E-04 3.35E-04 3.37E-04 3.65E-04 3.68E-04 3.80E-04 4.00E-04 4.02E-04 3.98E-04 4.43E-04 4.69E-04	
LEE_LIVER_CANCER_ACOX1_UP GAJATE_RESPONSE_TO_TRABECTEDIN_UP SENESE_HDAC2_TARGETS_UP CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP ELVIDGE_HYPOXIA_BY_DMOG_UP KEGG_COMPLEMENT_AND_COAGULATION_CASCADES SOUCEK_MYC_TARGETS SENESE_HDAC3_TARGETS_UP WILCOX_PRESPONSE_TO_ROGESTERONE_DN GOLUB_ALL_VS_AML_DN BERENJENO_TRANSFORMED_BY_RHOA_UP CROONQUIST_STROMAL_STIMULATION_UP HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP SWEET_LUNG_CANCER_KRAS_DN KEGG_CHEMOKINE_SIGNALING_PATHWAY DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN TAVAZOIE_METASTASIS NAKAJIMA_EOSINOPHIL WOO_LIVER_CANCER_RECURRENCE_UP ZUCCHI_METASTASIS_DN LEE_LIVER_CANCER_MYC_TGFA_UP RASHI_RESPONSE_TO_IONIZING_RADIATION_6 NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN ROSS_AML_WITH_MLL_FUSIONS GOZGIT_ESR1_TARGETS_DN RIGGI_EWING_SARCOMA_PROGENITOR_DN RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN REACTOME_METASDLISM_OF_CARBOHYDRATES KOBAYASHI_EGFR_SIGNALING_6HR_DN CERVERA_SDHB_TARGETS_2 BILBAN_B_CLL_LPL_DN RADMACHER_AML_PROGNOSIS BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS RODWELL_AGING_KIDNEY_NO_BLOOD_UP ENGELMANN_CANCER_PROGENITORS_DN	20 20 20 20 20 20 20 20 20 20 20 20 20 2	8.47E-03 8.55E-03 8.81E-03 9.77E-03 9.91E-03 1.00E-02 1.01E-02 1.05E-02 1.05E-02 1.05E-02 1.05E-02 1.07E-02 1.08E-02 1.09E-02 1.10E-02 1.11E-02 1.11E-02 1.11E-02 1.11E-02 1.11E-02 1.15E-02 1.17E-02 1.17E-02 1.26E-02 1.27E-02 1.56E-02 1.56E-02 1.56E-02 1.56E-02 1.56E-02 1.75E-02 1.77E-02 1.86E-02 1.97E-02	over over over over over over over over	6 6 8 7 8 5 3 17 5 4 21 5 14 10 4 6 4 7 7 7 7 7 8 6 8 8 8 9 8 9 8 9 8 9 8 9 8 8 9 8 8 9 8 9 8 8 9 8 9 8 9 8 8 9 8 9 8 8 9 8 8 8 9 8 8 8 8 9 8	44 45 94 64 92 34 8 368 37 18 444 32 245 246 139 19 72 18 47 68 34 70 445 99 56 98 10 58 37 59 22 97 38	5.30E-04 5.37E-04 5.56E-04 5.66E-04 6.23E-04 6.35E-04 6.45E-04 6.55E-04 6.52E-04 6.71E-04 6.98E-04 6.98E-04 6.91E-04 7.18E-04 7.22E-04 7.26E-04 7.37E-04 7.37E-04 7.38E-04 7.59E-04 7.59E-04 7.18E-04 7.18E-03 1.11E-03 1.18E-03 1.26E-03 1.34E-03 1.34E-03 1.34E-03 1.38E-03 1.38E-03 1.38E-03 1.38E-03 1.38E-03 1.38E-03 1.38E-03 1.38E-03	
GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_UP DORN_ADENOVIRUS_INFECTION_48HR_DN CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN ACEVEDO_LIVER_CANCER_DN JISON_SICKLE_CELL_DISEASE_UP KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION HORIUCHI_WTAP_TARGETS_UP ODONNELL_TFRC_TARGETS_UP TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP DORN_ADENOVIRUS_INFECTION_32HR_DN CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3 DORN_ADENOVIRUS_INFECTION_12HR_DN DASU_IL6_SIGNALING_UP	c2 c2 c2	1.97E-02 1.99E-02 2.07E-02 2.15E-02 2.16E-02 2.17E-02 2.20E-02 2.22E-02 2.22E-02 2.27E-02 2.36E-02 2.43E-02 2.45E-02	over over over over over over over over	3 4 4 4 18 11 6 12 13 9 4 21 4 5	11 23 24 22 370 168 56 219 241 128 24 509 24 39	1.44E-03 1.46E-03 1.53E-03 1.60E-03 1.61E-03 1.66E-03 1.69E-03 1.68E-03 1.73E-03 1.81E-03 1.87E-03 1.89E-03	
