#### SUPPLEMENTAL METHODS

#### Patient samples and healthy donor peripheral blood mononuclear cells

MCL primary samples used in this study belong to Hematopathology collection, registered in the Biobank of IDIBAPS-Hospital Clínic, Barcelona (R121004-094) and in the National Registry of Biobanks-ISCIII (C.0000397), according to *Real Decreto 1716/2011*. This collection corresponds to biological material remaining from the samples used for the diagnosis, according to the World Health Organization (WHO), in the Hematopathology Unit of Hospital Clinic de Barcelona (HCB, Barcelona, Spain). Informed consent has been obtained from each patient in accordance with the Institutional Ethics Committee of the HCB and the Declaration of Helsinki.

Peripheral blood mononuclear cells (PBMCs) were obtained from healthy donor buffy coats provided by Banc de Sang i Teixits (Barcelona, Spain) after Ficoll-Paque gradient separation (GE Healthcare, Chicago, IL, USA). Monocytes were purified using CD14<sup>+</sup> magnetic beads and LS columns (Miltenyi Biotec, Bergisch Gladbach, Germany) and purity >98% was verified by flow cytometry (FACS Fortessa (BD Biosciences, Franklin Lanes, NJ, USA)). Monocytes were cryopreserved with 10% DMSO (Sigma-Aldrich, St. Louis, MO, USA) and stored in liquid nitrogen until use at IDIBAPS Biobank.

#### **MCL-PDLS** imaging

PDLS formation and growth were monitored by brightfield illumination on the automated digital microscope Cytation 1 (Biotek, Agilent, Santa Clara, CA, USA) under temperature ( $37^{\circ}C$ ) and  $CO_2/O_2$  gas control. Z-stacking function (n=5) was always performed to account for the third dimension. Image analysis and Z-projection were done with manufacturer's software Gen 5 (Biotek).

PDLS were also characterized by Selective Plane Illumination Microscopy (SPIM). Day 7 PDLS were fixed in 4% paraformaldehyde (PFA) for 12h, then PFA was diluted to 0.5% with PBS after several rinse cycles, and finally replaced by blocking/permeabilization buffer (PBS + 2% FBS + 2% BSA + 0.6% Triton + 0.01% Azide) and incubated overnight (ON) with agitation at room temperature (RT). PDLS were then labeled with 10 µg/mL propidium iodide (Thermo Fisher Scientific) and incubated for 4h at RT with agitation, washed and included in agarose.

Then, PDLS included in agarose were cleared using methanol and Benzyl Alcohol/Benzyl Benzoate (BABB) reagent. Finally, PDLS included were imaged by SPIM microscope (ZEISS Lightsheet Z.7, Imactiv 3D, Toulouse) and image-processing algorithms were developed in MATLAB.

### Monocyte-Macrophage differentiation and polarization analysis

To assess MCL induced monocyte-macrophage differentiation /polarization, CD11b<sup>+</sup> Far Red<sup>+</sup> cells were recovered by cells sorting (FACS Aria, BD) from PDLS (day 7), and RNA isolated with TRIZol following manufacturer's protocol (Thermo Fisher Scientific). cDNA was synthetized using Preamp RT Master Mix (Fluidigm, San Francisco, CA, USA). Next, cDNA was pre-amplified for the following genes: *CXCL11, CCL5, MRC1, CCL22, PMAIP1, RSG2, GUSB, ACTB, B2M* using pre-designed TaqMan probes (Thermo Scientific) and PreAmp Master Mix (Fluidigm).

Quantitative real-time PCR (qPCR) was then performed on a StepOne Real-Time PCR System (Thermo Fisher Scientific) using the same probes as the preamplification. Samples were analyzed in duplicate and expression was normalized using the mean of the three endogenous genes: *GUSB, ACTB, B2M*.

To evaluate the degree of M1/M2 polarization MCL-macrophages were compared with M1 or M2-polarized macrophages generated as follows: monocytes obtained from PBMCs as previously described were seeded in 6-wells plates at 0.5x10<sup>6</sup> cells/mL in enriched medium supplemented with macrophage colony stimulating factor (M-CSF) (ThermoFisher Scientific) at 100 ng/mL. After 6 days, additional stimuli were provided to obtain M1-polarized macrophages ((20ng/mL IFNγ (Gibco, Thermo Fisher Scientific) + 100ng/mL LPS (Sigma-Aldrich)) or M2-polarized macrophages (20ng/mL IL-4 (PeproTech, Rocky Hill, NJ)) for 24h.

## MCL-PDLS immune profile and activation

MCL-PDLS (day 3 and day 7) immune profile were both characterized with several panels for B (CD20+) cells, T (CD4+ and CD8+) cells and monocytes/macrophages (CD11b+) using the following antibodies PD1, TIGIT, TIM-3, CD27, CD70, CD66a, CD112, CD155, PD-L1, CD47, SIRPα followed by flow cytometry analysis. PBMCs from healthy donors were used as controls. A complete list of antibodies is provided in supplemental table S1.

Granzyme B and interferon (IFN)-γ were used as read-out of T cell activation and were analyzed in cell culture supernatants using Cytometric Bead Array (CBA) kits and FACS Fortessa (BD Biosciences) following manufacturer's instructions. Data was analyzed using FCAP Array<sup>™</sup> v.3.0 Software (BD Biosciences).

## **RNA-seq and data analysis**

Day 7 PDLS was disaggregated, labelled with LIVE/DEAD Aqua, CD20 - eIF450 (Thermo Fisher Scientific) and CD3-FITC (BD Biosciences). CD20<sup>+</sup>, CD3<sup>-</sup> Aqua<sup>-</sup> cells were recovered using a BD FACSARIA II sorter (Cytometry and cell sorting facility, IDIBAPS) and RNA extracted as before. Likewise, CD20+, CD3- Aqua- cells isolated from the original MCL sample at thawing (day 0) were used as a comparator for RNA-seq studies.

RNA was assayed for quantity and quality using Qubit RNA HS Assay (Life Technologies) and RNA 6000 Nano Assay on a Bioanalyzer 2100. Stranded RNA-seq libraries were performed for 150 ng of mRNA using the TruSeq library kit (Illumina, San Diego, CA, USA). Libraries were sequenced on a NextSeq2000 (Illumina) in a 2x50bp length with a coverage of >40 million paired-reads per simple.

Sequencing reads were trimmed using trimmomatic (version 0.38),<sup>1</sup> and ribosomic RNA reads were filtered out using SortMeRNA (version 2.1b).<sup>2</sup> Gene-level counts (GRCh38.p13; Ensembl release 100) were calculated using kallisto (version 0.46.1)<sup>3</sup> and tximport (version 1.6.0).<sup>4</sup> Differential expression was conducted using DESeq2 (version 1.18.1).<sup>5</sup> Shrinkage of effect size was performed using the apeglm method.<sup>6</sup> Adjusted *P* value (*Q*) <0.10 and absolute log2-transformed fold change >0.5 were used to identify differentially expressed genes (DEGs).

Gene-set enrichment analyses (GSEAs) were conducted with GSEA software (version 4.2.3), <sup>7</sup> using the preranked modality and log2FC results obtained from DESeq2 as input data. Hallmark gene sets, the C2 curated gene sets, the C3 motif gene sets, the C5 gene ontology gene sets (Molecular Signature Database v7.5), and custom gene sets <sup>8,9</sup> were used. Heatmaps of selected genes were generated using GraphPad software. RNAseq data have been deposited at the European Genome-phenome Archive (accession number EGAS00001006964) and will be publicly accessible at the time of publication.

### Metadata comparative analysis

mRNA relative expression levels of selected immune checkpoints in whole lysates of Mantle Cell Lymphoma lymph nodes (MCL-LN, n=199) was compared with normal tonsils (TONSIL n=30) according to GEP public databases (GSE21452, GSE93291, GSE70910, GSE70927, GSE132929, GSE3526, GSE7307, GSE39503, GSE43346, GSE65135, GSE65136 and GSE71810). These selected data were all generated with Affymetrix Human Genome U133 Plus 2.0. Briefly, CEL files were normalized using the Expression Console <sup>™</sup> Software v1.4.1.46 (Affymetrix). To take in consideration the batch effect, join data were normalized using the Limma package included in Transcriptome Analysis console (Applied Biosystems).

### **Statistical analysis**

Data were analyzed using Prism Software 8.0 (GraphPad Software, San Diego, CA, USA). Depending on the assay and based on Shapiro-Wilk normality test, paired t test or Wilcoxon test were used. Data were represented as the mean values of the patients. Differences between the results of comparative tests were

considered significant if the two-sided P value was less than 0.05. The statistical significance convention used

along the manuscript was as follows: \* p<0.05, \*\*p<0.01, \*\*\*p<0.001 and \*\*\*\*p<0.0001.

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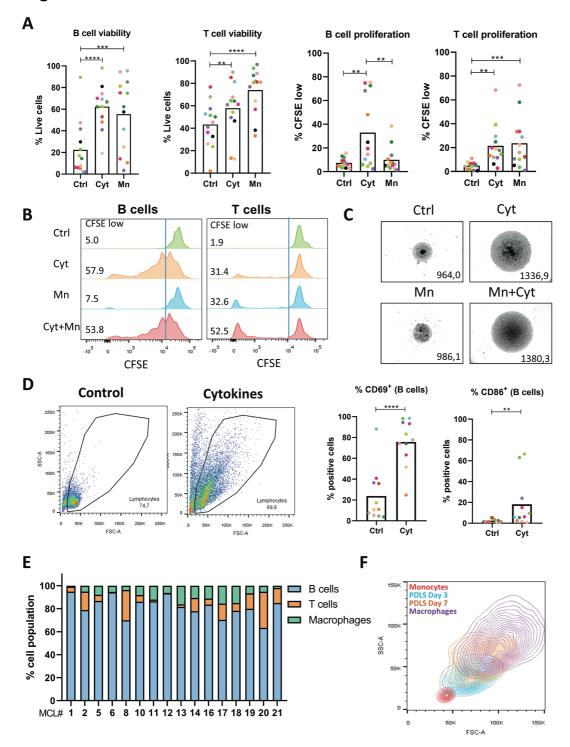
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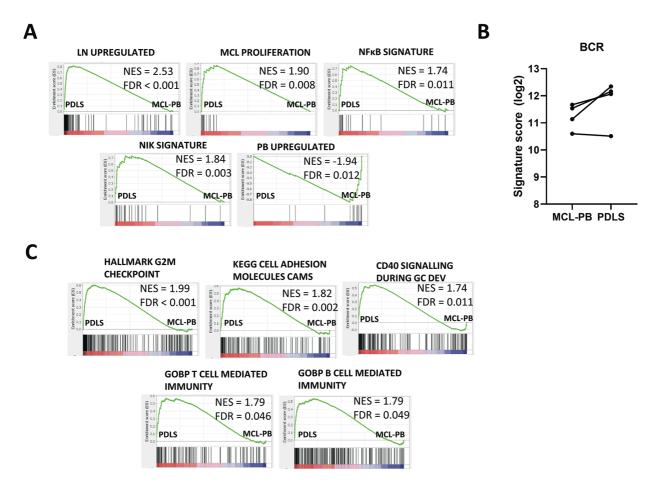
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## **Figure S1**



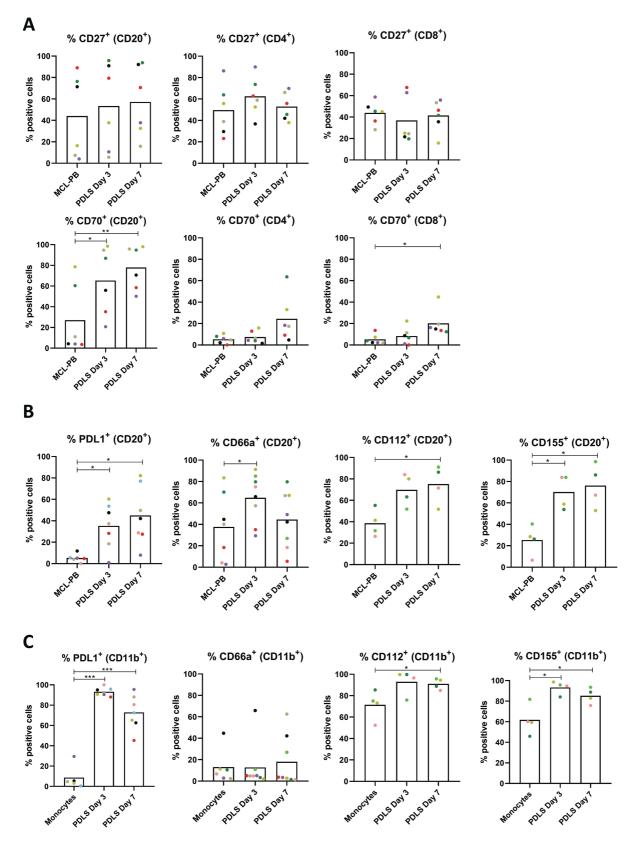
**Figure S1. Effect of cytokines and/or monocytes on PDLS culture**. **(A)** B/T cell viability and proliferation (%CFSE low) of MCL-PDLS cultured during 7 days with cytokines (Cyt) or monocytes (Mn) compared to the control (Ctrl) condition of non-stimulated PDLS. **(B)** Representative CFSE histogram (MCL10) plot showing B-and T cell proliferation when adding cytokines and/or monocytes. Percentage of CFSE low cells is indicated. **(C)** PDLS (MCL13) brightfield imaging (Cytation 1, x40 magnification) with cytokines (Cyt) and/or monocytes (Mn) stimuli compared to control (Ctrl) condition. Size in µm is indicated **(D)** Density plots illustrates the increase in cell growth (FSC-A) and cell complexity (SSC-A) of PDLS cultured with only cytokines for 7 days. B cell activation was assessed by the percentage of CD69 and CD86 positive cells. **(E)** B, T and monocyte distribution after 7 days with cytokines and monocytes. **(F)** Evolution in size (FSC-A) and complexity (SSC-A) of CD11b+ isolated from the PDLS (MCL13) after 3 or 7 days in PDLS media, compared to monocytes or to macrophages differentiated in 2D with M-CSF.

# Figure S2



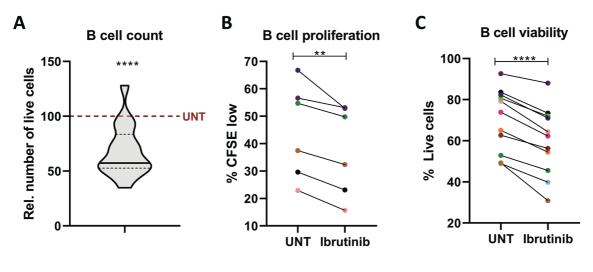
**Figure S2. MCL-PDLS GSEA analysis. (A)** GSEA enrichment plots representing relevant pathways in MCL pathogenesis, with significant increase or decrease in the signature score (Figure 2C). **(B)** BCR signature score calculated as explained in Figure 2C, detailed by each individual patient. **(C)** GSEA enrichment plots representing up-regulated pathways in the PDLS, related to cell cycle, adhesion and immune system.

Figure S3



**Figure S3. Up-regulation of immune modulators markers in MCL-PDLS**. (A) Percentage of positive cells for CD70 and CD27 in B cells and CD4/CD8 T cells from MCL-PDLS (n=6) . (B) Percentage of positive cells of PD-L1, CD66a, CD112 and CD155 in tumor B cell population in the PB sample and from MCL-PDLS at day 3 or day 7 of culture (n=4-8). (C) Percentage of positive cells of ICP ligands in monocytes and macrophages from PDLS after 3 or 7 days of culture (n=4-8).

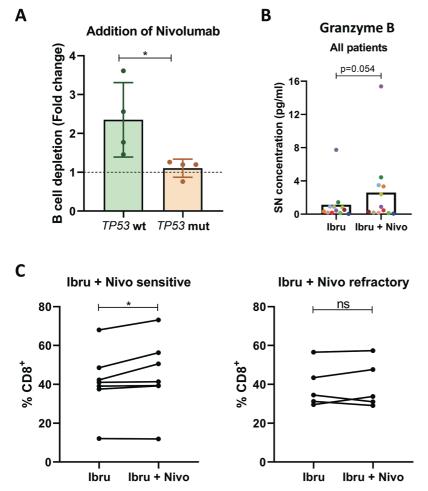
# **Figure S4**



Figure

**S4.** Ibrutinib is active in MCL-PDLS. MCL-PDLS were treated at day 3 with ibrutinib. B cell count (n=17) (A), B cell proliferation quantified by the percentage of CFSE low (B) and B cell viability measured by percentage of negative LIVE/DEAD (C) were assessed after 72h of ibrutinib treatment compared to untreated (UNT) samples.

# **Figure S5**



**Figure S5. Ibrutinib and nivolumab combination in MCL-PDLS. (A)** Effect of adding nivolumab to ibrutinib treatment in patients with *TP53* gene mutated (mut) or non-mutated (wild-type (wt)), represented as the fold change of B cell depletion. **(B)** Granzyme B concentration by CBA comparing ibrutinib monotherapy or in combination with nivolumab. **(C)** Percentage of CD8+ T cells (CD3+gated) after ibrutinib or ibrutinib +nivolumab in sensitive or resistant MCL-PDLS to the combination.

