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Appendix Table S1. Microarray analysis of the effect of HIV-1 infection on gene expression in CD4⁺ T-cells. Primary CD4⁺ T-cells were isolated from total blood of healthy individuals, activated for 72 h with α -CD3-CD28 beads and infected with HIV-1_{pNL4-3} or mock-infected. Both infected and mock-infected cells were cultured for two weeks to model different infection stages as described in (Shytaj *et al*, 2020). On days 7, 9 and 14 post-infection, HIV-1-infected and mock-infected cells were subjected to microarray analysis. Data from different time points were pooled for the analysis. Significantly enriched pathways in HIV-1 infected and mock-infected cells were identified by Gene Set Enrichment Analysis [GSEA (Subramanian *et al*, 2005)]. Number of donors = 2.

Gene set	NES	FDR q-value
Activated in infected	8.91	
CELL CYCLE MITOTIC	8.58	
DNA REPLICATION	8.45	
IMMUNE SYSTEM	8.04	
MITOTIC M M G1 PHASES	7.70	
HIV INFECTION	7.15	
S PHASE	7.01	
SYNTHESIS OF DNA	6.99	
MITOTIC G1 G1 S PHASES	6.84	
ADAPTIVE IMMUNE SYSTEM	6.76	
MRNA PROCESSING	6.71	
G1 S TRANSITION	6.56	
HOST INTERACTIONS OF HIV FACTORS	6.49	
ORC1 REMOVAL FROM CHROMATIN	6.44	
ASSEMBLY OF THE PRE REPLICATIVE COMPLEX	6.39	
M G1 TRANSITION	6.39	
PROCESSING OF CAPPED INTRON CONTAINING PRE MRNA	6.31	
TRANSCRIPTION	6.16	
METABOLISM OF RNA	5.87	
INTERFERON SIGNALING	5.79	
SIGNALING BY THE B CELL RECEPTOR BCR	5.77	
VIF MEDIATED DEGRADATION OF APOBEC3G	5.67	
RNA POL II TRANSCRIPTION	5.65	
CYTOKINE SIGNALING IN IMMUNE SYSTEM	5.64	
SCFSKP2 MEDIATED DEGRADATION OF P27 P21	5.62	
CDT1 ASSOCIATION WITH THE CDC8 ORC ORIGIN COMPLEX	5.59	
CYCLIN E ASSOCIATED EVENTS DURING G1 S TRANSITION	5.57	
CELL CYCLE CHECKPOINTS	5.55	
CDK MEDIATED PHOSPHORYLATION AND REMOVAL OF CDC6 REGULATION OF MRNA STABILITY BY PROTEINS THAT BIND AU	5.53	
RICH ELEMENTS	5.51	
ER PHAGOSOME PATHWAY	5.44	
P53 DEPENDENT G1 DNA DAMAGE RESPONSE	5.42	
LATE PHASE OF HIV LIFE CYCLE	5.41	
DESTABILIZATION OF MRNA BY AUF1 HNRNP D0	5.38	
AUTODEGRADATION OF THE E3 UBIQUITIN LIGASE COP1	5.29	
P53 INDEPENDENT G1 S DNA DAMAGE CHECKPOINT	5.29	
SCF BETA TRCP MEDIATED DEGRADATION OF EMI1	5.26	
MITOTIC PROMETAPHASE	5.20	
ACTIVATION OF NF KAPPAB IN B CELLS	5.20	
HIV LIFE CYCLE	5.17	
DOWNSTREAM SIGNALING EVENTS OF B CELL RECEPTOR BCR	5.10	
REGULATION OF MITOTIC CELL CYCLE	5.07	
CROSS PRESENTATION OF SOLUBLE EXOGENOUS ANTIGENS ENDOSOMES	5.02	
ANTIVIRAL MECHANISM BY IFN STIMULATED GENES	4.98	
APOPTOSIS	4.94	
ANTIGEN PROCESSING CROSS PRESENTATION	4.93	
APC C CDH1 MEDIATED DEGRADATION OF CDC20 AND OTHER APC C CDH1 TARGETED PROTEINS IN LATE MITOSIS EARLY G1	4.88	
REGULATION OF APOPTOSIS	4.84	
SIGNALING BY WNT	4.82	
METABOLISM OF PROTEINS	4.80	
CLASS I MHC MEDIATED ANTIGEN PROCESSING PRESENTATION	4.79	
AUTODEGRADATION OF CDH1 BY CDH1 APC C	4.70	
APC C CDC20 MEDIATED DEGRADATION OF MITOTIC PROTEINS	4.65	
METABOLISM OF MRNA ANTIGEN PROCESSING UBIQUITINATION PROTEASOME	4.62	
ANTIGEN PROCESSING UBIQUITINATION PROTEASOME DEGRADATION	4.61	
TRANSPORT OF MATURE TRANSCRIPT TO CYTOPLASM	4.59	
RNA POL I RNA POL III AND MITOCHONDRIAL TRANSCRIPTION	4.36	
FORMATION OF RNA POL II ELONGATION COMPLEX	4.33	
METABOLISM OF NON CODING RNA	4.30	
DNA REPAIR	4.20	
UNFOLDED PROTEIN RESPONSE TRANSPORT OF MATURE MRNA DERIVED FROM AN INTRONLESS	4.19	
TRANSCRIPT	4.15	
RNA POL II PRE TRANSCRIPTION EVENTS CLEAVAGE OF GROWING TRANSCRIPT IN THE TERMINATION	4.15	
REGION	4.09	
FORMATION OF THE HIV1 EARLY ELONGATION COMPLEX	4.02	
CHROMOSOME MAINTENANCE	4.02	
MITOTIC G2 G2 M PHASES	3.99	
TCA CYCLE AND RESPIRATORY ELECTRON TRANSPORT	3.94	
CHEMIOSMOTIC COURLING AND HEAT PRODUCTION BY	3.89	
CHEMIOSMOTIC COUPLING AND HEAT PRODUCTION BY UNCOUPLING PROTEINS		
UNCOUPLING PROTEINS	3.85	
UNCOUPLING PROTEINS RESPIRATORY ELECTRON TRANSPORT	3.85	
OHEMOSINC COUPLING AND HEAT PRODUCTION BY INSCOULENG PROTEINS RESPIRATORY ELECTRON TRANSPORT METABOLISM OF AMINO ACIDS AND DERIVATIVES DIABETES PATHYINYS		
UNCOUPLING PROTEINS RESPIRATORY ELECTRON TRANSPORT METABOLISM OF AMINO ACIDS AND DERIVATIVES	3.82	

Reactome							
q-value	Gene set	NES	FDR q-value				
	Activated in Mock						
0	3 UTR MEDIATED TRANSLATIONAL REGULATION	-5.75	0				
0	PEPTIDE CHAIN ELONGATION	-5.54	0				
0	TRANSLATION	-5.40	0				
0	SRP DEPENDENT COTRANSLATIONAL PROTEIN TARGETING TO MEMBRANE	-4.97	0				
0	NONSENSE MEDIATED DECAY ENHANCED BY THE EXON JUNCTION COMPLEX	-4.84	0				
0	INFLUENZA VIRAL RNA TRANSCRIPTION AND REPLICATION	-4.76	0				
0	INFLUENZA LIFE CYCLE	-3.79	0				
0	BINDING COMPLEX AND EIFS AND SUBSEQUENT BINDING TO	-3.78	0				
0	FORMATION OF THE TERNARY COMPLEX AND SUBSEQUENTLY THE 43S COMPLEX	-3.54	0				
0	OLFACTORY SIGNALING PATHWAY	-3.19	0				
0	GENERIC TRANSCRIPTION PATHWAY	-3.17	0				
0	GPCR DOWNSTREAM SIGNALING	-2.72	0.0006				
0	TCR SIGNALING	-2.68	0.0007				
0	GENERATION OF SECOND MESSENGER MOLECULES	-2.46	0.0033				
0	GLYCOLYSIS	-2.38	0.0055				
0	BINDING AND ENTRY OF HIV VIRION	-2.14	0.0266				
0	PROTEOLYTIC CLEAVAGE OF SNARE COMPLEX PROTEINS	-2.06	0.0440				
0	HS GAG DEGRADATION	-2.05	0.0445				

Gene set Activated in	NES Fi	OR q-value		NES Fl d in Mock	DR q-value
PROTEASOME PATHWAY	4.67	0	IL10 PATHWAY	-2.76	0.001
CELLCYCLE PATHWAY	3.39	0	PDGF PATHWAY	-2.36	0.011
CASPASE PATHWAY	3.16	0	EGF PATHWAY	-2.36	0.017
			TCRA PATHWAY		0.032
HIVNEF PATHWAY	2.72	0.0005	RELA PATHWAY	-2.05	0.033
FAS PATHWAY	2.51	0.0018	IL7 PATHWAY	-2.09	0.034
RANMS PATHWAY	2.53	0.0019	IL2 PATHWAY TCAPOPTOSIS	-2.10	0.036
ATRBRCA PATHWAY	2.54	0.0022	PATHWAY	-2.05	0.036
FCER1 PATHWAY BCELLSURVIVAL PATHWAY	2.58	0.0023	TCR PATHWAY	-2.15 -1.98	0.040
G1 PATHWAY	2.35	0.0065		I	
PGC1A PATHWAY	2.37	0.0068			
MITOCHONDRIA PATHWAY	2.35	0.0071			
RACCYCD PATHWAY	2.37	0.0073			
MAPK PATHWAY	2.30	0.0076			
G2 PATHWAY	2.27	0.0080			
DNAFRAGMENT PATHWAY	2.27	0.0084			
CHEMICAL PATHWAY	2.27	0.0088			
BCR PATHWAY	2.27	0.0092			
HDAC PATHWAY	2.22	0.0096			
EIF2 PATHWAY	2.22	0.0099			
NDKDYNAMIN PATHWAY	2.17	0.0102			
RHO PATHWAY	2.19	0.0102			
MPR PATHWAY	2.18	0.0105			
MEF2D PATHWAY	2.17	0.0105			
SRCRPTP PATHWAY	2.18	0.0106			
DEATH PATHWAY	2.13	0.0114			
SET PATHWAY	2.12	0.0116			
SKP2E2F PATHWAY	2.08	0.0148			
TNER1 PATHWAY	2.06	0.0166			
P35ALZHEIMERS PATHWAY	2.03	0.0188			
PTDINS PATHWAY	2.02	0.0193			
RNA PATHWAY	2.01	0.0199			
D4GDI PATHWAY	1.97	0.0245			
P27 PATHWAY	1.95	0.0270			
RB PATHWAY	1.94	0.0272			
ERK5 PATHWAY	1.93	0.0273			
PTC1 PATHWAY	1.95	0.0275			
MTOR PATHWAY	1.94	0.0275			
P53HYPOXIA PATHWAY	1.93	0.0278			
VDR PATHWAY	1.87	0.0356			
AKAP95 PATHWAY	1.87	0.0358			
CYTOKINE PATHWAY	1.87	0.0364			
MCALPAIN PATHWAY	1.86	0.0367			
NFAT PATHWAY	1.86	0.0368			
ETC PATHWAY	1.85	0.0371			
GCR PATHWAY	1.84	0.0390			
CARM ER PATHWAY	1.82	0.0424			
FMLP PATHWAY	1.81	0.0434			
EIF PATHWAY	1.81	0.0435			
IL3 PATHWAY	1.81	0.0437			
BLYMPHOCYTE PATHWAY	1.79	0.0472			

