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HGNC Symbol	
Ensembl ID	
Gene Description	
regulation_48h	
Ontology	
Group	
ratioDiff _8Tc vs 100Tc	Ratio of induction (signal at 8 ng/mL TC / signal at 100 ng/mL TC)
ratioDiff_6Tc vs 100Tc	Ratio of induction (signal at 6 ng/mL TC / signal at 100 ng/mL TC)
ratioDiff_5Tc vs 100Tc	Ratio of induction (signal at 5 ng/mL TC / signal at 100 ng/mL TC)
ratioDiff_4Tc vs 100Tc	Ratio of induction (signal at 4 ng/mL TC / signal at 100 ng/mL TC)
ratioDiff_3Tc vs 100Tc	Ratio of induction (signal at 3 ng/mL TC / signal at 100 ng/mL TC)
ratioDiff_2Tc vs 100Tc	Ratio of induction (signal at 2 ng/mL TC / signal at 100 ng/mL TC)
ratioDiff_1 5Tc vs 100Tc	Ratio of induction (signal at 1.5 ng/mL TC / signal at 100 ng/mL TC)
ratioDiff_1Tc vs 100Tc	Ratio of induction (signal at 1 ng/mL TC / signal at 100 ng/mL TC)
ratioDiff_0 5Tc vs 100Tc	Ratio of induction (signal at 0.5 ng/mL TC / signal at 100 ng/mL TC)
ratioDiff_0Tc vs 100Tc	Ratio of induction (signal at 0 ng/mL TC / signal at 100 ng/mL TC)
Ex_100Tc	Expression signal on filter (PhosphorImager data)
Ex_8Tc	Expression signal on filter (PhosphorImager data)
Ex_6Tc	Expression signal on filter (PhosphorImager data)
Ex_5Tc	Expression signal on filter (PhosphorImager data)
Ex_4Tc	Expression signal on filter (PhosphorImager data)
Ex_3Tc	Expression signal on filter (PhosphorImager data)
Ex_2Tc	Expression signal on filter (PhosphorImager data)
Ex_1 5Tc	Expression signal on filter (PhosphorImager data)
Ex_1Tc	Expression signal on filter (PhosphorImager data)
Ex_0 5Tc	Expression signal on filter (PhosphorImager data)
Ex_0Tc	Expression signal on filter (PhosphorImager data)
signDiff _8Tc vs 100Tc	Significance of the difference between signal at 8 ng/mL TC / signal at 100 ng/mL TC
signDiff_6Tc vs 100Tc	Significance of the difference between signal at 6 ng/mL TC / signal at 100 ng/mL TC
signDiff_5Tc vs 100Tc	Significance of the difference between signal at 5 ng/mL TC / signal at 100 ng/mL TC
signDiff_4Tc vs 100Tc	Significance of the difference between signal at 4 ng/mL TC / signal at 100 ng/mL TC
signDiff_3Tc vs 100Tc	Significance of the difference between signal at 3 ng/mL TC / signal at 100 ng/mL TC
signDiff_2Tc vs 100Tc	Significance of the difference between signal at 2 ng/mL TC / signal at 100 ng/mL TC
signDiff_1 5Tc vs 100Tc	Significance of the difference between signal at 1.5 ng/mL TC / signal at 100 ng/mL TC
signDiff_1Tc vs 100Tc	Significance of the difference between signal at 1 ng/mL TC / signal at 100 ng/mL TC
signDiff_0 5Tc vs 100Tc	Significance of the difference between signal at 0.5 ng/mL TC / signal at 100 ng/mL TC
signDiff_0Tc vs 100Tc	Significance of the difference between signal at 0 ng/mL TC / signal at 100 ng/mL TC
signEx_100Tc	Significant signal on filter (significant over background)
signEx_8Tc	Significant signal on filter (significant over background)
signEx_6Tc	Significant signal on filter (significant over background)
signEx_5Tc	Significant signal on filter (significant over background)
signEx_4Tc	Significant signal on filter (significant over background)
signEx_3Tc	Significant signal on filter (significant over background)
signEx_2Tc	Significant signal on filter (significant over background)
signEx_1 5Tc	Significant signal on filter (significant over background)
signEx_1Tc	Significant signal on filter (significant over background)
signEx_0 5Tc	Significant signal on filter (significant over background)
signEx_0Tc	Significant signal on filter (significant over background)

HGNC Symbol	Ensembl ID	Gene Description
MYC	ENSG00000136997	MYC PROTO-ONCOGENE PROTEIN (C-MYC). [Source:SWISSP
CACNA1G	ENSG00000006283	T-type calcium channel alpha1G (CACNA1G); low-voltage-activate
NME1	ENSG00000011052	NUCLEOSIDE DIPHOSPHATE KINASE A (EC 2.7.4.6) (NDK A) (N
ADCY2	ENSG00000078295	ADENYLATE CYCLASE, TYPE II (EC 4.6.1.1) (ATP PYROPHOSP
C4orf9	ENSG00000087269	chromosome 4 open reading frame 9Cluster Incl. AF040965:Homo
FKBP5	ENSG00000096060	FK506-BINDING PROTEIN 5 (EC 5.2.1.8) (PEPTIDYL-PROLYL C
CRKL	ENSG00000099942	CRK-LIKE PROTEINv-crk sarcoma virus CT10 oncogene homolog
RFC5	ENSG00000111445	ACTIVATOR 1 36 KDA SUBUNIT (REPLICATION FACTOR C 36 K
PPP2CA	ENSG00000113575	SERINE/THREONINE PROTEIN PHOSPHATASE 2A, CATALYTIC
TIMM8A	ENSG00000126953	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE
n.a.	ENSG00000132199	RTS BETA PROTEIN. [Source:RefSeq;Acc:NM_017512]rTS beta
MAD2L1	ENSG00000164109	MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A
MRPL12	---	Mrp17mitochondrial ribosomal protein L12 /// mitochondrial riboso
NME1	ENSG00000011052	NUCLEOSIDE DIPHOSPHATE KINASE A (EC 2.7.4.6) (NDK A) (N
METTL1	ENSG00000037897	METHYLTRANSFERASE-LIKE PROTEIN 1, ISOFORM C; D1075-
SLC7A5	ENSG00000103257	LARGE NEUTRAL AMINO ACIDS TRANSPORTER SMALL SUBU
SRM	ENSG00000116649	SPERMIDINE SYNTHASE (EC 2.5.1.16) (PUTRESCINE AMINOP
IL1B	ENSG00000125538	INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) (CATABOLIN).
PAICS	ENSG00000128050	MULTIFUNCTIONAL PROTEIN ADE2 [INCLUDES: PHOSPHORI
TOMM40	ENSG00000130204	PROBABLE MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT T
PYCR1	ENSG00000141548	PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5C
UMPK	ENSG00000143179	URIDINE-CYTIDINE KINASE 2 (EC 2.7.1.48) (UCK 2) (URIDINE
LRP8	ENSG00000157193	APOLIPOPROTEIN E RECEPTOR 2, ISOFORM 3 PRECURSOR;
DUSP14	ENSG00000161326	DUAL SPECIFICITY PROTEIN PHOSPHATASE 14 (EC 3.1.3.48)
METAP1	ENSG00000164024	METHIONINE AMINOPEPTIDASE 1 (EC 3.4.11.18) (METAP 1) (P
ABCE1	ENSG00000164163	ATP-BINDING CASSETTE SUB-FAMILY E MEMBER 1 (RNASE L
PA2G4	ENSG00000170515	PROLIFERATION-ASSOCIATED PROTEIN 2G4 (CELL CYCLE P
BOP1	ENSG00000170727	BLOCK OF PROLIFERATION 1. [Source:SWISSPROT;Acc:Q1413
RANBP1	ENSG00000170987	RAN binding protein 1Cluster Incl. D38076:Human mRNA for Ran
CTPS	ENSG00000171793	CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP S
TRAP1	ENSG00000178436	heat shock protein 75U12595 /FEATURE= /DEFINITION=HSU125
HSPD1	ENSG00000178461	SHORT HEAT SHOCK PROTEIN 60 HSP60S2. [Source:SPTREM
PFAS	ENSG00000178921	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC
TEAD4	ENSG00000179162	TRANSCRIPTIONAL ENHANCER FACTOR TEF-3 (TEA DOMAIN
MIF	ENSG00000179677	macrophage migration inhibitory factor (glycosylation-inhibiting fact
VARS2	ENSG00000180181	VALYL-TRNA SYNTHETASE 2 (EC 6.1.1.9) (VALINE--TRNA LIGA
CENTG1	ENSG00000181137	centaurin, gamma 1Cluster Incl. D79989:Human mRNA for KIAA01
DSCR2	---	leucine rich proteinDown syndrome critical region gene 2 /// Down
JAG2	---	Jagged 2jagged 2Cluster Incl. AF029778:Homo sapiens Jagged2 (
PRKAR1B	---	cAMP-dependent protein kinase type I beta regulatory subunit (PR
n.a.	---	MAC30hypothetical protein MAC30Cluster Incl. L19183:Human M
MATK	ENSG00000007264	MEGAKARYOCYTE-ASSOCIATED TYROSINE-PROTEIN KINAS
IARS	ENSG00000021374	ISOLEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.5) (
GAL	ENSG00000069482	GALANIN PRECURSOR [CONTAINS: GALANIN; GALANIN MESS
MCAM	ENSG00000076706	CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELA
CAD	ENSG00000084774	CAD PROTEIN [INCLUDES: GLUTAMINE-DEPENDENT CARBA
FH	ENSG00000091483	FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR (EC
SRPK1	ENSG00000096063	SFRS PROTEIN KINASE 1; SR PROTEIN KINASE 1. [Source:Ref
NEFH	ENSG00000100285	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILA
NP	ENSG00000100831	PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSIN
AHCY	ENSG00000101444	ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S-ADENOSYL-L-H
POLD2	ENSG00000106628	DNA POLYMERASE DELTA SUBUNIT 2 (EC 2.7.7.7). [Source:SW
C1QBP	ENSG00000108561	COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING
CAMKK2	ENSG00000110931	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE KINAS
n.a.	ENSG00000111234	PROTEIN PREDICTED BY CLONE 23733. [Source:RefSeq;Acc:N
BYSL	ENSG00000112578	BYSTIN. [Source:SWISSPROT;Acc:Q13895]bystin-like /// bystin-lik
NUP155	ENSG00000113569	NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORI

HGNC Symbol	Ensembl ID	Gene Description
IFRD2	ENSG00000114366	N-ACETYLTRANSFERASE 6 (EC 2.3.1.-) (FUS-2 PROTEIN) (FU
MRPL3	ENSG00000114686	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (L3MT). [Sour
HSPE1	ENSG00000115541	10 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10
HSPE1	ENSG00000115541	10 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10
n.a.	ENSG00000115946	PUTATATIVE 28 KDA PROTEIN. [Source:RefSeq;Acc:NM_020143
EBNA1BP2	ENSG00000117395	PROBABLE RRNA PROCESSING PROTEIN EBP2 (EBNA1 BIND
TNFRSF8	ENSG00000120949	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEM
PRDX4	ENSG00000123131	PEROXIREDOXIN 4 (EC 1.11.1.-) (PRX-IV) (THIOREDOXIN PER
CSE1L	ENSG00000124207	IMPORTIN-ALPHA RE-EXPORTER (CHROMOSOME SEGREGA
RPP40	ENSG00000124787	RIBONUCLEASE P PROTEIN SUBUNIT P40 (EC 3.1.26.5) (RNA
n.a.	ENSG00000125912	hypothetical protein from EUROIMAGE 2021883Cluster Incl. AI867
HRMT1L2	ENSG00000126457	PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-) (
n.a.	ENSG00000132877	KIAA1026 proteinCluster Incl. AB028949:Homo sapiens mRNA for
n.a.	ENSG00000136933	RAB9 EFFECTOR P40. [Source:RefSeq;Acc:NM_005833]Rab9 ef
MADH4	ENSG00000141646	MOTHERS AGAINST DECAPENTAPLEGIC HOMOLOG 4 (SMAD
IL9	ENSG00000145839	INTERLEUKIN-9 PRECURSOR (IL-9) (T-CELL GROWTH FACTO
PDCD11	ENSG00000148843	RRP5 PROTEIN HOMOLOG (FRAGMENT). [Source:SWISSPRO
HK2	ENSG00000159399	HEXOKINASE, TYPE II (EC 2.7.1.1) (HK II) (MUSCLE FORM HE
PWP2H	ENSG00000160220	PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG. [Source:SWI
n.a.	ENSG00000161813	C-MPL BINDING PROTEIN. [Source:RefSeq;Acc:NM_052879]c-M
NOLC1	ENSG00000166197	NUCLEOLAR PHOSPHOPROTEIN P130 (NUCLEOLAR 130 KDA
NOLC1	ENSG00000166197	NUCLEOLAR PHOSPHOPROTEIN P130 (NUCLEOLAR 130 KDA
CCT2	ENSG00000166226	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-B
DTYMK	ENSG00000168393	THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE). [Source:S
HNRPAB	ENSG00000169162	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN AB ISO
FASN	ENSG00000169710	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38;
FASN	ENSG00000169710	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38;
NMB	ENSG00000177279	NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN
CHC1	ENSG00000180198	RCC1chromosome condensation 1 /// chromosome condensation
		cDNA DKFZp586K1318Cluster Incl. AL049382:Homo sapiens mR
KIAA0179	---	KIAA0179KIAA0179Cluster Incl. D80001:Human mRNA for KIAA0
NTHL1	ENSG00000065057	NTH ENDONUCLEASE III-LIKE 1 (E. COLI); NTH (E.COLI ENDO
UNG	ENSG00000076248	URACIL-DNA GLYCOSYLASE, MITOCHONDRIAL PRECURSOR
KIAA0020	ENSG00000080608	KIAA0020Cluster Incl. D13645:Human mRNA for KIAA0020 gene,
n.a.	ENSG00000086189	PROBABLE DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-
n.a.	ENSG00000100304	KIAA0153 proteinCluster Incl. D63487:Human mRNA for KIAA015
POLE2	ENSG00000100479	DNA POLYMERASE EPSILON SUBUNIT B (EC 2.7.7.7) (DNA PO
MTHFD1	ENSG00000100714	C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-TH
NOL5A	ENSG00000101361	NUCLEOLAR PROTEIN NOP56 (NUCLEOLAR PROTEIN 5A). [S
PRPS2	ENSG00000101911	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE II (EC 2.7.6.1) (
RUVBL2	ENSG00000104818	CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIC
GPI	ENSG00000105220	GLUCOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.9) (GPI) (PHO
n.a.	ENSG00000106305	MULTISYNTHETASE COMPLEX AUXILIARY COMPONENT P38 (
NPM3	ENSG00000107833	NUCLEOPLASMIN 3. [Source:SWISSPROT;Acc:O75607]nucleop
n.a.	ENSG00000110104	hypothetical protein MGC2574Cluster Incl. AA195301:zr36g11.r1
CDC20	ENSG00000117399	CELL DIVISION CYCLE 20; CELL DIVISION CYCLE 20, S.CERE
n.a.	ENSG00000119812	DKFZP564F0522 proteinCluster Incl. AL049943:Homo sapiens m
PRKDC	ENSG00000121031	DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (EC
CKS2	ENSG00000123975	CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (CK
CSE1L	ENSG00000124207	IMPORTIN-ALPHA RE-EXPORTER (CHROMOSOME SEGREGA
EEF1E1	ENSG00000124802	MULTISYNTHETASE COMPLEX AUXILIARY COMPONENT P18.
HRMT1L2	ENSG00000126457	PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-) (
n.a.	ENSG00000127564	MEMBRANE-ASSOCIATED TYROSINE- AND THREONINE-SPE
TST	ENSG00000128311	THIOSULFATE SULFURTRANSFERASE (EC 2.8.1.1) (RHODAN
DKC1	ENSG00000130826	DYSKERIN (NUCLEOLAR PROTEIN NAP57) (CBF5 HOMOLOG)
RAN	ENSG00000132341	GTP-BINDING NUCLEAR PROTEIN RAN (TC4) (RAN GTPASE) (
PDGFRA	ENSG00000134853	ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR P

HGNC Symbol	**Ensembl ID**	**Gene Description**
CDK4	ENSG00000135446	CELL DIVISION PROTEIN KINASE 4 (EC 2.7.1.-) (CYCLIN-DEPE
ALDH1B1	ENSG00000137124	mitochondrial aldehyde dehydrogenase x genealdehyde dehydrog
SORD	ENSG00000140263	SORBITOL DEHYDROGENASE (EC 1.1.1.14) (L-IDITOL 2-DEHY
BDH	ENSG00000161267	D-BETA-HYDROXYBUTYRATE DEHYDROGENASE, MITOCHON
GMPS	ENSG00000163655	GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2) (GL
GPR30	ENSG00000164850	CHEMOKINE RECEPTOR-LIKE 2 (IL8-RELATED RECEPTOR D
PHB	ENSG00000167085	PROHIBITIN. [Source:SWISSPROT;Acc:P35232]prohibitinCluster
STRA13	ENSG00000169689	stimulated by retinoic acid 13Cluster Incl. U95006:Human D9 splic
XPOT	ENSG00000175719	exportin texportin, tRNA (nuclear export receptor for tRNAs)Cluste
SMN1	ENSG00000179850	SURVIVAL OF MOTOR NEURON (hSMN)survival of motor neuron
CHC1	ENSG00000180198	REGULATOR OF CHROMOSOME CONDENSATION (CELL CYC
PLK1	ENSG00000181598	SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1
n.a.	---	protein arginine N-methyltransferase 3 (PRMT3)protein arginine N-
AK2	ENSG00000004455	ADENYLATE KINASE ISOENZYME 2, MITOCHONDRIAL (EC 2.7
n.a.	ENSG00000006634	ACTIVATOR OF S PHASE KINASE. [Source:RefSeq;Acc:NM_006
MGST1	ENSG00000008394	MICROSOMAL GLUTATHIONE S-TRANSFERASE 1 (EC 2.5.1.18
CSDA	ENSG00000060138	DNA-BINDING PROTEIN A (COLD SHOCK DOMAIN PROTEIN A
n.a.	ENSG00000065485	PROTEIN DISULFIDE ISOMERASE A5 PRECURSOR (EC 5.3.4.1
ATP1B3	ENSG00000069849	SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN
BCS1L	ENSG00000074582	BCS1-LIKE (YEAST); BCS1 (YEAST HOMOLOG)-LIKE. [Source:
UNG	ENSG00000076248	URACIL-DNA GLYCOSYLASE, MITOCHONDRIAL PRECURSOR
PBP	ENSG00000089220	PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (PEBP) (
CDC6	ENSG00000094804	CDC6 HOMOLOG; CDC6 (CELL DIVISION CYCLE 6, S. CEREVI
CDC7	ENSG00000097046	CELL DIVISION CYCLE 7-RELATED PROTEIN KINASE (EC 2.7.1
MTAP	ENSG00000099810	5'-METHYLTHIOADENOSINE PHOSPHORYLASE (EC 2.4.2.28) (
ADSL	ENSG00000100357	ADENYLOSUCCINATE LYASE (EC 4.3.2.2) (ADENYLOSUCCINA
CDKN3	ENSG00000100526	CYCLIN-DEPENDENT KINASE INHIBITOR 3 (EC 3.1.3.48) (EC 3.
VRK1	ENSG00000100749	VACCINIA RELATED KINASE 1; VACCINIA-RELATED KINASE-1.
WFDC2	ENSG00000101443	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR (HE
GSPT1	ENSG00000103342	G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BI
SLC39A14	ENSG00000104635	KIAA0062solute carrier family 39 (zinc transporter), member 14Clu
n.a.	ENSG00000105677	SEVEN TRANSMEMBRANE DOMAIN PROTEIN. [Source:RefSeq
RLN2	ENSG00000107014	PRORELAXIN H2 PRECURSOR. [Source:SWISSPROT;Acc:P040
BAG2	ENSG00000112208	BAG-FAMILY MOLECULAR CHAPERONE REGULATOR-2. [Sour
HSD17B8	ENSG00000112474	ESTRADIOL 17 BETA-DEHYDROGENASE 8 (EC 1.1.1.62) (17-B
UCHL3	ENSG00000118939	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (
NME2	ENSG00000121054	NUCLEOSIDE DIPHOSPHATE KINASE B (EC 2.7.4.6) (NDK B) (
MRPS12	ENSG00000128626	28S RIBOSOMAL PROTEIN S12, MITOCHONDRIAL PRECURS
PCNA	ENSG00000132646	PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN).
DPH2L2	ENSG00000132768	DIPHTHAMIDE BIOSYNTHESIS-LIKE PROTEIN 2. [Source:RefS
CCNB1	ENSG00000134057	G2/MITOTIC-SPECIFIC CYCLIN B1. [Source:SWISSPROT;Acc:P
MC1R	ENSG00000141037	TUBULIN BETA-4 CHAIN (TUBULIN BETA-III). [Source:SWISSPR
SOD1	ENSG00000142168	SUPEROXIDE DISMUTASE [CU-ZN] (EC 1.15.1.1). [Source:SWIS
ATP5G3	ENSG00000154518	ATP SYNTHASE LIPID-BINDING PROTEIN, MITOCHONDRIAL P
CCT3	ENSG00000163468	T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA) (C
RFC4	ENSG00000163918	ACTIVATOR 1 37 KDA SUBUNIT (REPLICATION FACTOR C 37 K
CDC25A	ENSG00000164045	M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) (DUAL SPE
FRDA	ENSG00000165060	FRATAXIN, MITOCHONDRIAL PRECURSOR (FRIEDREICH'S AT
SNRPD1	ENSG00000167088	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1 (SNRNP COR
CHAF1A	ENSG00000167670	CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT A (CAF-1 SUBUN
PRDX2	ENSG00000167815	PEROXIREDOXIN 2 (EC 1.11.1.-) (THIOREDOXIN PEROXIDASE
BUB1	ENSG00000169679	MITOTIC CHECKPOINT SERINE/THREONINE-PROTEIN KINAS
CDC2	ENSG00000170312	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (
POLR1C	ENSG00000171453	DNA-DIRECTED RNA POLYMERASE I 40 KDA POLYPEPTIDE (
SLC19A1	ENSG00000173638	FOLATE TRANSPORTER 1 (PLACENTAL FOLATE TRANSPORT
TOMM20	ENSG00000173726	MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 HOM
MMP3	ENSG00000175007	STROMELYSIN-1 PRECURSOR (EC 3.4.24.17) (MATRIX METAL