AMIT_EGF_RESPONSE_60_MCF10A PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP LEE_LIVER_CANCER_MYC_E2F1_UP RICKMAN_HEAD_AND_NECK_CANCER_E VALK_AML_WITH_11023_REARRANGED HAHTOLA_CTCL_CUTANEOUS BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN TIAN_TNF_SIGNALING_NOT_VIA_NFKB KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_UP ENK_UV_RESPONSE_KERATINOCYTE_UP AMIT_DELAYED_EARLY_GENES MORI_MATURE_B_LYMPHOCYTE_UP BIOCARTA_PLATELETAPP_PATHWAY AMIT_EGF_RESPONSE_40_HELA COULOUARN_TEMPORAL_TGFB1_SIGNATURE_UP WILENSKY_RESPONSE_TO_DARAPLADIB TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN ELVIDGE_HYPOXIA_UP HAN_SATB1_TARGETS_DN HOSHIDA_LIVER_CANCER_SUBCLASS_S3 REACTOME_GLUCONEOGENESIS ROSS_AML_WITH_CBFB_MYH11_FUSION BIERIE_INFLAMMATORY_RESPONSE_TGFB1 LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN DORN_ADENOVIRUS_INFECTION_24HR_DN BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN KORKOLA_TERATOMA_UP WOTTON_RUNX_TARGETS_UP	62 62 63 63 64 65 65 64 65 65 65 65 65 65 65 65 65 65 65 65 65	2.49E-02 2.51E-02 2.53E-02 2.53E-02 2.55E-02 2.55E-02 2.56E-02 2.62E-02 2.62E-02 2.72E-02 2.72E-02 2.91E-02 2.97E-02 3.39E-02 3.39E-02 3.39E-02 3.39E-02 3.42E-02 3.59E-02 3.57E-02 3.59E-02 3.59E-02 3.59E-02 3.59E-02	over over over over over over over over	4 4 5 4 3 4 3 3 8 19 3 6 2 4 6 4 5 8 13 11 4 5 2 2 4 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	25 23 40 24 12 24 12 12 108 398 13 69 4 28 67 26 49 118 250 187 26 45 4 4 28 14	1.93E-03 1.99E-03 1.99E-03 1.99E-03 1.99E-03 2.02E-03 2.03E-03 2.10E-03 2.10E-03 2.20E-03 2.20E-03 2.20E-03 2.36E-03 2.42E-03 2.53E-03 2.72E-03 2.76E-03 2.82E-03 2.84E-03 2.84E-03 2.81E-03 2.87E-03 2.87E-03 3.01E-03 3.01E-03 3.07E-03 3.07E-03	
BROWNE_HCMV_INFECTION_2HR_UP CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN DUTTA_APOPTOSIS_VIA_NFKB KEGG_HEMATOPOIETIC_CELL_LINEAGE KOBAYASHI_EGFR_SIGNALING_24HR_UP HAN_SATB1_TARGETS_UP BROWNE_HCMV_INFECTION_1HR_UP DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_DN HOSHIDA_LIVER_CANCER_SURVIVAL_UP COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_UP BASSO_CD40_SIGNALING_UP HOOI_STT_TARGETS_DN SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_DN LIU_CDX2_TARGETS_UP AUJLA_IL22_AND_IL17A_SIGNALING BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN MITSIADES_RESPONSE_TO_APLIDIN_UP SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP KEGG_DORSO_VENTRAL_AXIS_FORMATION BECKER_TAMOXIFEN_RESISTANCE_DN LEONARD_HYPOXIA TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINDED_IN CHANG_IMMORTALIZED_BY_HPV31_DN	62 62 62 62 62 62 62 62 62 62 62 62 62 6	3.63E-02 3.63E-02 3.63E-02 3.63E-02 3.63E-02 3.64E-02 3.72E-02 3.77E-02 3.78E-02 3.79E-02 3.89E-02 3.90E-02 3.90E-02 3.90E-02 4.05E-02 4.10E-02 4.13E-02	over over over over over over over over	4 15 4 6 6 12 4 2 5 3 7 6 2 3 2 3 16 5 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	28 330 29 66 69 222 30 4 51 15 90 71 4 14 4 16 354 44 17 33 29 30 31	3.14E-03 3.14E-03 3.15E-03 3.17E-03 3.19E-03 3.28E-03 3.24E-03 3.34E-03 3.36E-03 3.46E-03 3.54E-03	
GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_UP WEST_ADRENOCORTICAL_TUMOR_DN AGARWAL_AKT_PATHWAY_TARGETS AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G CHEN_LUNG_CANCER_SURVIVAL CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP FERRANDO_T_ALL_WITH_MIL_ENL_FUSION_UP REACTOME_GLUCOSE_METABOLISM ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN WINTER_HYPOXIA_UP LI_PROSTATE_CANCER_EPIGENETIC FERNANDEZ_BOUND_BY_MYC BIOCARTA_MTA3_PATHWAY IVANOVA_HEMATOPOIESIS_MATURE_CELL LINDSTEDT_DENDRITIC_CELL_MATURATION_D CORRE_MULTIPLE_MYELOMA_DN BIOCARTA_FIBRINOLYSIS_PATHWAY ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP HAEGERSTRAND_RESPONSE_TO_IMATINIB KANG_IMMORTALIZED_BY_TERT_DN ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_UP LEE_LIVER_CANCER_MYC_E2F1_DN TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_MATTIOLI_MGUS_VS_PCL AMIT_SERUM_RESPONSE_120_MCF10A PUJANA_BRCA1_PCC_NETWORK RUNSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP VSAMIL_Q6 TATAAA_VSTATA_01	c2 c2 c2 c2 c2 c2 c3	4.13E-02 4.14E-02 4.19E-02 4.19E-02 4.19E-02 4.19E-02 4.19E-02 4.19E-02 4.22E-02 4.22E-02 4.25E-02 4.25E-02 4.26E-02 4.35E-02 4.47E-02 4.54E-03 3.06E-03 4.55E-03	over over over over over over over over	5 16 2 6 3 6 6 5 6 6 3 9 3 7 5 4 2 7 2 5 8 4 3 7 5 10 2 6 12 6 12 6 12 6 12 6 12 6 12 6 12	51 352 5 70 14 72 70 48 72 68 17 143 14 94 51 31 5 92 6 54 125 31 16 95 51 1439 718 1055 113 475	3.85E-03 3.87E-03 3.97E-03 3.97E-03 3.99E-03 3.99E-03 4.05E-03 4.04E-03 4.10E-03 4.13E-03 4.33E-03 4.37E-03 4.46E-03 4.46E-03 4.61E-03 4.81E-03	
V\$AP1_Q4 module_84 module_55 module_46 module_88 module_5 module_45 module_64 module_24 module_117 module_6 module_76 module_16 module_92 module_118 module_53 module_108 module_247 module_263 module_174	C3 C4 C4 C4 C4 C4 C4 C4 C4 C4 C4 C4 C4 C4	4.52E-02 7.50E-29 2.78E-23 2.93E-23 7.21E-23 2.60E-22 5.05E-22 5.15E-22 3.56E-20 2.95E-16 1.73E-15 2.58E-14 2.53E-13 1.53E-12 1.79E-10 1.80E-10 1.97E-09 8.09E-09 8.36E-09 8.36E-09 2.27E-08	over over over over over over over over	11 59 54 46 45 53 46 52 42 36 37 33 17 37 16 29 28 11 10 10	142 410 434 301 294 442 333 447 298 270 306 263 57 387 69 282 289 34 26 26 72	1.62E-04 8.53E-32 6.33E-26 1.00E-25 3.28E-25 1.48E-24 3.45E-24 4.10E-24 3.24E-22 3.02E-18 1.97E-17 3.23E-16 3.45E-15 2.26E-14 2.84E-12 3.06E-12 3.59E-11 1.56E-10 1.81E-10 1.77E-10 5.18E-10	