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RNA POL I TRANSCRIPTION TERMINATION 2.77 6.54E05 CEPOSITION OF NEW CERPA CONTAINING NUCLEOSOMES AT THE 2.78 8.69E 05 CERTORING OF NEW CERPA CONTAINING NUCLEOSOMES AT THE 2.78 8.69E 05 MEIOTIC RECOMBINATION 2.71 1.07E 04 PROCESSING OF INTROALESS PRE MENAS 2.70 1.08E 04 ASPARAGINE N. LINKED GLYCOSVLATION 2.88 1.14E 04 ADD SIGNALLING VIA TRAK PROM THE PLASMA MEMBRANE 2.70 1.16E 04 MAILHORGULATORY INTERACTIONS BETWEEN A LYMPHOID AND 2.70 1.17E 04 RNA POL I TRANSCRIPTION INTIATION 2.70 1.17E 04 COMPLEX 2.88 1.32E 04 COMPLEX 2.86 1.32E 04 COMPLEX 2.81 2.84E 04 CLOOS TRANSCRIPTION NOUPLED MER TO NER REPAIR 2.82 2.82 CLAGOIN STRAND SYNTHESIS	RNA.POL.ITRANSCRIPTION TERMINATION 2.77 6.54E 05 DEPOSITION OF NEW CENPA CONTAINING NUCLEOSOMES AT THE 2.78 8.69E 05 MEIOTO RECOMBINATION 2.71 1.07E 04 MEIOTO RECOMBINATION 2.71 1.07E 04 ASPARAGINE OF INTRONLESS PIE MENAS 2.73 1.08E 04 ASPARAGINE V LINKED GLYCOSYLATION 2.68 1.14E 04 ASPARAGINE V LINKED GLYCOSYLATION 2.68 1.14E 04 NON LYMPHOLO CELL 2.70 1.15E 04 MILLINGEQULATORY INTERACTONS BETWEEN A LYMPHOLO AND AND LYMPHOLO CELL 2.70 1.15E 04 NON LYMPHOLO CELL 2.76 1.35E 04 1.35E 04 CORMATION OF TRANSCRIPTION INITIATION 2.70 1.35E 04 1.35E 04 CORMATION OF TRANSCRIPTION COUPLED NER TO NER REPAIR 2.67 1.35E 04 CLOBAL CENOMIC NER GG NER 2.48 2.25E 04 1.62E 04 GLOBAL CENOMIC NER GG NER 2.48 2.25E 04 2.26E 04 GLOBAL CENOMIC NER GG NER TALING BY DNA POL IN TO NER 2.62 2.25E 04 MURIA MESSENGER RINA SYNTHESIS 2.43 4.47E 04 PIENK R	MEMBRANE TRAFFICKING	2.88	3.35E-05
DEPOSITION OF NEW CERPA CONTAINING NUCLEOSOMES AT THE 2.76 8.69E-05 CENTROLERE 2.71 1.07E-04 MEIOTIC RECOMBINATION 2.71 1.07E-04 PROCESSING OF INTROALESS PRE MENAS 2.73 1.08E-04 ASPARAGINE N LIKED CLOOSYLATION 2.88 1.14E-04 NGF SIGNALLING VIA TRICK PROM THE PLASMA MEMBRANE 2.70 1.15E-04 MIRNORECLILING VIA TRICK PROM THE PLASMA MEMBRANE 2.70 1.15E-04 MIRNORECLILING VIA TRICK PROM THE PLASMA MEMBRANE 2.70 1.15E-04 MIRNORECLILING VIA TRICK PROM THE PLASMA MEMBRANE 2.70 1.15E-04 ALMONITORY TRIANSCRIPTION INTIATION 2.70 1.15E-04 CI PHASE 2.66 1.23E-04 COMALEX 2.66 1.23E-04 COMALEX 2.66 1.23E-04 GLOOSE TRANSORT 2.66 1.02E-04 GLOOSE TRANSORT 2.61 2.62E 2.67E-04 REPAR SYNTHESIS 2.62 2.67E-04 MINES DAUTOTHENATE METABOLISM 2.61 2.24E-04 VITAMIN BS PANTOTHENATE METABOLISM 2.62 2.75E	DEPOSITION OF NEW CENPA CONTAINING NUCLEOSOME 8 AT THE 2.0 6.09E.05 DEITOSITIC RECOMBINATION 2.71 1.07E.04 MEIDTIC RECOMBINATION 2.71 1.07E.04 PROCESSING OF INTRON. ESS PRE MRNAS 2.73 1.08E.04 SASPARADEN LINKED GLYCOSYLATION 2.88 1.14E.04 NICH SIGNALLING VIA TRIKA FROM THE PLASMA MEMBRANE 2.70 1.14E.04 NICH SIGNALLING VIA TRIKA FROM THE PLASMA MEMBRANE 2.70 1.14E.04 NICH SIGNALLING VIA TRIKA FROM THE PLASMA MEMBRANE 2.70 1.14E.04 NICH VIPPOID CELL 2.70 1.14E.04 1.14E.04 ANON LYMPHOL CELL 2.70 1.14E.04 1.70 GI PHAGE 2.68 1.22E.04 1.22E.04 GLODGE TRANSCRIPTION INTIATION 2.70 1.15E.04 2.62 GLODGE TRANSCRIPTION COUPLED NET TO KER REPAR 2.67 1.32E.04 GLUDGE TRANSCRIPTION COUPLED NET TO KER REPAR 2.62 2.67E.04 LAGGING STRAND SYNTHESIS 2.64 2.67E.04 2.67E.04 GLUDGE TRANSCRIPTION 2.64 3.7CE.04 3.7CE.04 3.7CE.04	FORMATION OF TUBULIN FOLDING INTERMEDIATES BY CCT TRIC	2.81	5.46E-05
CENTRONERIE 2.76 8.89E05 AREIOTIC RECOMBINATION 2.71 1.07E04 PROCESSING OF INTRONLESS PRE MRNAS 2.73 1.08E04 ASPARAGRE N LINKED GLYGOSYLATION 2.88 1.14E04 NOF SIGNALING VIA TRAK FROM THE PLASMA MEMBRANE 2.70 1.15E04 NOF SIGNALING VIA TRAK FROM THE PLASMA MEMBRANE 2.70 1.15E04 NON L'IMPHOID CELL 2.70 1.16E04 RNA POL I TRANSCRIPTION INTRATION 2.70 1.15E04 COMPLEX 2.86 1.32E04 COMPLEX 2.86 1.32E04 COMPLEX 2.67 1.35E04 COMPLEX 2.68 1.32E04 COMPLEX 2.68 1.32E04 COMPLEX 2.68 1.32E04 CALOSE TRANSCRIPTION NUTLATION 2.64 2.015E04 LAGGING STRAND SYNTHESIS 2.62 2.67E04 REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER 2.65 3.40E04 LINEED CUIGOACHARDE LON TRANSFER TO A NASCENT 2.55 4.46E04 VIRAL MESSENGER RNA SYNTHESIS 2.55 5.4	CENTROMERE 2.76 8.696-05 DENTCOMERE 2.77 1.07E-04 PROCESSING OF INTRONLESS PREMINAS 2.77 1.07E-04 PROCESSING OF INTRONLESS PREMINAS 2.72 1.08E-04 NOT SIGNALLING VIA TIRKA FROM THE PLASMA MEMBRANE 2.70 1.15E-04 NEP SIGNALLING VIA TIRKA FROM THE PLASMA MEMBRANE 2.70 1.15E-04 NOT VIMPIODE GULVOSYLATION 2.86 1.12E-04 NOT VIMPIODE GULVOSYLATION 2.70 1.15E-04 OND VIM TIRKACTONS BETWEEN A LYMPHOL AND 2.70 1.17E-04 OLI TRANSCRIPTION INITIATION 2.70 1.17E-04 OLI TRANSCRIPTION COUPLED HER TO NER REPARE 2.80 1.23E-04 CLOBAL CENDMIC NER GG NER 2.60 2.07E-04 2.47 GLUGOSE TRANSORT 2.64 2.01E-04 2.61 2.25E-04 VITAMIN BE PANTOTHENATE METADLISM 2.61 2.24E-04 2.01E-04 LIAGGING STRAND SYNTHESIS 2.63 4.37E-04 2.65 SEPOLICIT TRANSCRIPTION 2.65 3.76E-04 3.36 SINDAL MESSENCER RNA SYNTHESIS 2.64 </td <td></td> <td>2.77</td> <td>6.54E-05</td>		2.77	6.54E-05
PROCESSING OF INTROMLESS PRE MINAS 2.73 1.08E-04 ASPARAGINE N LINKED CLYCOSYLATION 2.68 1.14E-04 NOF SIGNALING VIA TRAK AROM THE PLASMA MEMBRANE 2.70 1.15E-04 MINADROBECULATORY INTERACTIONS BETWEEN A LYMPHOID AND 2.70 1.15E-04 ANDIALING VIA TRAK AROM THE PLASMA MEMBRANE 2.70 1.15E-04 MINADROBECULATORY INTERACTIONS BETWEEN A LYMPHOID AND 2.70 1.17E-04 A NOLLYMPHOID CELL 2.70 1.17E-04 FORMATION OF TRANSCRIPTION INTATION 2.70 1.17E-04 FORMATION OF TRANSCRIPTION COUPLED NER TO NER REPAIR 2.60 1.25E-04 FORMATION OF TRANSCRIPTION COUPLED NER TO NER PAIR 2.67 1.35E-04 GLOBAL GENOMIC NER GG NER 2.68 1.05E-04 2.01E-04 GLOBAL STRAND SYNTHESIS 2.69 2.67E-04 2.01E-04 CAUCINE TRANSCRIPTION 2.64 2.01E-04 2.05E-04 CIVIAUN BS PANTOTHENATE METABOLISM 2.61 2.24E-04 2.05E-04 GLOBOSCHAMBELICID AND TRANSFER TO A NASCENT 2.53 4.37E-04 PROTEIN 2.50 5.40E-04 5.50E-0	PROCESSING OF INTRONLESS PIE MINAS 2.73 1.08E04 ASPARAGINE N LINKED GLYCOSYLATION 2.64 1.14E04 NOR SIGNALLING VIA TRKA FROM THE PLASMA MEMBRANE 2.70 1.15E04 MININGREGULATORY INTERACTIONS BETWEEN A LYMPHOID AND A NON LYMPHOID CELL 2.70 1.15E04 NNA POL ITAWASCRIPTION INITIATION 2.70 1.15E04 NA NOL LYMPHOID CELL 2.70 1.15E04 OF PMASE 2.80 1.25E04 GLOBAL GENOMIC NER GROM THE PLASMA MEMBRANE 2.70 1.15E04 ORIVERSITY 2.84 2.87 1.35E04 GLOBAL GENOMIC NER GG NER 2.66 1.62E04 1.052E04 GLOBAL GENOMIC NER GG NER 2.62 2.27E64 2.01E04 CALGING STAND SYNTHESIS 2.62 2.27E64 2.26E04 MIRINE STAND SYNTHESIS 2.66 3.70E64 3.70E64 VITAL MESSENGER RNA SYNTHESIS 2.61 3.70E64 3.70E64 VITAL MESSENGER RNA SYNTHESIS 2.53 4.44E04 2.44E04 SIGNALING SP SOF KIT 2.50 5.40E04 4.47E04 VITAL M		2.76	8.69E-05
ASPARGRE N LINKED GLYCOSYLATION 2.68 1.14E.04 NGF SIGNALLING VIA TRAK FROM THE PLASMA MEMBRANE 2.70 1.15E.04 MARD SIGNALLING VIA TRAK FROM THE PLASMA MEMBRANE 2.70 1.15E.04 MARD SIGNALLING VIA TRAK FROM THE PLASMA MEMBRANE 2.70 1.15E.04 MARD SIGNALTRAY FROM THE PLASMA MEMBRANE 2.70 1.15E.04 AND LYMPHOID CELL 2.70 1.17E.04 RNA POL LI TRANSCRIPTION INTIATION 2.70 1.37E.04 GI PHASE 2.66 1.32E.04 COMPLEX 2.67 1.33E.04 GOMALER 2.68 1.32E.04 GOMALER 2.65 1.32E.04 GOMALER 2.65 1.32E.04 GUIOSE TRANSPORT 2.64 2.01E.04 CLUGSE TRANSPORT 2.64 2.01E.04 LIGGING STRAND SYNTHESIS 2.62 2.75E.04 VITAMIN B5 PARTOTHENATE METABOLISM 2.61 2.84E.04 VITAMIN S5 PARTOTHENATE METABOLISM 2.61 2.84E.04 LINKED OLIGOSACCHARDE LLO AND TRANSFER TO A NASCENT 2.53 4.47E.04 PREK REGULATED	ASPARAGINE N LINED GLYCOSYLATION 2.66 1.14E04 NOR JEGUALLING VIA TRIKA FRODI THE PLASIMA MEMBRIANE 2.70 1.15E04 MIRNOREGULATORY INTERACTIONS BETWEEN ALYMPHOD AND 2.70 1.15E04 NANNARDEGULATORY INTERACTIONS BETWEEN ALYMPHOD AND 2.70 1.15E04 NAN, POLITRANGGRIPTION INTERACTIONS BETWEEN ALYMPHOD AND 2.70 1.15E04 NAN, POLITRANGGRIPTION INTERACTIONS BETWEEN ALYMPHOD AND 2.70 1.15E04 ORA ANDI, VEMPIOD CELL 2.81 2.82 1.22E04 ORDMARE 2.83 1.23E04 2.83 1.35E04 GLOBAL, GENOMIC NER GG KER 2.65 1.62E04 2.01E04 CLOBAL, GENOMIC NER GG KER 2.61 2.24E04 2.01E04 CLOGENTANDEORT 2.64 2.01E04 2.24E04 VITAMIN BS PANTOTHENATE METABOLISM 2.61 3.70E04 VITAMIN BS PANTOTHENATE METABOLISM 2.63 4.47E04 VIRAL MESSENGER RNA SYNTHESIS 2.53 4.47E04 VIRAL MESSENGER RNA SYNTHESIS 2.50 5.44E04 SIGNALING BY SCH KIT 2.50 5.46E04 <td< td=""><td>MEIOTIC RECOMBINATION</td><td>2.71</td><td>1.07E-04</td></td<>	MEIOTIC RECOMBINATION	2.71	1.07E-04
NGF SIGNALLING VIA TRKA FROM THE PLASMA MEMBRANE 2.70 1.15E.04 MARLING CELL 1.15E.04 2.70 1.15E.04 MARLING CELL 2.70 1.16E.04 2.70 RNA POLITORY INTERATONS BETWEEN A LYMPHOD AND 2.70 1.16E.04 ANDI LYMPHOD CALL 2.70 1.17E.04 RNA POLI TRANSCRIPTION INITATION 2.70 1.37E.04 GI PHASE 2.66 1.32E.04 COMPLEX 2.67 1.33E.04 GORAL CONTRANSCRIPTION COUPLED NER TO NER REPAIR 2.67 1.33E.04 COMPLEX 2.61 2.262 1.52E.04 CAUCOSE TRANSCRIPTION COUPLED NER TO NER REPAIR 2.61 2.267 2.55E.05 CAUCOSE TRANSPORT 2.64 2.01E.04 2.65 3.026.04 VITAMIN 85 PARTOTHERINE METABOLISM 2.61 2.26E.04 2.55 3.07E.04 VITAMIN 85 PARTOTHERINE MATABOLISM 2.53 4.34E.04 3.07E.04 3.07E.04 PROTEIN 2.55 4.34E.04 3.07E.04 3.07E.04 3.07E.04 VITAMIN 85 PARTOTHERINE MATABOLISM 2	NGF SIGNALLING VIA TIRKA FROM THE PLASMA MEMBRANE 2.70 1.156.04 MARLING ZULA TIGH INTERACTIONS BETWEEN A LYMPHOD AND MARLING ZULA TIGH INTERACTIONS BETWEEN A LYMPHOD AND NON YMMPHOD ZULA 2.70 1.156.04 SIGN ALLING VIA TIRKA FROM THE PLASMA MEMBRANE 2.70 1.156.04 SIGN ALLING VIA TIRKA FROM THE PLASMA MEMBRANE 2.70 1.156.04 SIGN ALLING VIA TIRKA FROM THE PLASMA MEMBRANE 2.70 1.156.04 SIGN ALLING VIA TIRKA FROM THE PLASMA MEMBRANE 2.70 1.156.04 SIGN ALLING VIA TIRKA FROM THE PLASMA MEMBRANE 2.60 1.256.04 SIGN ALLING OF TRANSCRIPTION COUPLED HER TO NER REPAIR 2.66 1.256.04 CLOBAL CENDMIC NER GO NER 2.60 1.256.04 2.2016.04 CLOBAL CENDMIC NER GO NER TO ALLING SU DNA POL IN TO NER 2.62 2.276.04 VITAMIN BS PANTOTHENATE METABLISM 2.64 2.456.04 VIRAL MESSENCER RNA SYNTHESIS 2.63 4.366.04 VIRAL MESSENCER RNA SYNTHESIS 2.63 4.476.04 VIRAL MESSENCER RNA SYNTHESIS 2.64 6.466.04 VIRAL MESSENCER RNA SYNTHESIS 2.64 6.466.04 SIGNALING BY SOF KIT <t< td=""><td>PROCESSING OF INTRONLESS PRE MRNAS</td><td>2.73</td><td>1.08E-04</td></t<>	PROCESSING OF INTRONLESS PRE MRNAS	2.73	1.08E-04