HGNC Symbol	**Ensembl ID**	**Gene Description**
UBE2C	ENSG00000175063	UBIQUITIN-CONJUGATING ENZYME E2 C (EC 6.3.2.19) (UBIQU
PTPN2	ENSG00000175354	PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE
RUVBL1	ENSG00000175792	TATA BINDING PROTEIN INTERACTING PROTEIN 49 KDA; RUV
TYMS	ENSG00000176890	THYMIDYLATE SYNTHASE (EC 2.1.1.45) (TS) (TSASE). [Source:
DDX10	ENSG00000178105	PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAD-B
TUFM	ENSG00000178952	ELONGATION FACTOR TU, MITOCHONDRIAL PRECURSOR (E
AURKB	ENSG00000178999	SERINE/THREONINE PROTEIN KINASE 12 (EC 2.7.1.37) (AUR
RRS1	ENSG00000179041	RIBOSOME BIOGENESIS REGULATORY PROTEIN HOMOLOG.
GEMIN4	ENSG00000179409	COMPONENT OF GEMS 4 (GEMIN4) (P97). [Source:SWISSPRO
PTMA	ENSG00000181571	PROTHYMOSIN A14. [Source:RefSeq;Acc:NM_016171]prothymos
CYP51A1	ENSG00000001630	CYTOCHROME P450 51 (EC 1.14.14.-) (CYPL1) (P450L1) (STER
ARHGEF5	ENSG00000050327	RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR 5 (GUANIN
KIAA0690	ENSG00000052749	KIAA0690Cluster Incl. AB014590:Homo sapiens mRNA for KIAA06
VDAC1	ENSG00000073905	VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEI
DDX1	ENSG00000079785	ATP-DEPENDENT HELICASE DDX1 (DEAD-BOX PROTEIN 1) (D
SCAMP1	ENSG00000085365	SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1.
DDX18	ENSG00000088205	ATP-DEPENDENT RNA HELICASE DDX18 (DEAD-BOX PROTEI
PES1	ENSG00000100029	PESCADILLO HOMOLOG 1. [Source:SWISSPROT;Acc:O00541]p
RANGAP1	ENSG00000100401	RAN-GTPASE ACTIVATING PROTEIN 1. [Source:SWISSPROT;A
APEX1	ENSG00000100823	DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE (EC 4.2.99.18)
MYBL2	ENSG00000101057	MYB-RELATED PROTEIN B (B-MYB). [Source:SWISSPROT;Acc:
USP10	ENSG00000103194	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 10 (EC 3.1.2.1
n.a.	ENSG00000104613	hypothetical protein FLJ10569Cluster Incl. W27152:23h11 Homo s
RPA3	ENSG00000106399	REPLICATION PROTEIN A 14 KDA SUBUNIT (RP-A) (RF-A) (RE
CXCL12	ENSG00000107562	stromal cell derived factor 1 precursor (SDF1); pre B-cell growth st
n.a.	ENSG00000109184	KIAA0276 proteinCluster Incl. D87466:Human mRNA for KIAA027
MCM3	ENSG00000112118	DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYME
GMNN	ENSG00000112312	GEMININ. [Source:SWISSPROT;Acc:O75496]
HSPA9B	ENSG00000113013	STRESS-70 PROTEIN, MITOCHONDRIAL PRECURSOR (75 KD
TCERG1	ENSG00000113649	TRANSCRIPTION ELONGATION REGULATOR 1; TRANSCRIPT
RNU3IP2	ENSG00000114767	U3 SNORNP-ASSOCIATED 55-KDA PROTEIN. [Source:RefSeq;A
SFRS7	ENSG00000115875	SPLICING FACTOR, ARGININE/SERINE-RICH 7 (SPLICING FAC
MSH6	ENSG00000116062	DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 K
CENPF	ENSG00000117724	CENP-F KINETOCHORE PROTEIN (CENTROMERE PROTEIN F
MXI1	ENSG00000119950	MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN). [Source:SWIS
AMD1	ENSG00000123505	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (
ELK1	ENSG00000126767	ETS-DOMAIN PROTEIN ELK-1. [Source:SWISSPROT;Acc:P1941
ILF3	ENSG00000129351	INTERLEUKIN ENHANCER-BINDING FACTOR 3 (NUCLEAR FA
TFDP1	ENSG00000130266	TRANSCRIPTION FACTOR DP-1 (E2F DIMERIZATION PARTNE
n.a.	ENSG00000130713	EXOSOME COMPLEX EXONUCLEASE RRP4 (EC 3.1.13.-) (RIB
TOP2A	ENSG00000131747	DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3). [Sou
EIF5A	ENSG00000132507	EUKARYOTIC TRANSLATION INITIATION FACTOR 5A (EIF-5A) (
n.a.	ENSG00000132763	DKFZP564I122 protein /// DKFZP564I122 proteinCluster Incl. AL0
n.a.	ENSG00000136718	U3 snoRNP protein 4 homologCluster Incl. AF054996:Homo sapie
ATIC	ENSG00000138363	BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH [INCL
ATIC	ENSG00000138363	BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH [INCL
PEX5	ENSG00000139197	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR (PEROXIS
TAF4B	ENSG00000141384	TRANSCRIPTION INITIATION FACTOR TFIID 105 KDA SUBUNIT
HDGF	ENSG00000143321	HEPATOMA-DERIVED GROWTH FACTOR (HDGF) (HIGH-MOBIL
HDGF	ENSG00000143321	HEPATOMA-DERIVED GROWTH FACTOR (HDGF) (HIGH-MOBIL
ILF2	ENSG00000143621	INTERLEUKIN ENHANCER BINDING FACTOR 2; NUCLEAR FA
CCNA2	ENSG00000145386	CYCLIN A2 (CYCLIN A). [Source:SWISSPROT;Acc:P20248]cyclin
MDH2	ENSG00000146701	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (
PEG10	ENSG00000146743	PATERNALLY EXPRESSED 10. [Source:RefSeq;Acc:NM_015068
PPRC1	ENSG00000148840	peroxisome proliferative activated receptor, gamma, coactivator-rel
SSRP1	ENSG00000149136	STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 (SSRP1) (R
PTK9	ENSG00000151239	PTK9 PROTEIN TYROSINE KINASE 9; PROTEIN TYROSINE KI

HGNC Symbol	**Ensembl ID**	**Gene Description**
ACSL1	ENSG00000151726	LONG-CHAIN-FATTY-ACID--COA LIGASE 2 (EC 6.2.1.3) (LONG-
PFKM	ENSG00000152556	6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE (EC 2.7.1.11) (PH
HNRPDL	ENSG00000152795	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D-LIKE;
RPIA	ENSG00000153574	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6) (PHOSPHOR
SLC16A1	ENSG00000155380	MONOCARBOXYLATE TRANSPORTER 1 (MCT 1). [Source:SWI
KCNJ6	ENSG00000157542	G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CH
SFRS2	ENSG00000161547	SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FAC
PRKCI	ENSG00000163558	PROTEIN KINASE C, IOTA TYPE (EC 2.7.1.-) (NPKC-IOTA). [Sou
POLR2H	ENSG00000163882	DNA-DIRECTED RNA POLYMERASES I, II, AND III 17.1 KDA PO
ABCE1	ENSG00000164163	ATP-BINDING CASSETTE SUB-FAMILY E MEMBER 1 (RNASE L
MELK	ENSG00000165304	MATERNAL EMBRYONIC LEUCINE ZIPPER KINASE. [Source:R
DDX21	ENSG00000165732	NUCLEOLAR RNA HELICASE II (NUCLEOLAR RNA HELICASE
SSSCA1	ENSG00000173465	SJOGREN'S SYNDROME/SCLERODERMA AUTOANTIGEN 1 (A
n.a.	ENSG00000175602	DELTA-INTERACTING PROTEIN A (HEPATITIS DELTA ANTIGEN
HSPCA	ENSG00000176668	HEAT SHOCK PROTEIN 86 (FRAGMENT). [Source:SPTREMBL;
DEAF1	ENSG00000177030	DEFORMED EPIDERMAL AUTOREGULATORY FACTOR 1 HOM
n.a.	ENSG00000177176	Cluster Incl. AL050035:Homo sapiens mRNA; cDNA DKFZp566H0
EIF1AX	ENSG00000179112	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A, X-CHRO
n.a.	ENSG00000180997	MY016 PROTEIN. [Source:SPTREMBL;Acc:Q9H3K6]hypothetical
n.a.	ENSG00000181708	DKFZP564K2062 proteinCluster Incl. AL080088:Homo sapiens m
SF3A3	---	splicing factor SF3a60splicing factor 3a, subunit 3, 60kDa /// splici
n.a.	---	cDNA clone EUROIMAGE 39515Cluster Incl. AL079283:Homo sa
AK2	ENSG00000004455	ADENYLATE KINASE ISOENZYME 2, MITOCHONDRIAL (EC 2.7
PLAUR	ENSG00000011422	UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTO
SCARB1	ENSG00000073060	SCAVENGER RECEPTOR CLASS B, MEMBER 1; CD36 ANTIGE
MCM2	ENSG00000073111	DNA REPLICATION LICENSING FACTOR MCM2 (NUCLEAR PR
EXOSC7	ENSG00000075914	EXOSOME COMPLEX EXONUCLEASE RRP42 (EC 3.1.13.-) (RI
KHSRP	ENSG00000088247	KH-TYPE SPLICING REGULATORY PROTEIN (FUSE BINDING
NUDC	ENSG00000090273	NUCLEAR DISTRIBUTION GENE C HOMOLOG (A. NIDULANS);
CGRRF1	ENSG00000100532	CELL GROWTH REGULATORY WITH RING FINGER DOMAIN. [
APEX1	ENSG00000100823	DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE (EC 4.2.99.18)
GARS	ENSG00000106105	GLYCYL-TRNA SYNTHETASE (EC 6.1.1.14) (GLYCINE--TRNA L
EIF3S9	ENSG00000106263	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT
IMPDH1	ENSG00000106348	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (EC 1.1.1
VEGF	ENSG00000112715	VASCULAR ENDOTHELIAL GROWTH FACTOR A PRECURSOR
TFDP2	ENSG00000114126	TRANSCRIPTION FACTOR DP-2 (E2F DIMERIZATION PARTNE
PRDX1	ENSG00000117450	PEROXIREDOXIN 1 (EC 1.11.1.-) (THIOREDOXIN PEROXIDASE
SCO2	ENSG00000130489	SCO2 PROTEIN HOMOLOG, MITOCHONDRIAL PRECURSOR. [
TUBG1	ENSG00000131462	TUBULIN GAMMA-1 CHAIN (GAMMA-1 TUBULIN) (GAMMA-TUB
MYCN	ENSG00000134323	N-MYC PROTO-ONCOGENE PROTEIN. [Source:SWISSPROT;A
ABL2	ENSG00000143322	TYROSINE-PROTEIN KINASE ABL2 (EC 2.7.1.112) (TYROSINE
SLC20A1	ENSG00000144136	SOLUTE CARRIER FAMILY 20 (PHOSPHATE TRANSPORTER),
CDKN2B	ENSG00000147883	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15
n.a.	ENSG00000162568	DKFZP564C186 proteinCluster Incl. AL050019:Homo sapiens mR
FANCG	ENSG00000165281	FANCONI ANEMIA GROUP G PROTEIN (FACG PROTEIN) (DNA-
PMPCA	ENSG00000165688	MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT,
PSMC3	ENSG00000165916	26S PROTEASE REGULATORY SUBUNIT 6A (TAT-BINDING PR
MCM7	ENSG00000166508	DNA REPLICATION LICENSING FACTOR MCM7 (CDC47 HOMO
ABCA3	ENSG00000167972	ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 3 (ATP-BIN
EIF4EBP1	ENSG00000169150	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E BINDING
TNFRSF4	ENSG00000174608	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEM
SRP72	ENSG00000174780	SIGNAL RECOGNITION PARTICLE 72 KDA PROTEIN (SRP72). [
ALG3	ENSG00000175142	DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL MANNOS
CKS1B	ENSG00000178556	CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (CK
NSEP1	ENSG00000178563	nuclease sensitive element binding protein 1 /// nuclease sensitive
FARSLA	ENSG00000179115	PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN (EC 6.1.1.
PRIM1	ENSG00000181494	DNA PRIMASE SMALL SUBUNIT (EC 2.7.7.-) (DNA PRIMASE 49

HGNC Symbol	Ensembl ID	Gene Description
TBL3	---	SazD (Transducin like protein)transducin (beta)-like 3Cluster Incl.
JUND	---	jun D proto-oncogeneCluster Incl. X56681:Human junD mRNA /cd
PTBP1	ENSG00000011304	POLYPYRIMIDINE TRACT-BINDING PROTEIN 1 (PTB) (HETER
MRE11A	ENSG00000020922	DOUBLE-STRAND BREAK REPAIR PROTEIN MRE11A (MRE11
HSPA5	ENSG00000044574	78 KDA GLUCOSE-REGULATED PROTEIN PRECURSOR (GRP
OAT	ENSG00000065154	ORNITHINE AMINOTRANSFERASE, MITOCHONDRIAL PRECU
TFRC	ENSG00000072274	TRANSFERRIN RECEPTOR PROTEIN 1 (TFR1) (TR) (TFR) (TR
SHMT1	ENSG00000072465	SERINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC (EC 2
CLNS1A	ENSG00000074201	CHLORIDE CONDUCTANCE REGULATORY PROTEIN ICLN (I(C
SEMA3C	ENSG00000075223	SEMAPHORIN 3C PRECURSOR (SEMAPHORIN E) (SEMA E). [
MCAM	ENSG00000076706	CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELA
MAPKAPK5	ENSG00000089022	MITOGEN-ACTIVATED PROTEIN KINASE-ACTIVATED PROTEI
SIP1	ENSG00000092208	SURVIVAL OF MOTOR NEURON PROTEIN-INTERACTING PRO
NF2	ENSG00000100305	MERLIN (SCHWANNOMIN) (NEUROFIBROMIN 2). [Source:SWIS
SLC1A5	ENSG00000105281	NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) (SODIUM
PSMA2	ENSG00000106588	PROTEASOME SUBUNIT ALPHA TYPE 2 (EC 3.4.25.1) (PROTE
RAD51C	ENSG00000108384	DNA REPAIR PROTEIN RAD51 HOMOLOG 3. [Source:SWISSPR
CTSC	ENSG00000109861	DIPEPTIDYL-PEPTIDASE I PRECURSOR (EC 3.4.14.1) (DPP-I)
HSPA8	ENSG00000109971	HEAT SHOCK COGNATE 71 KDA PROTEIN. [Source:SWISSPR
n.a.	ENSG00000110108	hypothetical protein MGC5508Cluster Incl. N53547:yv43b12.s1 Ho
IGFBP2	ENSG00000115457	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECU
DARS	ENSG00000115866	ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TR
UCHL3	ENSG00000118939	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3
GTF3A	ENSG00000122034	TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA). [Source:SW
RPL5	ENSG00000122406	60S RIBOSOMAL PROTEIN L5. [Source:SWISSPROT;Acc:P467
AMD1	ENSG00000123505	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (
HSPA1A	ENSG00000124567	HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-
SYNGR3	ENSG00000127561	SYNAPTOGYRIN 3. [Source:SWISSPROT;Acc:O43761]synaptog
NINJ1	ENSG00000131669	NINJURIN 1 (NERVE INJURY-INDUCED PROTEIN 1). [Source:S
SNRPA1	ENSG00000131876	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')
TAF9	ENSG00000134059	TRANSCRIPTION INITIATION FACTOR TFIID 31 KDA SUBUNIT
SYNCRIP	ENSG00000135316	NS1-ASSOCIATED PROTEIN 1. [Source:RefSeq;Acc:NM_006372
n.a.	ENSG00000136270	CELL CYCLE PROGRESSION 2 PROTEIN. [Source:RefSeq;Acc:
ITGB3BP	ENSG00000142856	INTEGRIN BETA 3 BINDING PROTEIN (BETA3-ENDONEXIN); B
PTPRF	ENSG00000142949	LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED
CHEK1	ENSG00000149554	SERINE/THREONINE-PROTEIN KINASE CHK1 (EC 2.7.1.-). [So
TCEB1	ENSG00000154582	ELONGIN C; TRANSCRIPTION ELONGATION FACTOR B (SIII),
n.a.	ENSG00000155506	likely ortholog of mouse la related proteinCluster Incl. AB018274:H
VBP1	ENSG00000155959	PREFOLDIN SUBUNIT 3 (VON HIPPEL-LINDAU BINDING PROT
BUB1B	ENSG00000156970	MITOTIC CHECKPOINT SERINE/THREONINE-PROTEIN KINAS
RACGAP1	ENSG00000161800	RAC GTPASE ACTIVATING PROTEIN 1; GTPASE ACTIVATING P
AK3	ENSG00000162433	ADENYLATE KINASE ISOENZYME 4, MITOCHONDRIAL (EC 2.7
HNRPF	ENSG00000169813	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNR
PDAP1	ENSG00000176672	PDGFA associated protein 1 /// PDGFA associated protein 1Cluste
SELE	ENSG00000007908	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHE
n.a.	ENSG00000048162	PROTEIN CGI-117 (PROTEIN HSPC111). [Source:SWISSPROT;A
RCN1	ENSG00000049449	RETICULOCALBIN 1 PRECURSOR. [Source:SWISSPROT;Acc:Q
GLDC	ENSG00000049496	GLYCINE DEHYDROGENASE [DECARBOXYLATING], MITOCH
PMS1	ENSG00000064933	PMS1 PROTEIN HOMOLOG 1 (DNA MISMATCH REPAIR PROTE
PFKP	ENSG00000067057	6-PHOSPHOFRUCTOKINASE, TYPE C (EC 2.7.1.11) (PHOSPH
PDCD2	ENSG00000071994	PROGRAMMED CELL DEATH PROTEIN 2 (ZINC FINGER PROT
MGST2	ENSG00000085871	MICROSOMAL GLUTATHIONE S-TRANSFERASE 2 (EC 2.5.1.18
NDUFB7	ENSG00000099795	NADH-UBIQUINONE OXIDOREDUCTASE B18 SUBUNIT (EC 1.6
G22P1	ENSG00000100419	ATP-DEPENDENT DNA HELICASE II, 70 KDA SUBUNIT (LUPUS
n.a.	ENSG00000103226	PROTEIN PM5 PRECURSOR. [Source:SWISSPROT;Acc:Q15155
PBEF1	ENSG00000105835	PRE-B CELL ENHANCING FACTOR PRECURSOR. [Source:SWI
TBL2	ENSG00000106638	TRANSDUCIN BETA-LIKE 2 PROTEIN (WS BETA-TRANSDUCIN