**Supplemental video 1.** Time-lapse video of MCL-PDLS (MCL1) evolution from D1 to D7. Images were taken every 12h in a Cytation 1 device (magnification x40).

**Supplemental video 2.** 3D reconstruction of MCL-PDLS (MCL1) by SPIM microscopy using MATLAB software.

## SUPPLEMENTARY TABLES

# Table S1. Antibodies used in flow cytometry

Target	Conjugate	Clone	Dilution
CD112	PE	R2.525	1/40
CD155	BV605	SKII.4	1/100
CD19	PE	SJ25C1	1/200
CD20	eFluor 450	2H7	1/50
CD27	PE-Cy7	LG.7F9	1/100
CD3	PE-Cy5	UCHT1	1.5/100
CD4	SB600	RPA-T4	1.5/100
CD47	PE-Cy7	B6H12	1/20
CD66a	AF488	283340	1/50
CD70	APC	REA292	1/20
CD8	APC-H7	SK1	1/100
PD-1	PE-Cy7	EH12.1	1/50
PD-L1	PE	MIH1	1/200
SIRPa	APC	15-414	1/200
TIGIT	APC	MBSA43	1/50
TIM-3	PE	F38-2E2	1/50

# Table S2. Leading edge genes of specific signatures from Figure 2C

LN	CENPA	KIF20A	PBK	РВ
	CENPE	KIF23	PLK4	
ANLN	CENPF	KIF2C	POLQ	CKAP4 KLF2
ASPM C170+F40	CENPM	KIFC1	PTPN7	KLF2
AURKA	CEP55	LTBP1	RRM2	MXI1
AURKE	CLSPN	MCM10	SIRPA	PCGF5
	CTNNAL1	MELK	SKA3	RIN3
BUBIN	DLGAP5	MKI67	SMC2	SEMA4B
BUBIB EPB411_4B	DTL	MND1	SPAG5	UCKL1
CCL22-TD HLA-DQA1	E2F8	MRPS14	TOP2A	OORET
CDCZOC	ESCO2	NCAPG	TOX	
CDCZ5A	ESPL1	NCAPG2	TPX2	NFKB
CDC45	EXO1	NCAPH	TYMS	
LICAM	FAM72A	NEIL3	UBE2C	BCL2A1
	FEN1	NEK2	UBE2T	CCL3
MGATS	FOXM1	NEURL1B	UHRF1	CCL4
RASGRP3	HJURP	NLRP3		DUSP2
ŞEMAAA	IPCEF1	NME1		EBI3
TRAF3IP3	KIF14	NUF2		ID2
				IL12B
				LTA
MCL Proli	H2AZ1	ODC1	SET	NFKBIE
CKAP4	HDAC2	PCNA	SF3B3	RGS1
AIMP2 KLE2	HDGF	POLD2	SLC25A3	TNF
KLE9	HNRNPA1	POLE3		
MAL	HNRNPA2B1	PPIA DDM10	SNRPA	
ECGF5	HNRNPA3 HNRNPC	PPM1G PRDX4	SNRPA1 SNRPB2	NIK
RING	HNRNPD	PRDA4 PRPF31	SNRPD1	
<u> ЗЕ</u> ФГА4В	HNRNPR	PSMA1	SNRPD2	ANXA4
ŬĊKI 1	HNRNPU	PSMA2	SNRPG	C17orf49
CCT5	HPRT1	PSMA4	SRM	CABLES1
CCT7	HSP90AB1	PSMA6	SRSF2	CCDC28B
CDC20	HSPD1	PSMA7	SRSF3	CFLAR
600 <del>2</del> 51	HSPE1	PSMB2	SRSF7	DOK5
EEK3	IARS1	PSMB3	SSB	EPB41L4B
<u> Ödvis</u> 1A	IFRD1	PSMC4	SSBP1	HLA-DQA1
ONBP2	ILF2	PSMC6	SYNCRIP	HLA-DRB1
EBBS5	KARS1	PSMD1	TARDBP	HVCN1 IL21R
₩¥5A	KPNA2	PSMD14	TCP1	L1CAM
QTP281	LDHA	PSMD3	TOMM70	LMCD1
₽₽₭	LSM7	PSMD7	TRA2B	MGAT3
RFFKBBE	MAD2L1	PTGES3	TRIM28	RASGRP3
FRE SAX	MCM2	PWP1	TUFM	SEMA4A
ENG2S1	MCM4	RAN	TXNL4A	TRAF3IP3
EIF2S2	MCM6	RANBP1	UBE2L3	
EIF3B	MCM7	RFC4	USP1	
EIF4A1	MRPL23	RPL18	VBP1	
EIF4E	MRPL9	RPL34	XRCC6	
ERH	MRPS18B	RPL6	YWHAE	AIMP2
EXOSC7 FBL		RPS2 RPS5		AP3S1
GLO1	NHP2 NME1	RPS5 RRM1		APEX1
GNL3	NOLC1	RRP9		C1QBP
GOT2	NOP16	RUVBL2		CBX3
GSPT1	NPM1	SERBP1		CCT2
20111				CCT3
				CCT4
				CCT5
				CCT7 CDC20
				CDC20 CDC45
				CDC45 CDK4
				CLNS1A
				CNBP
				COPS5

H2AZ HDAC HDGF HNRM HNRM HNRM HNRM HNRM HNRM HNRM HPRT HSP9 HSPD HSPE IARS<sup>2</sup> IFRD' ILF2

KARS

KPNA

COPS5

COX5A

FOX HJU IPCI KIF1 Table S3. Gene sets (by biological process) overrepresented in MCL-PDLS compared to unstimulated (MCL-PB) controls

Biological process	# of enriched gene sets	NES (max)	FDR, q value (min)
Proliferation			
Cell cycle regulation	18	2,31	<0,001
DNA replication	31	2	<0,001
MYC regulated genes	1	1.64	0.008
KRAS pathway	1	1.51	0.024
Immune pathways			
Chemokines	5	2,11	<0,001
Allograft reaction	3	2,02	<0,001
Immune checkpoint control	1	1,97	0.002
Antigen presentation	9	1,91	0,013
Interleukins	3	1,84	0,007
Cytokines	2	1,75	0,035
Immune response	22	1,75	0.020
CD40-CD40L signalling	1	1,74	0,011
Survival pathways			
ΝϜκΒ	8	1,94	0,001
TNF	3	1,75	0,037
Cellular processes			
Protein syntheis	10	3,01	0,001
RNA synthesis	4	1,87	0,006
Cell adhesion	2	1,82	0,002
Proteasome	2	1,71	0,011
Metabolic pathways			
Oxidative phosphorylation (OXPHOS)	13	1,96	0,002
Glucose metabolism	6	1,72	0,023
Fatty acid metabolism	4	1,72	0,023
Aminoacid metabolism	3	1,69	0,028
DNA damage			
DNA damage/repair	7	1,94	0,002
p53	1	1,65	0,04
Others			
Telomeres	2	1,77	0,016
Redox balance	4	1,73	0,017

GSEA was used to test for significant enrichment of defined gene signatures. NES indicates Normalized Enriched Score; FDR, False Discovery Rate. Threshold FDR<0.05 and NES>1.5. Custom genes set were experimentally derived and downloaded from <u>http://lymphochip.nih.gov/signaturedb/index.html</u>. C2CP, C3, C5 and H gene sets were obtained from the Molecular Signature Database (v2.5).