MANABOREGULATORY INTERACTIONS BETWEEN A LYMPHOD AND A NON LYMPHOD CELL 2.70 1.16E 04 NON LYMPHOD CELL 2.70 1.17E 04 RNA POL I TRANSCRIPTION INTATION 2.70 1.17E 04 GI PHASE 2.86 1.32E 04 COMPLEX 2.86 1.32E 04 COMPLEX 2.86 1.32E 04 COMPLEX 2.86 1.32E 04 COMPLEX 2.86 1.32E 04 CAGAL GENOMC NER GO NER 2.85 1.62E 04 CLOSE TRANSPORT 2.82 2.62 2.76E 04 REPAIR SYNTHESIS 2.82 2.85E 0.27E 04 2.81E 0.42E 04 REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER 2.62 2.76E 04 VITAMIN BS PANTOTHENATE METABOLISM 2.61 2.84E 04 INRED DUIGSOACCHARGE LLO AND TRANSFER TO A NASCENT 2.53 4.34E 04 PROTEIN 2.53 4.36E 04 4.47E 04 PROTEINS 2.50 5.40E 04 4.47E 04 PROTEINS 2.50 5.40E 04 4.47E 04 PROTEINS 2.50 5.40E 04 <t< td=""><td>MAILARGEGULATORY INTERACTORS BETWEEN AL YMPHOLD AND 2.70 1.16E04 NANL YMPHOLO CLLL 2.70 1.17E04 RNA POL ITRANSCRIPTION INITIATION 2.71 1.16E04 GI PHASE 2.80 1.2260 COMPLEX 2.81 1.2260 COMPLEX 2.81 1.32604 COMPLEX 2.86 2.86 CLOBAL GENOMIC NER 05 REP CILLING SV DIA POL IN TC NER 2.82 REPAIR SYNTHESIS 2.82 2.75604 VITALIN BS PANTOTHEINTE ME TABOLISM 2.61 2.384604 GI S SPECIFIC TRANSCRIPTION 2.56 3.370E04 VIRAL MESSENDER TRN. SYNTHESIS 2.53 4.45604 ACTIVATION OF INHONLY PROTEINS 2.50 5.45604 SIGNALING SYNTHESIS 2.45 5.45604 DESTABULZTION OF INHONLY PROTEINS 2.46 5.45604 DESTABULZTION OF MENDARY ASGRY 2.46<</td><td>ASPARAGINE N LINKED GLYCOSYLATION</td><td>2.68</td><td>1.14E-04</td></t<>	MAILARGEGULATORY INTERACTORS BETWEEN AL YMPHOLD AND 2.70 1.16E04 NANL YMPHOLO CLLL 2.70 1.17E04 RNA POL ITRANSCRIPTION INITIATION 2.71 1.16E04 GI PHASE 2.80 1.2260 COMPLEX 2.81 1.2260 COMPLEX 2.81 1.32604 COMPLEX 2.86 2.86 CLOBAL GENOMIC NER 05 REP CILLING SV DIA POL IN TC NER 2.82 REPAIR SYNTHESIS 2.82 2.75604 VITALIN BS PANTOTHEINTE ME TABOLISM 2.61 2.384604 GI S SPECIFIC TRANSCRIPTION 2.56 3.370E04 VIRAL MESSENDER TRN. SYNTHESIS 2.53 4.45604 ACTIVATION OF INHONLY PROTEINS 2.50 5.45604 SIGNALING SYNTHESIS 2.45 5.45604 DESTABULZTION OF INHONLY PROTEINS 2.46 5.45604 DESTABULZTION OF MENDARY ASGRY 2.46<	ASPARAGINE N LINKED GLYCOSYLATION	2.68	1.14E-04
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GI S SPECIFIC TRANSCRIPTION 2.56 3.70524 VIRAL MESSENGER RNA SYNTHESIS 2.53 4.34E-04 LINKED OLIGOSACCHARDE LLO AND TRANSFER TO A INSCENT 2.53 4.54E-04 PERK REGULATED GENE EXPRESSION 2.53 4.50E-04 ACTIVATION OF BHO NLY PROTEINS 2.50 5.64E-04 SIGNALING BY SCF KIT 2.50 5.64E-04 BESTABILIZATION OF MERA BY KSRP 2.49 5.78E-04 SIGNALING BY SCR IF PROCESSING OF REPLICATION DEPENDENT 5.82E-04 5.82E-04 ISSIGNALING BY LLS 2.48 6.44E-04 TOLL RECEPTOR CASCADES 2.47 6.44E-04 TOLL RECEPTOR CASCADES 2.46 6.74E-04 SIGNALING BY LLS 2.46 6.74E-04 TOLING BY REBS2 2.46 6.74E-04 SIGNALING BY LES 2.46 6.74E-04 SIGNALING BY ERBS2	G1 S SPECIFIC TRANSCRIPTION 2.6 3.766.40 VIRAL MESSENGER RWA SYNTHESIS 2.53 4.346.04 LINRED DUIGOSACCHARDE LLO AND TRANSFER TO A NASCENT 2.53 4.346.04 PERK REGULATED GENE EXPRESSION 2.53 4.346.04 ACTIVATION OF BH3 ONLY PROFESSION 2.53 4.566.04 ACTIVATION OF BH3 ONLY PROFESSION 2.50 5.466.04 SIGNALING BY SCF KIT 2.50 5.766.04 SLEP DEERIDENT PROCESSING OF REPLICATION DEPENDENT 3.240 5.326.04 SIGNALING BY LS 2.44 6.146.04 5.466.04 DUL RECEPTOR NA.5GALES 2.47 6.846.04 5.766.04 SIGNALING BY LS 2.46 6.786.04 7.706.04 SIGNALING BY ERBI2 2.46 <	GI PHASE FORMATION OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX CLOBAL GENOMIC NER GG NER CLUCOSE TRANSPORT LLGGING STRAND SYNTHESIS	2.70 2.68 2.67 2.65 2.64 2.62	1.33E-04 1.62E-04 2.01E-04 2.67E-04
VIRAL MESSENGER RNA SYNTHESIS 2.53 4.34E-04 LINKED DUGGSACCHARIDE LLO AND TRANSFER TO A NASCENT 2.53 4.47E-04 PORTEIN 2.53 4.50E-04 4.47E-04 PERK REGULATED GENE EXPRESSION 2.53 4.50E-04 4.47E-04 PERK REGULATED GENE EXPRESSION 2.53 5.60E-04 5.60E-04 SIGNALING BY SCF KIT 2.50 5.64E-04 5.82E-04 SIGNALING BY SCF KIT 2.49 5.78E-04 5.82E-04 SIGNALING BY LIS 2.48 6.14E-04 5.82E-04 SIGNALING BY LIS 2.48 6.14E-04 5.82E-04 TOLL RECEPTOR CASCADES 2.47 6.4EE-04 5.82E-04 SIGNALING BY LIS 2.48 6.14E-04 5.82E-04 TOLL RECEPTOR CASCADES 2.47 6.4EE-04 5.62E-04 SIGNALING BY LIS 2.48 6.14E-04 5.62E-04 SIGNALING BY LES 2.46 6.74E-04 5.74E-04 SIGNALING BY ERBB2 2.46 6.79E-04 6.74E-04 SIGNALING BY ERBB2 2.46 6.79E-04 <	VIRAL MESSENDER RNA SYNTHESIS 2.55 4.34E-04 LINRED CLIGGSACCHARDE LLO AND TRANSFER TO A NASCENT 2.53 4.47E-04 PREX RECLATED GENE EXPRESSION 2.53 4.47E-04 ACTIVATION OF BHO ONLY POPTINS 2.60 5.46E-04 SIGNALING BY SCF KIT 2.50 5.44E-04 SIGNALING BY SCF KIT 2.50 5.46E-04 SIGNALING BY LIS 2.44 6.14E-04 SIGNALING BY LIS 2.44 6.46E-04 NULLECTOTE BRING GOMMIN LEUCINE RICH REPEAT 6.77E-04 CONTAINNE RECEPTOR NAR RIGHALING PATHWAYS 2.46 6.77E-04 SIGNALING BY ERBB2 2.44 6.77E-04 TRAYS DEPENDENT FROCHSINGLEASE 2.45 7.06E-04 TRAYS DEPENDENT FROCHSINGLICLESE 2.46 7.06E-04 TRAYS DEPENDENT FROCHT RECEPTOR NAR REGRESIONUCLEASE 2.45 7.06E-04 TATA'S DEPENDENT FROCHT REPARTION PATHWAY 2.45 7.06E-04	GI PHASE FORMATION OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA. POL IN TC NER	2.70 2.68 2.67 2.65 2.64 2.62 2.62 2.62	1.33E-04 1.62E-04 2.01E-04 2.67E-04 2.75E-04
LINKED OLIGOBACCHARIDE LLO AND TRANSFER TO A NASCENT 2.5 PERK REGULATED GENE EXPRESSION 2.53 4.47E 04 PERK REGULATED GENE EXPRESSION 2.50 SADE OF SADE SADE SADE SADE SADE SADE SADE SADE	LINEED CUICOSACCUARDE LLO AND TRANSFER TO A NASCENT 2.25 4.47E-04 PERK REGULATED GENE EXPRESSION 2.25 4.50E-04 ACTIVATION OF BINS ONLY PROTEINS 2.50 5.40E-04 SIGNALING BY SCF KIT 2.60 5.84E-04 DEST DEPENDENT FROCKSING OF REPLICATION DEPENDENT 2.49 5.78E-04 SIGNALING BY LS 2.44 6.4EE-04 DEP DEFENDENT FREE MINNS 2.44 6.4EE-04 DIAL DECEPTION CASCADES 2.47 6.84E-04 NICL ECOFFOR CASCADES 2.46 6.78E-04 SIGNALING BY LS 2.46 6.78E-04 SIGNALING BY SIGNALING CONN IN SIGNALING PATHWAYS 2.46 6.78E-04 SIGNALING BY LS 1.5 SECOHEDNUCLEASE 2.45 7.06E-04 TRAFS DEPENDENT IRF AC	GI PHASE FORMATION OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUGOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER VITAMIN BS PANTOTHENATE METABOLISM	2.70 2.68 2.67 2.65 2.64 2.62 2.62 2.62 2.61	1.33E-04 1.62E-04 2.01E-04 2.67E-04 2.75E-04 2.84E-04
PERK REGULATED GENE EXPRESSION 2.53 4.50E-04 ACTIVATION OF BH3 ONLY PROTEINS 2.50 5.40E-04 SIGNALING BY SCF KIT 2.50 5.64E-04 DESTABLIZATION OF MENA BY KSRP 2.49 5.78E-04 SIGNALING BY SCF KIT 2.40 5.82E-04 SIGNALING BY SCF KIT 2.40 5.82E-04 SIGNALING BY SCF KIT 2.40 5.82E-04 SIGNALING BY LIS 2.48 6.14E-04 NICL EPICE PROCESSING OF REPLICATION DEPENDENT 8.82E-04 SIGNALING BY LIS 2.48 6.14E-04 NICL RECEIPTOR CASCADES 2.47 6.64E-04 OKTIVINION RECEIPTOR N.L'R SIGNALING PATHWAYS 2.46 6.78E-04 SIGNALING BY ERB82 2.46 6.78E-04 SIGNALING BY ERB82 2.45 7.08E-04 MINA DECAY BY 3 TO S EXORIBONICLEASE 2.45 7.08E-04 THAF3 DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E-04	PERK REGULATED GENE EXPRESSION 2.53 4.56E-04 ACTIVATION OF BH3 ONLY PROTEINS 2.50 5.46E-04 SIGNALING BY SOF KIT 2.50 5.84E-04 DESTABLIZATION OF MINA BY KISRP 2.49 5.78E-04 SUP OPENCENT REPORCISING OF REPLICATION DEPENDENT 2.49 5.78E-04 SIGNALING BY LIS 2.44 6.18E-04 OLL HECEPTOR CASADES 2.44 6.48E-04 NUCL EXTRING COMAIN LEUCHE RICH REPERT 2.46 6.78E-04 SURALING BY LIS 2.46 6.78E-04 SURD ENDING COMAIN LEUCHE RICH REPERT 2.46 6.78E-04 MENA CECAY BY 3 TO S EXORIBONUCLEASE 2.45 7.06E-04 TRAFS DEPENDENT IRF ACTIVATION PATHWAY 2.46 7.10E-04 CYCLIN A BY LASSOLITED EVENTS DURING 2M TRANSITION 2.44 7.49E-04	GI PIASE GI PIASE GOMPLEX COMPLEX GLOBAL GENOMIC NER GG NER GLOBAL FRANSPORT LAGGING STRAND SYNTHESIS REPAR SYNTHESIS OR GAP FILLING BY DNA. POL IN TC NER VITAMIN BS PANTOTHENATE METABOLISM GI S SPECIFIC TRANSCRIPTION	2.70 2.68 2.67 2.65 2.64 2.62 2.62 2.62 2.61 2.56	1.33E-04 1.62E-04 2.01E-04 2.67E-04 2.75E-04 2.84E-04 3.70E-04
ACTIVATION OF BHS ONLY PROTEINS 2.50 5.40E04 SIGNALING BY SCF KIT 2.50 5.64E04 DESTABLIZATION OF MENA BY KSRP 2.40 5.78E04 SIGN DEPERDENT 2.40 5.82E04 INSTORE PRE MENAS 2.48 5.82E04 SIGNALING BY ILS 2.48 6.14E04 NUCL EFORT CASCADES 2.47 6.64E04 NUCL EFORT CASCADES 2.46 6.74E04 SIGNALING BY ILS 2.46 7.06E04 SIGNALING BY ILS 2.46 7.06E04 SIGNALING BY ERB2 2.46 7.70E04 MINA DECAY BY 3 TO S EXORIBONICLEASE 2.45 7.00E04 TIMAF AR ECAY BY 3 TO S EXORIBONICLEASE 2.45 7.10E04	ACTIVATION OF BINS ONLY PROTEINS 2.50 5.40E64 SIGNALING BY SOF KIT 2.50 5.40E64 DESTABLIZATION OF MINA BY KISRP 2.40 5.78E.04 SUP OPENDENT PROCESSING OF REPLICATION DEPENDENT 2.40 5.78E.04 SUD OPENDENT PROCESSING OF REPLICATION DEPENDENT 2.40 5.82E.04 ILL INSCRIPTION CLASSADES 2.44 6.44E.04 NUCL EXTORE RINGH COMMALING PATHWAYS 2.44 6.44E.04 NUCL EXTORE RING CLASSADES 6.79E.04 6.77E.04 MENA CECAY BY 3 TO S EXORIBONUCLEASE 2.45 7.06E.04 TRAFS DEPENDENT IRF ACTIVATION PATHWAY 2.46 7.10E.04 CYCLIN A BY LASSOCIATED EVENTS DURING 20 MARANSTION 2.44 7.49E.04	GI PIASE GI PIASE GOWTEX GLOBAL GENOMIC NER GG NER GLOBE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER VITAMIN BE PANTOTHENATE METABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER RNA SYNTHESIS LINKED DI GRAGOCHARDE LLO AND TRANSPER TO A MASCENT	2.70 2.68 2.67 2.65 2.64 2.62 2.62 2.61 2.56 2.53	1.33E-04 1.62E-04 2.01E-04 2.67E-04 2.75E-04 2.84E-04 3.70E-04 4.34E-04
SIGNALING BY SCF KIT 2.50 5.64E.04 DESTABLIZATION OF MINA BY KERP 2.49 5.78E.04 SUB DEPENDENT PROCESSING OF REPLICATION DEPENDENT 2.49 5.82E.04 INST DEPENDENT PROCESSING OF REPLICATION DEPENDENT 2.49 5.82E.04 INST DEPENDENT PROCESSING OF REPLICATION DEPENDENT 2.49 5.82E.04 INST DEPENDENT RACEONES 2.41 6.14E.04 INCL ENDED BINDING DOMINI, LEICINE HICH EREFAT 2.46 6.78E.04 SIGNALING BY TERB2 2.46 6.78E.04 SIGNALING BY ERB2 2.46 7.08E.04 SIGNALING BY ERB2 2.45 7.06E.04 MINA DECAY BY 3 TO S EXORIBONICLEASE 2.45 7.08E.04 THAF3 DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E.04	SIGNALING BY SCF KIT 2.50 5.64E04 DEBTABLIZATION OF MINA BY KISRP 2.40 5.78E04 SUB POEPINGENG FROOTSING OF REPLICATION DEPENDENT 2.40 5.78E04 SIGNALING BY LIS 2.46 6.14E04 SUBALING BY LIS 2.46 6.14E04 TOLL RECEPTOR CASCADES 2.47 6.84E04 SURALING BY LIS 2.46 6.78E04 SURALING BY LIS 2.46 6.78E04 SURALING BY ERBRQ 2.46 6.78E04 SURALING BY ERBRQ 2.46 7.06E04 SURALING BY ERBRQ 2.46 7.06E04 TRAYS DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E04 CYCLIN A BI ASSOCIATED EVENTS DURING 22 M TRANSITION 2.44 7.49E04	GI PHASE FORMATION OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER VITAMIN BS PANTOTHENATE NETABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER FNA SYNTHESIS LINKED OLIGOSACCHARIDE LLO AND TRANSFER TO A NASCENT PROTEIN	2.70 2.68 2.67 2.65 2.64 2.62 2.62 2.61 2.56 2.53 2.53	1.33E-04 1.62E-04 2.01E-04 2.67E-04 2.75E-04 2.84E-04 3.70E-04 4.34E-04 4.47E-04
DISTRIBUTION OF MRMA BY KSR0 2.49 5.78E.04 Sab Dependency PROCESSING OF REPLICATION DEPENDENT 2.49 5.82E.04 NEXTONE PRE MRMAS 2.48 6.14E.04 SIGNALING BY LS 2.48 6.14E.04 NOLL RECEIPTOR CASCODES 2.47 6.64E.04 OVATIONE BROKEN COMMUNICATIONE PROH BEREAT 2.46 6.74E.04 SIGNALING RECEIPTOR N.E.R SIGNALING PATHWAYS 2.46 6.74E.04 SIGNALING SY ERBEZ 2.45 7.06E.04 MINA DECAY BY 3 TO 5 EXORIBONUCLEASE 2.45 7.06E.04 THAR'S DEPENDENT INFLACTIVATION PATHWAY 2.46 7.10E.04	DESTABLIZATION OF MRWA BY KSRP 2.49 5.78E.04 SLEP DEPENDENT PROCESSING OF REPLICATION DEPENDENT 2.40 5.82E.04 SIGNALING BY LIS 2.40 5.82E.04 SIGNALING BY LIS 2.40 6.84E.04 NULL RECEPTOR CASCADES 2.47 6.84E.04 NULL RECEPTOR NAS CADES 2.46 6.74E.04 SIGNALING BY ERBING GOMAIN LEUCINE RICH REPEAT 2.46 6.74E.04 SIGNALING RECEPTOR NAS CADALING PATHWAYS 2.46 6.74E.04 RIMA DECXI VS 13 TO 5 EXORIBONUCLEASE 2.45 7.06E.04 TRAYS DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E.04 CYCLIN A B1 ASSOCIATED EVENTS DURING 22 M TRANSITION 2.44 7.49E.04	GI PHASE FORWATION OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER VITAUM RESPONTOTHENATE METABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER RNA SYNTHESIS LINKED CHGOSACCHARDE LLO AND TRANSFER TO A NASCENT PORTEIN PERK REGULATED GENE EXPRESSION	2.70 2.68 2.67 2.65 2.64 2.62 2.62 2.61 2.56 2.53 2.53 2.53	1.33E-04 1.62E-04 2.01E-04 2.67E-04 2.75E-04 2.84E-04 3.70E-04 4.34E-04 4.50E-04