HGNC Symbol	Ensembl ID	Gene Description
GCN5L2	ENSG00000108773	GENERAL CONTROL OF AMINO ACID SYNTHESIS PROTEIN 5-
CDK2AP1	ENSG00000111328	CYCLIN-DEPENDENT KINASE 2-ASSOCIATED PROTEIN 1 (CD
NOL1	ENSG00000111641	PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFE
SLC29A1	ENSG00000112759	EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILIBRAT
BNIP1	ENSG00000113734	BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PRO
DBN1	ENSG00000113758	DREBRIN (DEVELOPMENTALLY REGULATED BRAIN PROTEIN
EIF4G1	ENSG00000114867	EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (E
B4GALT2	ENSG00000117411	BETA-1,4-GALACTOSYLTRANSFERASE 2 (EC 2.4.1.-) (BETA-1,4
TMEM5	ENSG00000118600	TRANSMEMBRANE PROTEIN 5; PUTATIVE TYPE II MEMBRANE
FVT1	ENSG00000119537	FOLLICULAR VARIANT TRANSLOCATION PROTEIN 1 PRECUR
ETF1	ENSG00000120705	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1
ATF4	ENSG00000128272	CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-4 (A
ILF3	ENSG00000129351	INTERLEUKIN ENHANCER-BINDING FACTOR 3 (NUCLEAR FA
RAMP1	ENSG00000132329	RECEPTOR ACTIVITY-MODIFYING PROTEIN 1 PRECURSOR (
n.a.	ENSG00000134697	AUTOANTIGEN NGP-1. [Source:SWISSPROT;Acc:Q13823]nucle
ADCY3	ENSG00000138031	ADENYLATE CYCLASE TYPE III (EC 4.6.1.1) (ADENYLATE CYC
AFG3L2	ENSG00000141385	AFG3-LIKE PROTEIN 2 (EC 3.4.24.-) (PARAPLEGIN-LIKE PROTE
PRPS1	ENSG00000147224	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE I (EC 2.7.6.1) (P
OPRS1	ENSG00000147955	TYPE I SIGMA RECEPTOR ISOFORM 1; SR31747 BINDING PR
TOMM70A	ENSG00000154174	MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTO
APRT	ENSG00000158581	ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) (AP
FGFR4	ENSG00000160867	FIBROBLAST GROWTH FACTOR RECEPTOR 4 PRECURSOR (
DEFA6	ENSG00000164822	DEFENSIN 6 PRECURSOR (DEFENSIN, ALPHA 6). [Source:SWIS
ZNF9	ENSG00000169714	CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP). [Source
RAC3	ENSG00000169750	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 3 (P21-RA
WNT10B	ENSG00000169884	WNT-10B PROTEIN PRECURSOR (WNT-12). [Source:SWISSPR
NFRKB	ENSG00000170322	NUCLEAR FACTOR RELATED TO KAPPA B BINDING PROTEIN.
CDK5R2	ENSG00000171450	CYCLIN-DEPENDENT KINASE 5 ACTIVATOR 2 PRECURSOR (C
CYCS	ENSG00000172115	CYTOCHROME C. [Source:SWISSPROT;Acc:P00001]
YES1	ENSG00000176105	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.
DLEU1	ENSG00000176124	LEUKEMIA ASSOCIATED PROTEIN 1. [Source:SWISSPROT;Acc
BNIP3	ENSG00000176643	BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PRO
RAD23A	ENSG00000179262	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A
		clone 121711 defective mariner transposon Hsmar2Cluster Incl. U
UBE2G2	---	ubiquitin conjugating enzyme G2 (UBE2G2)ubiquitin-conjugating e
KCNQ3	---	KCNQ3 potassium channel; epilepsy-involved (FRAGMENT).potas
MTA1	---	metastasis-associated MTA1metastasis associated 1Cluster Incl.
LIG3	ENSG00000005156	DNA LIGASE III (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE S
ITGA2B	ENSG00000005961	INTEGRIN ALPHA-IIB PRECURSOR (PLATELET MEMBRANE G
TOMM34	ENSG00000025772	MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM34 (TRA
ITIH4	ENSG00000055955	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECUR
POLD1	ENSG00000062822	DNA POLYMERASE DELTA CATALYTIC SUBUNIT (EC 2.7.7.7) (
IKBKAP	ENSG00000070061	IKAPPAB KINASE COMPLEX-ASSOCIATED PROTEIN (IKK CO
ASNS	ENSG00000070669	ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] (EC
MX1	ENSG00000075290	WNT-8B PROTEIN PRECURSOR. [Source:SWISSPROT;Acc:Q93
XRCC5	ENSG00000079246	ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT (LUPUS
XPO1	ENSG00000082898	EXPORTIN 1; CRM1, YEAST, HOMOLOG; EXPORTIN-1 (REQUI
RAD54L	ENSG00000085999	RAD54-LIKE PROTEIN; RAD54 HOMOLOG. [Source:RefSeq;Acc
PTHLH	ENSG00000087494	PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR (
MSH2	ENSG00000095002	DNA MISMATCH REPAIR PROTEIN MSH2. [Source:SWISSPROT
CDKL1	ENSG00000100490	SERINE/THREONINE-PROTEIN KINASE KKIALRE (EC 2.7.1.-) (
ADA	ENSG00000101093	ADENOSINE DEAMINASE (EC 3.5.4.4) (ADENOSINE AMINOHY
n.a.	ENSG00000103226	PROTEIN PM5 PRECURSOR. [Source:SWISSPROT;Acc:Q15155
TGFB1	ENSG00000105329	TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TG
NPTX2	ENSG00000106236	NEURONAL PENTRAXIN II PRECURSOR (NP-II) (NP2). [Source:
BAG1	ENSG00000107262	BAG-FAMILY MOLECULAR CHAPERONE REGULATOR-1 (BCL-
BAG1	ENSG00000107262	BAG-FAMILY MOLECULAR CHAPERONE REGULATOR-1 (BCL-

HGNC Symbol	Ensembl ID	Gene Description
SHB	ENSG00000107338	SHB (SRC HOMOLOGY 2 DOMAIN CONTAINING) ADAPTOR PR
EIF3S10	ENSG00000107581	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT
HTATIP2	ENSG00000109854	HIV-1 TAT INTERACTIVE PROTEIN 2, 30KDA; TAT-INTERACTIN
CALCA	ENSG00000110680	CALCITONIN PRECURSOR [CONTAINS: CALCITONIN; KATACA
C6orf108	ENSG00000112667	PUTATIVE C-MYC-RESPONSIVE. [Source:RefSeq;Acc:NM_0064
ACY1	ENSG00000114786	AMINOACYLASE-1 (EC 3.5.1.14) (N-ACYL-L-AMINO-ACID AMID
PASK	ENSG00000115687	PAS DOMAIN CONTAINING SERINE/THREONINE KINASE; PAS-
CEBPZ	ENSG00000115816	CCAAT-BOX-BINDING TRANSCRIPTION FACTOR (CCAAT-BIND
RAP1A	ENSG00000116473	RAS-RELATED PROTEIN RAP-1A (C21KG) (KREV-1 PROTEIN) (
NID	ENSG00000116962	NIDOGEN PRECURSOR (ENTACTIN). [Source:SWISSPROT;Acc
IDE	ENSG00000119912	INSULIN-DEGRADING ENZYME (EC 3.4.24.56) (INSULYSIN) (IN
HOXB7	ENSG00000120087	HOMEOBOX PROTEIN HOX-B7 (HOX-2C) (HHO.C1). [Source:S
GUCY1B2	ENSG00000123201	GUANYLATE CYCLASE SOLUBLE, BETA-2 CHAIN (EC 4.6.1.2) (
SERPINA7	ENSG00000123561	THYROXINE-BINDING GLOBULIN PRECURSOR (T4-BINDING
FPRL2	ENSG00000123859	FMLP-RELATED RECEPTOR II (FMLP-R-II). [Source:SWISSPRO
MTRR	ENSG00000124275	METHIONINE SYNTHASE REDUCTASE, MITOCHONDRIAL PRE
THRA	ENSG00000126351	THYROID HORMONE RECEPTOR ALPHA (C-ERBA-ALPHA) (C-
POR	ENSG00000127948	NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) (
YWHAH	ENSG00000128245	14-3-3 PROTEIN ETA (PROTEIN AS1). [Source:SWISSPROT;Acc
TRIM28	ENSG00000130726	TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (TIF1-BETA
DHX30	ENSG00000132153	DEAD/H (ASP-GLU-ALA-ASP/HIS) BOX POLYPEPTIDE 30 ISOF
CDK8	ENSG00000132964	CELL DIVISION PROTEIN KINASE 8 (EC 2.7.1.-) (PROTEIN KIN
CCNH	ENSG00000134480	CYCLIN H (MO15-ASSOCIATED PROTEIN) (P37) (P34). [Source
RFK	ENSG00000135002	riboflavin kinaseCluster Incl. AF038172:Homo sapiens clone 2392
RABGGTB	ENSG00000137955	GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (E
PLK4	ENSG00000142731	SERINE/THREONINE KINASE 18; SNK AKIN KINASE. [Source:R
CYP4B1	ENSG00000142973	CYTOCHROME P450 4B1 (EC 1.14.14.1) (CYPIVB1) (P450-HP).
TP53BP2	ENSG00000143514	TUMOR SUPPRESSOR P53-BINDING PROTEIN 2 (P53-BINDIN
NVL	ENSG00000143748	NUCLEAR VCP-LIKE; NUCLEAR VALOSIN-CONTAINING PROT
ARF1	ENSG00000143761	ADP-RIBOSYLATION FACTOR 1. [Source:SWISSPROT;Acc:P32
PLK2	ENSG00000145632	SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SER
GZMA	ENSG00000145649	GRANZYME A PRECURSOR (EC 3.4.21.78) (CYTOTOXIC T-LYM
NOLA2	ENSG00000145912	NUCLEOLAR PROTEIN FAMILY A, MEMBER 2; LIKELY HOMOL
HMBS	ENSG00000149397	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8) (HYDROXYMET
ITIH2	ENSG00000151655	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECUR
SACS	ENSG00000151835	spastic ataxia of Charlevoix-Saguenay (sacsin)Cluster Incl. AB018
GABPA	ENSG00000154727	GA-binding protein alpha subunit (GABP-alpha); transcription facto
ETS2	ENSG00000157557	C-ETS-2 PROTEIN.v-ets erythroblastosis virus E26 oncogene ho
IL8RA	ENSG00000163464	HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 R
API5	ENSG00000166181	APOPTOSIS INHIBITOR 5; FIBROBLAST GROWTH FACTOR 2-I
n.a.	ENSG00000166557	MEMBRANE PROTEIN P24B PRECURSOR. [Source:SWISSPRO
ICT1	ENSG00000167862	IMMATURE COLON CARCINOMA TRANSCRIPT 1 (DIGESTION
DFFB	ENSG00000169598	DNA FRAGMENTATION FACTOR 40 KDA SUBUNIT (EC 3.-.-.-) (
USP7	ENSG00000171616	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15
PAP	ENSG00000172016	PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR. [Sourc
BSG	ENSG00000172270	BASIGIN PRECURSOR (LEUKOCYTE ACTIVATION ANTIGEN M
YIF1	ENSG00000174851	YIP1P-INTERACTING FACTOR; PUTATIVE RAB5-INTERACTING
POLE	ENSG00000177084	DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A (EC 2.7.7
		cDNA DKFZp586E1120Cluster Incl. AL049437:Homo sapiens mR