# Table S4. Complete GSEA results of MCL-PDLS compared to unstimulated (MCL-PB) controls

Aligge Presention         Image Presention         Image Presention           Aligge Present Construct And Construct	GENE SET	SIZE	NES	FDR q-val
NEGE_GRAT_VERSUS_HOST DEFASE         39         2.02         0.000           NEGE_GALUGERAT_REJECTION         19         1.77         0.002           MULMARK_ALLODRAFT_REJECTION         195         1.77         0.002           MULMARK_ALLODRAFT_REJECTION         195         1.77         0.002           MURIDAGES         118         1.64         0.023           REG_MURIT_VERADUSIN         40         1.83         0.0225           Angiogenesis				
REG. ALLOGANF. REIECTON         37         1.94         0.000           Amminoadds Metabolism		39	2.02	0.000
NALLMARK_ALQCRAFT_REJECTION         195         1.77         0.002           NUMINOACISM METABOLISM         44         1.64         0.023           KEG_TIVETOPMAN_METABOLISM         16         1.69         0.028           REACTOME_SELENCAMINO_ACID_METABOLISM         116         1.69         0.028           REACTOME_SELENCAMINO_ACID_METABOLISM         116         1.61         0.010           Antigen presentation		37	1.94	0.000
KEG_MUNE_LEUCINE_DEGRADATION         44         1.64         0.023           KEG_TYPTOPHAN_METAGOUSM         40         1.63         0.023           REACTOME_SELENOAMINO_ACID_METABOLISM         118         1.63         0.028           Angiogenesis		195	1.77	
HEG TWYTOPHAN, METABOLISM         40         1.63         0.025           Reactorum, Eschenovanito, ACID, METABOLISM         1         0.025           Angiogenesis				
HEG TWYTOPHAN, METABOLISM         40         1.63         0.025           Reactorum, Eschenovanito, ACID, METABOLISM         1         0.025           Angiogenesis		44	1.64	0.023
REACTOME_SELERIOAMINO_ACID_METABOLISM         116         1.69         0.028           Andgeneris		40		
Angiogenesis		118		0.028
HALLMARK_ANGIOGENESIS         33         1.61         0.020           Antigen presentation			,	
GOBF_AMTIGEN_PROCESSING_AND_PRESENTATION         107         1.91         0.013           REACTOME_ANTIGEN_PROCESSING_AND_PRESENTATION         106         1.84         0.032           GOBF_AMTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN         47         1.82         0.034           GOBP_ANTIGEN_ASSEMBLY_WITH_MIC_CASS_IPROTEIN_COMPLEX         20         1.82         0.036           GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MIC_CASS_IPROTEIN_COMPLEX         20         1.82         0.036           GOBP_ANTIGEN_SSEMBLY_WITH_MIC_CASS_IPROTEIN_COMPLEX         20         1.82         0.036           GOBP_SERTIDE_ANTIGEN_SSEMBLY_WITH_MIC_PROTEIN_COMPLEX         20         1.86         0.012           CENDACOMED_SPERSENTATION         73         1.76         0.006           KEGG_CALLADES_PRESENTATION         73         1.76         0.011           CENDACOME_SPERSENTATION         1.71         0.021         EMACOME_COSS_PRESENTATION         0.71           CENDACOMES_PRESENTATION         0.73         1.76         0.011         EMACOME_COSS           CENDACOME_SPERSENTATION         1.74         0.011         EMACOME COSS         0.011         EMACOME COSS           CENDACOME_SPERSENTATION         1.72         1.72         0.021         EMACOME COSS         0.013         EMACOME COSS <td></td> <td>33</td> <td>1.61</td> <td>0.010</td>		33	1.61	0.010
GOBF_AMTIGEN_PROCESSING_AND_PRESENTATION         107         1.91         0.013           REACTOME_ANTIGEN_PROCESSING_AND_PRESENTATION         106         1.84         0.032           GOBF_AMTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN         47         1.82         0.034           GOBP_ANTIGEN_ASSEMBLY_WITH_MIC_CASS_IPROTEIN_COMPLEX         20         1.82         0.036           GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MIC_CASS_IPROTEIN_COMPLEX         20         1.82         0.036           GOBP_ANTIGEN_SSEMBLY_WITH_MIC_CASS_IPROTEIN_COMPLEX         20         1.82         0.036           GOBP_SERTIDE_ANTIGEN_SSEMBLY_WITH_MIC_PROTEIN_COMPLEX         20         1.86         0.012           CENDACOMED_SPERSENTATION         73         1.76         0.006           KEGG_CALLADES_PRESENTATION         73         1.76         0.011           CENDACOME_SPERSENTATION         1.71         0.021         EMACOME_COSS_PRESENTATION         0.71           CENDACOMES_PRESENTATION         0.73         1.76         0.011         EMACOME_COSS           CENDACOME_SPERSENTATION         1.74         0.011         EMACOME COSS         0.011         EMACOME COSS           CENDACOME_SPERSENTATION         1.72         1.72         0.021         EMACOME COSS         0.013         EMACOME COSS <td>Antigen presentation</td> <td></td> <td></td> <td></td>	Antigen presentation			
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION         106         1.8.6         0.006           GORP_ANTEGIN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         47         1.8.2         0.034           GORP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         47         1.8.2         0.034           GORP_PETIDE_ANTIGEN_ASSEMBLY_WITH_MIC_CLASS_IL_PROTEIN_COMPLEX         10         1.8.2         0.034           GORP_PETIDE_ANTIGEN_ASSEMBLY_WITH_MIC_CLASS_IL_PROTEIN_COMPLEX         20         1.8.2         0.034           KEGG_ANTIGEN PROCESSING_AND_PRESENTATION         7         1.5.0         0.006           REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGEN_ENDOSOMES         50         1.7.4         0.011           COLDGI SIGNALLING DURING GC DEV         101         1.7.4         0.011           Call Admesion		107	1.91	0.013
GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN         26         1.8         0.032           GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         47         1.82         0.034           GOBP_PTEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         16         1.83         0.036           GOBP_PTEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         20         1.82         0.034           MIC CLASS         50         1.6         0.096         1.50         0.096           KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION         73         1.76         0.0096           REACTOME_CROSS PRESENTATION OF_SOLUBLE_EXOBENOUS_ANTIGENS_ENDOSOMES         50         1.8         0.012           CD40 SIGNALING DURING GC DEV         150         1.74         0.011         1.82         0.002           CD40 SIGNALING DURING GC DEV         197         1.55         0.018         1.866         0.002           REACTOME_CROSSON MOLECULS CAMS         191         1.82         0.002         1.81         0.002           REALIMARE_PICA_UNICTION         199         1.99         0.000         1.41LMARE_PICA_TARGETS         160         1.73         0.021           REALIMARE_PICAL_UNICTION         199         1.99         0.0002         1.84         0.002		106	1,86	0.006
GOBP_ATTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOCENOUS_ANTIGEN         47         1.82         0.034           GOBP_PEPTDE_ANTIGEN_ASSEMALY_WITH_MHC_CASS_IL_PROTEIN_COMPLEX         16         1.83         0.036           GOBP_PEPTDE_ANTIGEN_ASSEMALY_WITH_MHC_CASS_IL_PROTEIN_COMPLEX         20         1.82         0.034           MHC CLASS I         FRACTOME_CROSS_PRESENTATION         7         1.76         0.006           REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES         50         1.8         0.012           CD40-CD40Lagranding		26		0.032
GOBE_DPERTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         16         1.83         0.036           GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         20         1.82         0.034           MICC CLASS I         7         1.50         0.096           KEGG_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         73         1.76         0.096           KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION         73         1.76         0.001           CD40-OLDAL signalling         73         1.76         0.001           CD40-SIGNALLING DURING GC DEV         150         1.74         0.011           Cell Adhesion         197         1.55         0.018           KEGG_CELL_ONESION MOLECULES CAMS         131         1.82         0.002           HALLMARK_ZET_ARGETS         20         2.31         0.000           HALLMARK_SCET_ARGETS         160         1.73         0.221           REACTOME_PCCL_IKE (INASE_MEDIATED_EVENTS         166         1.73         0.021           REACTOME_CYCLE         MC4L_PORTES         165         1.87         0.002           REACTOME_CYCLE, MEGRADATION OF_CELL_CYCLE PROTEINS         88         1.94         0.002           REACTOME_CYCL, MEGRADATION OF_CELL_CYCLE PROTEINS         88         1.94         0.002 </td <td></td> <td>47</td> <td></td> <td>0.034</td>		47		0.034
GOBP_DPETDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         20         1.82         0.034           MHC CLASS I         7         1.50         0.096           KEGG_ANTIGN_PROCESSING_AND_PRESENTATION         73         1.76         0.006           REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES         50         1.8         0.012           CD40-C040_apailing		16		
MIC CLASS I         7         1.50         0.096           KEGG ANTIGEN PROCESSING_AND PRESENTATION         73         1.76         0.006           RECTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES         50         1.8         0.012           CD40 - GROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES         50         1.74         0.011           CC40 - SIGNALLING DURING GC DEV         155         0.013         KEGG         0.022           Cell Adhesion         197         1.55         0.013           KEGG CELL ADHESION_MOLECULES_CAMS         131         1.82         0.002           Cell cyde regulation         199         1.99         0.000           HALLMARK 152T_ARGETS         200         2.31         0.002           REACTOME_CC_C, MEDIATED_EVENTS         16         1.73         0.021           REACTOME_CC_C, MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS         88         1.94         0.002           REACTOME_CC_C, MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS         88         1.94         0.002           REACTOME_CC_C, MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS         88         1.94         0.002           REACTOME_CC_L, CYCLE_C LHECKPOINTS         165         1.87         0.006           REACTOME_TESS_REGULATES_EXAND_G				
KIGG_ANTIGEN_PROCESSING_AND_PRESENTATION         73         1.76         0.006           REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES         50         1.74         0.011           CD40-CD40: signalling		7		
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES         50         1,8         0.012           CD40-CO40L signalling	KEGG ANTIGEN PROCESSING AND PRESENTATION	73		
CD40-C040. signalling         150         1.74         0.011           CD40 SIGNALLING DURING GC DEV         150         1.74         0.011           CCD40 SIGNALLING DURING GC DEV         150         1.74         0.011           CCD40 SIGNALLING DURING GC DEV         157         1.55         0.018           KEGG CELL ADHESION, MOLECULES, CAMS         131         1.82         0.000           Cell Avdhesion, MOLECULES, CAMS         131         1.82         0.000           HALLMARK, CAR, TARGETS         200         2.31         0.000           HALLMARK, CAR, CHECKPOINT         199         1.99         0.013           KEGG CELL, CYCLE         124         1.65         0.023           REACTOME, CUCLE         166         1.73         0.021           REACTOME, CUCLE         CCLE, CYCLE         166         1.73         0.021           REACTOME, CUCLE         CUCLE, CREVOINTS         289         1.92         0.003           REACTOME, COL, CYCLE, ARTS         165         1.87         0.006           REACTOME, COYCLIN, A. BL B2, ASSOCIATED, EVENTS, DURING, G2, M, TRANSITION         149         0.112           REACTOME, CYCLIN, A. BL B2, ASSOCIATED, EVENTS, DURING, G2, M, TRANSITION         1.81         0.011           R				
CD40 SIGNALLING DURING GC DEV         150         1.74         0.011           Cell Adhesion				
Cell Adhesion         197         1.55         0.018           HALLMARK APICAL_JUNCTION         197         1.55         0.018           KEG_CELL_ADHESION_MOLECULES_CAMS         131         1.82         0.002           Cell orgulation         200         2.31         0.000           HALLMARK_E2F_TARGETS         200         2.31         0.000           HALLMARK_GCM_CHECKPOINT         199         1.99         0.021           REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS         16         1.73         0.021           REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS         16         1.73         0.021           REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS         165         1.87         0.006           REACTOME_CIL_CYCLE         CHECKPOINTS         289         1.92         0.003           REACTOME_GI_S_PHASE         162         1.84         0.001           REACTOME_GI_S_PHASE         162         1.84         0.012           REACTOME_GI_S_SPECIFIC_TRANSCRIPTION         29         1.82         0.013           REACTOME_GI_S_SPECIFIC_TRANSCRIPTION_CF_GENES_INVOLVED_IN_G2_CELL_         18         1.71         0.023           REACTOME_TRES_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         1.82         0.035 <td< td=""><td></td><td>150</td><td>1.74</td><td>0.011</td></td<>		150	1.74	0.011
HALLMARK_APICAL_JUNCTION         197         1.55         0.018           KEGG_CELL ADHESION_MOLECULES_CAMS         131         1.82         0.002           Cell cycle regulation         199         1.90         0.000           HALLMARK_G2M_CHECKPOINT         199         1.99         0.000           HALLMARK_G2M_CHECKPOINT         199         1.99         0.001           KEGG_CELL_CYCLE         124         1.65         0.021           REACTOME_POL_LIKE_KINASE_MEDIATED_EVENTS         16         1.73         0.021           REACTOME_OL, LIKE,KINASE_MEDIATED_EVENTS         165         1.87         0.006           REACTOME_GU_LWE,KINASE_MEDIATED_EVENTS         165         1.87         0.006           REACTOME_GU_M_CILL_CYCLE_CHECKPOINTS         165         1.87         0.006           REACTOME_GU_M_CILL_CYCLEC,CARDENTS         162         1.84         0.007           REACTOME_GU_M_CILL_CYCLEC,CARDENTS         181         0.011         REACTOME_MITOTIC_GI_PHASE_AND_GI_S_TRANSITION         149         1.81         0.012           REACTOME_MITOTIC_GI_PHASE_AND_GI_S_TRANSITION         25         1.72         0.023           REACTOME_MITOTIC_GI_PHASE_AND_ANAPHASE         23         1.71         0.023           REACTOME_MEDACTON_CO_CHROMOSOME_S			•	
KEGG_CELL_ADHESION_MOLECULES_CAMS         131         1.82         0.002           Cell cycle regulation		197	1.55	0.018
Cell cycle regulation         200         2.31         0.000           HALLMARK, E2F, TARGETS         200         2.31         0.000           HALLMARK, ZM, CHECKPOINT         199         1.99         0.000           HALLMARK, ZM, CHECKPOINT         199         1.59         0.013           KEGG, CELL, CYCLE         124         1.65         0.023           REACTOME, POLO, LIKE, KINASE, MEDIATED_EVENTS         16         1.73         0.021           REACTOME, COL, LIKE, KINASE, MEDIATED_EVENTS         16         1.73         0.021           REACTOME, COL, LIKE, KINASE, MEDIATED_EVENTS         165         1.87         0.002           REACTOME, CJ, CHECKPOINTS         188         1.94         0.002           REACTOME, GL, SCHEL, CYCLE, CHECKPOINTS         165         1.87         0.006           REACTOME, GL, SCHECHT, TRANSCRIPTION         19         1.82         0.011           REACTOME, MITOTIC, GL, PHASE, AND, GL S, TRANSITION         149         1.81         0.012           REACTOME, MEDIATES, TRANSCRIPTION_OF, GENES_INVOLVED_IN_G2_CELL_18         1.72         0.023           REACTOME, MITOTIC, GL, TAPHASE, AND_ANAPHASE         236         1.64         0.445           GOBP, MITOTI, OUCLART DIASINON         126         1.79         0.010				
HALLMARK_E2F_TARGETS         200         2.31         0.000           HALLMARK_G2M_CHECKPOINT         199         1.99         0.000           HALLMARK_MITOTIC_SPINDLE         199         1.59         0.013           KEGG_CEL_CYCLE         124         1.65         0.023           REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS         16         1.73         0.021           REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS         88         1.94         0.002           REACTOME_CC_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS         88         1.94         0.002           REACTOME_CC_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS         88         1.92         0.003           REACTOME_CC_MEDIATED_DEGRADATED_EVENTS         165         1.87         0.006           REACTOME_GL_S_SPECIFIC_TRANSCRIPTION         29         1.82         0.011           REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION         149         1.81         0.012           REACTOME_TP33_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1.71         0.023           REACTOME_TP33_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         0.011           REACTOME_TP33_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         0.023           GOBP_REGULATION_OF_CH				
HALLMARK_G2M_CHECKPOINT       199       1.99       0.000         HALLMARK_MITOTIC_SPINDLE       199       1.59       0.013         KEGG_CELL_CYCLE       124       1.65       0.023         REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS       88       1.94       0.002         REACTOME_CLL_CYCLE_CHECKPOINTS       289       1.92       0.003         REACTOME_CLL_CYCLE_CHECKPOINTS       165       1.87       0.006         REACTOME_G1_S_PERICL_TRANSCRIPTION       29       1.82       0.001         REACTOME_G1_S_SPECIFL_TRANSCRIPTION       29       1.82       0.011         REACTOME_G1_S_SPECIFL_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_       18       1.71       0.023         REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_       18       1.71       0.023         CYCLE_ARREST       18       1.71       0.023         CYCLE_ARREST       18       1.71       0.023         GOBP_MITOTIC_OMETAPHASE_AND_ANAPHASE       236       1.64       0.045         GOBP_MICTOTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS       153       1.83       0.036         GOBP_MITOTIC_NUCLEAR_DIVISION       291       1.82       0.035         GOME_CHEMOKINE_RECEPTOR_BINDING       34		200	2.31	0.000
HALLMARK_MITOTIC_SPINDLE       199       1.59       0.013         KEGG_CELL_CYCLE       124       1.65       0.023         REACTOME_COLQ_LIKE_KINASE_MEDIATED_EVENTS       16       1.73       0.021         REACTOME_COLQ_LIKE_KINASE_MEDIATED_EVENTS       88       1.94       0.002         REACTOME_CELL_CYCLE_CHECKPOINTS       289       1.92       0.003         REACTOME_S_PHASE       162       1.84       0.007         REACTOME_S_PHASE       162       1.84       0.001         REACTOME_S_PHASE       162       1.84       0.001         REACTOME_GI_S_PECIFIC_TRANSCRIPTION       29       1.82       0.011         REACTOME_CYCLIN_A_BT_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION       25       1.72       0.023         REACTOME_CYCLIAR_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_       18       1.71       0.023         CYCLE_ARREST       REACTOME_GI_PHASE_AND_ANAPHASE       236       1.64       0.045         GOBP_MICTIC_MUCLAR_DIVISION       291       1.83       0.036         GOBP_MICTIC_NUCLEAR_DIVISION       291       1.82       0.037         GOBP_MICTIC_NUCLEAR_DIVISION       291       1.82       0.044         ChemoKine_CCHEMOKINE_RECEPTOR_BINDLOHEMOKINES       53       1.86 </td <td></td> <td></td> <td></td> <td></td>				
KEGG_CELL_CYCLE         124         1.65         0.023           REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS         16         1.73         0.021           REACTOME_POLO_LIKE_KINASE_MEDIATED_EGRADATION_OF_CELL_CYCLE_PROTEINS         88         1.94         0.002           REACTOME_CC_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS         88         1.94         0.003           REACTOME_G2_M_CHECKPOINTS         165         1.87         0.006           REACTOME_G1_S_PECIFIC_TRANSCRIPTION         29         1.82         0.011           REACTOME_G1_G1_PHASE_AND_G1_S_TRANSITION         29         1.82         0.0023           REACTOME_CYCLIN_A_B1 B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION         25         1.72         0.023           REACTOME_TPS3_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1.71         0.023           REACTOME_MITOTIC_G1_PHASE_AND_ANAPHASE         236         1.64         0.045           GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MICTOT_SUNCIAR_DECEPTOR_BIND_CHEMOKINES         53         1.86         0.0006           GOMF_CICLEMOKINE_RECEPTOR_BINDING         54         2.08         0.0001           GOMF_CICLEMOKINE_RECEPTOR_BINDING         54         2.08         0.0001 <td></td> <td></td> <td></td> <td></td>				
REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS         16         1,73         0.021           REACTOME_ARC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS         88         1,94         0.002           REACTOME_CEL_CYCLE_CHECKPOINTS         165         1,87         0.006           REACTOME_S_PHASE         165         1,87         0.001           REACTOME_S_PHASE         162         1,84         0.001           REACTOME_MITORIC_G_PHASE_AND_G1_S_TRANSITION         29         1,82         0.011           REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION         25         1,72         0.023           REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1,71         0.023           REACTOME_INTON_METAPHASE_AND_ANAPHASE         236         1,64         0.045           GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MICROTUBULE_CYTOSKELETON_RGANIZATION         291         1.82         0.035           GOMF_CREMOKINE_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.000           GOMF_CREMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CREMOKINE_RECEPTOR_BINDING         34         2.07         0.000           GOMF_CREMOK				
REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS         88         1,94         0.002           REACTOME_CELL_CYCLE_CHECKPOINTS         289         1,92         0.003           REACTOME_GEL_MCCHECKPOINTS         165         1,87         0.006           REACTOME_S_PHASE         162         1,84         0.007           REACTOME_GI_S_SPECIFIC_TRANSCRIPTION         29         1,82         0.011           REACTOME_MITOTIC_G_I_PHASE_AND_G1_S_TRANSITION         25         1,72         0.023           REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1,71         0.023           REACTOME_MITOTIC_G_LREPAPHASE_AND_ANAPHASE         236         1,64         0.045           GOBP_REGULATION_OF_CHROMOSOME_SEPARATION         69         1.97         0.010           GOBP_MICROTUBULE_OTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_SPINDLE_ORGANIZATION         126         1.79         0.044           Chemokines         53         1.86         0.000           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDIG         54         2.08         0.000           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         20 <td></td> <td></td> <td></td> <td></td>				