SLBP DEPROBENT PROCESSING OF REPLICATION DEPENDENT 2.49 5.82E-04 ISTONE PRE WIRAS 2.48 5.82E-04 SIGNULING BY ILS 2.48 6.14E-04 TOLL RECEPTOR CASCADES 2.47 6.64E-04 NUCLEONDE BINCING DOMAIN LECHNER INCH REPEAT 2.46 6.74E-04 SIGNULING BY ERBS2 2.46 6.79E-04 MRWA DECAY BY 3 TO 5 EXORIBONUCLEASE 2.45 7.08E-04 TMAFS DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E-04	SLEP DEERNDENT PROCESSING OF REPLICATION DEPENDENT 2.40 5.32E.04 SIGNALING BY ILS 2.40 6.14E.04 SIGNALING BY ILS 2.40 6.14E.04 DILL RECEPTION CASCADES 2.47 6.84E.04 NUCLEDTOE BRONG DOWN IL LEUCHE RICH REPEAT 2.46 6.78E.04 SIGNALING BY ILS 2.40 6.78E.04 WINN RECEPTION N.R SIGNALING PATHWAYS 2.46 6.78E.04 RIWA DECX VS 10 TO EXCIVATION NATHWAY 2.45 7.06E.04 TRAYS DEPENDENT IRF ACTIVATION PATHWAY 2.46 7.10E.04 CYCLIN A BI ASSOCIATED EVENTS DURING G2 M TRANSITION 2.44 7.49E.04	GI PHASE FORWITCH OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER VITAMIN BS PANTOTHENATE METABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER RNA SYNTHESIS LINKED OLIGOSACCHARDE LLO AND TRANSPER TO A NASCENT PROTEIN PERK REGULATED GENE EXPRESSION ACTIVATION OF BHS ONLY PROTEINS	2.70 2.68 2.67 2.65 2.64 2.62 2.62 2.62 2.61 2.56 2.53 2.53 2.53 2.53	1.33E-04 1.62E-04 2.01E-04 2.67E-04 2.87E-04 3.70E-04 4.34E-04 4.34E-04 4.47E-04 4.50E-04 5.40E-04
SIGNALING BY ILS 2.48 6.14E-04 TOLL RECEPTOR CASCADES 2.47 6.84E-04 NUCL FONDE BINDING DOWNI LEUCINE RICH REPEAT 2.46 6.74E-04 SIGNALING BY ERBS2 2.48 6.79E-04 SIGNALING BY ERBS2 2.48 6.79E-04 MINA DECAY BY 3 TO 5 EXORIBONUCLEASE 2.45 7.06E-04 TMAFS DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E-04	SIGNALING BY ILS 2.46 6.14E04 TOLL RECEPTOR CASCADES 2.47 6.64E04 NUCLE DIDE BROING DOMINI LEUCINE RICH REPEAT 2.46 6.74E04 SIGNALING BY ERBB2 2.46 6.74E04 SIGNALING BY ERBB2 2.46 6.79E04 MRNA DECAY BY 3 TO 5 EXORIBONUCLEASE 2.45 7.08E04 TRAFS DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E04 CYCLIN A B1 ASSOCIATED EVENTS DURING 22 M TRANSITION 2.44 7.49E04	GI PHASE FORWATION OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER VITAMIN BS PANTOTHENATE NETABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER RNA SYNTHESIS LINKED OLIGOSACCHARIDE LLO AND TRANSPER TO A NASCENT PROTEIN PERK REGULATED GENE EXPRESSION ACTIVATION OF BHG ONLY PROTEINS SIGNALING BY SCF KIT DESTABILIZATION OF MENA BY KSRP	2.70 2.68 2.67 2.65 2.64 2.62 2.62 2.62 2.63 2.53 2.53 2.53 2.53 2.50 2.50	1.33E04 1.82E04 2.01E04 2.87E04 2.87E04 2.84E04 3.70E04 4.34E04 4.34E04 4.47E04 5.40E04 5.64E04
NUCLEOTIDE BINDING DOMAIN LEUCINE RICH REPEAT 246 CONTINING RECEPTOR N.R. SIGNALING PATHWAYS 2.46 6.74E.04 SIGNALING BY ERBB2 2.46 6.78E.04 MINA DECAY BY 3 TO 5 EXORIBONUCLEASE 2.45 7.08E.04 THAF3 DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E.04	NUCLE OTDE BIKINK DOMAIN LEUCINE RICH REPAT 6.74E-04 SIGNALING BY ERBB2 2.46 6.78E-04 SIGNALING BY ERBB2 2.46 6.78E-04 MRNA DECAY BY 3 TO 5 EXORIBONUCLEASE 2.45 7.00E-04 TRAF3 DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E-04 CYCLIN A B1 ASSOCIATED EVENTS DURING 22 M TRANSITION 2.44 7.49E-04	GI PHASE GI PHASE GOMPLEX COMPLEX GOMPLEX GLOBAL GENOMIC NER GG NER GLUGSE TRANSPORT LAGGING STRAND SYNTHESIS REPAR SYNTHESIS FOR GAP FILLING BY DNA. POL IN TC NER VITAMIN BS PANTOTHENATE METABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER INA. SYNTHESIS LINKED OLIGOSCHARDE LLO AND TRANSPER TO A NASCENT PROTEIN PROTEINS FIGURATED GENE EXPRESSION ACTIVATION OF BHG ON Y PROTEINS SIGNALING BY SCF KIT DESTABILIZATION OF MENNA BY SRP SIGNALING BY SCF KIT	2.70 2.68 2.67 2.65 2.64 2.62 2.62 2.62 2.63 2.53 2.53 2.53 2.53 2.50 2.50 2.49	1.33E04 1.62E04 2.01E04 2.07E04 2.75E04 2.84E04 3.70E04 4.34E04 4.37E04 4.37E04 4.50E04 5.60E04 5.64E04 5.76E04
CONTAINING RECEPTOR NLR SIGNALING PATHWAYS 2.46 6.74E04 SIGNALING BY ERBB2 2.46 6.79E04 MRNA DECAY BY 3 TO 5 EXORIBONUCLEASE 2.45 7.06E04 TRAF3 DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E04	CONTAINING RECEPTOR NLR SIGNALING PATHWAYS 2.46 6.74E.04 SIGNALING BY ERBB2 2.46 6.79E.04 MRNA DECAY BY 3 TO \$ EXORIBONUCLEASE 2.45 7.06E.04 TRAF3 DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E.04 CYCLIN A 81 ASSOCIATED EVENTS DURING G2 M TRANSITION 2.44 7.49E.04	GL PHASE GL PHASE GRAFACHON OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER VITAMIN BS PANTOTHENATE METABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER RNA SYNTHESIS LINKED DUIGSOCHARDE LLO AND TRANSPER TO A NASCENT PROTEIN PERN REGULATED GENE EXPRESSION ACTIVATION OF EHIS ONLY PROTEINS SIGNALING BY SCF KIT DESTABLIZATION OF MEM BY RSDP SIGNALING BY SCF KIT DESTABLIZATION OF MEM BY RSDP SIGNALING BY SCF KIT	2.70 2.88 2.67 2.65 2.64 2.62 2.62 2.62 2.53 2.53 2.53 2.53 2.53 2.53 2.53 2.5	1.33E04 1.62E04 2.01E04 2.07E04 2.75E04 2.84E04 3.70E04 4.370E04 4.370E04 4.370E04 5.84E04 5.84E04 5.84E04 5.87E04
NRNA DECAY BY 3 TO 5 EXORIBONUCLEASE 2.45 7.08E-04 TRAFS DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E-04	MRNA DECAY BY 3 TO 5 EXORIBONUCLEASE 2.45 7.06E04 TRAFS DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E04 CYCLIN A B1 ASSOCIATED EVENTS DURING 62 M TRANSITION 2.44 7.49E04	GI PHASE GI PHASE FORWITION OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER VITAMIN BS PANTOTHENATE METABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER RNA SYNTHESIS LINKED OLIGOSACCHARDE LLO AND TRANSPER TO A NASCENT PROTEIN PERK REGULATED GENE EXPRESSION ACTIVATION OF BH3 ONLY PROTEINS SIGNALING BY SCF KIT DESTABILIZATION OF RM30 BY KSRP SIGNALING BY ILS SIGNALING ST ILS SIGNALING ST ILS SIGNALING ST ILS	2.70 2.88 2.67 2.65 2.64 2.62 2.62 2.53 2.53 2.53 2.53 2.53 2.53 2.50 2.50 2.50 2.49 2.49 2.48	1.33E04 1.62E04 2.01E04 2.07E04 2.75E04 2.84E04 3.70E04 4.34E04 4.34E04 4.34E04 4.34E04 5.40E04 5.64E04 5.78E04 5.82E04 6.14E04
TRAF3 DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E-04	TRAF3 DEPENDENT IRF ACTIVATION PATHWAY 2.45 7.10E-04 CYCLIN A B1 ASSOCIATED EVENTS DURING G2 M TRANSITION 2.44 7.49E-04	GI PHASE GI PHASE GI PHASE GRANNER ON OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER UTAIN BS PANTOTHENATE NETABOLISM GI S SPECIFIC TRANSCRIPTION YIRAL MESSENGER FNA SYNTHESIS LINKED OLIGOSACCHARDE LLO AND TRANSPER TO A NASCENT PROTEINS SIGNALING BY SCF KIT DESTABILIZATION OF MRVA BY KSRP SLIB DEPRORT PROCESSING OF REPLICATION DEPENDENT HISTORE PRE MRVAS SIGNALING BY ILS TOLL RECEPTOR CASCADES NUCLEDTOE INFORM DOMINI LUCINE RICH REPEAT	2.70 2.88 2.67 2.65 2.62 2.62 2.62 2.53 2.53 2.53 2.53 2.53 2.53 2.55 2.53 2.54 2.49 2.49 2.48 2.49	1.33E-04 1.62E-04 2.01E-04 2.01E-04 2.75E-04 2.75E-04 3.70E-04 4.34E-04 4.34E-04 4.34E-04 4.34E-04 5.40E-04 5.76E-
	CYCLIN A B1 ASSOCIATED EVENTS DURING G2 M TRANSITION 2.44 7.49E-04	GI PHASE FORWATION OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER WITHAUM SE SPATTOHENATE NETABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER RNA SYNTHESIS LINKED DUIGDSACCHARDE LLO AND TRANSFER TO A NASCENT POTEIN PERK REGULATED GENE EXPRESSION ACTIVATION OF BHG ONLY PROTEINS SIGNALING SY SCF KIT DESTABILIZATION OF MRVA BY KSRP SLIB DEPRINENT PROCESSING OF REPLICATION DEPENDENT HISTORE PIRE NERVAS SIGNALING SY ILS	2.70 2.68 2.67 2.65 2.64 2.62 2.64 2.64 2.64 2.53 2.53 2.53 2.53 2.53 2.50 2.50 2.49 2.49 2.48 2.47 2.46	1.33E04 1.62E04 2.01E04 2.75E04 2.87E04 2.84E04 4.34E04 4.34E04 4.34E04 4.47E04 5.64E04 5.64E04 6.74E04 6.74E04
		GI PHASE FORWATION OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GG NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER (I S SPECIFIC TRANSCRIPTION) VIRAL MESSENGER RNA SYNTHESIS LINKED OLIGOSACCHARBELLO AND TRANSFER TO A NASCENT PROTEIN PERK REGULATED GENE EXPRESSION ACTIVATION OF BHS ON Y PROTEINS SIGNALING BY SCR ILS SIGNALING BY SCR ILS SIGNALING BY LIS TOLL RECEPTOR CASCADES NUCLEOTICE BIRDING DOMAIN LEUCINE RICH REPAT CONTRIME NERFORN SIGNALING PATHWAYS SIGNALING BY LIS	2.70 2.68 2.67 2.65 2.64 2.62 2.64 2.64 2.65 2.53 2.53 2.53 2.53 2.53 2.50 2.50 2.49 2.49 2.49 2.48 2.47 2.46	1.33E-04 1.62E-04 2.01E-04 2.01E-04 2.07E-04 2.07E-04 2.07E-04 3.70E-04 4.34E-04 4.34E-04 4.34E-04 4.37E-04 5.64E-04 5.64E-04 5.64E-04 6.74E-04 6.74E-04 6.74E-04 6.75E-04
		GI PHASE GI PHASE GOMPLEX GOMPLEX GLOBAL GENOMIC NER GG NER GLUGSE TRANSPORT LAGGING STRAND SYNTHESIS REPAR SYNTHESIS FOR GAP FILLING BY DNA. POL IN TC NER VITAMIN BS PANTOTHENATE METABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER INN. SYNTHESIS LINKED OLIGSOCHANDE LLO AND TRANSPER TO A NASCENT PROTEIN PROTEINS BIONALING BY SCF KIT DESTABLIZATION OF BHG ON Y PROTEINS SIGNALING BY LSCF KIT DESTABLIZATION OF BHG ON Y PROTEINS SIGNALING BY LSCF KIT DESTABLIZATION OF MENNA BY KSRP SIGNALING BY LSC SIGNALING BY EBB2 MINA DECAY BY 3 TO S EXORIBONJICLEASE	2.70 2.88 2.67 2.65 2.64 2.62 2.62 2.53 2.53 2.53 2.53 2.53 2.53 2.53 2.5	1.33E-04 1.62E-04 2.01E-04 2.07E-04 2.75E-04 2.75E-04 2.75E-04 3.77EE-04 4.34E-04 4.47E-04 4.47E-04 4.47E-04 5.64E-04 5.64E-04 5.64E-04 6.64E-04 6.64E-04 6.74E-04 6.74E-04 6.77E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.76E-04 7.77E
POL SWITCHING 2.43 8.51E-04	POL SWITCHING 2.43 8.51E-04	GI PHASE GI PHASE GI PHASE GI PHASE GRANDA OF TRANSCRIPTION COUPLED NER TC NER REPAIR COMPLEX GLOBAL GENOMIC NER GO NER GLUCOSE TRANSPORT LAGGING STRAND SYNTHESIS REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER VITAMIN 85 PANTOTHENATE NETABOLISM GI S SPECIFIC TRANSCRIPTION VIRAL MESSENGER RNA SYNTHESIS INKED DI GROGACCHARDE LLO AND TRANSPER TO A NASCENT PROTEIN EXTRA DE SOR APP FILLING BY KARP SLED DEPROSENT ON A VARCH SING OF REPLICATION DEPENDENT SLED DEPROSENT PROCESSING OF REPLICATION DEPENDENT SLED DEPROSENT ON ANY REVISE SIGNALING BY SCF HIT DESTABILIZATION OF MRVA BY KSRP SIGNALING BY SCF HIT TOLL RECEPTOR CASCADES NUCLEOTIOE BINDAD DOWNING LEUNIRE RICH REPEAT CONTINING RECEPTOR A R SIGNALING PATHWAYS SIGNALING BY ERB2 MINND ECXY BY 3 TO 5 EXORIBIONUCLEASE TRAPS DEPENDENT RACTIVATION PATHWAY CYCLIN A BI ASSOCIATED EVENTS DURING G2 M TRANSITION	2.70 2.88 2.67 2.65 2.64 2.62 2.62 2.53 2.53 2.53 2.53 2.53 2.53 2.53 2.5	1.33E04 1.62E04 2.07E04 2.77E04 2.87E04 3.70E04 4.34E04 4.34E04 4.34E04 4.34E04 4.34E04 4.34E04 4.34E04 4.34E04 5.54E04 5.54E04 5.78E04 6.14E04 6.44E04 6.74E04 6.74E04 7.06E04 7.10E04

FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND		r f
FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND PLATELET PRODUCTION	2.42	9.34E-04
TRIGLYCERIDE BIOSYNTHESIS	2.40	0.0010
POST TRANSLATIONAL PROTEIN MODIFICATION	2.37	0.0014
METABOLISM OF CARBOHYDRATES	2.36	0.0014
DEADENVLATION DEPENDENT MRNA DECAY	2.34	0.0016
HEMOSTASIS	2.30	0.0021
DARPP 32 EVENTS	2.30	0.0021
MITOCHONDRIAL TRNA AMINOACYLATION	2.30	0.0021
FATTY ACID TRIACYLGLYCEROL AND KETONE BODY METABOLISM	2.29	0.0022
DOUBLE STRAND BREAK REPAIR RECYCLING PATHWAY OF L1	2.29	0.0022
CITRIC ACID CYCLE TCA CYCLE	2.28	0.0022
PURINE RIBONUCLEOSIDE MONOPHOSPHATE BIOSYNTHESIS	2.28	0.0024
MEIOTIC SYNAPSIS	2.26	0.0027
GAB1 SIGNALOSOME	2.24	0.0030
INNATE IMMUNE SYSTEM	2.25	0.0030
NRAGE SIGNALS DEATH THROUGH JNK	2.23	0.0034
ACTIVATION OF GENES BY ATF4 DOWNSTREAM SIGNAL TRANSDUCTION	2.22	0.0036
REMOVAL OF THE FLAP INTERMEDIATE FROM THE C STRAND	2.17	0.0048
DESTABILIZATION OF MRNA BY TRISTETRAPROLIN TTP	2.17	0.0050
TRAF6 MEDIATED IRF7 ACTIVATION IN TLR7 8 OR 9 SIGNALING	2.16	0.0050
RNA POL I PROMOTER OPENING	2.14	0.0056
P75 NTR RECEPTOR MEDIATED SIGNALLING	2.14	0.0057
	2.13	0.0060
PROCESSIVE SYNTHESIS ON THE LAGGING STRAND SHC1 EVENTS IN EGFR SIGNALING	2.12	0.0062
CD28 CO STIMULATION	2.12	0.0065
NOD1 2 SIGNALING PATHWAY	2.10	0.0072
TRIF MEDIATED TLR3 SIGNALING	2.10	0.0073
DESTABILIZATION OF MRNA BY BRF1	2.10	0.0074
FANCONI ANEMIA PATHWAY	2.09	0.0077
TRANS GOLGI NETWORK VESICLE BUDDING OPIOID SIGNALLING	2.04	0.0101
COSTIMULATION BY THE CD28 FAMILY	2.04	0.0108
RIG I MDA5 MEDIATED INDUCTION OF IFN ALPHA BETA PATHWAYS	2.02	0.0115
NFKB ACTIVATION THROUGH FADD RIP1 PATHWAY MEDIATED BY CASPASE 8 AND10	2.00	0.0127
IL 2 SIGNALING	1.99	0.0139
ACTIVATED TLR4 SIGNALLING	1.98	0.0143
ACTIVATION OF CHAPERONES BY ATF6 ALPHA	1.98	0.0143
ACTIVATION OF CHAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING	1.98	0.0143
ACTIVATION OF CHAPERONES BY ATF8 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE	1.98 1.97 1.97	0.0143 0.0147 0.0150
ACTIVATION OF CHAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE METABOLISM OF NUCLEOTIDES	1.98 1.97 1.97 1.96	0.0143 0.0147 0.0150 0.0160
ACTUATION OF CHAPERONES BY ATF0 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM CHEMOKINE RECEPTORS BIND CHEMOKINES CDC0 ASSOCIATION WITH THE ORC ORIGIN COMPLEX	1.98 1.97 1.97 1.95 1.95 1.95	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0166
ACTUATION OF CHAPERONES BY ATF0 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OFEMOKINE RECEPTORS BIND CHEMOKINES COCR ASSOCIATION WITH THE ORC ORGIN COMPLEX IL RECEPTOR SING SIGNALING NET MEDIATES DOWN MODULATION OF CELL SURFACE	1.98 1.97 1.97 1.96 1.95 1.95 1.95 1.94	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0162 0.0166
ACTIVATION OF CHAPERONES BY ATF0 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OFEMOKINE RECEPTORS BIND CHEMOKINES COEMOKINE RECEPTORS BIND CHEMOKINES LI RECEPTOR SIGN WITH THE ORC ORGIN COMPLEX LI RECEPTOR SIGN CHEMOKINES	1.98 1.97 1.97 1.95 1.95 1.95	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0166
ACTIVATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FORT IN DIGEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF CHECKIER CECEPTORS BIND CHEMOKINES COC6 ASSOCIATION WITH THE ORC ORGIN COMPLEX & INCERED ASSOCIATION WITH THE ORC ORGIN COMPLEX & INCERED ASSOCIATION WITH THE ORC ORGIN COMPLEX & INCERED ASSOCIATION WITH THE ORC ORGIN COMPLEX RECEPTORS BY RECRUITING THEM TO CLATHERN ADAPTERS	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.94	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0162 0.0172 0.0175
ACTIVATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FORT IN DIGEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF CHECKIER CECEPTORS BIND CHEMOKINES COC6 ASSOCIATION WITH THE ORC ORGIN COMPLEX & INCERED ASSOCIATION WITH THE ORC ORGIN COMPLEX & INCERED ASSOCIATION WITH THE ORC ORGIN COMPLEX & INCERED ASSOCIATION WITH THE ORC ORGIN COMPLEX RECEPTORS BY RECRUITING THEM TO CLATHERN ADAPTERS	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.95	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0162 0.0172 0.0175
ACTUATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FORT IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES CODE ASSOCIATION WITH THE ORC ORGIN COMPLEX LINEGENTS OSINI ADDIA TO FOLL SUBFACE RECEPTORS BY RECRUITING THEM TO CLATHERN ADAPTERS LYSGOSOWE VESICLE BIOGENESIS SIGNALING TO PRAS SIGNALING TO PRAS	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.94 1.93 1.93 1.93	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0166 0.0172 0.0175 0.0184 0.0194
ACTUATION OF CHAPERONES BY ATF0 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OKEMOKINE RECEPTORS BIND CHEMOKINES CDC8 ASSOCIATION WITH THE ONC CORGIN COMPLEX IL INCEPTORS IS COMMUNICATION OF CELL SUPFACE RECEPTORS BY REGRATING THEM TO CLATHERN ADAPTERS LYSGORUE VESICLE BIOGENESIS SIGNALLING TO RAS SIGNALLING BY PGPR RESOLUTION OF AST STAY THE MULTIPLE NUCLEOTIDE PATCH REPLACEMENT PATHWAY	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.94 1.93 1.93 1.93 1.92 1.91 1.90	0.0143 0.0147 0.0150 0.0162 0.0162 0.0162 0.0175 0.0164 0.0175 0.0164 0.0175 0.0164 0.0175 0.0164 0.0201 0.0201
ACTUATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FORT IN DIGEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES CODE ASSOCIATION WITH THE ORC ORGIN COMPLEX LINEGENTS SOM HODIA ATOM OF CELL SUBFACE RECEPTORS BY RECRUITING THEM TO CLATHERN ADAPTERS LYSGSOWE VESICLE BIOCENESIS SIGNALING TO PAS SIGNALING TO PAS SIGNALING BY GPCR RESOLUTION OF AP SITES VIX. THE MULTIPLE NUCLEOTIDE PRICE NUCLEOTION	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.92 1.91 1.90	0.0143 0.0147 0.0150 0.0162 0.0162 0.0162 0.0162 0.0175 0.0184 0.0274 0.0267 0.0272
ACTUATION OF CHAPERONES BY ATF0 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OKEMOKINE RECEPTORS BIND CHEMOKINES CDC8 ASSOCIATION WITH THE ONC CORGIN COMPLEX IL INCEPTORS IS COMMUNDI NER MEDIATIS GOWIN MODULATION OF CELL SURFACE RECEPTORS BY REGRALING SIGNALLING TO RAS SIGNALLING BY OPCR RESOLUTION OF AS SIGNALLING SY PERF.	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.94 1.93 1.93 1.93 1.92 1.91 1.90	0.0143 0.0147 0.0150 0.0162 0.0162 0.0162 0.0175 0.0164 0.0175 0.0164 0.0175 0.0164 0.0175 0.0164 0.0201 0.0201
ACTUATION OF GRAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FOR IN DIGEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OREMOKINE RECEPTORS BIND OFEMOKINES COED ASSOCIATION WITH THE ORE ORGINI COMPLEX LI RECEPTORS SING SIGNALING NET MEDIATIS DOWN MODULATION OF CELL SUPFACE RECEPTORS SING SIGNALING SIGNALING TO PAS SIGNALING TO PAS SIGNALING TO PROP RESOLUTION OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PROVICE PLOCED TO A FRAGMENTATION PP3 ACTIVATES AKT SIGNALING	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.93 1.92 1.91 1.90 1.90	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0172 0.0175 0.0175 0.0176 0.0175 0.0184 0.0204 0.0224 0.0221
ACTUATION OF GRAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FOR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF ONCLEOTIDES OF METABOLISM OF ONCLEOTIDES CODE ASSOCIATION WITH THE ORC ORGIN COMPLEX LI RECEPTORS BIND COLUMNOTO FOELL SUBFACE METABOLISM OF NUCLEOTIDE SIGNALING METABOLISM OF ORCH DISEASE SIGNALING TO PAS SIGNALING TO PAS	1.98 1.97 1.97 1.97 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.93 1.90 1.90 1.90 1.89	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0162 0.0175 0.0175 0.0175 0.0175 0.0174 0.0204 0.0204 0.0201 0.0212 0.0213
ACTIVATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE HETABOLISM OF NUCLEOTIDES PI METABOLISM OF MONTH AND ADDRESSION OF MONTH AND ADDRESSION OF MONTH AND ADDRESSION IN PROFENSION WITH THE ORC ORGIN COMPLEX IL RECEPTORS BY ACTEMATING OF CELL SURFACE RECOFTORS BY EACHTMAN THE MULTIPLE NUCLEOTIDE SIGNALLING TO PAS SIGNALLING TO PAS SIGNALLING TO PAS SIGNALLING SIGNALLING TO PAS SIGNALLING SIGNALLING TO PAS SIGNALLING SIGNALLING TO PAS SIGNALLING SIGNALLING TO PAS SIGNALING SIGNALLING TO PAS SIGNALING SIGNALLING TO PAS SIGNALING SIGNAL SIGNALLING SIGNAL COMPLEX ANT SIGNALING GOLGI ASSOCIATED VESICLE BIOGENESIS SIGNALING TO PAR SIGNALING SIGNAL SIGNAL SIGNALING SIGNAL SIGNAL SIGNALING SIGNAL	1.98 1.97 1.97 1.97 1.96 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.93 1.90 1.90 1.90 1.89 1.89	0.0143 0.0147 0.0150 0.0162 0.0162 0.0162 0.0162 0.0175 0.0175 0.0175 0.0174 0.0174 0.0174 0.0204 0.0204 0.0201 0.0221 0.0213 0.0213
ACTUVATION OF GRAPERQNES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FORE IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES CODE ASSOCIATION WITH THE ORC ORGIN COMPLEX LENEERFORTS GOVINGUA ATOM OF CELL SUBPACE NET REDATES GOVINGUA ATOM OF CELL SUBPACE RECEPTORS BY RECRUITING THEM TO CLATHEIN ADAPTERS LYSGEOME VESICLE BIOCENESIS SIGNALING BY GORE NESOLITION OF AP SITES VIX. THE MULTIPLE NUCLEOTIDE PREDATES GOVINGUA ATOM APOPTOSIS INDUCED DNA FRAGMENTATION PRP ACTIVATES AKT SIGNALING COLGI ASSOCIATED VESICLE BIOCENESIS SIGNALING OF GRAPTING THEM TO CLATHEIN ADAPTERS LYSGEOMENT PATHAWY APOPTOSIS INDUCED DNA FRAGMENTATION PRP ACTIVATES AKT SIGNALING COLGI ASSOCIATED VESICLE BIOCENESIS SIGNALING OF GRAPTING THEM TO ADAPTERS LYSGEOMENT AT HAWY APOPTOSIS INDUCED DNA FRAGMENTATION PR ACTIVATES AKT SIGNALING COLGI ASSOCIATED VESICLE BIOCENESIS SIGNALING OF GRAPTING THEM ADAPTOR LS JANO GUC SF SIGNALING TRUNSPORT OF INORGANIC CATIONS AND ANNO ACIDS COLGOPERT OF INORGANIC CATIONS AND ANNO ACIDS SIGNALING DISCOMENTIONS AND ANNO ACIDS SIGNALING DISCOMENTION AND ANNO ACIDS SIGNALING DISCOMENTIONS AND AND AND AC	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.93 1.93 1.90 1.90 1.90 1.89 1.89 1.89	0.0143 0.0147 0.0160 0.0162 0.0162 0.0162 0.0162 0.0175 0.0164 0.0275 0.0184 0.0207 0.0207 0.0207 0.0201 0.0201 0.0213 0.0213 0.0213
ACTUATION OF GRAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FOR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OPEMOKINE RECEPTORS BIND OFEMOKINES COSC ASSOCIATION WITH THE ORC ORDIN COMPLEX LI RECEPTORS SHI SIGNALING NET MEDIATES DOWN MODULATION OF CELL SUPFACE RECEPTORS SHI CAUTION OF CELL SUPFACE RECOVER SHILLING SUPPACE SIGNALING TO RAS SIGNALING TO RAS SIGNALING TO PROR RESOLUTION OF AP SITES VIX THE MILITIPLE NUCLEOTIDE PROVINCE ANT SIGNALING COLGI ASSICIATED TRIMALING COLGI ASSICIATED TRIMALING COLGI ASSICIATED TRIMALING COLGI ASSICIATED TRIMALING COLGI CONTROLANCE CATIONS AND AMINO ACIDS SIC MEDIATED SIGNALING COLGI CONTROLANCE CATIONS AND AMINO ACIDS SIC MEDIATED SIGNALING COLGI DEGATED SIGNALING COLGI DEGATED SIGNALING COLGI DEGATED SIGNALING COLGI DEGATED SIGNALING COLGI CAUTION OF APPER AND AND ACIDS SIC MEDIATED SIGNALING COLGI DEGATED SIGNALING COLGI DEGATED SIGNALING COLGI DEGATED SIGNALING COLGI DEGATED SIGNALING COLGI DEGATED SIGNALING CELL DEATH SIGNALLING VIA NRACE NRIF AND NADE	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.93 1.93 1.93 1.93	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0175 0.0166 0.0175 0.0166 0.0275 0.0184 0.0226 0.02213 0.0213 0.0213 0.0213 0.0221 0.0221 0.0225
ACTUATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DIGEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES DIEMACKINE RECEPTORS BIND CHEMOKINES COEMAKINE RECEPTORS OF COEMAKINE S COEMAKINE RECEPTORS OF MEDIATION OF CELL SURFACE RECEPTORS OF COEMAKINE OF CALIFORM ADAPTERS LYSOBOME VESICLE BIOGENESIS SIGNALING TO PARS SOS MEDIATED SIGNALLING SOCIAL RED VESICLE BIOGENESIS SIGNALING VORC RESOLUTION OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PATO/I REPLACEMENT PATHWAY APOPTOSIS INDUCED DNA FRAGMENTATION PIP3 ACTIVATES AKT SIGNALING GOLG ASSOCIATED VESICLE BIOGENESIS SLC MEDIATED TRANSMEMBRANE TWANSPORT LI 5 3 NO GUES DIANA INC ATTONS AND AMON ACDES COLORDEPTIONES SIC MEDIATED SIGNALING VIA NARGE INIF AND NADE DOWNSTREAM SIGNALING OF ACTIVATED PGR	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.93 1.99 1.99 1.89 1.89 1.89 1.89 1.89 1.89	0.0143 0.0147 0.0150 0.0162 0.0162 0.0172 0.0175 0.0175 0.0174 0.0277 0.0226 0.0213 0.0213 0.0213 0.0213 0.0213 0.0213 0.0223 0.0223
ACTUATION OF GRAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FOR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES CODE ASSOCIATION WITH THE ORC ORGIN COMPLEX LI RECEPTIONS BIND CHEMOKINES CODE ASSOCIATION WITH THE ORC ORGIN COMPLEX LI RECEPTIONS BY RECRUITING THEM TO CLATHERN ADAPTERS VISIONAL UNDER THE AND OF CELL SUBFACE REFERENTES SOMEWORK REFERENTES SOMEWORK SIGNALLING TO PAS SIGNALING TO PAS SIGNALLING TO PAS SIGNALING	1.98 1.97 1.97 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.93 1.93 1.93 1.93	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0175 0.0166 0.0175 0.0166 0.0275 0.0184 0.0226 0.02213 0.0213 0.0213 0.0213 0.0221 0.0221 0.0225
ACTUATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FOR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES DIEMOKINE RECEPTORS BIRD OFENOKINES COSC ASSOCIATION WITH THE ORC ORIGIN COMPLEX LI RECEPTORS SHI'S GIGNALING DIEMOKINE RECEPTORS BIRD OFENOKINES COSC ASSOCIATED SIGNALING DISOLATES DOWN MODULATION OF CELL SUPFACE REFORMS BY RECENTING THEM TO CLAINING ADAPTERS LYSOGOME VESICLE BIOGENESIS SIGNALING TO PAS SIGNALING TO PAS SIGNALING TO PAS MEDIATED SIGNALING COLGI ASSOCIATED VESICE BIOGENESIS SIC MEDIATED TRANSMEMBRANE TRANSPORT LL 3 FADO GMG STINALING COLGI ASSOCIATED VESICE BIOGENESIS SIC MEDIATED TRANSMEMBRANE TRANSPORT LL 3 FADO GMG STINALING COLGI CONTRELANCE CATIONS AND AMINO ACIDE COLOPOETIDES SIC MEDIATED SIGNALING CELL DEATH SIGNALLING VIA INVEGE INFI AND NADE DOWNSTREAM SIGNALING OF ACTUVATED FOR SYNTHESIS OF A THANSPORT OF INDRIGANCE CATIONE AND AMP FINASES UPON THANSPORT OF INDRIGANCE OF OF CHEM AND MAP FINASES UPON THANSPORT OF INDRIGANCE OF CONTINUES AND AMINO ACIDE CONTRESS OF A THANSPORT OF INDRIGANCE OF OF THE AND MAP FINASES UPON THAT'S 0 OF A OTATION	1.98 1.97 1.97 1.96 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.90 1.99 1.99 1.99 1.89 1.89 1.89 1.89 1.89	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0162 0.0172 0.0172 0.0174 0.0174 0.0204 0.0204 0.0204 0.0217 0.0212 0.0213 0.0213 0.02213 0.02213 0.0227 0.0227 0.0227 0.0227 0.0227
ACTIVATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OPEMOKINE RECEPTORS BIND CHEMOKINES COEMOKINE RECEPTORS BIND CHEMOKINES INFORMATIS DOWN MODULATION OF CELL SURFACE RECEPTORS BY EXECUTING THEMOKINES SIGNALING TO RAS SIGNALING TO RAS SIGNALING TO RAS SIGNALING TO RAS STEES VITHE MALTIPLE INCLEOTIDE PATOR REPLACEMENT PATHAWING COLG I ASSOCIATED VESICLE BIOGENESIS SIGNALING COEMOKINE CHANSPORT IL 3 5 AND GM CSF SIGNALING COLG I ASSOCIATED VESICLE BIOGENESIS SIGN MEDIATED TRANSFEMBRARE TRANSPORT IL 3 5 AND GM CSF SIGNALING COLG LEATIS IGNALLING COLG LEATIS IGNALLING COLG LEATIS IGNALLING COLG LEATIS IGNALLING COLG LEATIS IGNALLING COLG LEATIS IGNALLING COLG DISTINGTING OF ACTIVATED PARTING MINING OF AND COLOR OF NOR AND AND AND ACDS CLICEPTIES SYNTHESIS OF PA THE NER'S IMPLAMASDOME THE NER'S IMPLAMASDOME THE NER'S INFORMATION	1.88 1.97 1.97 1.95 1.95 1.95 1.95 1.94 1.93 1.93 1.93 1.93 1.93 1.93 1.93 1.93	0.0143 0.0147 0.0150 0.0162 0.0162 0.0162 0.0162 0.0175 0.0175 0.0175 0.0174 0.0204 0.0204 0.0204 0.0207 0.0213 0.0213 0.0213 0.0213 0.0221 0.0221 0.0221 0.0223 0.0226