HGNC Symbol	regulation_48h	Ontology	Group	ratioDiff _8Tc vs 100Tc
MYC	induced (448)		[Not included]	2.3764
CACNA1G	induced (448)	Miscellanous	group01_(11)	4.84187
NME1	induced (448)	Cell cycle	group01_(11)	2.30844
ADCY2	induced (448)	Signal Transductic	group01_(11)	3.61493
C4orf9	induced (448)	Miscellanous	group01_(11)	3.96701
FKBP5	induced (448)	Miscellanous	group01_(11)	2.24702
CRKL	induced (448)	Miscellanous	group01_(11)	2.46796
RFC5	induced (448)	Cell cycle	group01_(11)	5.25137
PPP2CA	induced (448)	Signal Transductic	group01_(11)	2.70384
TIMM8A	induced (448)	Metabolism	group01_(11)	4.01599
n.a.	induced (448)	Metabolism	group01_(11)	2.25686
MAD2L1	induced (448)	Cell cycle	group01_(11)	5.52907
MRPL12	induced (448)	Protein Synthesis	group02_(25)	1.50055
NME1	induced (448)	Cell cycle	group02_(25)	1.89026
METTL1	induced (448)	Protein Synthesis	group02_(25)	1.35741
SLC7A5	induced (448)	Protein Synthesis	group02_(25)	1.51645
SRM	induced (448)	Metabolism	group02_(25)	1.57055
IL1B	induced (448)	Signal Transductic	group02_(25)	1.62763
PAICS	induced (448)	Cell cycle	group02_(25)	1.59223
TOMM40	induced (448)	Metabolism	group02_(25)	1.66341
PYCR1	induced (448)	Metabolism	group02_(25)	1.86158
UMPK	induced (448)	Cell cycle	group02_(25)	1.54319
LRP8	induced (448)	Metabolism	group02_(25)	0.45412
DUSP14	induced (448)	Signal Transductic	group02_(25)	0.52046
METAP1	induced (448)	Metabolism	group02_(25)	1.61905
ABCE1	induced (448)	Metabolism	group02_(25)	1.86434
PA2G4	induced (448)	Cell cycle	group02_(25)	1.44826
BOP1	induced (448)	Protein Synthesis	group02_(25)	1.48379
RANBP1	induced (448)	Signal Transductic	group02_(25)	1.5814
CTPS	induced (448)	Cell cycle	group02_(25)	1.89059
TRAP1	induced (448)	Apoptosis	group02_(25)	1.70988
HSPD1	induced (448)	Metabolism	group02_(25)	1.56801
PFAS	induced (448)	Cell cycle	group02_(25)	1.45025
TEAD4	induced (448)	Transcription	group02_(25)	1.48622
MIF	induced (448)	Signal Transductic	group02_(25)	1.5809
VARS2	induced (448)	Protein Synthesis	group02_(25)	1.60541
CENTG1	induced (448)	Signal Transductic	group02_(25)	1.63124
DSCR2	induced (448)	Miscellanous	group03_(50)	1.34626
JAG2	induced (448)	Signal Transductic	group03_(50)	1.20535
PRKAR1B	induced (448)	Signal Transductic	group03_(50)	1.2126
n.a.	induced (448)	Signal Transductic	group03_(50)	0.99649
MATK	induced (448)	Signal Transductic	group03_(50)	0.36648
IARS	induced (448)	Protein Synthesis	group03_(50)	1.2073
GAL	induced (448)	Signal Transductic	group03_(50)	1.92922
MCAM	induced (448)	Adhesion	group03_(50)	1.73848
CAD	induced (448)	Cell cycle	group03_(50)	1.28346
FH	induced (448)	Metabolism	group03_(50)	1.34544
SRPK1	induced (448)	Signal Transductic	group03_(50)	1.26191
NEFH	induced (448)	Miscellanous	group03_(50)	13.4611
NP	induced (448)	Cell cycle	group03_(50)	1.36814
AHCY	induced (448)	Metabolism	group03_(50)	1.3206
POLD2	induced (448)	Cell cycle	group03_(50)	1.13536
C1QBP	induced (448)	Immunity/Inflamma	group03_(50)	1.42593
CAMKK2	induced (448)	Signal Transductic	group03_(50)	1.45735
n.a.	induced (448)	Miscellanous	group03_(50)	1.4522
BYSL	induced (448)	Adhesion	group03_(50)	1.52071
NUP155	induced (448)	Metabolism	group03_(50)	0.71143

HGNC Symbol	**regulation_48h**	**Ontology**	**Group**	**ratioDiff _8Tc vs 100Tc**
IFRD2	induced (448)	Metabolism	group03_(50)	1.37324
MRPL3	induced (448)	Protein Synthesis	group03_(50)	1.39505
HSPE1	induced (448)	Metabolism	group03_(50)	1.47264
HSPE1	induced (448)	Metabolism	group03_(50)	1.31557
n.a.	induced (448)	Miscellanous	group03_(50)	1.06385
EBNA1BP2	induced (448)	Protein Synthesis	group03_(50)	1.38291
TNFRSF8	induced (448)	Signal Transductic	group03_(50)	0.84576
PRDX4	induced (448)	Metabolism	group03_(50)	1.61226
CSE1L	induced (448)	Metabolism	group03_(50)	1.00579
RPP40	induced (448)	Protein Synthesis	group03_(50)	1.40911
n.a.	induced (448)	Miscellanous	group03_(50)	4.22989
HRMT1L2	induced (448)	Signal Transductic	group03_(50)	1.36716
n.a.	induced (448)	Miscellanous	group03_(50)	1.16959
n.a.	induced (448)	Metabolism	group03_(50)	0.93658
MADH4	induced (448)	Signal Transductic	group03_(50)	1.29848
IL9	induced (448)	Signal Transductic	group03_(50)	1.44342
PDCD11	induced (448)	Miscellanous	group03_(50)	1.41629
HK2	induced (448)	Metabolism	group03_(50)	0.12912
PWP2H	induced (448)	Signal Transductic	group03_(50)	1.42152
n.a.	induced (448)	Signal Transductic	group03_(50)	1.87657
NOLC1	induced (448)	Protein Synthesis	group03_(50)	1.42724
NOLC1	induced (448)	Protein Synthesis	group03_(50)	1.58858
CCT2	induced (448)	Metabolism	group03_(50)	1.17485
DTYMK	induced (448)	Cell cycle	group03_(50)	1.60379
HNRPAB	induced (448)	Metabolism	group03_(50)	1.42246
FASN	induced (448)	Metabolism	group03_(50)	1.42041
FASN	induced (448)	Metabolism	group03_(50)	1.64671
NMB	induced (448)	Signal Transductic	group03_(50)	2.16172
CHC1	induced (448)	Cell cycle	group03_(50)	1.57608
	induced (448)	Miscellanous	group03_(50)	1.54568
KIAA0179	induced (448)	Metabolism	group04_(39)	0.93285
NTHL1	induced (448)	Cell cycle	group04_(39)	1.3775
UNG	induced (448)	Metabolism	group04_(39)	1.10324
KIAA0020	induced (448)	Miscellanous	group04_(39)	1.22065
n.a.	induced (448)	Protein Synthesis	group04_(39)	1.40369
n.a.	induced (448)	Miscellanous	group04_(39)	1.18203
POLE2	induced (448)	Cell cycle	group04_(39)	1.19014
MTHFD1	induced (448)	Metabolism	group04_(39)	1.51045
NOL5A	induced (448)	Protein Synthesis	group04_(39)	1.27464
PRPS2	induced (448)	Cell cycle	group04_(39)	1.1839
RUVBL2	induced (448)	Cell cycle	group04_(39)	1.26719
GPI	induced (448)	Metabolism	group04_(39)	1.24742
n.a.	induced (448)	Transcription	group04_(39)	1.43075
NPM3	induced (448)	Protein Synthesis	group04_(39)	1.50033
n.a.	induced (448)	Miscellanous	group04_(39)	1.03437
CDC20	induced (448)	Cell cycle	group04_(39)	1.38226
n.a.	induced (448)	Miscellanous	group04_(39)	1.19051
PRKDC	induced (448)	Signal Transductic	group04_(39)	1.33767
CKS2	induced (448)	Cell cycle	group04_(39)	0.97911
CSE1L	induced (448)	Metabolism	group04_(39)	1.18278
EEF1E1	induced (448)	Protein Synthesis	group04_(39)	1.52508
HRMT1L2	induced (448)	Signal Transductic	group04_(39)	1.10747
n.a.	induced (448)	Cell cycle	group04_(39)	1.78281
TST	induced (448)	Metabolism	group04_(39)	1.6905
DKC1	induced (448)	Protein Synthesis	group04_(39)	1.21105
RAN	induced (448)	Signal Transductic	group04_(39)	1.38926
PDGFRA	induced (448)	Signal Transductic	group04_(39)	1.32091

HGNC Symbol	**regulation_48h**	**Ontology**	**Group**	**ratioDiff _8Tc vs 100Tc**
CDK4	induced (448)	Cell cycle	group04_(39)	3.17761
ALDH1B1	induced (448)	Metabolism	group04_(39)	1.45133
SORD	induced (448)	Metabolism	group04_(39)	1.35875
BDH	induced (448)	Metabolism	group04_(39)	1.26823
GMPS	induced (448)	Cell cycle	group04_(39)	1.22531
GPR30	induced (448)	Signal Transductic	group04_(39)	0.9772
PHB	induced (448)	Miscellanous	group04_(39)	1.19489
STRA13	induced (448)	Miscellanous	group04_(39)	1.75175
XPOT	induced (448)	Metabolism	group04_(39)	1.13386
SMN1	induced (448)	Metabolism	group04_(39)	1.29156
CHC1	induced (448)	Cell cycle	group04_(39)	1.16129
PLK1	induced (448)	Cell cycle	group04_(39)	1.08143
n.a.	induced (448)	Metabolism	group05_(55)	1.21388
AK2	induced (448)	Metabolism	group05_(55)	1.21653
n.a.	induced (448)	Cell cycle	group05_(55)	1.15509
MGST1	induced (448)	Metabolism	group05_(55)	1.26971
CSDA	induced (448)	Transcription	group05_(55)	1.1875
n.a.	induced (448)	Metabolism	group05_(55)	0.83981
ATP1B3	induced (448)	Metabolism	group05_(55)	1.17977
BCS1L	induced (448)	Miscellanous	group05_(55)	1.15293
UNG	induced (448)	Cell cycle	group05_(55)	1.44215
PBP	induced (448)	Metabolism	group05_(55)	1.04448
CDC6	induced (448)	Cell cycle	group05_(55)	1.34424
CDC7	induced (448)	Cell cycle	group05_(55)	1.1793
MTAP	induced (448)	Cell cycle	group05_(55)	0.63939
ADSL	induced (448)	Cell cycle	group05_(55)	1.29939
CDKN3	induced (448)	Cell cycle	group05_(55)	1.36766
VRK1	induced (448)	Signal Transductic	group05_(55)	1.05866
WFDC2	induced (448)	Miscellanous	group05_(55)	0.95987
GSPT1	induced (448)	Miscellanous	group05_(55)	1.2805
SLC39A14	induced (448)	Metabolism	group05_(55)	0.92228
n.a.	induced (448)	Signal Transductic	group05_(55)	1.36447
RLN2	induced (448)	Signal Transductic	group05_(55)	1.71085
BAG2	induced (448)	Apoptosis	group05_(55)	0.92007
HSD17B8	induced (448)	Metabolism	group05_(55)	0.83211
UCHL3	induced (448)	Metabolism	group05_(55)	0.98653
NME2	induced (448)	Cell cycle	group05_(55)	1.37431
MRPS12	induced (448)	Protein Synthesis	group05_(55)	1.27927
PCNA	induced (448)	Cell cycle	group05_(55)	1.26589
DPH2L2	induced (448)	Metabolism	group05_(55)	0.93668
CCNB1	induced (448)	Cell cycle	group05_(55)	1.07985
MC1R	induced (448)	Metabolism	group05_(55)	0.93349
SOD1	induced (448)	Metabolism	group05_(55)	1.33609
ATP5G3	induced (448)	Metabolism	group05_(55)	1.27248
CCT3	induced (448)	Metabolism	group05_(55)	1.19447
RFC4	induced (448)	Cell cycle	group05_(55)	1.30828
CDC25A	induced (448)	Cell cycle	group05_(55)	1.06288
FRDA	induced (448)	Metabolism	group05_(55)	1.04946
SNRPD1	induced (448)	Metabolism	group05_(55)	1.16123
CHAF1A	induced (448)	Cell cycle	group05_(55)	1.3222
PRDX2	induced (448)	Metabolism	group05_(55)	1.28746
BUB1	induced (448)	Cell cycle	group05_(55)	1.0375
CDC2	induced (448)	Cell cycle	group05_(55)	1.24944
POLR1C	induced (448)	Protein Synthesis	group05_(55)	1.3731
SLC19A1	induced (448)	Metabolism	group05_(55)	0.11568
TOMM20	induced (448)	Metabolism	group05_(55)	1.23424
MMP3	induced (448)	Signal Transductic	group05_(55)	1.18776