REACTOME_CELL_CYCLE_CHECKPOINTS         289         1,92         0.003           REACTOME_G2_M_CHECKPOINTS         165         1,87         0.006           REACTOME_G1_S_SPECIFIC_TRANSCRIPTION         29         1,82         0.011           REACTOME_G1_S_PECIFIC_TRANSCRIPTION         29         1,82         0.023           REACTOME_TP53_REQULATES_TRANSTOP         149         1,81         0.012           REACTOME_TP53_REQULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1,71         0.023           REACTOME_TP53_REQULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1,71         0.023           REACTOME_TOME_TP53_REQULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1,71         0.023           REACTOME_TOME_TOTIC_METAPHASE_AND_ANAPHASE         236         1,64         0.045           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.036           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.036           GOMF_CCR_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         29         1.73         0.041           GOMF_CHEMOKINE_REC				
REACTOME_G2_M_CHECKPOINTS         165         1,87         0.006           REACTOME_G1_PHASE         162         1,84         0.007           REACTOME_G1_S_SPECIFIC_TRANSCRIPTION         29         1,82         0.011           REACTOME_G1_S_PHASE_AND_G1_S_TRANSITION         149         1,81         0.012           REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION         25         1,72         0.023           REACTOME_MITOTIC_G1_PHASE_AND_ANAPHASE         236         1,64         0.045           GOBP_REGULATION_OF_CHROMOSOME_SEPARATION         69         1.97         0.010           GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_SPINDLE_ORGANIZATION         126         1.79         0.044           Chemokines         53         1.86         0.006           GOMF_CCR_CHEMOKINE_RECEPTOR_BIND_CHEMOKINES         53         1.86         0.000           GOMF_CR_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CR_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CR_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CR_CHEMOKINE_RECEPTOR_BINDING         54         2.08 <td></td> <td></td> <td></td> <td></td>				
REACTOME_S_PHASE         162         1,84         0.007           REACTOME_G1_S_SPECIFIC_TRANSCRIPTION         29         1,82         0.011           REACTOME_G1_S_SPECIFIC_TRANSCRIPTION         149         1,81         0.012           REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION         25         1,72         0.023           REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1,71         0.023           REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE         236         1,64         0.045           GOBP_MITOTIC_NUCLEAR_DIVISION         69         1.97         0.010           GOBP_MITOTIC_VOLUEAR_DIVISION         291         1.82         0.035           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.036           GOMF_CCR_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.000           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CCHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CCHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.				
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION         29         1,82         0.011           REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION         149         1,81         0.012           REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1,71         0.023           CYCLE_ARREST         18         1,71         0.023           REACTOME_INTOL_METAPHASE_AND_ANAPHASE         236         1,64         0.045           GOBP_REGULATION_OF_CHROMOSOME SEPARATION         69         1.97         0.010           GOBP_MICTOTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.035           GOBP_MITOTIC_SPINDL_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_SPINDL_ORGANIZATION         126         1.79         0.044           Chemokine_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.006           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         40         2.07         0.001           GOMF_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.002           GOMF_CHEMOKINE_RECEPTOR_INTERACTION				
REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION         149         1,81         0.012           REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION         25         1,72         0.023           REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1,71         0.023           REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE         236         1,64         0.045           GOBP_REGULATION_OF_CHROMOSOME_SEPARATION         69         1.97         0.010           GOBP_MICROTUBULE_CYTOSKELETON_RGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_SPINDLE_ORGANIZATION         291         1.82         0.035           GOBP_MITOTIC_SPINDLE_ORGANIZATION         126         1.79         0.044           Chemokines         53         1.86         0.006           GOMF_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_ACTIVITY         40         2.07         0.000           GOMF_CHEMOKINE_ACTIVITY         29         1.73         0.047           Cytokines         -         -         -         -           GOMF_CYTOKINE_ACTIVITY         205				
REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION         25         1,72         0.023           REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_ CYCLE_ARREST         18         1,71         0.023           REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_ CYCLE_ARREST         18         1,71         0.023           REACTOME_MITOTIO_METAPHASE_AND_ANAPHASE         236         1,64         0.045           GOBP_REGULATION_OF_CHROMOSOME_SEPARATION         69         1.97         0.010           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.035           GOBP_MITOTIC_SPINDLE_ORGANIZATION         126         1.79         0.044           Chemokines         126         1.79         0.044           Chemokine_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CHEMOKINE_ACTIVITY         40         2.07         0.000           GOMF_CHEMOKINE_ACTIVITY         29         1.73         0.047           CYTOKINE_CHTOKINE_RECEPTOR_INTERACTION         240         1.57         0.035           DNA damage/repair         X <td></td> <td></td> <td></td> <td></td>				
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_         18         1,71         0.023           CYCLE_ARREST         1.64         0.045           CYCLE_ARREST         236         1.64         0.045           CYCLE_ARREST         69         1.97         0.010           GOBP_REGULATION_OF_CHROMOSOME_SEPARATION         69         1.97         0.010           GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.035           GOBP_MITOTIC_SINDLE_ORGANIZATION         126         1.79         0.044           Chemokines         53         1.86         0.006           GOMF_CCR_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         29         1.73         0.041           GOMF_CHEMOKINE_RECEPTOR_BINDING         29         1.75         0.035           GOMF_CHEMOKINE_ACTIVITY         205         1.75         0.035           DNA damage/repair         XEGG_V				
CYCLE_ARREST         10         1,71         0.023           REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE         236         1,64         0.045           GOBP_REGULATION_OF_CHROMOSOME_SEPARATION         69         1.97         0.010           GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.035           GOBP_MITOTIC_SPINDLE_ORGANIZATION         126         1.79         0.044           Chemokines         53         1.86         0.006           GOMF_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         205         1.73         0.047           GOMF_CHEMOKINE_RECEPTOR_BINDING         204         2.07         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         240         1.57         0.041           GOMF_CHEMOKINE_RECEPTOR_INTERACTION         240         1.57         0.041           GOMF_CYTOKINE_ACTIVITY         29         1.73         0.047           GOMF_CYT				
GOBP_REGULATION_OF_CHROMOSOME_SEPARATION         69         1.97         0.010           GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.035           GOBP_MITOTIC_SPINDLE_ORGANIZATION         126         1.79         0.044           Chemokines         291         1.82         0.035           REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.006           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.07         0.000           GOMF_CHEMOKINE_ACTIVITY         40         2.07         0.000           GOMF_CHEMOKINE_RECEPTOR_INTERACTION         240         1.57         0.041           GOMF_CYTOKINE_CTOKINE_RECEPTOR_INTERACTION         240         1.57         0.041           GOME_CYTOKINE_ACTIVITY         205         1.75         0.035		18	1,71	0.023
GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.035           GOBP_MITOTIC_SPINDLE_ORGANIZATION         126         1.79         0.044           Chemokines          126         1.79         0.044           Chemokine_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.006           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.08         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         40         2.07         0.000           GOMF_CHEMOKINE_ACTIVITY         40         2.07         0.001           GOMF_CHEMOKINE_ACTIVITY         29         1.73         0.047           Cytokines           1.57         0.035           DMA damage/repair         205         1.75         0.035           DNA damage/repair         23         1.77         0.005           KEGG_NUCLEOTIDE_EXCISION_REPAIR         34         1.67         0.016           KEGG_NUCLEOTIDE_EXCISION_REPAIR         34         1.67         0.016           REACTOME_BASE_EXCISION_REPA	REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	236	1,64	0.045
GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS         153         1.83         0.036           GOBP_MITOTIC_NUCLEAR_DIVISION         291         1.82         0.035           GOBP_MITOTIC_SPINDLE_ORGANIZATION         126         1.79         0.044           Chemokines          126         1.79         0.044           Chemokine_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES         53         1.86         0.006           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         34         2.08         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         40         2.07         0.000           GOMF_CHEMOKINE_ACTIVITY         40         2.07         0.001           GOMF_CHEMOKINE_ACTIVITY         29         1.73         0.047           Cytokines           1.57         0.035           DMA damage/repair         205         1.75         0.035           DNA damage/repair         23         1.77         0.005           KEGG_NUCLEOTIDE_EXCISION_REPAIR         34         1.67         0.016           KEGG_NUCLEOTIDE_EXCISION_REPAIR         34         1.67         0.016           REACTOME_BASE_EXCISION_REPA	GOBP_REGULATION_OF_CHROMOSOME_SEPARATION	69	1.97	0.010
GOBP_MITOTIC_SPINDLE_ORGANIZATION         126         1.79         0.044           Chemokines	GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS	153	1.83	0.036
Chemokines         53         1,86         0.006           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CHEMOKINE_ACTIVITY         40         2.07         0.000           GOMF_CHEMOATRACTANT_ACTIVITY         29         1.73         0.047           Cytokines           240         1.57         0.041           GOMF_CYTOKINE_ACTIVITY         205         1.75         0.035            DNA damage/repair         23         1.77         0.0016            KEGG_NUCLEOTIDE_EXCISION_REPAIR         23         1.67         0.016           KEGG_NUCLEOTIDE_EXCISION_REPAIR         34         1.67         0.016           KEGG_NUCLEOTIDE_EXCISION_REPAIR         44         1.58         0.040           REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS         37         1.94         0.002           REACTOME_BASE_EXCISION_REPAIR         86         1.7         0.024           REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR         164         1.63         0.046		291		
Chemokines         53         1,86         0.006           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING         34         2.11         0.000           GOMF_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CHEMOKINE_ACTIVITY         40         2.07         0.000           GOMF_CHEMOATRACTANT_ACTIVITY         29         1.73         0.047           Cytokines           240         1.57         0.041           GOMF_CYTOKINE_ACTIVITY         205         1.75         0.035            DNA damage/repair           23         1.77         0.0016           KEGG_NUCLEOTIDE_EXCISION_REPAIR         34         1.67         0.016 <td></td> <td></td> <td></td> <td></td>				
GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING       34       2.11       0.000         GOMF_CHEMOKINE_RECEPTOR_BINDING       54       2.08       0.000         GOMF_CHEMOKINE_ACTIVITY       40       2.07       0.000         GOMF_CHEMOATTRACTANT_ACTIVITY       29       1.73       0.047         Cytokines       29       1.73       0.041         GOMF_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION       240       1.57       0.035         DNA damage/repair       205       1.75       0.035         EKEG_NISMATCH_REPAIR       23       1.77       0.005         KEGG_NUCLEOTIDE_EXCISION_REPAIR       34       1.67       0.016         KEGG_NUCLEOTIDE_EXCISION_REPAIR       44       1.58       0.040         REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS       37       1.94       0.002         REACTOME_BASE_EXCISION_REPAIR       86       1.7       0.024         REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR       164       1.63       0.046         REACTOME_MISMATCH_REPAIR       164       1.62       0.050         DMA replication       15       1.62       0.050	Chemokines			
GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING       34       2.11       0.000         GOMF_CHEMOKINE_RECEPTOR_BINDING       54       2.08       0.000         GOMF_CHEMOKINE_ACTIVITY       40       2.07       0.000         GOMF_CHEMOATTRACTANT_ACTIVITY       29       1.73       0.047         Cytokines       29       1.73       0.041         GOMF_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION       240       1.57       0.035         DNA damage/repair       205       1.75       0.035         EKEG_NISMATCH_REPAIR       23       1.77       0.005         KEGG_NUCLEOTIDE_EXCISION_REPAIR       34       1.67       0.016         KEGG_NUCLEOTIDE_EXCISION_REPAIR       44       1.58       0.040         REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS       37       1.94       0.002         REACTOME_BASE_EXCISION_REPAIR       86       1.7       0.024         REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR       164       1.63       0.046         REACTOME_MISMATCH_REPAIR       164       1.62       0.050         DMA replication       15       1.62       0.050	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	53	1,86	0.006
GOMF_CHEMOKINE_RECEPTOR_BINDING         54         2.08         0.000           GOMF_CHEMOKINE_ACTIVITY         40         2.07         0.000           GOMF_CHEMOKINE_ACTIVITY         29         1.73         0.047           Cytokines           1.57         0.041           GOMF_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION         240         1.57         0.041           GOMF_CYTOKINE_ACTIVITY         205         1.75         0.035           DNA damage/repair         23         1.77         0.005           KEGG_INISMATCH_REPAIR         23         1.67         0.016           KEGG_NUCLEOTIDE_EXCISION_REPAIR         34         1.67         0.016           KEGG_NUCLEOTIDE_EXCISION_REPAIR         44         1.58         0.040           REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS         37         1,94         0.002           REACTOME_BASE_EXCISION_REPAIR         86         1,7         0.024           REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR         164         1.63         0.046           REACTOME_MISMATCH_REPAIR         15         1.62         0.050           DNA replication         15         1.62         0.050				
GOMF_CHEMOKINE_ACTIVITY       40       2.07       0.000         GOMF_CHEMOATTRACTANT_ACTIVITY       29       1.73       0.047         Cytokines             KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION       240       1.57       0.041         GOMF_CYTOKINE_ACTIVITY       205       1.75       0.035         DNA damage/repair       23       1.77       0.005         KEGG_INISMATCH_REPAIR       23       1.67       0.016         KEGG_NUCLEOTIDE_EXCISION_REPAIR       34       1.67       0.016         KEGG_NUCLEOTIDE_EXCISION_REPAIR       44       1.58       0.040         REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS       37       1,94       0.002         REACTOME_BASE_EXCISION_REPAIR       86       1,7       0.024         REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR       164       1,63       0.046         REACTOME_MISMATCH_REPAIR       15       1,62       0.050         DNA replication       15       1,62       0.050         DNA replication       15       0.000       0.000		54		
GOMF_CHEMOATTRACTANT_ACTIVITY         29         1.73         0.047           Cytokines				
Cytokines           KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION         240         1.57         0.041           GOMF_CYTOKINE_ACTIVITY         205         1.75         0.035           DNA damage/repair				
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION       240       1.57       0.041         GOMF_CYTOKINE_ACTIVITY       205       1.75       0.035         DNA damage/repair       23       1.77       0.005         KEGG_MISMATCH_REPAIR       23       1.67       0.016         KEGG_BASE_EXCISION_REPAIR       34       1.67       0.016         KEGG_NUCLEOTIDE_EXCISION_REPAIR       44       1.58       0.040         REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS       37       1,94       0.002         REACTOME_BASE_EXCISION_REPAIR       86       1,7       0.024         REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR       164       1,63       0.046         REACTOME_MISMATCH_REPAIR       15       1,62       0.050         DNA replication       KEGG_DNA_REPLICATION       36       2.00       0.000				
GOMF_CYTOKINE_ACTIVITY         205         1.75         0.035           DNA damage/repair         KEGG_MISMATCH_REPAIR         23         1.77         0.005           KEGG_BASE_EXCISION_REPAIR         34         1.67         0.016           KEGG_NUCLEOTIDE_EXCISION_REPAIR         44         1.58         0.040           REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS         37         1,94         0.002           REACTOME_BASE_EXCISION_REPAIR         86         1,7         0.024           REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR         164         1,63         0.046           REACTOME_MISMATCH_REPAIR         15         1,62         0.050           DNA replication         15         1,62         0.050		240	1.57	0.041
DNA damage/repair           KEGG_MISMATCH_REPAIR         23         1.77         0.005           KEGG_BASE_EXCISION_REPAIR         34         1.67         0.016           KEGG_NUCLEOTIDE_EXCISION_REPAIR         44         1.58         0.040           REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS         37         1,94         0.002           REACTOME_BASE_EXCISION_REPAIR         86         1,7         0.024           REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR         164         1,63         0.046           REACTOME_MISMATCH_REPAIR         15         1,62         0.050           DNA replication           V         V				
KEGG_MISMATCH_REPAIR       23       1.77       0.005         KEGG_BASE_EXCISION_REPAIR       34       1.67       0.016         KEGG_NUCLEOTIDE_EXCISION_REPAIR       44       1.58       0.040         REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS       37       1,94       0.002         REACTOME_BASE_EXCISION_REPAIR       86       1,7       0.024         REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR       164       1,63       0.046         REACTOME_MISMATCH_REPAIR       15       1,62       0.050         DNA replication             KEGG_DNA_REPLICATION       36       2.00       0.000				
KEGG_BASE_EXCISION_REPAIR       34       1.67       0.016         KEGG_NUCLEOTIDE_EXCISION_REPAIR       44       1.58       0.040         REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS       37       1,94       0.002         REACTOME_BASE_EXCISION_REPAIR       86       1,7       0.024         REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR       164       1,63       0.046         REACTOME_MISMATCH_REPAIR       15       1,62       0.050         DNA replication       KEGG_DNA_REPLICATION		23	1.77	0.005
KEGG_NUCLEOTIDE_EXCISION_REPAIR       44       1.58       0.040         REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS       37       1,94       0.002         REACTOME_BASE_EXCISION_REPAIR       86       1,7       0.024         REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR       164       1,63       0.046         REACTOME_MISMATCH_REPAIR       15       1,62       0.050         DNA replication             KEGG_DNA_REPLICATION       36       2.00       0.000				
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS         37         1,94         0.002           REACTOME_BASE_EXCISION_REPAIR         86         1,7         0.024           REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR         164         1,63         0.046           REACTOME_MISMATCH_REPAIR         15         1,62         0.050           DNA replication               KEGG_DNA_REPLICATION         36         2.00         0.000				
REACTOME_BASE_EXCISION_REPAIR         86         1,7         0.024           REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR         164         1,63         0.046           REACTOME_MISMATCH_REPAIR         15         1,62         0.050           DNA replication         V           KEGG_DNA_REPLICATION         36         2.00         0.000				
REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR         164         1,63         0.046           REACTOME_MISMATCH_REPAIR         15         1,62         0.050           DNA replication         5         5         5         5         5         5         6         6         6         6         6         6         6         6         6         6         6         6         7 <th7< th=""> <th7< th=""> <th7< th=""></th7<></th7<></th7<>				
REACTOME_MISMATCH_REPAIR         15         1,62         0.050           DNA replication         5<				
DNA replication     KEGG_DNA_REPLICATION     36     2.00     0.000				
KEGG_DNA_REPLICATION         36         2.00         0.000			.,	2.000
		36	2 00	0.000