ACTUATION OF GRAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FOR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES OF METABOLISM OF NUCLEOTIDES CODE ASSOCIATION WITH THE ORC ORGIN COMPLEX LI RECEPTOR SHO SIGNALING MET MEDIATES DOWN MODULATION OF CELL SUBFACE METABOLISM OF MEDIATES DOWN MODULATION OF CELL SUBFACE METABOLISM SIGNALING TO RAS SIGNALING TO RAS SIGNALING TO PROP RESOLUTION OF APE SITES VIN THE MILITPLE NUCLEOTIDE PRESIDENTIAL OF OPEN RESOLUTION OF APE SITES VIN THE MILITPLE NUCLEOTIDE PROVINCE AND SITES VIN THE MILITPLE NUCLEOTIDE PROVINCE OF APEN RESOLUTION OF APE SITES VIN THE MILITPLE NUCLEOTIDE PROVINCE AND SIGNALING OLGI ASSOCIATED VESICLE BIOGENESIS SIC MEDIATED TRANSMEMBERANE TRANSPORT LI S AND GOLG SIGNALING CILLOCETH SIGNALLING CILLOCETH SIGNALLING CILLOCETH SIGNALLING CILLOCETH SIGNALLING OF APRA AND MAP KINASES UPON THARE ON A OF ANTANON ENDEGRAAL SORTING COMPLEX REQUIRED FOR TRANSPORT LIAR ON PROVINTION	1.88 1.97 1.97 1.97 1.95 1.95 1.95 1.94 1.93 1.93 1.93 1.93 1.93 1.90 1.90 1.90 1.90 1.90 1.90 1.89 1.89 1.89 1.89 1.89 1.89 1.89 1.89	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0175 0.0175 0.0184 0.0271 0.0284 0.0227 0.0213 0.0213 0.0213 0.0213 0.0227 0.0223 0.0223 0.0224 0.0226 0.0226 0.0225 0.0226
ACTUATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FOR IN DIGEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES DIEGNALING TO RAS METABOLISM OF NUCLEOTIDES METABOLISM COLOR ASSOCIATION WITH THE ORC ORGIN COMPLEX LI RECEPTORS SIE SIGNALING METABOLISM OF NUCLEOTIDE SIE SIGNALING TO RAS SIGNALING TO RAS SIGNALING TO PARS SIGNALING TO PARS METABOLISM APOPTOSIS INCLICED DNA FRAGMENTATION PIP3 ACTIVATES AKT SIGNALING GOLG ASSOCIATED VESICE BIOGENESIS SIGNALING TO FINDRANIC CATIONS AND ANNO ACDE ODIGOPEPTIES SIGNALING OF ARTIS SIGNALING CELL DEATH SIGNALLING OF ACTIVATED FRIFAND NADE DOWNSTREAM SIGNALING OF ACTIVATED FOR SIGNALING SIGNALING CELL DEATH SIGNALING OF ACTIVATED FOR SIGNALING OF ARTIS SIGNALING DOWNSTREAM SIGNALING OF ACTIVATED FOR SIGNALING OF ARTIS SIGNALING DOWNSTREAM SIGNALING OF ACTIVATED FOR SIGNALING SIGNALING OF ACTIVATED FOR THANSPORT THAP SIGNAL SIGNALING OF ACTIVATED FOR THANSPORT THAP SIGNAL SIGNALING OF ACTIVATED FOR THANSPORT THAP SIGNAL SIGNAL SIGNAL SIGNAL FOR SIGNAL S	1.88 1.97 1.87 1.97 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.90 1.90 1.90 1.90 1.90 1.90 1.90 1.90	0.0143 0.0147 0.0160 0.0162 0.0162 0.0162 0.0172 0.0175 0.0175 0.0175 0.0174 0.0207 0.0201 0.0217 0.0217 0.0217 0.0213 0.0213 0.0213 0.0213 0.0212 0.0223 0.0223 0.0225 0.0226 0.0227 0.0228 0.0225 0.0225 0.0225
ACTIVATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DIGEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES SIGNALING TO FAS SIGNALING TO FAS SIGNALING TO PAS SIGNALING TO PAS SIGNALING TO PAS PI SIGNALING OF OPO RESOLUTION OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PATO/REPLACEMENT PATHAWAY APOPTOSIS INDUCED DNA FRAGMENTATION PIP3 ACTIVATES AKT SIGNALING GOLI ABSOCIATED VESICLE BIOGENESIS SIGNALING TO FINGRANIC CATIONS AND AMON ACIDS OLIGOPEPTIOES SIC MEDIATED SIGNALING CELL DEATH SIGNALING OF ACTIVATED PGPR SIVINESIS OF PA SIVINESIS OF PA THE NLIP3 INFLAMAGOME THMAS MEDIATED SIGNALING OF ACTIVATED FOR THANSPORT HE NLIP3 INFLAMAGOME THMAS MEDIATED INCLICION OF INFRE AND MADE INFLAMASES UPON TRANSPORT OF INORGANIC CATIONS AND AND KINASES UPON THMAS MEDIATED SIGNALING OF ACTIVATED FOR THANSPORT ENDEDAMAS OF PA SIGNALING BY PDGF MEMA DECAY BY STO 3 EXORIBODINGLEASE	1.88 1.97 1.96 1.95 1.95 1.95 1.95 1.94 1.93 1.93 1.93 1.93 1.93 1.93 1.90 1.90 1.90 1.90 1.90 1.89 1.89 1.89 1.89 1.89 1.89 1.89 1.89	0.0143 0.0147 0.0160 0.0162 0.0162 0.0162 0.0175 0.0175 0.0175 0.0174 0.0276 0.0201 0.0213 0.0213 0.0213 0.0213 0.0213 0.0213 0.0223 0.0223 0.0223 0.0225 0.0226 0.0256 0.
ACTUATION OF GRAPERORES BY ATF9 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES COEMAKINE RECEPTORS BIND CHEMOKINES COEMAKINE STORM MOULTATION OF CELL SURFACE RECEPTORS SH'C SIGNALING SIGNALING TO RAS SIGNALING OF SIGNALING CILL DEATH SIGNALING CILL DEATH SIGNALING SIGNALING OF FANNER SIGNALING OF PA THE NLERS INFLUMASIONE THEN ALES INFLAMASIONE THEN ALES INFLAMASIONE THEN ALES INFLAMASIONE THEN ALES INFLAMASIONE THEN ALES INFLAMASIONE THEN ALES INFLAMASIONE THEN ALES INFLAMASIONE SIGNALING BY PEREM SIGNALING BY EREMAINTIONE AND DOWNSTREAM EVENTS SIGNALING BY PEREMAINTIONE SIGNALING BY PEREMAINTI	1.88 1.97 1.87 1.97 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.90 1.90 1.90 1.90 1.90 1.90 1.90 1.90	0.0143 0.0147 0.0160 0.0162 0.0162 0.0162 0.0172 0.0175 0.0175 0.0175 0.0174 0.0207 0.0201 0.0217 0.0217 0.0213 0.0213 0.0213 0.0213 0.0213 0.0212 0.0223 0.0223 0.0225 0.0226 0.0227 0.0228 0.0225 0.0225 0.0225
ACTIVATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DIGEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES SIGNALING TO FAS SIGNALING TO FAS SIGNALING TO PAS SIGNALING TO PAS SIGNALING TO PAS PI SIGNALING OF OPO RESOLUTION OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PATO/REPLACEMENT PATHAWAY APOPTOSIS INDUCED DNA FRAGMENTATION PIP3 ACTIVATES AKT SIGNALING GOLI ABSOCIATED VESICLE BIOGENESIS SIGNALING TO FINGRANIC CATIONS AND AMON ACIDS OLIGOPEPTIOES SIC MEDIATED SIGNALING CELL DEATH SIGNALING OF ACTIVATED PGPR SIVINESIS OF PA SIVINESIS OF PA THE NLIP3 INFLAMAGOME THMAS MEDIATED SIGNALING OF ACTIVATED FOR THANSPORT HE NLIP3 INFLAMAGOME THMAS MEDIATED INCLICION OF INFRE AND MADE INFLAMASES UPON TRANSPORT OF INORGANIC CATIONS AND AND KINASES UPON THMAS MEDIATED SIGNALING OF ACTIVATED FOR THANSPORT ENDEDAMAS OF PA SIGNALING BY PDGF MEMA DECAY BY STO 3 EXORIBODINGLEASE	1.88 1.97 1.97 1.95 1.95 1.95 1.94 1.93 1.93 1.93 1.93 1.93 1.93 1.93 1.99 1.99	0.0143 0.0147 0.0150 0.0160 0.0162 0.0162 0.0162 0.0172 0.0175 0.0174 0.0274 0.0271 0.02213 0.02213 0.02213 0.02213 0.02213 0.02213 0.02213 0.02213 0.0225 0.0225 0.0225 0.0225 0.0225 0.0225 0.0225 0.0225 0.0325 0.0335
ACTUATION OF GRAPERONES BY ATTE ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FORT IN DIEEASE METABOLISM OF NUCLEOTDES PI METABOLISM OF NUCLEOTDES PI METABOLISM OF NUCLEOTDES COCI ASSOCIATION WITH THE ORC ORGIN COMPLEX LI RECEPTORS BIRD CHEMOKINES COCI ASSOCIATION WITH THE ORC ORGIN COMPLEX LI RECEPTORS BIRD CHEMOKINES COCI ASSOCIATION WITH THE ORC ORGIN COMPLEX LI RECEPTORS BIRD CHEMOKINES COCI ASSOCIATION WITH THE ORC ORGIN COMPLEX LI RECEPTORS BY RECRUITING THEM TO CLATHERN ADAPTERS VISSIONUE VESICLE BIOGENESIS SIGNALLING TO RAS SIGNALLING BY GPCR RESOLITION OF APE SIGNALING GIGNALING BY OPCR RESOLITION OF APE SIGNALING COLGI ASSOCIATED VESICLE BIOGENESIS SIGNALING BY OPCR RESOLITION OF APE SIGNALING COLGI ASSOCIATED VESICLE BIOGENESIS SIGNALING COLGED DIA FRAGMENTATION PIP 3 ACTIVATES ART SIGNALING COLGI ASSOCIATED VESICLE BIOGENESIS SIGNALING COP SIGNALING COLGI ASSOCIATED VESICLE BIOGENESIS SIGNALING COP SIGNALING COLGI ASSOCIATED VESICLE BIOGENESIS SIGNALING COP SIGNALING COLDITO FRAMEWERRARE TRANSPORT LL 3 AND GM CSP SIGNALING COLDITION SIGNALING CONTREAM NON AND AND AND ADDS SIM MEDIATED SIGNALING COLDITION SIGNAL ON OF RIFES AND MAD FRAMESOURD DOWNSTREAM SIGNALING ON FIRES AND MAD FRAMESOURD TRANSPORTED SIGNALING COMPLEX REQUIRED FOR TRANSPORT TRANSPORTED SIGNALING ON FIRES AND MAD FRAMESOURD SIGNALING SOFTING COMPLEX REQUIRED FOR TRANSPORT TRANSPORTED SIGNALING ON FIRES AND MAD FRAMESOURD TRANSPORTED SIGNALING ON FIRES AND MAD FRAMESOURD SIGNALING SOFTING COMPLEX REQUIRED FOR TRANSPORT SIGNALING SOFTING COM	1.88 1.97 1.97 1.95 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.90 1.90 1.90 1.90 1.90 1.90 1.89 1.89 1.89 1.89 1.89 1.89 1.89 1.89	0.0143 0.0147 0.0150 0.0162 0.0162 0.0162 0.0172 0.0175 0.0184 0.0271 0.0271 0.0271 0.0271 0.0271 0.0271 0.0271 0.0272 0.0273 0.0228 0.0203 0.0228 0.0204 0.0272 0.0228 0.0205 0.0272
ACTUATION OF GRAPERORES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FORT IN DISEASE INCLUSING OF NUCLEOTIDES PI METABOLISM OF NUCLEOTIDES SIGNALING BY GORD RESOLUTION OF AP SITES VIX. THE MILITIPLE NUCLEOTIDE PITOL RESOLUCIENT FAITHANY APOPTOSIS INSUED DIAN FRAGMENTATION PIP 3 ACTIVATES ARE SIGNALING GOLGI ASSOCIATED VESICLE BIOGENESIS SIGNALING BY GORD RESOLUTION OF AP SITES VIX. THE MILITIPLE NUCLEOTIDE PITOL RESOLUCIENT FAITHANY APOPTOSIS INSUED DIAN FRAGMENTATION PIP 3 ACTIVATES ARE SIGNALING GOLGI ASSOCIATED VESICLE BIOGENESIS SIGNALING COLORISANS AND ANION ACIDS GOLGI ASSOCIATED VESICLE BIOGENESIS SIGNALING AL SIGNALING CELL DEATH SIGNALLING CELL DEATH SIGNALLING CELL DEATH SIGNALLING CATIVATED FGFR SIGNALING BY PDGT THANE POLOTION OF AREA AND MAY KINASES UPON THANE ON A ACTIVATION POLICIAL DE SIGNALING CELL DEATH SIGNALLING CATIVATED FGFR SIGNALING BY PDGT MENNESIS OF PA	1.88 1.97 1.97 1.97 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.93 1.93 1.93 1.93 1.93	0.0143 0.0147 0.0160 0.0162 0.0162 0.0162 0.0175 0.0184 0.0175 0.0184 0.0207 0.0207 0.0207 0.0207 0.0201 0.0207 0.0201 0.0201 0.0201 0.0201 0.0202 0.0201 0.0202 0.
ACTIVATION OF CHAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FGFR IN DISEASE METABOLISM OF MOXING RECEPTORS BIND CHEMOKINE'S COCCA ASSOCIATION WITH THE ORC ORIGIN COMPLEX IL RECEPTORS BHC SIGNALING COCCA ASSOCIATION WITH THE ORC ORIGIN COMPLEX IL RECEPTORS BHC SIGNALING SIGNALING TO RAS SIGNALING TO RAS SIGNALING TO GRAS SIGNALING SIGNALING OLICIASSOCIATED VESICE BIOGENESIS SIGNALED TRANSMEMARIANE TRANSPORT IL 3 AND GRAS SIGNALING CILLIDEATH SIGNALLING CATIONS ANIONS AND AMINO ACIDS OLICOPEPTORES SIC MEDIATED SIGNALLING CILLIDEATH SIGNALLING OF ACTIVATED FORR SYNTHESIS OF PA TRANSPORT OF INORGANIC CATIONS ANIONS AND AMINO ACIDS OLICOPEPTORES SIC MEDIATED SIGNALLING CILLIDEATH SIGNALLING OF ACTIVATED FORR SYNTHESIS OF PA THARS MEGATED INCLETION OF FIRE AND MAP KINASES UPON TIARS DEGATED NORGENON OF MERS AND MAP KINASES UPON THAFF DEGATED NERGATED NERGATED NOR MERS AND DOWNSTREAM EVENTS SIGNALING BY ERBA THAFF MEDIATED NERGA ACTIVATION PHOSPHOLIPLE METABOLISM DEVELOPMENTAL BINDING AND DOWNSTREAM EVENTS SIGNALING BY E	1.88 1.97 1.87 1.97 1.95 1.95 1.95 1.95 1.95 1.93 1.93 1.93 1.90 1.90 1.90 1.90 1.90 1.90 1.90 1.90	0.0143 0.0147 0.0160 0.0162 0.0162 0.0162 0.0172 0.0175 0.0175 0.0174 0.0277 0.0220 0.0213 0.0213 0.0213 0.0213 0.0213 0.0213 0.0213 0.0223 0.0223 0.0225 0.0228 0.0225 0.0225 0.0225 0.0325 0.0344 0.0345 0.0345 0.0345
ACTIVATION OF CHAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FORF IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OLEMOXINE RECEPTORS BIND CHEMOKINES COCEA ASSOCIATION WITH THE ORC ORIGIN COMPLEX IL RECEPTOR SHC SIGNALING COEMOXINE RECEPTORS BIND CHEMOKINES COCEA ASSOCIATION WITH THE ORC ORIGIN COMPLEX IL RECEPTOR SHC SIGNALING NEF MEDATES DOWN MODULATION OF CELL SURFACE RECEPTOR SHC SIGNALING SIGNALING TO RAS SOS MEDIATED SIGNALING SIGNALING TO RAS SOS MEDIATED SIGNALING SIGNALING TO RAS SOS MEDIATED SIGNALING SIGNALING TO RAS SOS MEDIATED SIGNALING OF DISIS INDUCED DNA FRAGMENTATION PIP3 ACTIVATES AKT SIGNALING GOLI ASSOCIATED VESICLE BIOGENESIS SIC MEDIATED SIGNALING GOLI ASSOCIATED VESICLE BIOGENESIS SIC MEDIATED SIGNALING CELL DEATH SIGNALING OF ACTIVATED FARA SIGNALING SIGNALING OF ACTIVATED FRAG SIGNALING SIGNALING OF ACTIVATED FRAG SIGNALING SIGNALING OF ACTIVATED FRAG SIGNALING SIGNALING OF ACTIVATED FOR SIGNALING SIGNALING OF ACTIVATE	1.88 1.97 1.96 1.95 1.95 1.95 1.94 1.93 1.93 1.92 1.93 1.92 1.99 1.99 1.99 1.89 1.89 1.89 1.89 1.89	0.0143 0.0147 0.0150 0.0162 0.0162 0.0162 0.0172 0.0175 0.0175 0.0175 0.0174 0.0201 0.0201 0.0212 0.0213 0.0213 0.0213 0.0213 0.0213 0.0213 0.0213 0.0225 0.0227 0.0227 0.0227 0.0227 0.0225 0.0201 0.0205 0.0205 0.0205 0.0205 0.0325 0.0325 0.0334 0.0345 0.0345 0.0345 0.0345 0.0345
ACTIVATION OF CHAPERONES BY ATF6 ALPHA PRE NOTCH EXPRESSION AND PROCESSING SIGNALING BY FORR IN DISEASE METABOLISM OF NUCLEOTIDES PI METABOLISM OF ADVISION OF NUCLEOTIDES PI METABOLISM OF EXPRESSION AND PROCESSING COGE ASSOCIATION WITH THE ORC ORGIN COMPLEX L RECEPTORS BY SIGNALING INFERENTES OF NON INDOLATION OF CELL SUPFACE RECEPTORS BY RECRUITING THEM TO CLATHRIN ADAPTERS UNSOSOME VESICLE BIOGENESIS SIGNALING TO RAS SIGNALING TO RAS SIGNALING OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PRESSULTION OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PRESSULTON OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PRESSULTON OF AP SITES VIA THE MULTIPLE NUCLEOTIDE SIGNALING BY GFCR RESOLITON OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PRESSULTON OF AP SITES VIA THE MULTIPLE NUCLEOTIDE SIGNALING BY OFCR COUNTERESSON AND AND AND ADDITATION PI A ATTIVATES ART SIGNALING CELL DECITIES SIGNALLING CELL DECITIES SIGNALLING CELL DECITIES INDUCED DIA PRAGENERT FAND NADE DOWNSTREAM SIGNALLING OF ACTIVATED FORR SIGNALING OF PA THE RUBDATED TRANSFORME TRAFF MEDIATED NERBALTING OD OWNSTREAM EVENTS SIGNALING BY PDGF MIND DECAY BY ST O 3 EXORIBIONULEASE SIGNALING BY ENBAL THAFF MEDIATED NERBALCTIVATION PROSPHOLIPID METABOLISM DEVELOPMENTAL BOLOGY ECFF DOWNREGULATION GAP JUNCTION TRAFFICKING PACHAGING OF TELOMERE ENDS	1.88 1.97 1.97 1.96 1.95 1.95 1.95 1.95 1.95 1.95 1.93 1.90 1.90 1.90 1.90 1.90 1.90 1.90 1.90	0.0143 0.0147 0.0150 0.0162 0.0162 0.0162 0.0172 0.0175 0.0184 0.0277 0.0271 0.0271 0.0271 0.0271 0.0271 0.0271 0.0271 0.0272 0.0273 0.0272 0.0273 0.0272 0.0273 0.0272 0.0273 0.0272 0.0273 0.0275 0.0273 0.0275 0.0375 0.0355 0.0345 0.0355 0.
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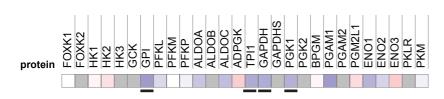
P38MAPK EVENTS	1.76	0.0400
HOMOLOGOUS RECOMBINATION REPAIR OF REPLICATION		
INDEPENDENT DOUBLE STRAND BREAKS	1.76	0.0402
ASSOCIATION OF LICENSING FACTORS WITH THE PRE		
REPLICATIVE COMPLEX	1.75	0.0413
TETRAHYDROBIOPTERIN BH4 SYNTHESIS RECYCLING SALVAGE		
AND REGULATION	1.75	0.0414
CELL CELL JUNCTION ORGANIZATION	1.75	0.0417
INTEGRIN CELL SURFACE INTERACTIONS	1 74	0.0417
INTEGRIN CELL SORFACE INTERACTIONS	1.74	0.0417
SPRY REGULATION OF FGF SIGNALING	1.74	0.0422
FORMATION OF INCISION COMPLEX IN GG NER	1.74	0.0424
INTEGRIN ALPHAIIB BETA3 SIGNALING	1.74	0.0426
FATTY ACYL COA BIOSYNTHESIS	1.74	0.0427
SHC1 EVENTS IN ERBB4 SIGNALING	1.73	0.0430
AMYLOIDS	1.72	0.0450
TRANSMEMBRANE TRANSPORT OF SMALL MOLECULES	1.72	0.0451
ENOS ACTIVATION AND REGULATION	1.72	0.0452
EXTRACELULI AR MATRIX ORGANIZATION	1 72	0.0453
ENTROLEEDERS INFITUX ONORALIZATION	1.12	3.0403
MAP KINASE ACTIVATION IN TLR CASCADE	1.72	0.0458
SYNTHESIS OF SUBSTRATES IN N GLYCAN BIOSYTHESIS	1.71	0.0480
SIGNALLING TO ERKS	1.70	0.0492
COPI MEDIATED TRANSPORT	1.70	0.0492