HGNC Symbol	regulation_48h	Ontology	Group	ratioDiff _8Tc vs 100Tc
UBE2C	induced (448)	Miscellanous	group05_(55)	1.2387
PTPN2	induced (448)	Signal Transductic	group05_(55)	1.5487
RUVBL1	induced (448)	Transcription	group05_(55)	1.24152
TYMS	induced (448)	Cell cycle	group05_(55)	1.30425
DDX10	induced (448)	Protein Synthesis	group05_(55)	0.92391
TUFM	induced (448)	Protein Synthesis	group05_(55)	1.3219
AURKB	induced (448)	Cell cycle	group05_(55)	1.65691
RRS1	induced (448)	Protein Synthesis	group05_(55)	0.72559
GEMIN4	induced (448)	Metabolism	group05_(55)	1.25902
PTMA	induced (448)	Miscellanous	group05_(55)	1.36491
CYP51A1	induced (448)	Metabolism	group06_(67)	1.04909
ARHGEF5	induced (448)	Signal Transductic	group06_(67)	1.6733
KIAA0690	induced (448)	Miscellanous	group06_(67)	0.95603
VDAC1	induced (448)	Metabolism	group06_(67)	1.00989
DDX1	induced (448)	Protein Synthesis	group06_(67)	1.25202
SCAMP1	induced (448)	Metabolism	group06_(67)	0.57469
DDX18	induced (448)	Protein Synthesis	group06_(67)	1.15068
PES1	induced (448)	Protein Synthesis	group06_(67)	1.14414
RANGAP1	induced (448)	Signal Transductic	group06_(67)	1.01559
APEX1	induced (448)	Cell cycle	group06_(67)	1.33419
MYBL2	induced (448)	Transcription	group06_(67)	1.29557
USP10	induced (448)	Metabolism	group06_(67)	1.01975
n.a.	induced (448)	Miscellanous	group06_(67)	0.76092
RPA3	induced (448)	Cell cycle	group06_(67)	1.41483
CXCL12	induced (448)	Signal Transductic	group06_(67)	1.00046
n.a.	induced (448)	Miscellanous	group06_(67)	0.97915
MCM3	induced (448)	Cell cycle	group06_(67)	1.79011
GMNN	induced (448)	Miscellanous	group06_(67)	0.99417
HSPA9B	induced (448)	Metabolism	group06_(67)	1.04121
TCERG1	induced (448)	Transcription	group06_(67)	0.80809
RNU3IP2	induced (448)	Metabolism	group06_(67)	1.0667
SFRS7	induced (448)	Metabolism	group06_(67)	1.22445
MSH6	induced (448)	Cell cycle	group06_(67)	1.15211
CENPF	induced (448)	Cell cycle	group06_(67)	1.08356
MXI1	induced (448)	Transcription	group06_(67)	1.24438
AMD1	induced (448)	Metabolism	group06_(67)	0.97734
ELK1	induced (448)	Transcription	group06_(67)	0.99305
ILF3	induced (448)	Signal Transductic	group06_(67)	1.23164
TFDP1	induced (448)	Transcription	group06_(67)	1.03834
n.a.	induced (448)	Protein Synthesis	group06_(67)	1.00754
TOP2A	induced (448)	Cell cycle	group06_(67)	1.12853
EIF5A	induced (448)	Protein Synthesis	group06_(67)	1.12484
n.a.	induced (448)	Miscellanous	group06_(67)	1.02357
n.a.	induced (448)	Metabolism	group06_(67)	1.23476
ATIC	induced (448)	Cell cycle	group06_(67)	1.12373
ATIC	induced (448)	Cell cycle	group06_(67)	1.21664
PEX5	induced (448)	Metabolism	group06_(67)	1.07918
TAF4B	induced (448)	Transcription	group06_(67)	1.02797
HDGF	induced (448)	Signal Transductic	group06_(67)	1.22358
HDGF	induced (448)	Signal Transductic	group06_(67)	1.28071
ILF2	induced (448)	Signal Transductic	group06_(67)	1.20744
CCNA2	induced (448)	Cell cycle	group06_(67)	1.19313
MDH2	induced (448)	Metabolism	group06_(67)	1.22058
PEG10	induced (448)	Miscellanous	group06_(67)	1.44959
PPRC1	induced (448)	Signal Transductic	group06_(67)	0.94437
SSRP1	induced (448)	Transcription	group06_(67)	1.24561
PTK9	induced (448)	Signal Transductic	group06_(67)	1.34615

HGNC Symbol	**regulation_48h**	**Ontology**	**Group**	**ratioDiff _8Tc vs 100Tc**
ACSL1	induced (448)	Metabolism	group06_(67)	0.91687
PFKM	induced (448)	Metabolism	group06_(67)	1.28262
HNRPDL	induced (448)	Metabolism	group06_(67)	1.04157
RPIA	induced (448)	Metabolism	group06_(67)	0.94101
SLC16A1	induced (448)	Metabolism	group06_(67)	0.41351
KCNJ6	induced (448)	Metabolism	group06_(67)	1.2786
SFRS2	induced (448)	Metabolism	group06_(67)	1.02704
PRKCI	induced (448)	Signal Transductic	group06_(67)	0.84682
POLR2H	induced (448)	Transcription	group06_(67)	1.32116
ABCE1	induced (448)	Metabolism	group06_(67)	0.6866
MELK	induced (448)	Signal Transductic	group06_(67)	1.27441
DDX21	induced (448)	Protein Synthesis	group06_(67)	0.74002
SSSCA1	induced (448)	Miscellanous	group06_(67)	1.12711
n.a.	induced (448)	Miscellanous	group06_(67)	1.21357
HSPCA	induced (448)	Metabolism	group06_(67)	0.98101
DEAF1	induced (448)	Transcription	group06_(67)	1.06629
n.a.	induced (448)	Miscellanous	group06_(67)	1.0083
EIF1AX	induced (448)	Protein Synthesis	group06_(67)	0.8281
n.a.	induced (448)	Miscellanous	group06_(67)	1.21652
n.a.	induced (448)	Miscellanous	group06_(67)	1.09651
SF3A3	induced (448)	Metabolism	group07_(37)	1.05147
n.a.	induced (448)	Miscellanous	group07_(37)	1.42716
AK2	induced (448)	Cell cycle	group07_(37)	0.89803
PLAUR	induced (448)	Signal Transductic	group07_(37)	1.02257
SCARB1	induced (448)	Adhesion	group07_(37)	0.77152
MCM2	induced (448)	Cell cycle	group07_(37)	1.24398
EXOSC7	induced (448)	Protein Synthesis	group07_(37)	1.21598
KHSRP	induced (448)	Metabolism	group07_(37)	1.03021
NUDC	induced (448)	Miscellanous	group07_(37)	1.26719
CGRRF1	induced (448)	Cell cycle	group07_(37)	1.0118
APEX1	induced (448)	Cell cycle	group07_(37)	1.09852
GARS	induced (448)	Protein Synthesis	group07_(37)	1.19488
EIF3S9	induced (448)	Protein Synthesis	group07_(37)	1.21527
IMPDH1	induced (448)	Metabolism	group07_(37)	1.16639
VEGF	induced (448)	Signal Transductic	group07_(37)	1.87363
TFDP2	induced (448)	Transcription	group07_(37)	1.10912
PRDX1	induced (448)	Metabolism	group07_(37)	1.05206
SCO2	induced (448)	Metabolism	group07_(37)	1.11537
TUBG1	induced (448)	Metabolism	group07_(37)	1.14335
MYCN	induced (448)	Transcription	group07_(37)	1.12384
ABL2	induced (448)	Signal Transductic	group07_(37)	1.42956
SLC20A1	induced (448)	Metabolism	group07_(37)	1.1411
CDKN2B	induced (448)	Cell cycle	group07_(37)	1.64573
n.a.	induced (448)	Miscellanous	group07_(37)	1.10775
FANCG	induced (448)	Cell cycle	group07_(37)	1.35147
PMPCA	induced (448)	Metabolism	group07_(37)	1.12328
PSMC3	induced (448)	Metabolism	group07_(37)	1.32879
MCM7	induced (448)	Cell cycle	group07_(37)	1.48747
ABCA3	induced (448)	Metabolism	group07_(37)	0.9891
EIF4EBP1	induced (448)	Protein Synthesis	group07_(37)	1.151
TNFRSF4	induced (448)	Signal Transductic	group07_(37)	1.27171
SRP72	induced (448)	Metabolism	group07_(37)	1.00404
ALG3	induced (448)	Metabolism	group07_(37)	0.90013
CKS1B	induced (448)	Cell cycle	group07_(37)	1.08272
NSEP1	induced (448)	Transcription	group07_(37)	1.00877
FARSLA	induced (448)	Protein Synthesis	group07_(37)	1.12775
PRIM1	induced (448)	Cell cycle	group07_(37)	1.01017