	100	0.04	0.000
REACTOME_SYNTHESIS_OF_DNA	120	2,01	0.000
	135	1,97	0.002
REACTOME_DNA_REPLICATION	186	1,96	0.002
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	68	1,91	0.003
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	33	1,9	0.003
REACTOME_DNA_REPLICATION_PRE_INITIATION	143	1,88	0.005
	111	1,84	0.007
REACTOME_SEPARATION_OF_SISTER_CHROMATIDS	191	1,72	0.023
REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION	126	1,72	0.023
REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES	69	1,67	0.034
REACTOME_MITOTIC_PROMETAPHASE	203	1,67	0.035
GOBP_MONOCYTE_CHEMOTAXIS	62	2.08	0.000
GOBP_MITOTIC_SISTER_CHROMATID_SEGREGATION	171	1.98	0.012
GOBP_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE	63	1.96	0.009
GOBP_REGULATION_OF_CHROMOSOME_SEGREGATION	86	1.96	0.008
GOBP_SISTER_CHROMATID_SEGREGATION	203	1.96	0.007
GOBP_CENTROMERE_COMPLEX_ASSEMBLY	31	1.94	0.008
GOBP_KINETOCHORE_ORGANIZATION	23	1.93	0.010
GOBP_REGULATION_OF_MITOTIC_SISTER_CHROMATID_SEGREGATION	45	1.92	0.011
GOBP_CHROMOSOME_SEPARATION	94	1.91	0.013
GOBP_CHROMOSOME_SEGREGATION	343	1.89	0.017
GOBP_NUCLEAR_CHROMOSOME_SEGREGATION	284	1.89	0.016
GOBP_NEGATIVE_REGULATION_OF_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE	41	1.86	0.026
GOBP_DNA_REPLICATION_INITIATION	38	1.81	0.037
GOCC_NUCLEAR_REPLICATION_FORK	28	1.85	0.007
GOCC_REPLICATION_FORK	60	1.84	0.007
GOCC_CONDENSED_CHROMOSOME_CENTROMERIC_REGION	156	1.83	0.006
GOCC_CHROMOSOME_CENTROMERIC_REGION	226	1.76	0.014
GOCC_REPLISOME	15	1.69	0.023
Fatty Acid metabolism			
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	22	1.60	0.037
KEGG_FATTY_ACID_METABOLISM	42	1.59	0.042
REACTOME FATTY ACID METABOLISM	177	1,72	0.023
REACTOME_FATTY_ACID_METABOLISM		,	
REACTOME_FATTT_ACID_METABOLISM REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION	37	1,64	0.044
			0.044
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION			0.044
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION Glucose metabolism	37	1,64	
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION Glucose metabolism HALLMARK_GLYCOLYSIS	37 199	1,64	0.015
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION Glucose metabolism HALLMARK_GLYCOLYSIS KEGG_GLYCOLYSIS_GLUCONEOGENESIS	37 199 61	1,64 1.57 1.56	0.015 0.046
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION Glucose metabolism HALLMARK_GLYCOLYSIS KEGG_GLYCOLYSIS_GLUCONEOGENESIS KEGG_ONE_CARBON_POOL_BY_FOLATE	37 199 61 17	1,64 1.57 1.56 1.55	0.015 0.046 0.050
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION Glucose metabolism HALLMARK_GLYCOLYSIS KEGG_GLYCOLYSIS_GLUCONEOGENESIS KEGG_ONE_CARBON_POOL_BY_FOLATE KEGG_PENTOSE_PHOSPHATE_PATHWAY	37 199 61 17 26	1,64 1.57 1.56 1.55 1.54	0.015 0.046 0.050 0.050
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION Glucose metabolism HALLMARK_GLYCOLYSIS KEGG_GLYCOLYSIS_GLUCONEOGENESIS KEGG_ONE_CARBON_POOL_BY_FOLATE KEGG_PENTOSE_PHOSPHATE_PATHWAY REACTOME_GLUCONEOGENESIS	37 199 61 17 26 33	1,64 1.57 1.56 1.55 1.54 1,72	0.015 0.046 0.050 0.050 0.023
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION Glucose metabolism HALLMARK_GLYCOLYSIS KEGG_GLYCOLYSIS_GLUCONEOGENESIS KEGG_ONE_CARBON_POOL_BY_FOLATE KEGG_PENTOSE_PHOSPHATE_PATHWAY REACTOME_GLUCONEOGENESIS KEGG_PYRUVATE_METABOLISM	37 199 61 17 26 33	1,64 1.57 1.56 1.55 1.54 1,72	0.015 0.046 0.050 0.050 0.023
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response	37 199 61 17 26 33 40 23	1,64 1.57 1.56 1.55 1.54 1,72 1.58	0.015 0.046 0.050 0.050 0.023 0.041
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING	37 199 61 17 26 33 40 23	1,64 1.57 1.56 1.55 1.54 1,72 1.58	0.015 0.046 0.050 0.050 0.023 0.041
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response	37 199 61 17 26 33 40 23	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97	0.015 0.046 0.050 0.050 0.023 0.041 0.002
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH	37 199 61 17 26 33 40 23 23 C 184	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75	0.015 0.046 0.050 0.050 0.023 0.041 0.002 0.002
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING	37 199 61 17 26 33 40 23 23 40 40 23 40 40 23	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,74	0.015 0.046 0.050 0.050 0.023 0.041 0.002 0.020 0.021
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION	37 199 61 17 26 33 40 23 23 40 40 23 40 40 23 40 40 40 23 40 40 40 23 40 40 40 40 40 40 40 40 40 40 40 40 40	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,74 1,91	0.015 0.046 0.050 0.050 0.023 0.041 0.002 0.020 0.021 0.021 0.013
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN	37 199 61 17 26 33 40 23 23 40 23 40 40 23 40 40 23 40 40 23 23 40 40 23 23 23 40 23 23 40 23 23 40 23 23 40 23 24 25 26 26 27 26 26 27 26 26 27 26 27 26 26 27 26 26 27 27 26 27 27 26 27 27 26 27 27 27 27 27 27 27 27 27 27 27 27 27	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,74 1.91 1.84	0.015 0.046 0.050 0.050 0.023 0.041 0.002 0.020 0.021 0.021 0.013 0.032
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY	37 199 61 17 26 33 40 23 40 40 23 40 40 40 40 40 40 40 40 40 40	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,74 1.91 1.84 1.83	0.015 0.046 0.050 0.050 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX	37 199 61 17 26 33 40 23 40 40 23 40 40 23 40 40 23 40 40 23 40 40 40 40 40 40 40 40 40 40	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,74 1.91 1.84 1.83 1.83	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.036
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX	37 199 61 17 26 33 40 23 40 23 40 40 23 40 40 23 40 40 23 40 40 40 40 40 40 40 40 40 40	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,74 1.91 1.84 1.83 1.83 1.83 1.82	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.020 0.021 0.013 0.032 0.034 0.036 0.034
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_INMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	37 199 61 17 26 33 40 23 23 40 23 40 107 26 351 16 20 357	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,74 1.91 1.84 1.83 1.83 1.82 1.82	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_INMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN	37         199         61         17         26         33         40         23         40         40         40         23         40         40         51         16         20         357         47	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,74 1.91 1.84 1.83 1.83 1.82 1.82 1.82 1.82	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_INMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_MACROPHAGE_MIGRATION	37         199         61         17         26         33         40         23         40         40         53	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,75 1,74 1.91 1.84 1.83 1.83 1.82 1.82 1.82 1.82 1.80	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_INJUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_MACROPHAGE_MIGRATION         GOBP_MACROPHAGE_MIGRATION         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_B_CELL_MEDIATED_IMMUNITY	37         199         61         17         26         33         40         23         40         23         40         23         40         53         107         26         351         16         20         357         47         53         113	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,97 1,75 1,74 1.91 1.84 1.83 1.83 1.82 1.82 1.82 1.82 1.80 1.80	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034 0.034 0.034 0.042 0.043
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_ROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_ROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_ROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_MACROPHAGE_MIGRATION         GOBP_MACROPHAGE_MIGRATION         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_T_CELL_MEDIATED_IMMUNITY	37         199         61         17         26         33         40         23         40         23         40         23         40         53         113         111	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,97 1,75 1,74 1.91 1.84 1.83 1.82 1.82 1.82 1.82 1.82 1.82 1.80 1.80 1.79	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034 0.034 0.043 0.046
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_INJUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_MACROPHAGE_MIGRATION         GOBP_MACROPHAGE_MIGRATION         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_B_CELL_MEDIATED_IMMUNITY	37         199         61         17         26         33         40         23         40         23         40         23         40         23         40         23         40         23         40         53         113         111         208	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,75 1,74 1.91 1.84 1.83 1.83 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.80 1.79 1.79	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034 0.034 0.042 0.043 0.046 0.049
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         GOBP_NORCOPHAGE_MIGRATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_MACROPHAGE_MIGRATION         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_T_CELL_MEDIATED_IMMUNITY         GOBP_B_CELL_MEDIATED_IMMUNITY         GOBP_B_CELL_MEDIATED_IMMUNITY	37         199         61         17         26         33         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         53         113         111         208         26	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,97 1,75 1,74 1.91 1.84 1.83 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.80 1.80 1.79 1.79 1.79 1.91	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034 0.034 0.042 0.043 0.046 0.049 0.003
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_PD_1_SIGNALING         Immune response         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_MACROPHAGE_MIGRATION         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_T_CELL_MEDIATED_IMMUNITY         GOBP_B_CELL_MEDIATED_IMMUNITY         GOBP_	37         199         61         17         26         33         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         53         113         111         208         26         67	1,64 1,57 1,56 1,55 1,54 1,72 1,58 1,97 1,97 1,75 1,74 1,91 1,84 1,83 1,82 1,80 1,97 1,79 1,83 1,82 1,82 1,82 1,82 1,82 1,80 1,79 1,79 1,79 1,80 1,80 1,80 1,80 1,80 1,80 1,91 1,91 1,80 1,80 1,80 1,91 1,91 1,80 1,80 1,80 1,91 1,91 1,91 1,80 1,80 1,91 1,91 1,91 1,91 1,91 1,91 1,91 1,91 1,91 1,85 1	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034 0.034 0.042 0.043 0.046 0.049 0.003 0.007
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_ID_SIGNALING         Immune response         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_PETIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS         GOBP_MACROPHAGE_MIGRATION         GOBP_MACROPHAGE_MIGRATION         GOBP_MACROPHAGE_MIGRATION         GOBP_TCELL_LARESPONSE_TO_INTERFERON_GAMMA         GOBP_TCELL_LAREDIATED_IMMUNITY         GOCC_MHC_PROTEIN_COMPLEX_CIRCULATING         GOCC_IMMUNOGLOBULIN_COMPLEX_CIRCULATING	37         199         61         17         26         33         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         53         113         111         208         26         67         39	1,64 1,57 1,56 1,55 1,54 1,72 1,58 1,97 1,97 1,75 1,74 1,91 1,84 1,83 1,83 1,82 1,82 1,82 1,80 1,80 1,79 1,79 1,91 1,85 1,84	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034 0.042 0.043 0.046 0.049 0.003 0.007 0.006
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_ID_SIGNALING         Immune response         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_ROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_ANTIGEN_PROCESSING_AND_	37         199         61         17         26         33         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         23         47         53         113         111         208         26         67         39         17	1,64 1,57 1,56 1,55 1,54 1,72 1,58 1,97 1,97 1,75 1,74 1,91 1,84 1,83 1,82 1,82 1,82 1,82 1,82 1,82 1,82 1,82 1,80 1,79 1,79 1,79 1,91 1,85 1,84 1,78	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034 0.042 0.043 0.046 0.049 0.003 0.007 0.006 0.011
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_INITMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH         REACTOME_INTERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN         GOBP_MACROPHAGE_MIGRATION         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_T_CELL_MEDIATED_IMMUNITY         GOBP_T_CELL_MEDIATED_IMMUNITY         GOBP_B_CELL_MEDIATED_IMMUNITY         GOBP_B_CELL_MEDIATED_IMMUNITY         GOCC_IMMUNOGLOBULIN_COMPLEX_CIRCULATING         GOCC_IMMUNOGLOBULIN_COMPLEX	37         199         61         17         26         33         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         23         40         23         4107         26         357         47         53         113         111         208         26         67         39         17         146	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,97 1,75 1,74 1.91 1.84 1.83 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.80 1.79 1.79 1.79 1.91 1.85 1.84 1.78 1.76	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034 0.042 0.043 0.046 0.049 0.003 0.007 0.006 0.011 0.014
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION         Glucose metabolism         HALLMARK_GLYCOLYSIS         KEGG_GLYCOLYSIS_GLUCONEOGENESIS         KEGG_ONE_CARBON_POOL_BY_FOLATE         KEGG_PENTOSE_PHOSPHATE_PATHWAY         REACTOME_GLUCONEOGENESIS         KEGG_PYRUVATE_METABOLISM         Immune checkpoint control         REACTOME_INITERFERON_GAMMA_SIGNALING         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION         GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY         GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_IL_PROTEIN_COMPLEX         EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_CCELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_CCELLULAR_RESPONSE_TO_INTERFERON_GAMMA         GOBP_COC_IMMEDIATED_IMMUNITY         GOBP_B_CELL_MEDIATED_IMMUNITY         GOCC_MHC_PROTEIN_COMPLEX         GOCC_IMMUNOGLOBULIN_COMPLEX         GOCC_IMMUNOGLOBULIN_COMPLEX         GOCC_IMHC_CLASS_II_PROTEIN_COMPLEX         GOCC_IMHC_LOASS_II_PROTEIN_COMPLEX	37         199         61         17         26         33         40         23         107         26         351         16         20         357         47         53         111         208         26         67         39         17         146         156	1,64 1.57 1.56 1.55 1.54 1,72 1.58 1,97 1,97 1,75 1,74 1.91 1.84 1.83 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.80 1.79 1.79 1.79 1.91 1.85 1.84 1.78 1.76 1.87	0.015 0.046 0.050 0.023 0.023 0.041 0.002 0.020 0.021 0.021 0.013 0.032 0.034 0.034 0.034 0.034 0.034 0.034 0.042 0.043 0.046 0.049 0.003 0.007 0.006 0.011 0.014 0.012
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION Glucose metabolism HALLMARK_GLYCOLYSIS KEGG_GLYCOLYSIS_GLUCONEOGENESIS KEGG_ONE_CARBON_POOL_BY_FOLATE KEGG_PENTOSE_PHOSPHATE_PATHWAY REACTOME_GLUCONEOGENESIS KEGG_PYRUVATE_METABOLISM Immune checkpoint control REACTOME_PD_1_SIGNALING Immune response REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPH REACTOME_INTERFERON_GAMMA_SIGNALING GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_PROTEIN_COMPLEX EPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMAA GOBP_CELLULAR_GE_MIGRATION GOBP_CELLULAR_GE_MIGRATION GOBP_CELLULAR_GE_MIGRATION GOBP_CCELL_MEDIATED_IMMUNITY GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMAA GOBP_T_CELL_MEDIATED_IMMUNITY GOBP_CELLULAR_DIATED_IMMUNITY GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA GOBP_CELL_MEDIATED_IMMUNITY GOCC_MHC_CLASS_II_PROTEIN_COMPLEX GOCC_IMMUNOGLOBULIN_COMPLEX_CIRCULATING GOCC_T_CELL_RECEPTOR_COMPLEX GOCC_IMMUNOGLOBULIN_COMPLEX_BINDING GOMF_ANTIGEN_BINDING GOMF_ANTIGEN_BINDING	37         199         61         17         26         33         40         23         107         26         351         16         20         357         47         53         113         111         208         26         67         39         17         146         156         36	1,64 1,57 1,56 1,55 1,54 1,72 1,58 1,97 1,97 1,75 1,74 1,91 1,84 1.83 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.80 1.79 1.79 1.79 1.79 1.91 1.85 1.84 1.78 1.76 1.87 1.83	0.015 0.046 0.050 0.023 0.023 0.024 0.002 0.021 0.021 0.021 0.034 0.034 0.034 0.034 0.034 0.034 0.034 0.034 0.042 0.043 0.046 0.049 0.003 0.007 0.006 0.011 0.014 0.012 0.022