Appendix Table S1

Appendix Table S2. Characteristics of PLWH enrolled for collection of blood used to assess the *ex-vivo* efficacy of AF and BSO.

Patient ID	Age at sampling	Sex	Stage in which treatment was initiated	Number of years from diagnosis until sampling	Type of ART at initiation (NRTi + protease inhibitor or NNRTi)	CD4 count	Viremia	CD4/CD8 ratio
donor 1	52.2	F	A2, Treated undetectable	24.41	AZT	657	<20	1.07
donor 2	41.1	М	A3, Treated undetectable	15.88	Retrovir - Invirase - Viracept	323	<20	1.03
donor 3	34	F	B1, Treated undetectable	0.18	Dolutégravir/Abacavir/Lamivudine	972	<20	0.97
donor 4	38	М	C3, Treated undetectable	5.7	Efavirenz/Emtricitabine/Tenofovir	235	<20	0.209
donor 5	58.3	М	B3, Treated undetectable	13.35	AZT-3TC-EFV	664	22	0.68
donor 6	43.6	F	B2, Treated undetectable	11.85	Lamivudin + Lopinavir/Ritonavir + Abacavir	1114	<20	1.37
donor 7	49.5	М	A3, Treated undetectable	9.16	AZT + 3TC + EFV	543	<20	0.71
donor 8	27.7	F	C3, Treated undetectable	8.03	Emtricitabine/tenofovir, Nevirapine	481	<20	1.1

Appendix Table S2





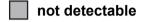
Log₂ fold change expression (HIV-1 infected vs mock infected)

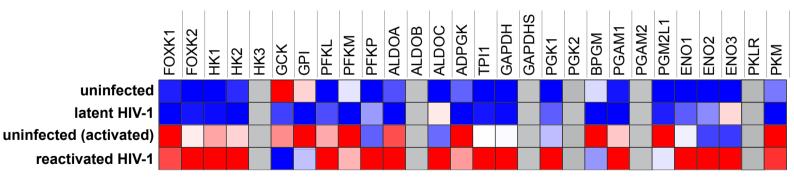
p value < 0.05</p>

not detectable

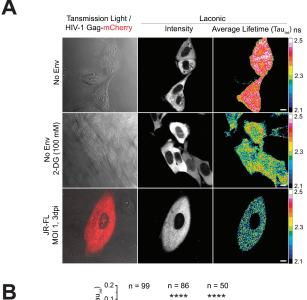
Appendix Figure S1. Modulation of glycolytic pathway in the CD4⁺ T-cell proteome. Heatmap of the expression of the glycolytic pathway in HIV-1 infected vs mock-infected cells. Cells were activated for 72 h with α -CD3-CD28 beads and infected with HIV-1_{pNL4-3} or mock-infected. Both infected and mock-infected cells were cultured for two weeks to model different infection stages as described in (Shytaj *et al*, 2020). On days 3, 7, 9 and 14 post-infection, HIV-1 infected and mock-infected cells were subjected to proteomic analysis (Shytaj *et al*, 2020). Data were analyzed by Student's t-test after pooling the different time points.