module_291 module_324 module_165 module_33 module_241 module_154 module_297 module_357 module_27 module_38 module_433 module_23 module_23 module_47 module_63 module_47 module_63 module_122 module_112 module_112 module_176 module_176 module_439 module_439 module_39 module_208 module_208 module_208 module_208 module_209 module_104 module_102 module_102 module_104 module_102 module_104 module_104 module_128 module_79	04 04 04 04 04 04 04 04 04 04 04 04 04 0	3.27E-08 5.23E-08 5.92E-08 9.35E-08 1.00E-07 1.22E-07 2.02E-07 9.17E-07 9.17E-07 2.54E-06 2.75E-06 2.75E-06 4.02E-06 4.21E-06 5.65E-06 7.42E-06 2.33E-05 4.04E-05 6.50E-05 9.53E-05 1.23E-04 1.23E-04 1.31E-04 1.31E-04 1.44E-04 1.44E-04	over over over over over over over over	12 14 12 23 12 10 10 10 20 24 8 24 21 15 14 14 20 6 13 12 19 11 6 7 11 8 14	50 78 53 242 56 35 37 37 207 303 27 305 257 130 114 111 249 14 113 100 250 84 19 32 94 46 154 13 80 80	7.81E-10 1.31E-09 1.55E-09 2.55E-09 2.85E-09 3.60E-09 6.42E-09 6.42E-09 3.05E-08 3.13E-08 8.96E-08 9.96E-08 1.06E-07 1.03E-07 1.60E-07 1.72E-07 2.38E-07 3.21E-07 1.03E-06 1.84E-06 6.191E-06 3.10E-06 3.18E-06 6.38E-06 6.38E-06 6.38E-06 6.39E-06 7.14E-06 8.19E-06 8.19E-06	
module_170 module_157 module_41 module_164 module_191 module_15 module_209 module_121 module_280 module_171 module_96 CAR_HPX module_511 module_410 module_172 module_172 module_12 module_12 module_1342 GNF2_CEBPA module_573 GNF2_CARD15	04 04 04 04 04 04 04 04 04 04 04 04 04 0	1.61E-04 1.69E-04 1.72E-04 1.72E-04 1.78E-04 2.04E-04 2.29E-04 2.66E-04 2.69E-04 2.89E-04 3.27E-04 3.48E-04 3.83E-04 5.24E-04 6.52E-04 6.73E-04	over over over over over over over over	10 8 19 7 5 20 8 9 6 11 6 5 5 6 8 19 15 10 6 5 8	81 49 278 35 14 307 50 68 25 106 24 15 18 25 54 290 213 94 28 19 59	9.32E-06 1.01E-05 1.02E-05 1.06E-05 1.12E-05 1.30E-05 1.48E-05 1.53E-05 1.87E-05 1.87E-05 1.84E-05 1.98E-05 2.11E-05 2.38E-05 2.57E-05 2.88E-05 3.99E-05 4.84E-05 5.14E-05 5.14E-05 5.14E-05 5.19E-05 5.43E-05	
GNF2_SPI1 module_52 module_436 GNF2_HPX module_220 module_265 GNF2_LCAT module_212 GNF2_HPN module_112 module_345 module_411 module_545 module_179 module_179 module_181 module_292 module_341 module_292 module_341 module_293 module_181 GNF2_TST module_73 GNF2_GSTM1 module_213 GNF2_GSTM1 module_213 GNF2_TSF10 module_456 GNF2_SERPINB5 module_321 GNF2_CDH3 module_134 GNF2_CVP2B6 module_134 GNF2_CVP2B6 module_136 module_459 module_459 module_459 module_459 module_469 module_47 module_489 