HGNC Symbol	regulation_48h	Ontology	Group	ratioDiff _8Tc vs 100Tc
TBL3	induced (448)	Signal Transductic	group08_(44)	1.03572
JUND	induced (448)	Transcription	group08_(44)	1.29562
PTBP1	induced (448)	Metabolism	group08_(44)	1.1253
MRE11A	induced (448)	Cell cycle	group08_(44)	1.12138
HSPA5	induced (448)	Metabolism	group08_(44)	1.12893
OAT	induced (448)	Metabolism	group08_(44)	1.0997
TFRC	induced (448)	Metabolism	group08_(44)	1.04406
SHMT1	induced (448)	Metabolism	group08_(44)	1.01202
CLNS1A	induced (448)	Metabolism	group08_(44)	1.17999
SEMA3C	induced (448)	Immunity/Inflamma	group08_(44)	1.4029
MCAM	induced (448)	Adhesion	group08_(44)	0.98349
MAPKAPK5	induced (448)	Signal Transductic	group08_(44)	1.18476
SIP1	induced (448)	Metabolism	group08_(44)	1.06483
NF2	induced (448)	Metabolism	group08_(44)	1.15812
SLC1A5	induced (448)	Metabolism	group08_(44)	1.47504
PSMA2	induced (448)	Metabolism	group08_(44)	1.18952
RAD51C	induced (448)	Cell cycle	group08_(44)	1.07359
CTSC	induced (448)	Apoptosis	group08_(44)	0.95852
HSPA8	induced (448)	Metabolism	group08_(44)	1.08507
n.a.	induced (448)	Miscellanous	group08_(44)	0.511
IGFBP2	induced (448)	Signal Transductic	group08_(44)	1.05091
DARS	induced (448)	Protein Synthesis	group08_(44)	1.08118
UCHL3	induced (448)	Metabolism	group08_(44)	1.02202
GTF3A	induced (448)	Transcription	group08_(44)	0.97068
RPL5	induced (448)	Protein Synthesis	group08_(44)	1.12898
AMD1	induced (448)	Metabolism	group08_(44)	0.73975
HSPA1A	induced (448)	Metabolism	group08_(44)	2.23581
SYNGR3	induced (448)	Miscellanous	group08_(44)	0.89946
NINJ1	induced (448)	Adhesion	group08_(44)	0.24112
SNRPA1	induced (448)	Metabolism	group08_(44)	1.1024
TAF9	induced (448)	Transcription	group08_(44)	1.12279
SYNCRIP	induced (448)	Metabolism	group08_(44)	1.32004
n.a.	induced (448)	Cell cycle	group08_(44)	1.22827
ITGB3BP	induced (448)	Adhesion	group08_(44)	1.11119
PTPRF	induced (448)	Signal Transductic	group08_(44)	1.07111
CHEK1	induced (448)	Cell cycle	group08_(44)	1.01791
TCEB1	induced (448)	Transcription	group08_(44)	1.05153
n.a.	induced (448)	Miscellanous	group08_(44)	0.90476
VBP1	induced (448)	Metabolism	group08_(44)	0.914
BUB1B	induced (448)	Cell cycle	group08_(44)	1.15887
RACGAP1	induced (448)	Signal Transductic	group08_(44)	0.88986
AK3	induced (448)	Cell cycle	group08_(44)	1.69248
HNRPF	induced (448)	Metabolism	group08_(44)	1.23193
PDAP1	induced (448)	Signal Transductic	group08_(44)	1.03511
SELE	induced (448)	Adhesion	group09_(47)	1.27826
n.a.	induced (448)	Miscellanous	group09_(47)	1.14839
RCN1	induced (448)	Metabolism	group09_(47)	0.23216
GLDC	induced (448)	Metabolism	group09_(47)	0.53743
PMS1	induced (448)	Cell cycle	group09_(47)	1.07045
PFKP	induced (448)	Metabolism	group09_(47)	0.90664
PDCD2	induced (448)	Apoptosis	group09_(47)	1.04283
MGST2	induced (448)	Metabolism	group09_(47)	1.28168
NDUFB7	induced (448)	Metabolism	group09_(47)	1.16558
G22P1	induced (448)	Cell cycle	group09_(47)	1.21622
n.a.	induced (448)	Miscellanous	group09_(47)	1.32008
PBEF1	induced (448)	Signal Transductic	group09_(47)	0.68784
TBL2	induced (448)	Miscellanous	group09_(47)	0.98072

HGNC Symbol	**regulation_48h**	**Ontology**	**Group**	**ratioDiff _8Tc vs 100Tc**
GCN5L2	induced (448)	Protein Synthesis	group09_(47)	0.81582
CDK2AP1	induced (448)	Cell cycle	group09_(47)	1.21604
NOL1	induced (448)	Protein Synthesis	group09_(47)	1.17826
SLC29A1	induced (448)	Metabolism	group09_(47)	1.03641
BNIP1	induced (448)	Apoptosis	group09_(47)	1.51801
DBN1	induced (448)	Metabolism	group09_(47)	0.97252
EIF4G1	induced (448)	Protein Synthesis	group09_(47)	1.11453
B4GALT2	induced (448)	Metabolism	group09_(47)	0.55927
TMEM5	induced (448)	Signal Transductic	group09_(47)	0.85335
FVT1	induced (448)	Miscellanous	group09_(47)	0.2208
ETF1	induced (448)	Protein Synthesis	group09_(47)	0.96041
ATF4	induced (448)	Transcription	group09_(47)	1.05744
ILF3	induced (448)	Transcription	group09_(47)	1.16996
RAMP1	induced (448)	Metabolism	group09_(47)	1.42907
n.a.	induced (448)	Signal Transductic	group09_(47)	1.08658
ADCY3	induced (448)	Signal Transductic	group09_(47)	0.61993
AFG3L2	induced (448)	Metabolism	group09_(47)	1.12675
PRPS1	induced (448)	Cell cycle	group09_(47)	1.13059
OPRS1	induced (448)	Metabolism	group09_(47)	0.37851
TOMM70A	induced (448)	Metabolism	group09_(47)	1.21096
APRT	induced (448)	Cell cycle	group09_(47)	1.29353
FGFR4	induced (448)	Signal Transductic	group09_(47)	0.69969
DEFA6	induced (448)	Miscellanous	group09_(47)	1.18016
ZNF9	induced (448)	Transcription	group09_(47)	1.6475
RAC3	induced (448)	Signal Transductic	group09_(47)	0.12015
WNT10B	induced (448)	Signal Transductic	group09_(47)	3.05265
NFRKB	induced (448)	Transcription	group09_(47)	1.30406
CDK5R2	induced (448)	Cell cycle	group09_(47)	1.17064
CYCS	induced (448)	Metabolism	group09_(47)	0.13868
YES1	induced (448)	Signal Transductic	group09_(47)	1.00449
DLEU1	induced (448)	Miscellanous	group09_(47)	1.07807
BNIP3	induced (448)	Apoptosis	group09_(47)	0.95028
RAD23A	induced (448)	Cell cycle	group09_(47)	1.12355
	induced (448)	Miscellanous	group09_(47)	0.41569
UBE2G2	induced (448)	Metabolism	group10_(72)	1.25227
KCNQ3	induced (448)	Metabolism	group10_(72)	0.8407
MTA1	induced (448)	Transcription	group10_(72)	1.11265
LIG3	induced (448)	Cell cycle	group10_(72)	1.30475
ITGA2B	induced (448)	Signal Transductic	group10_(72)	1.37088
TOMM34	induced (448)	Metabolism	group10_(72)	1.16749
ITIH4	induced (448)	Miscellanous	group10_(72)	1.03377
POLD1	induced (448)	Cell cycle	group10_(72)	1.21528
IKBKAP	induced (448)	Signal Transductic	group10_(72)	1.08096
ASNS	induced (448)	Protein Synthesis	group10_(72)	0.78433
MX1	induced (448)	Signal Transductic	group10_(72)	1.21969
XRCC5	induced (448)	Cell cycle	group10_(72)	1.63313
XPO1	induced (448)	Metabolism	group10_(72)	1.0894
RAD54L	induced (448)	Cell cycle	group10_(72)	1.30816
PTHLH	induced (448)	Signal Transductic	group10_(72)	0.58548
MSH2	induced (448)	Cell cycle	group10_(72)	1.17264
CDKL1	induced (448)	Cell cycle	group10_(72)	0.9063
ADA	induced (448)	Metabolism	group10_(72)	1.08888
n.a.	induced (448)	Miscellanous	group10_(72)	1.08238
TGFB1	induced (448)	Signal Transductic	group10_(72)	0.72051
NPTX2	induced (448)	Adhesion	group10_(72)	0.41935
BAG1	induced (448)	Apoptosis	group10_(72)	1.2899
BAG1	induced (448)	Apoptosis	group10_(72)	1.15374

HGNC Symbol	regulation_48h	Ontology	Group	ratioDiff _8Tc vs 100Tc
SHB	induced (448)	Signal Transductic	group10_(72)	0.86843
EIF3S10	induced (448)	Protein Synthesis	group10_(72)	0.92623
HTATIP2	induced (448)	Transcription	group10_(72)	1.45903
CALCA	induced (448)	Signal Transductic	group10_(72)	1.13444
C6orf108	induced (448)	Miscellanous	group10_(72)	1.19198
ACY1	induced (448)	Metabolism	group10_(72)	1.49339
PASK	induced (448)	Signal Transductic	group10_(72)	0.78773
CEBPZ	induced (448)	Transcription	group10_(72)	0.9466
RAP1A	induced (448)	Signal Transductic	group10_(72)	0.76155
NID	induced (448)	Adhesion	group10_(72)	1.25385
IDE	induced (448)	Signal Transductic	group10_(72)	1.05635
HOXB7	induced (448)	Transcription	group10_(72)	1.26641
GUCY1B2	induced (448)	Signal Transductic	group10_(72)	1.2161
SERPINA7	induced (448)	Miscellanous	group10_(72)	0.87814
FPRL2	induced (448)	Signal Transductic	group10_(72)	1.14439
MTRR	induced (448)	Metabolism	group10_(72)	0.87687
THRA	induced (448)	Signal Transductic	group10_(72)	0.99733
POR	induced (448)	Metabolism	group10_(72)	1.141
YWHAH	induced (448)	Signal Transductic	group10_(72)	1.02239
TRIM28	induced (448)	Transcription	group10_(72)	1.3573
DHX30	induced (448)	Miscellanous	group10_(72)	1.06363
CDK8	induced (448)	Transcription	group10_(72)	0.56615
CCNH	induced (448)	Transcription	group10_(72)	1.06268
RFK	induced (448)	Metabolism	group10_(72)	1.23926
RABGGTB	induced (448)	Metabolism	group10_(72)	1.16822
PLK4	induced (448)	Signal Transductic	group10_(72)	1.14971
CYP4B1	induced (448)	Metabolism	group10_(72)	1.21661
TP53BP2	induced (448)	Signal Transductic	group10_(72)	2.73204
NVL	induced (448)	Miscellanous	group10_(72)	0.92542
ARF1	induced (448)	Signal Transductic	group10_(72)	1.08929
PLK2	induced (448)	Signal Transductic	group10_(72)	0.91806
GZMA	induced (448)	Immunity/Inflamma	group10_(72)	1.76904
NOLA2	induced (448)	Protein Synthesis	group10_(72)	3.37019
HMBS	induced (448)	Metabolism	group10_(72)	1.21367
ITIH2	induced (448)	Miscellanous	group10_(72)	0.8581
SACS	induced (448)	Metabolism	group10_(72)	0.29733
GABPA	induced (448)	Transcription	group10_(72)	1.17483
ETS2	induced (448)	Transcription	group10_(72)	0.68972
IL8RA	induced (448)	Signal Transductic	group10_(72)	1.03057
API5	induced (448)	Apoptosis	group10_(72)	0.993
n.a.	induced (448)	Metabolism	group10_(72)	1.04228
ICT1	induced (448)	Protein Synthesis	group10_(72)	0.9037
DFFB	induced (448)	Apoptosis	group10_(72)	0.9399
USP7	induced (448)	Metabolism	group10_(72)	1.01493
PAP	induced (448)	Immunity/Inflamma	group10_(72)	1.02525
BSG	induced (448)	Signal Transductic	group10_(72)	0.86176
YIF1	induced (448)	Signal Transductic	group10_(72)	1.24813
POLE	induced (448)	Cell cycle	group10_(72)	1.09589
	induced (448)	Miscellanous	group10_(72)	0.35856

HGNC Symbol	ratioDiff_6Tc vs 100Tc	ratioDiff_5Tc vs 100Tc	ratioDiff_4Tc vs 100Tc
MYC	4.81549	6.66592	9.56934
CACNA1G	6.71896	9.27174	4.78749
NME1	3.75328	4.66457	5.73212
ADCY2	2.94268	8.1558	2.17108
C4orf9	2.11863	2.07955	2.42135
FKBP5	4.19037	3.37186	4.83496
CRKL	2.25103	2.99466	4.1095
RFC5	3.76623	7.70054	9.4519
PPP2CA	2.54673	3.85817	4.42124
TIMM8A	4.70979	4.93726	15.42908
n.a.	4.48987	3.55254	5.82794
MAD2L1	15.54284	13.6743	14.60326
MRPL12	2.07637	2.22999	2.65853
NME1	3.26224	3.69856	4.88817
METTL1	2.19881	3.19541	3.88134
SLC7A5	2.69691	2.43193	3.66158
SRM	2.59134	3.29691	3.56176
IL1B	2.07153	2.10507	2.3458
PAICS	2.73837	3.37929	3.91134
TOMM40	2.04021	2.73932	2.72483
PYCR1	2.62304	3.25362	3.87065
UMPK	2.08307	2.52457	2.74736
LRP8	2.24522	4.38339	2.30539
DUSP14	2.60904	5.48787	2.65001
METAP1	2.80028	2.59915	3.22885
ABCE1	2.40818	2.80154	2.43602
PA2G4	2.19245	2.75535	3.12647
BOP1	2.12655	2.40387	2.53434
RANBP1	2.0889	2.69317	2.79258
CTPS	2.17632	2.96327	3.04084
TRAP1	2.76006	2.89325	3.4475
HSPD1	2.38861	3.10118	3.88176
PFAS	2.30469	2.85753	3.12945
TEAD4	2.11858	2.54551	2.64704
MIF	2.15543	2.01053	2.4144
VARS2	2.07228	2.2788	2.42498
CENTG1	2.05212	2.5154	2.9446
DSCR2	1.9494	2.34422	2.83542
JAG2	1.89737	2.4156	2.60547
PRKAR1B	1.82421	3.0025	2.15551
n.a.	1.72121	2.11201	2.49754
MATK	1.70159	2.37402	2.45864
IARS	1.47277	2.09977	2.03272
GAL	1.95403	2.37595	3.6872
MCAM	1.55853	2.36932	2.17634
CAD	1.82868	2.39415	2.6133
FH	1.49852	2.13702	2.32288
SRPK1	1.78077	2.37834	2.58474
NEFH	1.79537	83.04585	22.94621
NP	1.712	2.06789	2.12232
AHCY	1.76625	2.13765	2.65962
POLD2	1.62243	2.27814	2.62605
C1QBP	1.97132	2.35206	2.63978
CAMKK2	1.8368	2.47737	2.97843
n.a.	1.65886	3.06294	2.96822
BYSL	1.9524	2.1623	2.25914
NUP155	0.79647	2.39668	2.38242