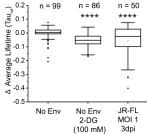






Appendix Figure S2. Modulation of glycolytic pathway transcription during productive or latent HIV-1 infection of microglia. Heatmap of the relative gene expression of the glycolytic pathway in C20/HC69 microglial cells (Garcia-Mesa *et al*, 2017) is shown. Microglial cells were subjected to RNA-Seq analysis under four conditions: uninfected (C20), uninfected and activated (C20-TNF), latently HIV-1 infected (HC69) and reactivated HIV-1 infection (HC69-TNF). Expression data were analyzed by Deseq2 (Love *et al*, 2014).



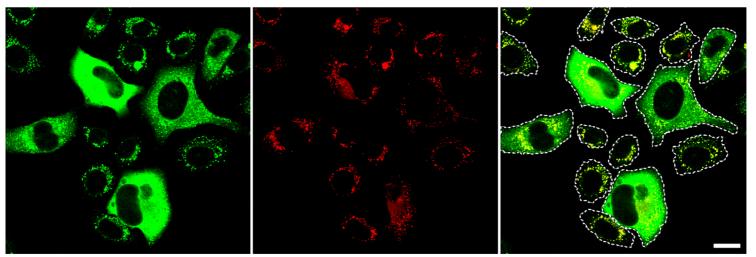


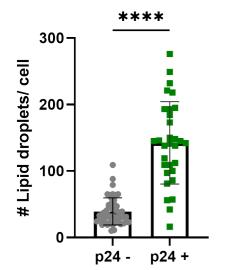
Appendix Figure S3. Single-cell lactate level in HIV-1 infected and uninfected TZM-bl cells. Panel A) micrograph showing TZM-bl cells expressing Laconic FRET-based biosensor infected with HIV-1 Gag-mCherry pseudoviruses (No Env or JR-FL Env, as indicated), in the absence or presence of the glycolysis inhibitor D-deoxy D-glucose (2-DG). Left column: merge of transmission light image and Gag-mCherry fluorescence showing TZM-bl cells negative (-mCherry) or positive for HIV-1 infection (+mCherry). Middle column: intensity image of Laconic fluorescence. Right column: pixel-by-pixel average lifetime (TauInt) image of Laconic expressing cells represented in 16-colors Look-up Table (LUT). Calibration color bar shows values from 2.1 to 2.5 ns. Scale bar = 10 μ m. Panel B) Box and whisker plot showing results from individual TZM-bl cells from 3 independent experiments. Total number of cells analyzed per condition is indicated above each box. Results were analyzed by one-way ANOVA and Sidak post-hoc test **** p < 0.0001.

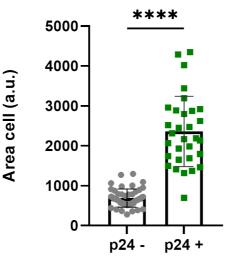
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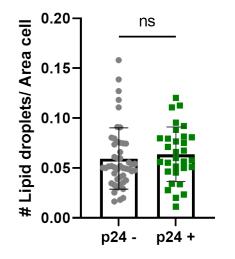
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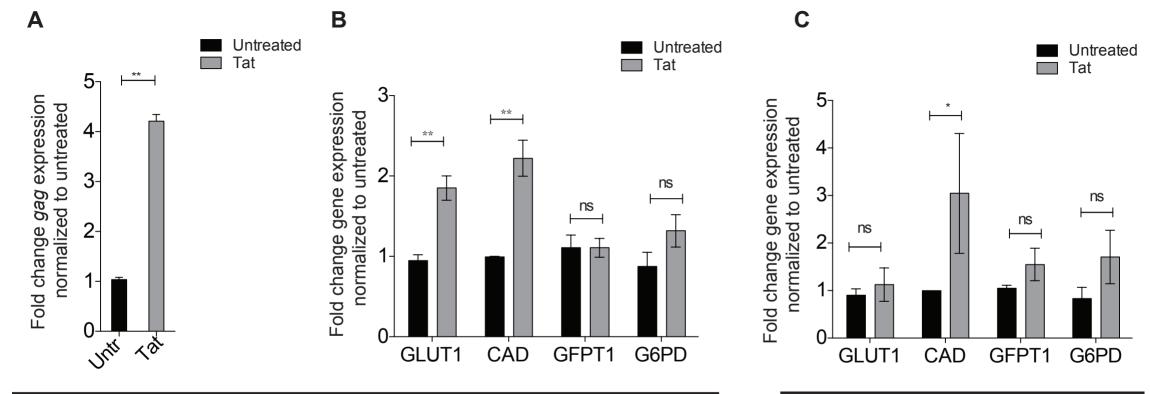








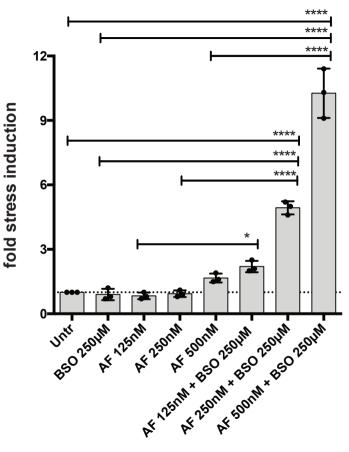
Appendix Figure S4. Single-cell lipid droplet content in HIV-1 infected and uninfected TZM-bl cells. Panel A) Micrograph showing TZM-bl cells expressing HIV-1 p24 3 days post-infection (Alexa 488 positive cells; emission 500 nm -550 nm, left column) and stained with Nile Red dye for lipid droplet detection (emission 650 nm – 690 nm, middle column). Merge of green and red channels is shown on the right column. Dashed lines indicate the cytoplasm contour of each cell. Scale bar = 20μ m. Panels B-D) Scatter plots showing the comparative analysis of infected (A488 positive) vs non-infected cells (A488 negative) cells. Each dot represents the value obtained for a single cell. Bars represent the mean and error bars the standard deviation of at least 30 cells per condition. (B) Quantification of the absolute number of lipid droplets per cell. (C) Quantification of the size (area) of individual cells. (D) Quantification of the number of lipid droplets detected per cell normalized by the size of each cell. Results were analysed using unpaired t-test. **** p< 0.0001.



HIV-1 infected U1 cells

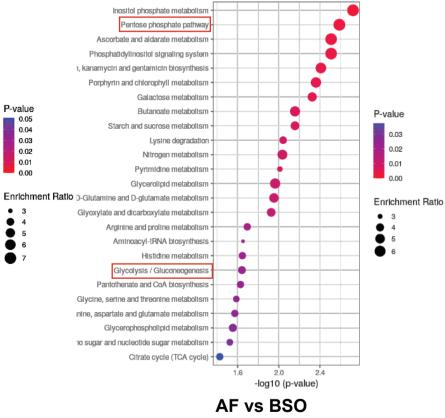
Uninfected U937 cells

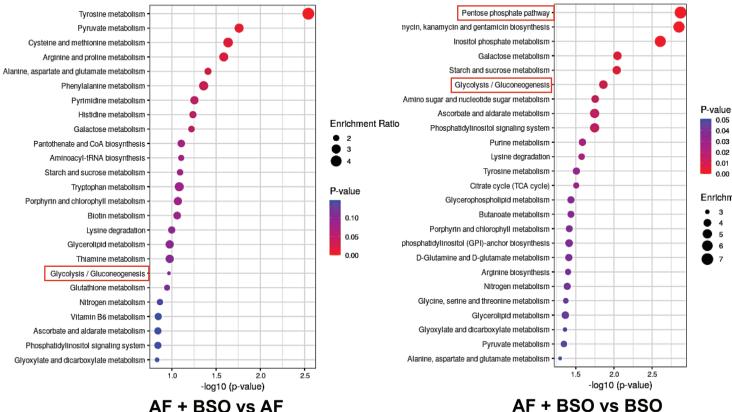
Appendix Figure S5. Viro-metabolic effects of exogenous Tat administration in HIV-1 infected and uninfected cells. The HIV-1 infected (U1, Panels A,B) and uninfected (U937, Panel C) cell lines, both deficient for Tat signaling, were left untreated or treated with HIV subtype-B Tat protein (800 ng/ml) for 72 h. Panel A. HIV-1 reactivation as measured by qPCR of gag expression in infected cells. Panels B,C. Expression of key metabolic genes of glycolysis (GLUT1), the pentose phosphate pathway pyrimidine biosynthesis/glutamate metabolism hexosamine (G6PD),(CAD)and biosynthesis/glutamate metabolism (GFPT1) as measured by qPCR in both infected (B) and uninfected cells (C). Fold change variations over the untreated control were calculated using the 2- $\Delta\Delta$ CT method as in (Livak & Schmittgen, 2001). Results are expressed as mean ± SD and are representative of data from two independent experiments (N=2). Results were analyzed by unpaired t-test with Welch's correction (A) or two-way ANOVA followed by Bonferroni's multiple comparison test (B,C). *p<0.05; **p<0.01.



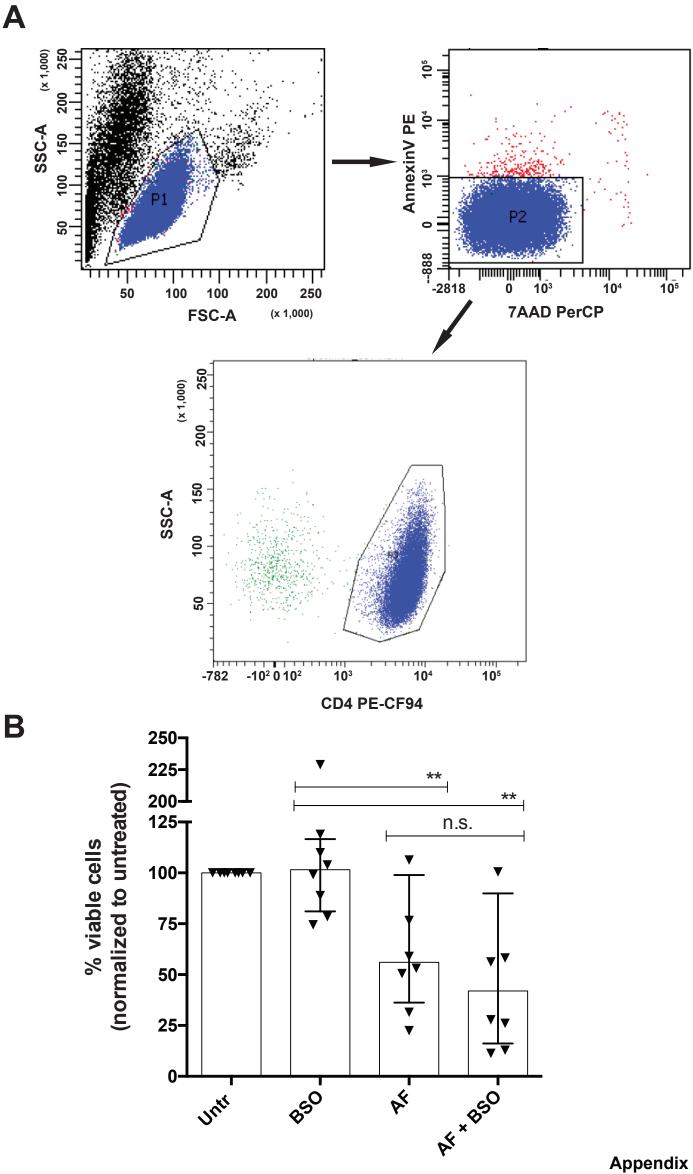
Appendix Figure S6. Auranofin (AF) and buthionine sulfoximine (BSO) co-treatment induces synergistic oxidative stress in U1 cells. U1 cells expressing the redox sensor Grx1-roGFP2 (Bhaskar *et al*, 2015) were exposed to various combinations of AF and/or BSO and the roGFP2 ratio (405/488 nm) was measured 24 h post-treatment. Fold change was calculated by dividing the roGFP2 ratios under treated conditions with the untreated cells. Data (mean \pm SD of three experiments) were analyzed by One Way ANOVA followed by Tukey's post-test (only comparisons between matching drug dosages are shown for simplicity's sake).

* p< 0.05, **** p< 0.0001.

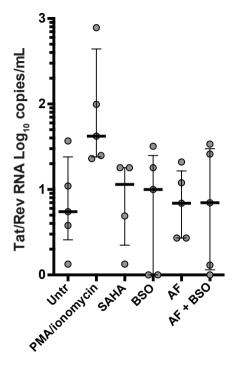




Appendix Figure S7. Modulation of glycolytic metabolites in cells of PLWH treated with auranofin (AF) and/or buthionine sulfoximine (BSO). Peripheral blood mononuclear cells (PBMC), isolated from total blood of PLWH, were treated with auranofin AF (500 nM), BSO (250 μ M) or a combination of the two, for 24 h. PBMC donors were selected from PLWH enrolled in trial NCT02961829 (Diaz *et al*, 2019). Cells were subjected to metabolomic analysis and the top enriched pathways were ordered according to p values obtained with Q statistics for metabolic datasets performed with Globaltest (MetaboAnalyst) (Xia *et al*, 2009). Number of donors = 6.



Appendix Figure S8. Gating strategy and viability of CD4⁺ T-cells of PLWH under ART left untreated or treated with auranofin (AF) and/or buthionine sulfoximine (BSO). CD4+ T-cells were treated with auranofin AF (500 nM), BSO (250 μ M) or a combination of the two, for 24 h. Viable CD4⁺ T-cells were sorted according to the gating strategy shown in Panel A. Viability data are shown as mean \pm SD (Panel B). Data were analyzed by repeated measures one-way ANOVA followed by Tukey's posttest ** p< 0.01.



CD4⁺T-cells from PLWH under suppressive ART

Appendix Figure S9. HIV-1 reactivation in CD4⁺ T-cells of PLWH under ART following treatment with auranofin (AF) and buthionine sulfoximine (BSO). CD4⁺ T-cells were isolated from total blood of PLWH under suppressive ART and left untreated or treated with AF (500 nM), BSO (250 μ M) or a combination of the two for 48 h. Viral reactivation was measured by Tat/rev Induced Limiting Dilution Assay [TILDA (CD4⁺ T-cells of PLWH)] (Procopio *et al*, 2015). Data are expressed as medians and interquartile ranges.