module_378 module_378 module_378 module_388 module_398 module_1148 module_316 module_148 module_288 module_94 module_194 module_11 module_148 module_11 module_148 module_11 module_148 module_235 module_288 module_94 module_11 module_148 module_235 module_462 GNF2_PECAM1 module_109	04 04 04 04 04 04 04 04 04 04 04 04 04 0	9.18E-04 9.78E-04 1.17E-03 1.40E-03 1.40E-03 1.40E-03 1.57E-03 2.00E-03 2.03E-03 3.02E-03 3.02E-03 3.53E-03 4.13E-03 4.44E-03 4.44E-03 4.44E-03 4.64E-03 5.86E-03 5.86E-03 5.86E-03 5.89E-03 6.89E-03 6.89E-03 6.89E-03 6.81E-03 6.77E-03 6.84E-03 7.78E-03 8.75E-03 8.75E-03 8.75E-03 8.75E-03 1.16E-02 1.17E-02 1.17E-02 1.27E-02	over over over over over over over over	6 18 10 7 11 5 7 16 7 8 9 6 3 6 18 6 4 9 10 6 4 6 6 4 5 8 3 8 4 15 3 3 4 3 6 3 14 4 6 3 5 3 12 14 4 6 3 5 3	32 295 105 47 131 24 48 252 50 77 97 44 7 42 291 82 47 18 105 128 44 19 44 48 18 30 92 8 93 19 279 9 9 19 10 53 10 266 267 127 11 270 11 12 270 11 270 170 170 170 170 170 170 170 170 170 1	7.52E-05 8.12E-05 9.83E-05 1.22E-04 1.21E-04 1.20E-04 1.39E-04 1.80E-04 1.84E-04 2.17E-04 2.89E-04 2.85E-04 3.41E-04 4.04E-04 4.44E-04 4.70E-04 4.81E-04 6.36E-04 6.36E-04 6.36E-04 6.36E-04 7.08E-04 7.08E-03 1.05E-03 1.05E-03 1.05E-03 1.64E-03 1.66E-03 1.66E-03 2.80E-03 2.80E-03 2.80E-03 3.18E-03 3.28E-03 3.18E-03 3.28E-03	
module_248 module_385 module_100 module_499 module_499 module_491 module_390 module_311 GNF2_SPRR1B module_300 module_119 module_131 module_137 RESPONSE_TO_EXTERNAL_STIMULUS DEFENSE_RESPONSE EXTRACELLULAR_REGION EXTRACELLULAR_REGION PART INFLAMMATORY_RESPONSE RESPONSE_TO_WOUNDING LOCOMOTORY_BEHAVIOR PLASMA_MEMBRANE BEHAVIOR IMMUNE_SYSTEM_PROCESS INTEGRAL_TO_PLASMA_MEMBRANE INTRINSIC_TO_PLASMA_MEMBRANE INTRINSIC_TO_MEMBRANE RESPONSE_TO_BOTIC_STIMULUS CYTOKINE_PRODUCTION PLASMA_MEMBRANE_PART RESPONSE_TO_BOTIC_STIMULUS INTEGRAL_TO_MEMBRANE INTRINSIC_TO_MEMBRANE INTRINSIC_TO_MEMBRANE RESPONSE_TO_BACTERIUM O_PERNSE_RESPONSE_TO_BACTERIUM O_PERNSE_RESPONSE_TO_BACTERIUM G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHW MEMBRANE_PART CHEMOKINE_ACTIVITY RESPONSE_TO_STRESS CHEMOKINE_RECEPTOR_BINDING MEMBRANE_PART CHEMOKINE_ACTIVITY RESPONSE_TO_STRESS CHEMOKINE_RECEPTOR_BINDING KERATINOCYTE_DIFFERENTIATION MULTI_ORGANISM_PROCESS MULTICELLULAR_ORGANISMAL_DEVELOPMENT SECOND_MEMSSENGER_MEDIATED_SIGNALING CYTOKINE_ACTIVITY POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS G_PROTEIN_COUPLED_RECEPTOR_BINDING POSITIVE_REGULATION_OF_TRANSLATION	c5 c5 c5 c5 c5 c5 c5 c5 c5	3.11E-02 3.37E-02 3.79E-02 3.80E-02 3.96E-02 3.96E-02 4.11E-02 4.23E-02 4.42E-02 4.86E-02 1.25E-14 1.70E-13 1.70E-13 4.08E-11 8.09E-10 4.76E-08 6.82E-08 1.55E-07 2.40E-07 2.53E-07 2.40E-07 3.64E-08 6.63E-06 1.31E-07 5.21E-07 5.21E-07 5.42E-07 6.20E-07 