INTERTATION         14         16.4         0.007           REACTOME_INTERLEUKIN 10_SIGNALING         16         1.84         0.007           REACTOME_INTERLEUKIN 10_SIGNALING         110         1.83         0.048           REACTOME_INTERLEUKIN 10_SIGNALING         110         1.83         0.048           REACTOME_INTERLEUKIN 10_ACMON INTERLEUKIN 13_SIGNALING         110         1.83         0.048           REACTOME_INTERLEUKIN 14_ABCTS_VI         200         1.64         0.008           NINS         NINS GLARAGET SUBJ         23         1.98         0.000           NINS GLARAGET GENES         23         1.98         0.000         NINS GLARATURE         26         1.64         0.003           NINS GLARATURE         26         1.84         0.011         0.014         0.011           NINS GLARATURE         26         1.84         0.011         0.011         0.011           NINS GLARATURE         NINS GLARATURE         200         1.86         0.001         1.86         0.001           NINS GLARATURE         NINS GLARATURE         0.011         0.011         0.011         0.011         0.011         0.011         0.011         0.011         0.011         0.011         0.011         0.011	Interleukins			
BACTOME_INTERLEUKIN_13_SIGNALING         46         1.84         0.007           REACTOME_INTERLEUKIN_13_SIGNALING         110         1.63         0.048 <b>WRAS pahway</b> 95         1.51         0.024 <b>WRAS pahway</b> 200         1.64         0.008 <b>WRS</b> 201         1.64         0.008 <b>WRS</b> 23         1.98         0.000           NRNE ATCHE ZOB_COMPAGNO         109         1.84         0.001           NRNE ATCHE ZOB_COMPAGNO         109         1.84         0.003           NRS BATCHE ZOB_COMPAGNO         109         1.84         0.001           NRNE BLOIDEN ANTURE 2009_COMPAGNO         109         1.84         0.001           NRS BATCHE         26         1.84         0.001           NRE BOTHOCITASANDU YODULATED BY IBRUTINIB         39         1.78         0.011           NRE BOTHOCITASANDU YODULATED MORCANONICAL NF KB SIGNALING         20         1.86         0.011           NRE BOTHOCITANDINAL FENDSMORTATION         200         1.86         0.021           NRE BOTHOCITANDINAL FENDSMORTATION         218         0.011           NRECTOME_EXERTION NALASSIATORY (TEAN COMPLEX SEMBLY         9         1.86         0.022 </td <td></td> <td>14</td> <td>1.64</td> <td>0,031</td>		14	1.64	0,031
BEACTONE_INTERLEURIN_1A_AND_INTERLEURIN_13_SIGNALING         110         1.63         0.048           MASA pathway         195         1.51         0.024           MAILMARK XRAS SIGNALING UP         200         1.64         0.008           MAILMARK XRAS SIGNALING UP         200         1.64         0.008           MRG         CAMBARK XMC, LARCEN KVI         200         1.64         0.001           NRG TARCET GENES         3         1.98         0.001           NRG TARCET ANTHRE 2005, COMPAGNO         109         1.93         0.003           NRG DIGTANTURE         26         1.84         0.001           NRG DIGTANTURE         26         1.84         0.001           NRG DIGTANTURE         26         1.84         0.001           NRG DIGTANTURE         20         1.86         0.001           NRG DIGTANTURE         0.001         1.66         0.001           RESCONDATIVE, PHOSHOWICATION         200         1.86         0.001           RESCONDATIVE, PHOSHOWICATION         201         1.76         0.012           RESCONDATIVE, PHOSHOWICATION         210         1.71         0.012           RESCONDATIVE, PHOSHOWICATION         218         1.84         0.032				
KRASpathany				
HALLMARK, KRAS, SIGNALING, UP         195         1.51         0.024           MVC regulars genes         0.008           HALLMARK, MYC, TARGETS, VI         200         1.64         0.008           NHB         23         1.88         0.000           NYKB, DLDCL, NATURE 2009_COMPAGNO         109         1.44         0.001           NYKB, CLDCL, NATURE 2009_COMPAGNO         109         1.44         0.001           NYKB, CLDCL, NATURE 2009_COMPAGNO         109         1.44         0.001           NYKB, CALLOC, VALUE         26         1.24         0.003           NYKB, DATURE         26         1.24         0.011           NYKB, SIGNATURE         18         1.74         0.011           NYKB, SIGNATURE         18         1.74         0.011           REG_ONDATIVE         NORCHONDRIAL TRANSPORT         200         1.86         0.001           REG_ONDATIVE, PHOSPHORYLATION         200         1.86         0.001         86         0.022           GORD, MONTIVE, PHOSPHORYLATION         100         1.78         0.002         86         0.025           GORD, MONTIVE, PHOSPHORYLATION         126         1.79         0.002         86         0.002           GOLD, MONTIVE, PHOSP			1,00	0.0 +0
MYC regulates genes		195	1.51	0.024
HALLMARK, MC, TARGETS, VI         200         3.64         0.008           NHS		155	1.51	0.021
NHS		200	1.64	0,008
NRKB TARGET GENES         23         1.88         0.000           NRKB DLECL, NUTRE ZOUG_COMPAGNO         109         1.94         0.001           NRKB DLECL, NUTRE ZOUG_COMPAGNO         57         1.87         0.003           NRK BJALL_OCILY3_LY10         57         1.87         0.003           NRK BJANTURE         26         1.84         0.004           NRKB DATAUXE         28         1.74         0.010           NRKB SIGNATURE         18         1.74         0.011           MALMARK_DUDATIVE         18         1.74         0.011           REG_CONDATIVE_PROSPHORYNATION         200         1.86         0.002           REG_CONDATIVE_PROSPHORYNATION         103         1.73         0.002           REACTOME_RESPIRATORY_CHAILTON         200         1.86         0.022           GOBP_MICTCHONDRIAL_RESPIRATORY_CHAILCOMPLEX ASSEMBLY         94         1.66         0.022           GOBP_MICTCHONDRIAL_RESPIRATORY_CHAILCOMPLEX ASSEMBLY         94         1.66         0.022           GOBP_MICTCHONDRIAL_RESPIRATORY_CHAIL COMPLEX ASSEMBLY         94         1.66         0.023           GOCC_INDRIAL_RESPIRATORY_CHAIL COMPLEX ASSEMBLY         94         1.66         0.024           GOCC_INDRIAL_RESPIRATORON_CHAIL COMPLEX ASSE		200	1.04	0.000
NFKB_DLBCL         NATURE 2009_COMPAGNO         109         1.84         0.001           NFKB_ALL_OCILY3_LY10         57         1.87         0.003           NFKB_GALL_OCILY3_LY10         33         1.75         0.001           NFKB_GOTHOCIY3ANDLY10         33         1.75         0.010           NFKB_GOTHOCIYANDLY10         33         1.76         0.011           CALCTOME_DECIYANDLY10         33         1.76         0.011           CALCTOME_DECIYANDLY10         20         1.86         0.001           NEGGONDATIVE_PHOSPHORYLATION         200         1.86         0.001           REACTOME_ENDERNOTWE_PHOSPHORYLATION         200         1.86         0.001           REACTOME_ENDERNOTWE_PHOSPHORYLATION         200         1.86         0.002           GODP_ONDATVE_PHOSPHORYLATION         136         1.84         0.034           GODP_ONDATVE_PHOSPHORYLATION         136         1.84         0.034           GODE_MICCHONDAL_RESPIRATORY_LECRON_REANDORT         133         1.84         0.034           GODE_MICCHONDAL_RESPIRATION         165         1.78         0.040           GODE_MICCHONDAL_RESPIRATION         165         1.78         0.040           GOCC_MINTERANDORIAL_REANDER         1.71		23	1 98	0.000
NRKB_ALL_OCLV3_LY10         57         18.7         0.003           NRKB SIGNATURE         26         18.4         0.003           NRKB PATHWAY MODULATED BY IBRUTINIB         39         1.83         0.004           NRKB SIGNATURE         18         1.7.4         0.011           REACTOME DECTIN 1_MEDIATED NONCANONICAL NF KB SIGNALING         62         1.81         0.011           REACTOME DECTIN 1_MEDIATED NONCANONICAL NF KB SIGNALING         200         1.86         0.001           REACTOME SPECTIN 1_MEDIATED NONCANONICAL NF KB SIGNALING         200         1.86         0.001           REACTOME RESPIRATORY_LECTORN TRANSPORT         103         1.7.4         0.011           REACTOME RESPIRATORY_LECTORN TRANSPORT         103         1.84         0.002           GOBP_INTOCHONDRIAL_TRANSLATION         129         1.73         0.022           GOBP_INTOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX         128         1.73         0.022           GOBP_INTOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX         136         1.81         0.003           GOCC_CINTERNITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX         153         1.81         0.004           GOCC_CINTERNITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX         153         0.014         0.002           GOCC_CINTERNITOCHONDRIAL_RESPIRATORY_CHAI				
NIK SIGNATURE       26       1.8.4       0.003         NIKB PATHARY MODULATE DE YIBUTINIB       39       1.7.6       0.001         NIKR PATHARY MODULATE DE YIBUTINIB       33       1.7.6       0.011         REACTOME ECINIMEDIATE_NORCANONICAL_MF_K8_SIGNALING       62       1.8.1       0.011         Gadiative phosphorylation				
NRKB PATHWAY MODULATED BY IBRUTINIB         39         1.83         0.004           NRKB SIGNATURE         18         1.74         0.011           REACTONE DECTIN 1_MEDIATED_NONCANONICAL NF KB SIGNALING         62         1.81         0.011           REACTONE DECTIN 1_MEDIATED_NONCANONICAL NF KB SIGNALING         62         1.81         0.011           REACTONE DECTIN 1_MEDIATED_NONCANONICAL NF KB SIGNALING         200         1.86         0.001           KEG_ONDATIVE_PHOSPHORYLATION         200         1.86         0.002           REACTOME_RISPIRATORY_ELECTRON TRANSPORT         103         1.73         0.022           GOBP_INCTONONAL_RESPIRATORY_CHAIN_COMPLEX         258         0.025         0.025           GOBP_SILCTRON TRANSPORTICHAIN         186         1.84         0.034           GODE_CINTER, MICHORNAL_RESPIRATORY_CHAIN         185         1.78         0.049           GOCC, INDEL MICHORNAL_RESPIRATORY_CHAIN         186         1.78         0.049           GOCC, INDEL MICHORNAL_RESPIRATORY_CHAIN         186         1.78         0.049           GOCC, INDEL MICHORNAL_RESPIRATORY_CHAIN         181         1.04         1.025           GOCC, INDEL MICHORNAL_RESPIRATORY_CHAIN         124         1.77         0.030           GOCC, PROTON TRANSPORTING_ATP_SYMTHAS				
NFKB_BOTHOCIL Y3ANDLY10         33         1.76         0.010           NFKB_SIGNATURE         18         1.74         0.011           RACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING         62         1.81         0.011           Oddative phosphorylation         20         1.86         0.001           KEGG_DIDATIVE_PHOSPHORYLATION         200         1.86         0.001           KEGG_DROME_RESPIRATORY_FLICETON_TRANSPORT         103         1.73         0.022           GORP_MICHONDRUAL_ESPIRATORY_FLICETON_TRANSPORT         103         1.74         0.031           GORP_MICHONDRUAL_ESPIRATORY_FLICETON_TRANSPORT         103         1.73         0.022           GORP_MICHONDRUAL_ESPIRATORY_FLICETON_TRANSPORT         103         1.73         0.022           GOC_MINER_MICHONDRUA_ESPIRATORY_FLICETON         165         1.78         0.049           GOC_MINER_MICHONDRUAL_RESPIRATORY_COMPLEX         153         1.81         0.002           GOC_MINER_MICHONDRUAL_SEGNAL_PROTEIN_COMPLEX         153         1.81         0.002           GOC_COMPLEX         27         1.73         0.017         0.022           GOC_MINER_MICHONDRUAL_SEGNAL_PROTEIN_COMPLEX         17         0.016         0.022           GOC_MINER_MICHONDRUAL_SEGNAL_PROTEINCOMPLEX <td< td=""><td></td><td></td><td></td><td></td></td<>				
NRK6_GIONATURE         18         1.74         0.011           REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF,KS_SIGNALING         62         1.81         0.011           COLDATUE_DESONPOYLATION         200         1.86         0.0011           KEG_OXIDATIVE_PHOSPHORYLATION         200         1.86         0.0011           REACTOME_RESPIRATORY_LECTRON_TRANSPORT         103         1.73         0.022           GOBP_INTICCHONORIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY         94         1.86         0.023           GOBP_MITICCHONORIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY         94         1.86         0.024           GODE_DISTICHON_TRANSPORT_CHAIN         106         1.78         0.049           GOCC_INTRE,MITICCHONDRIAL_RESPIRATORY_CHAIN <complex< td="">         279         1.93         0.002           GOCC_INTRE,MITICCHONDRIAL_PROTEIN_COMPLEX         153         1.81         0.003           GOCC_INTRE,MITICCHONDRIAL_REMEMARE_PROTEIN_COMPLEX         121         1.73         0.017           GOCC_RESPIRASOME         100         1.71         0.018         GOCC_RESPIRASOME         100         1.71         0.011           GOCC_RESPIRASOME         101         1.77         0.021         0.022         1.70         0.022           POIDERISOME         14         <t< td=""><td></td><td></td><td></td><td></td></t<></complex<>				
REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING         62         1.81         0.011           Dadative phosphorytation	-			
Oxidative phosphorylation         v           HALLMARK_OXIDATIVE_PHOSPHORYLATION         200         1.86         0.001           REG_OXIDATIVE_PHOSPHORYLATION         129         1.71         0.011           RRACTOME_RISPIRATORY_ELECTION_TRANSPORT         103         1.73         0.022           GOBP_INTICCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY         94         1.86         0.023           GOBP_MITTCCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY         94         1.86         0.034           GOBP_INTICCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY         94         1.86         0.034           GOC_COMPLEX_HONSPIRAL_RESPIRATORY_CHAINING_COMPLEX         279         1.93         0.002           GOCC_INTRANSPORTIN_CATAINING_COMPLEX         153         1.81         0.004           GOCC_INTRANSPORTING_ATP_SYNTHASE_COMPLEX         100         1.71         0.018           GOCC_RESPIRASOME         100         1.77         0.030           GOCC_RESPIRASOME         14         1.90         0.002           PROTEINTERNATION_SIGNATURE         14         1.90         0.002           Protessome         -         -         -         -           KEGG_RIBOSOMAL_SUBUNT         177         2.01         0.001           GOCC_PROTEASOME<				
HALLMARE, OXIDATIVE, PHOSPHORYLATION KEGG, DXIDATIVE, PHOSPHORYLATION KEGG, DXIDATIVE, PHOSPHORYLATION REACTOME, MITCCHONDRIAL, ITRANSLATION REACTOME, MITCCHONDRIAL, ITRANSLATION REACTOME, MITCCHONDRIAL, ITRANSLATION REACTOME, PHOSPHORYLATION GOBP_MITCCHONDRIAL, ESPIRATORY, CHAIN_COMPLEX, ASSEMBLY 94 165 17.8 17.8 18.4 18.4 19.6 19.6 19.7 19.6 19.6 19.7 19.6 19.7 19.8 19.7 19.8 19.8 19.8 19.8 19.9 19			1,01	0.011
KEGG_OXIDATIVE_PHOSPHORYLATION         129         1,71         0.011           REACTOME_MITCCHONDRIAL_TRANSLATION         94         1,96         0.002           REACTOME_MERSPIRATORY_LELCRION_TRANSPORT         103         1,73         0.022           GOBP_MITCCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY         94         1.86         0.025           GOBP_CINDERLY_PHOSPHORYLATION         136         1.84         0.034           GORE_CINTERLY_PHOSPHORYLATION         136         1.84         0.034           GOCC_MINTERLY_PHOSPHORYLATION         165         1.78         0.049           GOCC_MINTERLY_PROTEIN_CONTAINING_COMPLEX         279         1.81         0.002           GOCC_INTERLANDORTING_ATP_SYNTHASE_COMPLEX         13         1.81         0.002           GOCC_RESPIRATION_SORTING_ATP_SYNTHASE_COMPLEX         14         1.77         0.030           GOCC_RESPIRATION_SIGNATURE         14         1.90         0.002           Proteinspiration         -         -         -           KEGG_RIDESOMAL_SUBUNT         14         1.90         0.002           GOCC_INSCIALAR_R RIGOSOMAL_SUBUNT         177         0.012         -           GOCC_RIDESOMAL_SUBUNT         177         0.012         -         -		200	1.86	0.001
REACTOME_MITCCHONDRIAL_TRANSLATION         94         1,96         0.002           REACTOME_RESPIRATORY_LECTRON_TRANSPORT         103         1,73         0.022           GOBP_MITCCHONDRIAL_ESPIRATORY_LECTRON_TRANSPORT         136         1,74         0.034           GOBP_MITCCHONDRIAL_PROTEXTORY_CHAIN_COMPLEX_ASSEMBLY         136         1,78         0.049           GOCC_INITCHONDRIAL_PROTEIN_CONTAINING_COMPLEX         279         1,93         0.002           GOCC_ININER_MITCCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX         153         1.81         0.008           GOCC_PROTONDRIAL_PROTEIN_CONTAINING_COMPLEX         100         1.71         0.018           GOCC_PROTONDRIAL_SENDER         100         1.71         0.018           GOCC_RESPIRASOME         100         1.71         0.018           GOCC_ROTON REANSER ACTIVITY         124         1.77         0.044           GOCC_PROTON REANSER ACTIVITY         124         1.77         0.011           GOCC_PROTON REANSER ACTIVITY         124         1.77         0.022           Protessome				
REACTOME_RESPIRATORY_LECTRON_TRANSPORT         103         1,73         0.022           GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY         94         1.86         0.025           GOBP_CXIDATIVE_PHOSPHORYLATION         136         1.84         0.034           GODP_CXIDATIVE_PHOSPHORYLATION         155         1.78         0.049           GOCC_INTECNONTRANSPORT_CHAIN         155         1.81         0.008           GOCC_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX         153         1.81         0.008           GOCC_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX         100         1.71         0.017           GOCC_RESPIRATORYDORING_ATP_SYNTHASE_COMPLEX         100         1.71         0.017           GOCC_RESPIRATORYDORING_ATP_SYNTHASE_COMPLEX         11         1.73         0.017           GOCC_RESPIRATORY TRANSPER_ACTIVITY         124         1.77         0.032           PS3          14         1.90         0.002           Proteasome          14         1.71         0.011           GOCC_RESPIRATION_SIGNATURE         44         1.71         0.011           GOCC_RIDSOMAL_SUBUNIT         177         2.01         0.002           GOCC_RIDSOME         88         1.82         0.001				
GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY         94         1.86         0.025           GOBP_LECETRON_TRANSPORT_CHAIN         136         1.84         0.034           GOCP_DIDENTOR_TRANSPORT_CHAIN         165         1.78         0.049           GOCC_INNER_MITOCHONDRIAL_PROTEIN_COMPLEX         279         1.93         0.002           GOCC_INNER_MITOCHONDRIAL_PROTEIN_COMPLEX         121         1.73         0.017           GOCC_RONT TRANSPORTING_ATP_SYNTHASE_COMPLEX         21         1.73         0.017           GOCC_RONT TRANSPORTING_ATP_SYNTHASE_COMPLEX         49         1.62         0.044           GOMF_ELECTRON_TRANSPER_ACTIVITY         124         1.77         0.030           p3           1.90         0.002           Proliferation           1.90         0.002           Proteasome           1.90         0.002           Proteasome           1.91         0.01           GOCC_ROBONA_SUBUNIT         14         1.90         0.001           GOCC_ROBONA_SUBUNIT         177         2.01         0.001           GOCC_ROBONA_SUBUNIT         177         0.01         0.01           GOCC_ROBONA_SUBUNIT				
GOB_OXIDATIVE_PHOSPHORYLATION         136         1.84         0.034           GODE_DXIDATIVE_PHOSPHORYLATION         165         1.78         0.049           GODE_DXIDATIVE_PHOSPHORYLATION_COMPLIANING_COMPLEX         279         1.93         0.002           GOCC_INTECNONDRIAL_MEMBRANE_PROTEIN_COMPLEX         153         1.81         0.008           GOCC_INSER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX         21         1.73         0.017           GOCC_INSER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX         49         1.62         0.044           GOCC_INSERMANCE         49         1.62         0.044           GOMF_ELECTRON_TRANSPER_ACTIVITY         124         1.77         0.030           Pollferation				
GOBP_ELECTRON_TRANSPORT_CHAIN         165         1.78         0.049           GOCC_MITOCHONDRIAL_PROTEIN_CONTAINING_COMPLEX         279         1.93         0.002           GOCC_INNER_MITOCHONDRIAL_MEMBRARE_PROTEIN_COMPLEX         153         1.81         0.008           GOCC_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX         21         1.73         0.017           GOCC_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX         49         1.62         0.044           GOCC_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX         49         1.62         0.040           FGGC_RESPIRASOME         49         1.62         0.040           FGGC_RESTRABULIZATION_OF_P53         57         1.65         0.040           Protessome				
GOCC_MITOCHONDRIAL_PROTEIN_COMPLEX         279         1.93         0.002           GOCC_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX         153         1.81         0.008           GOCC_ROTONDRIAL_MEMBRANE_PROTEIN_COMPLEX         100         1.71         0.017           GOCC_RESPIRASOME         100         1.71         0.018           GOCC_ROTOND_TRANSPORTING_ATP_SYNTHASE_COMPLEX         49         1.62         0.044           GOCC_INDE_NTRANSPER_ACTIVITY         124         1.77         0.030 <b>p53</b>				
GOCC_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX         153         1.81         0.008           GOCC_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX         100         1.71         0.017           GOCC_RESPIRASOME         100         1.71         0.018           GOCC_RESPIRASOME         49         1.62         0.044           GOME_LECTRON_TRANSFER_ACTIVITY         124         1.77         0.030           PSJ				
GOCC_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX         21         1.73         0.017           GOCC_RESPIRASOME         100         1.71         0.018           GOCC_RESPIRASOME         49         1.62         0.044           GOMF_ELECTRON_TRANSFER_ACTIVITY         124         1.77         0.030           pS3				
GOCC_RESPIRASOME         100         1.71         0.018           GOCC_NADH_DEHYDROGENASE_COMPLEX         49         1.62         0.044           GOC_NADH_DEHYDROGENASE_COMPLEX         49         1.62         0.040           ps3				
GOCC_NADH_DEHYDROGENASE_COMPLEX         49         1.62         0.044           GOME_LECTRON_TRANSFER_ACTIVITY         124         1.77         0.030           pS3              REACTOME_STABILIZATION_OF_P53         57         1.65         0.040           Proliferation               MCL_PROLIFERATION_SIGNATURE         44         1.71         0.011           GOCC_PROTEASOME_CORE_COMPLEX         20         1.70         0.022           Proteinsymtheis          44         1.71         0.011           GOCC_RIBOSOMAL_SUBUNIT         88         1.82         0.002           GOCC_RIBOSOMAL_SUBUNIT         1177         2.01         0.011           GOCC_RIBOSOMAL_SUBUNIT         111         1.96         0.001           GOCC_RIBOSOMAL_SUBUNIT         54         1.90         0.003           GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         69         1.74         0.015           GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         57         1.69         0.040           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1.65         0.040           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         1.69         0.040				
GOMF_ELECTRON_TRANSFER_ACTIVITY         124         1.77         0.030           p53	-			
p33         57         1,65         0.040           REACTOME_STABILIZATION_OF_P53         57         1,65         0.040           Proliferation         MCL_PROLIFERATION_SIGNATURE         14         1.90         0.002           Proteasome         20         1.70         0.022           Protein syntheis         20         1.70         0.022           Protein syntheis         88         1.82         0.002           GOCC_ROBOME_SUBUNIT         177         2.01         0.001           GOCC_ROBOMAL_SUBUNIT         177         2.01         0.001           GOCC_ROBOMAL_SUBUNIT         111         1.96         0.001           GOCC_ROBOSOMAL_SUBUNIT         54         1.90         0.003           GOCC_ROBOSOME         208         1.83         0.007           GOCC_SMALL_RIBOSOMAL_SUBUNIT         69         1.74         0.019           GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         57         1.69         0.023           GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         57         1.69         0.040           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1.65         0.040           REACTOME_EUKARYOTIC_TRANSLATION_OF_REACTIVE_OXYGEN_SPECIES         36         1.64 <t< td=""><td></td><td></td><td></td><td></td></t<>				
REACTOME_STABILIZATION_OF_P53         57         1,65         0.040           Proliferation		124	1.77	0.030
Proliferation	-	57	1.65	0.040
MCL_PROLIFERATION_SIGNATURE         14         1.90         0.002           Proteasome		57	1,05	0.040
Proteasome           KEGG_PROTEASOME         44         1.71         0.011           GOC_PROTEASOME_CORE_COMPLEX         20         1.70         0.022           Protein syntheis	Proliferation			
GOCC_PROTEASOME_CORE_COMPLEX         20         1.70         0.022           Protein syntheis		14	1.90	0.002
GOCC_PROTEASOME_CORE_COMPLEX         20         1.70         0.022           Protein syntheis	MCL_PROLIFERATION_SIGNATURE	14	1.90	0.002
Protein syntheis           KEGG_RIBOSOME         88         1.82         0.002           GOCC_RIBOSOMAL_SUBUNIT         177         2.01         0.001           GOCC_RGARELLAR_RIBOSOME         81         1.99         0.000           GOCC_RGARELLAR_RIBOSOMAL_SUBUNIT         111         1.96         0.001           GOCC_ARGE_RIBOSOMAL_SUBUNIT         54         1.90         0.003           GOCC_SMAL_RIBOSOMAL_SUBUNIT         54         1.90         0.003           GOCC_SMAL_REDSOMAL_SUBUNIT         69         1.74         0.015           GOCC_YTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         57         1.69         0.023           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1.65         0.040           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1.65         0.040           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1.73         0.017           AS_ACCEPTOR         78         1.59         0.040           REACTOME_DEDUCTASE_COMPLEX         120         1.73         0.046           REACTOME_LAGGING_STRAND_SYNTHESIS         20         1.87         0.006           REACTOME_LAGGING_STRAND_LAGGING_STRAND_SYNTHESIS         34         1.82         0.010	MCL_PROLIFERATION_SIGNATURE Proteasome			
GOC_RIBOSOMAL_SUBUNIT         177         2.01         0.001           GOCC_ORGANELLAR_RIBOSOMAL_SUBUNIT         81         1.99         0.000           GOCC_LARGE_RIBOSOMAL_SUBUNIT         111         1.96         0.001           GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         54         1.90         0.003           GOCC_RIBOSOME         208         1.83         0.007           GOCC_STRALL_RIBOSOMAL_SUBUNIT         69         1.74         0.015           GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         69         1.74         0.019           GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         57         1.69         0.023           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1.65         0.040 <b>Redot balance</b> 1.64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         78         1.59         0.040           REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1.64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         120         1.73         0.017           A_ACCEPTOR         7         1.73         0.046           REACTOME_LAGGING_STRAND_SYNTHESIS         34         1.82         0.010           REACTOME_TRANSLATION_ELONGATION </td <td>MCL_PROLIFERATION_SIGNATURE  Proteasome  KEGG_PROTEASOME</td> <td>44</td> <td>1.71</td> <td>0.011</td>	MCL_PROLIFERATION_SIGNATURE  Proteasome  KEGG_PROTEASOME	44	1.71	0.011