9.32E-07 3.64E-06 8.63E-06 1.31E-05 1.42E-05 1.57E-05 1.78E-05 3.42E-05 1.57E-05 1.78E-05 3.42E-04 4.40E-04 4.40E-04 4.44E-04 4.44E-04 4.44E-04 4.46E-04 4.60E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04 4.78E-04	over over over over over over over over	6 3 3 13 2 2 2 13 8 11 3 6 29 28 28 19 20 15 17 12 42 13 23 23 23 21 19 20 10 33 10 12 37 37 6 5 12 48 9 9 14 16 16 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18	71 16 17 274 6 5 5 5 5 279 127 216 19 78 178 181 175 89 122 80 115 51 717 67 245 462 464 169 194 48 556 53 82 689 694 16 11 102 1138 59 920 21 385 522 7 83 512 49 47 16 26 20	4.35E-03 4.76E-03 5.39E-03 5.49E-03 5.49E-03 5.74E-03 5.86E-03 6.12E-03 6.12E-03 6.69E-03 7.37E-03 7.47E-03 8.64E-18 3.51E-16 2.37E-16 1.12E-13 2.78E-12 1.96E-10 3.29E-10 8.56E-10 1.49E-09 1.74E-09 3.53E-09 4.30E-09 4.85E-09 5.97E-09 9.63E-09 4.01E-08 1.01E-07 1.63E-07 2.16E-07 2.57E-07 5.18E-07 1.37E-06 5.61E-06 7.35E-06 8.13E-06 9.16E-06 9.78E-06	
CATION_BINDING RECEPTOR_BINDING OYTOKINE_SECRETION CELL_CELL_SIGNALING REGULATION_OF_SECRETION REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS RECEPTOR_ACTIVITY CHEMICAL_HOMEOSTASIS CYTOKINE_BIOSYNTHETIC_PROCESS OYTOKINE_METABOLIC_PROCESS ION_BINDING PATTERN_BINDING CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO METALLOPEPTIDASE_ACTIVITY O_PROTEIN_SIGNALING_COUPLED_TO_IP3_SECOND_MESSENGE DETECTION_OF_BIOTIC_STIMULUS PHOSPHOINOSITIDE_MEDIATED_SIGNALING INTERLEUKIN_1_SECRETION SYSTEM_DEVELOPMENT SECRETION ANATOMICAL_STRUCTURE_DEVELOPMENT SIGNAL_TRANSDUCTION REGULATION_OF_CYTOKINE_SECRETION ORGAN_DEVELOPMENT ION_HOMEOSTASIS HETEROCYCLE_METABOLIC_PROCESS REGULATION_OF_BIOLOGICAL_QUALITY PROTEIN_SECRETION CELLULAR_CATION_HOMEOSTASIS HOMEOSTATIC_PROCESS PROTEIN_METABOLIC_PROCESS PROTEIN_METABOLIC_PROCESS PROTEIN_METABOLIC_PROCESS REGULATION_OF_BROCESS HOMEOSTATIC_PROCESS REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS CATION_HOMEOSTASIS CELLULAR_HOMEOSTASIS CELLULAR_HOMEOSTASIS	c5	1.93E-03 2.06E-03 2.30E-03 2.46E-03 3.30E-03 3.46E-03 3.40E-03 4.50E-03 4.50E-03 4.50E-03 5.52E-03 5.74E-03 6.93E-03 7.89E-03 8.41E-03 1.05E-02 1.12E-02 1.43E-02 2.13E-02 2.23E-02 2.27E-02 3.00E-02 3.13E-02 3.52E-02 3.52E-02 3.52E-02 3.52E-02 3.52E-02 4.06E-02 4.43E-02	over over over over over over over over	12 14 4 12 5 5 17 9 5 13 5 17 5 4 3 4 3 20 9 22 37 3 15 7 4 14 4 6 9 9 34 4 2 6 7	141 188 12 139 21 23 279 85 25 25 184 25 299 26 14 7 15 8 400 107 478 1004 10 281 69 22 258 24 56 123 947 23 3 880	5.19E-05 5.68E-05 6.48E-05 7.12E-05 7.57E-05 9.98E-05 1.07E-04 1.23E-04 1.52E-04 1.47E-04 1.62E-04 1.99E-04 2.09E-04 2.61E-04 3.04E-04 3.04E-04 4.17E-04 4.57E-04 5.91E-04 9.82E-04 1.34E-03 1.34E-03 1.42E-03 1.65E-03 1.67E-03 1.65E-03 1.70E-03 1.80E-03 2.22E-03	