GOCC_ORGANELLAR_RIBOSOME         81         1.99         0.000           GOCC_LARGE_RIBOSOMAL_SUBUNIT         111         1.96         0.001           GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         54         1.90         0.003           GOCC_NIBOSOME         208         1.83         0.007           GOCC_SMALL_RIBOSOMAL_SUBUNIT         69         1.74         0.015           GOCC_CYTOSOLIC_RAGE_RIBOSOMAL_SUBUNIT         57         1.69         0.023           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1,65         0.040 <b>Redot balance</b> 78         1.59         0.040           REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1,64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         120         1.73         0.017           AS_ACCEPTOR         57         1.73         0.040           REACTOME_LAGGING_STRAND_SYNTHESIS         20         1.87         0.017           REACTOME_TRANSLATION_ELONGATION         94         1.86         0.006           REACTOME_TRANSLATION_ELONGATION         94         1.86         0.006           REACTOME_TRANSLATION_ELONGATION         94         1.86         0.013           REACTOME_TRANSLATION_OF_TELOMERES	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX	44	1.71	0.011
GOCC_ORGANELLAR_RIBOSOME         81         1.99         0.000           GOCC_LARGE_RIBOSOMAL_SUBUNIT         111         1.96         0.001           GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         54         1.90         0.003           GOCC_NIBOSOME         208         1.83         0.007           GOCC_SMALL_RIBOSOMAL_SUBUNIT         69         1.74         0.015           GOCC_CYTOSOLIC_RAGE_RIBOSOMAL_SUBUNIT         57         1.69         0.023           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1,65         0.040 <b>Redot balance</b> 78         1.59         0.040           REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1,64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         120         1.73         0.017           AS_ACCEPTOR         57         1.73         0.040           REACTOME_LAGGING_STRAND_SYNTHESIS         20         1.87         0.017           REACTOME_TRANSLATION_ELONGATION         94         1.86         0.006           REACTOME_TRANSLATION_ELONGATION         94         1.86         0.006           REACTOME_TRANSLATION_ELONGATION         94         1.86         0.013           REACTOME_TRANSLATION_OF_TELOMERES	MCL_PROLIFERATION_SIGNATURE  Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis	44 20	1.71 1.70	0.011 0.022
GOCC_LARGE_RIBOSOMAL_SUBUNIT       111       1.96       0.001         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT       54       1.90       0.003         GOCC_RIBOSOME       208       1.83       0.007         GOCC_SMALL_RIBOSOMAL_SUBUNIT       69       1.74       0.015         GOCC_CYTOSOLIC_RIBOSOME       101       1.71       0.019         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT       57       1.69       0.023         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION       120       1,65       0.040         Redox balance       78       1.59       0.040         REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES       36       1,64       0.042         GOCC_OXIDOREDUCTASE_COMPLEX       120       1.73       0.017         AS_ACCEPTOR       78       1.59       0.040         REACTOME_LAGGING_STRAND_SYNTHESIS       20       1.87       0.046         REACTOME_LAGGING_STRAND_SYNTHESIS       20       1.87       0.006         REACTOME_TRANSLATION_LAGGING_STRAND_SYNTHESIS       34       1.82       0.010         REACTOME_TRANSLATION       293       1.8       0.013         Telomeres       11       1.77       0.016         REACTOME_TRANSLATION_OF_TELOMERES       51	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME	44 20 88	1.71 1.70 1.82	0.011 0.022 0.002
GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         54         1.90         0.003           GOCC_RIBOSOME         208         1.83         0.007           GOCC_SMALL_RIBOSOMAL_SUBUNIT         69         1.74         0.015           GOCC_CYTOSOLIC_RIBOSOME         101         1.71         0.019           GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         57         1.69         0.023           REACTOME_ELKARYOTIC_TRANSLATION_INITIATION         120         1.65         0.040           REACTOME_DEXARYOTIC_TRANSLATION_INITIATION         120         1.65         0.040           REACTOME_DEXARYOTIC_TRANSLATION_INITIATION         120         1.73         0.040           REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1.64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         120         1.73         0.046           REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1.64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         120         1.73         0.046           REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1.64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         120         1.73         0.046           REACTOME_LAGGING_STRAND_SYNTHESIS         20         1.87	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT	44 20 88 177	1.71 1.70 1.82 2.01	0.011 0.022 0.002 0.001
GOCC_RIBOSOME         208         1.83         0.007           GOCC_SMALL_RIBOSOMAL_SUBUNIT         69         1.74         0.015           GOCC_CYTOSOLIC_RIBOSOME         101         1.71         0.019           GOCC_CYTOSOLIC_RAGE_RIBOSOMAL_SUBUNIT         57         1.69         0.023           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1.65         0.040           Redox balance           78         1.59         0.040           Redox balance         78         1.59         0.040             REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1.64         0.042            GOCC_XIDOREDUCTASE_COMPLEX         120         1.73         0.017                  0.040	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT GOCC_ORGANELLAR_RIBOSOME	44 20 88 177 81	1.71 1.70 1.82 2.01 1.99	0.011 0.022 0.002 0.001 0.000
GOCC_SMALL_RIBOSOMAL_SUBUNIT       69       1.74       0.015         GOCC_CYTOSOLIC_RIBOSOME       101       1.71       0.019         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT       57       1.69       0.023         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION       120       1,65       0.040         Redox balance	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT GOCC_ORGANELLAR_RIBOSOME GOCC_LARGE_RIBOSOMAL_SUBUNIT	44 20 88 177 81 111	1.71 1.70 1.82 2.01 1.99 1.96	0.011 0.022 0.002 0.001 0.000 0.001
GOCC_CYTOSOLIC_RIBOSOME         101         1.71         0.019           GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         57         1.69         0.023           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1,65         0.040           Redox balance         78         1.59         0.040           REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1,64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         120         1.73         0.017           AS_ACCEPTOR         57         1.73         0.046           RNA synthesis         120         1.73         0.046           REACTOME_LAGGING_STRAND_SYNTHESIS         20         1,87         0.006           REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         34         1,86         0.006           REACTOME_TRANSLATION         94         1,86         0.010           REACTOME_TRANSLATION_LAGGING_STRAND_SYNTHESIS         34         1,82         0.010           REACTOME_TRANSLATION         293         1,8         0.013           Telomeres         108         1,75         0.016           REACTOME_TRELOMERE_MAINTENANCE         108         1,75         0.018           TF         1         1.69         0	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT GOCC_ORGANELLAR_RIBOSOME GOCC_LARGE_RIBOSOMAL_SUBUNIT GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT	44 20 88 177 81 111 54	1.71 1.70 1.82 2.01 1.99 1.96 1.90	0.011 0.022 0.002 0.001 0.000 0.001 0.003
GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         57         1.69         0.023           REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1,65         0.040           Redox balance	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT GOCC_ORGANELLAR_RIBOSOME GOCC_LARGE_RIBOSOMAL_SUBUNIT GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT GOCC_RIBOSOME	44 20 88 177 81 111 54 208	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007
REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         120         1,65         0.040           Redox balance	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT GOCC_ORGANELLAR_RIBOSOME GOCC_LARGE_RIBOSOMAL_SUBUNIT GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT GOCC_RIBOSOME GOCC_SMALL_RIBOSOMAL_SUBUNIT	44 20 88 177 81 111 54 208 69	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015
Redox balance         78         1.59         0.040           REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1,64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         120         1.73         0.017           AS_ACCEPTOR         57         1.73         0.046           RNA synthesis         78         1.64         0.042           REACTOME_LAGGING_STRAND_SYNTHESIS         20         1.73         0.017           REACTOME_EQUARRYOTIC_TRANSLATION_ELONGATION         94         1.86         0.006           REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         34         1.82         0.010           REACTOME_TRANSLATION         293         1.8         0.013         Telomeres           REACTOME_TRANSLATION         1.77         0.016         REACTOME_TELOMERES         51         1.77         0.016           REACTOME_TELOMERE_MAINTENANCE         108         1.75         0.018         TMF         TMF         TME	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT GOCC_ORGANELLAR_RIBOSOME GOCC_LARGE_RIBOSOMAL_SUBUNIT GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT GOCC_RIBOSOME GOCC_SMALL_RIBOSOMAL_SUBUNIT GOCC_CYTOSOLIC_RIBOSOME	44 20 88 177 81 111 54 208 69 101	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019
KEGG_PEROXISOME         78         1.59         0.040           REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         36         1,64         0.042           GOCC_OXIDOREDUCTASE_COMPLEX         120         1.73         0.017           AS_ACCEPTOR         57         1.73         0.046           RNA synthesis         57         1.73         0.046           REACTOME_LAGGING_STRAND_SYNTHESIS         20         1,87         0.006           REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         94         1,86         0.006           REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         34         1,82         0.010           REACTOME_TRANSLATION         293         1,8         0.013           Telomeres         7         1.77         0.016           REACTOME_TELOMERE_MAINTENANCE         108         1,75         0.018           TNF         7         1.69         0.027           REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS         29         1,69         0.027           REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY         101         1,67         0.033	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT GOCC_ORGANELLAR_RIBOSOME GOCC_LARGE_RIBOSOMAL_SUBUNIT GOCC_RIBOSOME GOCC_RIBOSOME GOCC_SMALL_RIBOSOMAL_SUBUNIT GOCC_CYTOSOLIC_RIBOSOME GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	44 20 88 177 81 111 54 208 69 101 57	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023
REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES       36       1,64       0.042         GOCC_OXIDOREDUCTASE_COMPLEX       120       1.73       0.017         AS_ACCEPTOR       57       1.73       0.046         RNA synthesis       20       1,87       0.006         REACTOME_LAGGING_STRAND_SYNTHESIS       20       1,87       0.006         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION       94       1,86       0.006         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS       34       1,82       0.010         REACTOME_TRANSLATION       293       1,8       0.013         Telomeres       7       0.016       7         REACTOME_EXTENSION_OF_TELOMERES       51       1,77       0.016         REACTOME_TRANSLATION_ELONGICAL_RECEPTORS       29       1,69       0.027         REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY       101       1,67       0.033	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT GOCC_ORGANELLAR_RIBOSOME GOCC_LARGE_RIBOSOMAL_SUBUNIT GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT GOCC_RIBOSOME GOCC_SMALL_RIBOSOMAL_SUBUNIT GOCC_CYTOSOLIC_RIBOSOME GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT REACTOME_EUKARYOTIC_TRANSLATION_INITIATION	44 20 88 177 81 111 54 208 69 101 57	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023
GOCC_OXIDOREDUCTASE_COMPLEX       120       1.73       0.017         AS_ACCEPTOR       57       1.73       0.046         RNA synthesis       20       1.87       0.006         REACTOME_LAGGING_STRAND_SYNTHESIS       20       1.87       0.006         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION       94       1.86       0.006         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS       34       1.82       0.010         REACTOME_TRANSLATION       293       1.8       0.013         Telomeres       293       1.8       0.016         REACTOME_EXTENSION_OF_TELOMERES       51       1.77       0.016         REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS       29       1.69       0.027         REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY       101       1.67       0.033	MCL_PROLIFERATION_SIGNATURE Proteasome KEGG_PROTEASOME GOCC_PROTEASOME_CORE_COMPLEX Protein syntheis KEGG_RIBOSOME GOCC_RIBOSOMAL_SUBUNIT GOCC_ORGANELLAR_RIBOSOME GOCC_LARGE_RIBOSOMAL_SUBUNIT GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT GOCC_RIBOSOME GOCC_SMALL_RIBOSOMAL_SUBUNIT GOCC_CYTOSOLIC_RIBOSOME GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT REACTOME_EUKARYOTIC_TRANSLATION_INITIATION Redox balance	44 20 88 177 81 111 54 208 69 101 57 120	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1,65	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040
AS_ACCEPTOR       57       1.73       0.046         RNA synthesis       20       1.87       0.006         REACTOME_LAGGING_STRAND_SYNTHESIS       20       1.87       0.006         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION       94       1.86       0.006         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS       34       1.82       0.010         REACTOME_TRANSLATION       293       1.8       0.013         Telomeres       293       1.8       0.016         REACTOME_EXTENSION_OF_TELOMERES       51       1.77       0.016         REACTOME_TRANSLATION       108       1.75       0.018         Th       T       0.016       1.69       0.027         REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS       29       1.69       0.027         REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY       101       1.67       0.033	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_SMALL_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME	44 20 88 177 81 111 54 208 69 101 57 120 78	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1,65 1.59	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040
RNA synthesis         20         1,87         0.006           REACTOME_LAGGING_STRAND_SYNTHESIS         20         1,87         0.006           REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         94         1,86         0.006           REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         34         1,82         0.010           REACTOME_TRANSLATION         293         1,8         0.013           Telomeres         293         1,77         0.016           REACTOME_TELOMERE_MAINTENANCE         108         1,75         0.018           TNF         TREACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS         29         1,69         0.027           REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY         101         1,67         0.033	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_SMALL_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES	44 20 88 177 81 111 54 208 69 101 57 120 78 36	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1,65 1.59 1,64	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.042
REACTOME_LAGGING_STRAND_SYNTHESIS         20         1,87         0.006           REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         94         1,86         0.006           REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         34         1,82         0.010           REACTOME_TRANSLATION         293         1,8         0.013           Telomeres         20         1,77         0.016           REACTOME_TELOMERE_MAINTENANCE         51         1,77         0.018           TFF         20         1,69         0.027           REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS         29         1,69         0.023	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_SMALL_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         GOCC_OXIDOREDUCTASE_COMPLEX	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1.65 1.59 1.64 1.73	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.042 0.047
REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         94         1,86         0.006           REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         34         1,82         0.010           REACTOME_TRANSLATION         293         1,8         0.013           Telomeres         51         1,77         0.016           REACTOME_TELOMERE_MAINTENANCE         108         1,75         0.018           The         The         The         The         The           REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS         29         1,69         0.027           REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY         101         1,67         0.033	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_RIBOSOME         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         GOCC_OXIDOREDUCTASE_COMPLEX         AS_ACCEPTOR	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1.65 1.59 1.64 1.73	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.042 0.047
REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         34         1,82         0.010           REACTOME_TRANSLATION         293         1,8         0.013           Telomeres         51         1,77         0.016           REACTOME_TELOMERE_MAINTENANCE         108         1,75         0.018           THE         700         700         700         700           REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS         29         1,69         0.027           REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY         101         1,67         0.033	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_RIBOSOME         GOCC_SMALL_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         RCC_OXIDOREDUCTASE_COMPLEX         AS_ACCEPTOR         RNA synthesis	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1.65 1.59 1.65 1.59 1.64 1.73 1.73	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.040 0.042 0.017 0.046
REACTOME_TRANSLATION         293         1,8         0.013           Telomeres	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_RIBOSOMAL         GOCC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES         GOCC_OXIDOREDUCTASE_COMPLEX         AS_ACCEPTOR         RNA synthesis         REACTOME_LAGGING_STRAND_SYNTHESIS	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57 20	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1.65 1.65 1.59 1.64 1.73 1.73 1.73	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.040 0.042 0.017 0.046
Telomeres         51         1,77         0.016           REACTOME_EXTENSION_OF_TELOMERES         51         1,75         0.018           REACTOME_TELOMERE_MAINTENANCE         108         1,75         0.018           TNF	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         GOCC_OXIDOREDUCTASE_COMPLEX         AS_ACCEPTOR         RNA synthesis         REACTOME_LAGGING_STRAND_SYNTHESIS         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57 20 94	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1.65 1.59 1.64 1.73 1.73 1.73	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.040 0.042 0.017 0.046
REACTOME_EXTENSION_OF_TELOMERES         51         1,77         0.016           REACTOME_TELOMERE_MAINTENANCE         108         1,75         0.018           TNF         REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS         29         1,69         0.027           REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY         101         1,67         0.033	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_SMALL_RIBOSOME         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         RCC_OXIDOREDUCTASE_COMPLEX         AS_ACCEPTOR         RNA synthesis         REACTOME_LAGGING_STRAND_SYNTHESIS         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         REACTOME_LAGGING_STRAND_SYNTHESIS	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57 7 20 94 34	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1.65 1.59 1.64 1.73 1.73 1.73 1.87 1.86 1.82	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.040 0.042 0.017 0.046 0.006 0.006 0.010
REACTOME_TELOMERE_MAINTENANCE         108         1,75         0.018           TNF	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_SMALL_RIBOSOME         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         RCC_OXIDOREDUCTASE_COMPLEX         As_ACCEPTOR         RNA synthesis         REACTOME_LAGGING_STRAND_SYNTHESIS         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57 7 20 94 34	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1.65 1.59 1.64 1.73 1.73 1.73 1.87 1.86 1.82	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.040 0.042 0.017 0.046 0.006 0.006 0.010
TNF         29         1,69         0.027           REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS         29         1,69         0.027           REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY         101         1,67         0.033	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_ORGANELLAR_RIBOSOME         GOCC_ORGANELLAR_RIBOSOMAL_SUBUNIT         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_RIBOSOME         GOCC_RIBOSOME         GOCC_RIBOSOME         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         GOCC_OXIDOREDUCTASE_COMPLEX         AS_ACCEPTOR         RNA synthesis         REACTOME_LAGGING_STRAND_SYNTHESIS         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         REACTOME_TRANSLATION	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57 7 20 94 34 293	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1,65 1.59 1,64 1.73 1.73 1.73 1.87 1,86 1,82 1,8	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.042 0.017 0.046 0.006 0.006 0.006 0.010 0.013
REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS291,690.027REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY1011,670.033	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_SMALL_RIBOSOMAL_SUBUNIT         GOCC_SMALL_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         GOCC_OXIDOREDUCTASE_COMPLEX         AS_ACCEPTOR         RNA synthesis         REACTOME_LAGGING_STRAND_SYNTHESIS         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         REACTOME_TRANSLATION         REACTOME_TRANSLATION         REACTOME_TRANSLATION	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57 7 20 94 34 293 51	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1,65 1.59 1,64 1.73 1.73 1.87 1,86 1,82 1,8 1,82 1,8	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.040 0.042 0.017 0.046 0.006 0.006 0.006 0.010 0.013
REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY 101 1,67 0.033	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_ORGANELLAR_RIBOSOME         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_LARGE_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         RCC_OXIDOREDUCTASE_COMPLEX         AS_ACCEPTOR         RNA synthesis         REACTOME_LAGGING_STRAND_SYNTHESIS         REACTOME_LAGGING_STRAND_SYNTHESIS         REACTOME_LAGGING_STRAND_LAGGING_STRAND_SYNTHESIS         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         REACTOME_TRANSLATION         Telomeres         REACTOME_TRANSLATION	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57 7 20 94 34 293 51	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1,65 1.59 1,64 1.73 1.73 1.87 1,86 1,82 1,8 1,82 1,8	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.040 0.042 0.017 0.046 0.006 0.006 0.006 0.010 0.013
	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_ORGANELLAR_RIBOSOME         GOCC_ORGANELLAR_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOMAL_SUBUNIT         GOCC_CARIDCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOME         GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         GOCC_OXIDOREDUCTASE_COMPLEX         AS_ACCEPTOR         RNA synthesis         REACTOME_LAGGING_STRAND_SYNTHESIS         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS         REACTOME_TRANSLATION         Telomeres         REACTOME_EXTENSION_OF_TELOMERES         REACTOME_TELOMERE_MAINTENANCE         TNF	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57 20 94 34 293 51 108	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1,65 1.59 1,64 1.73 1.73 1.73 1.87 1,86 1,82 1,8 1,82 1,8	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.023 0.040 0.040 0.042 0.017 0.046 0.006 0.006 0.006 0.010 0.013 0.016 0.018
	MCL_PROLIFERATION_SIGNATURE         Proteasome         KEGG_PROTEASOME         GOCC_PROTEASOME_CORE_COMPLEX         Protein syntheis         KEGG_RIBOSOME         GOCC_RIBOSOMAL_SUBUNIT         GOCC_ORGANELLAR_RIBOSOME         GOCC_ORGANELLAR_RIBOSOME         GOCC_CORGANELLAR_RIBOSOMAL_SUBUNIT         GOCC_RIBOSOMAL_SUBUNIT         GOCC_RIBOSOMAL_SUBUNIT         GOCC_RIBOSOME         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         GOCC_CYTOSOLIC_RIBOSOMAL_SUBUNIT         REACTOME_EUKARYOTIC_TRANSLATION_INITIATION         Redox balance         KEGG_PEROXISOME         GOCC_OXIDOREDUCTASE_COMPLEX         As_ACCEPTOR         RNA synthesis         REACTOME_LAGGING_STRAND_SYNTHESIS         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         REACTOME_TRANSLATION         REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION         REACTOME_TRANSLATION         REACTOME_TRANSLATION         REACTOME_TRANSLATION         REACTOME_TRANSLATION         REACTOME_TRANSLATION         REACTOME_TRANSLATION         REACTOME_TRANSLATION         REACTOME_TRANSLATION         REACTOME_TRANSLATION     <	44 20 88 177 81 111 54 208 69 101 57 120 78 36 120 57 20 94 34 293 51 108 29	1.71 1.70 1.82 2.01 1.99 1.96 1.90 1.83 1.74 1.71 1.69 1,65 1.59 1,64 1.73 1.73 1.73 1.87 1,86 1,82 1,87 1,86 1,82 1,8 1,77 1,75	0.011 0.022 0.002 0.001 0.000 0.001 0.003 0.007 0.015 0.019 0.023 0.040 0.040 0.040 0.042 0.017 0.046 0.006 0.006 0.006 0.010 0.013 0.016 0.018

## Table S5. Complete GSEA results of MCL-PDLS compared to MCL-2D co-cultures

GENE SET	SIZ E	NES	FDR q-val	CLASS
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_E NDOSOMES	50	1.88	0.048	Ag presentation
HALLMARK_ANGIOGENESIS	33	1.72	0.042	Angiogenesis
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	33	1.91	0.028	Cell adhesion
REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21	60	1.87	0.044	Cell cycle
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	59	1.90	0.032	DNA replication
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	295	1.98	0.003	Extracellular matrix
REACTOME_ACTIVATION_OF_MATRIX_METALLOPROTEINASES	31	1.89	0.038	Extracellular matrix
GOCC_COLLAGEN_CONTAINING_EXTRACELLULAR_MATRIX	413	2.03	<0.001	Extracellular matrix
GOCC_COLLAGEN_TRIMER	84	1.94	0.009	Extracellular matrix
GOMF_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	165	2.08	<0.001	Extracellular matrix
GOMF_COLLAGEN_BINDING	65	2.01	0.002	Extracellular matrix
REACTOME_DECTIN_2_FAMILY	26	1.89	0.039	Immune response
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	198	1.72	0.034	Metastasis
BIOCARTA_RACC_PATHWAY	15	1.90	0.048	Ion channel activity
GOMF_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	73	1.93	0.023	Ion channel activity
GOMF_LIGAND_GATED_ION_CHANNEL_ACTIVITY	144	1.90	0.044	Ion channel activity
GOCC_ION_CHANNEL_COMPLEX	286	1.93	0.009	Ion channel activity
HALLMARK_KRAS_SIGNALING_UP	195	1.84	0.015	KRAS
HALLMARK_MYC_TARGETS_V1	200	1.83	0.010	МҮС
REACTOME_NEGATIVE_REGULATION_OF_NOTCH4_SIGNALING	54	1.88	0.042	Notch pathway
E47_02	249	1.72	0.014	Stemness
KEGG_PROTEASOME	44	1.97	0.004	Proteasome
REACTOME_DISEASES_ASSOCIATED_WITH_O_GLYCOSYLATION_OF_PROTEIN S	68	1.98	0.003	Protein glycosylation
REACTOME_O_GLYCOSYLATION_OF_TSR_DOMAIN_CONTAINING_PROTEINS	39	1.94	0.012	Protein glycosylation
REACTOME_DEFECTIVE_GALNT3_CAUSES_HFTC	16	1.92	0.026	Protein glycosylation
REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	23	1.91	0.028	Protein glycosylation
REACTOME_DEFECTIVE_C1GALT1C1_CAUSES_TNPS	17	1.87	0.046	Protein glycosylation

GSEA was used to test for significant enrichment of defined gene signatures. NES indicates Normalized Enriched Score; FDR, False Discovery Rate. Threshold FDR<0.05 and NES>1.5. Custom genes set were experimentally derived and downloaded from <a href="http://lymphochip.nih.gov/signaturedb/index.html">http://lymphochip.nih.gov/signaturedb/index.html</a>. C2CP, C3, C5 and H gene sets were obtained from the Molecular Signature Database (v2.5).

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AIMP2 AP3S1 APEX1 C1QBP CBX3 CCT2 CCT3 CCT4 CCT5 CCT7 CDC20 CDC45 CDK4 CLNS1A CNBP COPS5 COX5A CTPS1 DEK EEF1B2 EIF1AX EIF2S1 EIF2S2 EIF3B EIF4A1 EIF2S2 EIF3B EIF4A1 EIF4E ERH EXOSC7 FBL GLO1 GNL3 GOT2 GSPT1	H2AZ1 HDAC2 HDGF HNRNPA1 HNRNPA2B1 HNRNPA3 HNRNPC HNRNPD HNRNPR HNRNPU HPRT1 HSP90AB1 HSPD1 HSPE1 IARS1 IFRD1 ILF2 KARS1 IFRD1 ILF2 KARS1 KPNA2 LDHA LSM7 MAD2L1 MCM2 MCM4 MCM6 MCM7 MRPL23 MRPL23 MRPL9 MRPS18B NDUFAB1 NHP2 NME1 NOLC1	NOP16 NPM1 ODC1 PCNA POLD2 POLE3 PPIA PPM1G PRDX4 PRPF31 PSMA1 PSMA2 PSMA4 PSMA2 PSMA4 PSMA6 PSMA7 PSMB2 PSMB3 PSMC4 PSMB3 PSMC4 PSMC6 PSMD1 PSMD14 PSMD14 PSMD14 PSMD14 PSMD3 PSMD7 PTGES3 PWP1 RAN RANBP1 RFC4 RPL18 RPL34 RPL34 RPL34 RPL34 RPL5	RRM1 RRP9 RUVBL2 SERBP1 SET SF3B3 SLC25A3 SNRPA SNRPA1 SNRPB2 SNRPD1 SNRPD2 SNRPD2 SNRPG SRM SRSF2 SRSF3 SRSF7 SSB SSBP1 SYNCRIP TARDBP TCP1 TOMM70 TRA2B TRIM28 TUFM TXNL4A UBE2L3 USP1 VBP1 XRCC6 YWHAE
Collagen C1QB C1QC CCDC80 COL12A1 COL6A3	COL7A1 CRELD1 CTSL EGFLAM FRAS1 HSP90B1 ITIH4	LGALS9 LTBP3 MMP9 PTPRZ1 S100A4 SEMA3B THBS1	TNC USH2A VWF WNT5B ZP3
ECM org	E47_02		
COL12A1 COL22A1 COL6A3 COL7A1 CTSL LRP4 MMP16 MMP19 MMP9 NRXN1 SPP1 THBS1 TNC VWF	GABRE COL22A1 MMP16 DOC2B BTBD3 CASKIN2 FGF13 ELP5 ERBB3 SNAP25 TPI1		