HGNC Symbol	**ratioDiff_6Tc vs 100Tc**	**ratioDiff_5Tc vs 100Tc**	**ratioDiff_4Tc vs 100Tc**
IFRD2	1.91314	2.31554	3.36477
MRPL3	1.47536	2.58579	2.71718
HSPE1	1.95572	2.46401	2.81177
HSPE1	1.83745	2.45599	2.90171
n.a.	1.12173	2.0534	2.10568
EBNA1BP2	1.78181	2.31217	2.55573
TNFRSF8	1.90649	2.10192	3.23506
PRDX4	1.92888	2.22135	2.56848
CSE1L	1.56971	2.21557	2.54962
RPP40	0.47104	3.15682	2.93052
n.a.	0.18787	4.97927	5.36059
HRMT1L2	1.83353	2.1637	2.26084
n.a.	1.77896	2.44741	2.14863
n.a.	1.61808	2.10926	2.2726
MADH4	1.72555	2.16611	2.61201
IL9	1.99284	2.05263	2.14009
PDCD11	1.5329	2.07363	2.10016
HK2	1.48275	3.45872	2.9279
PWP2H	1.56456	2.02778	2.06541
n.a.	1.40521	4.18783	3.5851
NOLC1	1.84493	2.20351	2.83921
NOLC1	1.90047	2.27739	2.26511
CCT2	1.51384	2.02355	2.2315
DTYMK	1.90031	2.06492	2.15035
HNRPAB	1.7638	2.1771	2.37648
FASN	1.69942	2.82226	3.38783
FASN	1.8119	2.02061	2.61375
NMB	1.63689	2.68896	2.36896
CHC1	1.72504	2.19078	2.80687
	1.24192	3.02726	3.20113
KIAA0179	1.10468	1.7302	2.29587
NTHL1	1.73718	1.81578	2.44866
UNG	1.62943	1.93033	2.1892
KIAA0020	1.51149	1.95995	2.05543
n.a.	1.76138	1.92484	2.09881
n.a.	1.77363	1.90119	2.27456
POLE2	1.64511	1.64511	2.25067
MTHFD1	1.52793	1.84837	2.16734
NOL5A	1.56604	1.98401	2.14148
PRPS2	1.47776	1.87085	2.04232
RUVBL2	1.71392	1.87034	2.13365
GPI	1.63725	1.80246	2.10822
n.a.	1.8862	1.945	2.18251
NPM3	2.44565	1.94807	2.34684
n.a.	1.74896	1.93653	2.33734
CDC20	2.01262	1.95725	2.45444
n.a.	1.35448	1.80728	2.19751
PRKDC	1.71524	1.9643	2.38681
CKS2	1.51532	1.64931	2.00999
CSE1L	1.65046	1.80897	2.37117
EEF1E1	2.02514	1.88755	2.42838
HRMT1L2	1.51373	1.79676	2.09275
n.a.	1.92799	1.59738	2.44071
TST	2.14819	1.67757	2.06398
DKC1	1.68122	1.89721	2.06805
RAN	1.70135	1.76479	2.24487
PDGFRA	1.45678	1.63785	2.14063

HGNC Symbol	**ratioDiff_6Tc vs 100Tc**	**ratioDiff_5Tc vs 100Tc**	**ratioDiff_4Tc vs 100Tc**
CDK4	5.36344	0.32002	5.43797
ALDH1B1	1.91156	1.73122	2.31769
SORD	2.05131	1.84885	2.47132
BDH	1.13868	1.83818	2.2574
GMPS	1.73284	1.92543	2.16261
GPR30	1.58977	1.51319	2.01867
PHB	1.92382	1.96119	2.10028
STRA13	1.77909	1.94096	2.29173
XPOT	1.83347	1.64499	2.44741
SMN1	1.35767	1.41486	2.08633
CHC1	1.68933	1.79879	2.18224
PLK1	1.49987	1.72055	2.08511
n.a.	1.97105	2.03541	1.84092
AK2	1.51634	1.64201	1.73135
n.a.	1.48892	1.58587	1.93437
MGST1	1.39779	1.62596	1.91053
CSDA	1.49072	1.58357	1.78478
n.a.	1.21551	1.4205	1.57653
ATP1B3	1.4471	1.80614	1.85421
BCS1L	1.53397	1.55436	1.78733
UNG	1.4841	1.68728	1.91587
PBP	1.73045	1.76598	1.92542
CDC6	1.74289	1.54987	1.76963
CDC7	1.66452	2.02226	1.83287
MTAP	1.31137	2.18955	1.95793
ADSL	1.40683	1.73825	1.71136
CDKN3	1.63709	1.8574	1.97721
VRK1	1.26603	1.64609	1.73945
WFDC2	1.26226	1.53946	1.61014
GSPT1	1.42812	1.56346	1.80976
SLC39A14	1.43645	1.78144	1.86249
n.a.	1.74825	1.664	1.83822
RLN2	1.52571	1.63963	1.56957
BAG2	1.3436	1.39729	1.62894
HSD17B8	1.87999	1.68966	1.74418
UCHL3	1.2763	1.66739	1.70436
NME2	1.67396	1.75913	1.92993
MRPS12	1.61773	1.60752	1.9294
PCNA	1.53414	1.75076	1.80126
DPH2L2	1.44138	1.33836	1.89954
CCNB1	1.44683	1.61157	1.90329
MC1R	1.43667	1.97308	1.98634
SOD1	1.43178	1.73899	1.81352
ATP5G3	1.29221	1.69593	1.85203
CCT3	1.61989	1.99064	1.97193
RFC4	1.37322	1.77171	1.88905
CDC25A	2.17229	1.62117	1.56237
FRDA	1.55664	1.65995	1.93501
SNRPD1	1.64985	2.13432	1.99208
CHAF1A	1.66285	1.53828	1.6267
PRDX2	1.57668	1.82956	1.91019
BUB1	1.28399	1.58465	1.69996
CDC2	1.6531	1.85679	1.98708
POLR1C	1.6381	1.64767	1.91436
SLC19A1	0.83645	1.04821	1.47966
TOMM20	1.35635	1.59622	1.80767
MMP3	1.88298	1.97448	1.97642

HGNC Symbol	ratioDiff_6Tc vs 100Tc	ratioDiff_5Tc vs 100Tc	ratioDiff_4Tc vs 100Tc
UBE2C	1.57778	1.74948	1.96342
PTPN2	1.70427	1.94261	1.87898
RUVBL1	1.54869	1.79738	1.90429
TYMS	1.63058	1.70477	1.99201
DDX10	1.29899	1.66308	1.68951
TUFM	1.36602	1.71366	1.77032
AURKB	1.74438	1.5449	1.75756
RRS1	1.38947	1.55856	1.64316
GEMIN4	1.65714	1.9546	1.90466
PTMA	1.48539	1.69408	1.97339
CYP51A1	1.0858	1.37852	1.3979
ARHGEF5	1.19298	0.29935	1.24134
KIAA0690	1.14765	1.5509	1.72484
VDAC1	1.22339	1.33462	1.6755
DDX1	1.25017	1.62039	1.61687
SCAMP1	0.85166	1.35067	1.54701
DDX18	1.18135	1.50316	1.54127
PES1	1.47171	1.71151	1.71442
RANGAP1	1.37388	1.44133	1.48451
APEX1	1.54085	1.67068	1.86064
MYBL2	1.40542	1.52269	1.65744
USP10	0.63669	2.03409	1.69649
n.a.	1.16301	1.73467	1.40168
RPA3	1.65984	1.54568	1.84241
CXCL12	1.41663	1.1107	1.81305
n.a.	1.4152	0.93186	1.92143
MCM3	1.0957	1.7133	1.62388
GMNN	1.49957	1.38504	1.65636
HSPA9B	1.41819	1.50618	1.68934
TCERG1	1.43166	1.41557	1.54893
RNU3IP2	1.37878	1.45174	1.6849
SFRS7	1.36419	1.65024	1.71178
MSH6	1.29411	1.52402	1.84194
CENPF	1.3468	1.72191	1.71199
MXI1	1.3135	1.31743	1.19626
AMD1	1.46884	1.75988	1.81387
ELK1	1.25578	1.25589	1.53549
ILF3	1.27684	1.69743	1.45194
TFDP1	1.30899	1.19587	1.54643
n.a.	1.46097	1.43448	1.63248
TOP2A	1.32611	1.33342	1.72915
EIF5A	1.4407	1.31863	1.61858
n.a.	1.3424	1.48857	2.53246
n.a.	1.26981	1.47297	1.59543
ATIC	1.31938	1.6846	1.784
ATIC	1.34126	1.44386	1.60867
PEX5	1.02944	1.43278	1.44383
TAF4B	1.27715	0.78418	1.59577
HDGF	1.40911	1.43719	1.51037
HDGF	1.40055	1.70753	1.58303
ILF2	1.39121	1.55236	1.55894
CCNA2	1.65893	1.32234	1.69948
MDH2	1.42357	1.73773	1.74186
PEG10	2.46209	2.23414	1.70597
PPRC1	1.31446	1.49879	1.73975
SSRP1	1.35381	1.49549	1.75099
PTK9	0.78374	1.1719	1.95839

HGNC Symbol	ratioDiff_6Tc vs 100Tc	ratioDiff_5Tc vs 100Tc	ratioDiff_4Tc vs 100Tc
ACSL1	1.05562	1.3981	1.38136
PFKM	1.53198	1.85416	1.84244
HNRPDL	1.18311	1.38335	1.43917
RPIA	1.17079	1.51594	1.79342
SLC16A1	1.49252	0.65561	1.86384
KCNJ6	1.44304	1.5021	1.71109
SFRS2	1.11256	1.35913	1.45094
PRKCI	1.32665	1.20011	1.5112
POLR2H	1.68864	1.69291	1.76266
ABCE1	0.96334	1.46254	2.75349
MELK	1.1531	1.28846	1.56933
DDX21	1.68681	1.52334	3.37362
SSSCA1	1.34237	1.48112	1.57811
n.a.	1.32206	1.476	1.63967
HSPCA	1.54057	1.41137	2.02849
DEAF1	1.23974	1.42025	1.57268
n.a.	1.20198	1.71333	1.63954
EIF1AX	1.42727	1.54594	2.14374
n.a.	1.37967	1.55072	1.67411
n.a.	1.18893	1.20466	1.34098
SF3A3	1.3409	1.25199	1.42738
n.a.	1.95846	1.8929	1.52947
AK2	1.03793	1.33934	1.58498
PLAUR	2.31965	4.95749	4.31479
SCARB1	1.34649	1.49581	1.44399
MCM2	1.41763	1.60275	1.58334
EXOSC7	1.49572	1.43067	1.56325
KHSRP	1.19079	1.44352	1.53272
NUDC	1.43608	1.48229	1.47768
CGRRF1	1.34957	1.76849	1.54921
APEX1	1.34581	1.54524	1.63411
GARS	1.19508	1.41018	1.44792
EIF3S9	1.39024	1.52765	1.6301
IMPDH1	1.24664	1.49884	1.44751
VEGF	1.03044	0.96363	1.564
TFDP2	1.01517	1.05677	1.67127
PRDX1	1.26841	1.40978	1.54272
SCO2	1.74361	1.61204	1.97416
TUBG1	1.23565	1.61129	1.80625
MYCN	1.41986	1.40047	1.67606
ABL2	0.96056	1.21173	1.24694
SLC20A1	1.45071	1.99997	1.63072
CDKN2B	2.64784	1.761	1.7792
n.a.	1.21262	1.66423	1.57628
FANCG	1.44508	1.48016	1.65057
PMPCA	1.19616	1.49273	1.29986
PSMC3	1.38664	1.30797	1.52169
MCM7	1.46905	1.57033	1.60345
ABCA3	1.16464	1.64454	1.46588
EIF4EBP1	1.2625	1.32854	1.33156
TNFRSF4	1.31431	1.14723	1.28288
SRP72	1.29724	1.33775	1.58723
ALG3	1.2302	1.2188	1.32756
CKS1B	1.30073	1.56062	1.54686
NSEP1	1.35999	1.42518	1.56026
FARSLA	1.32818	1.3299	1.5047
PRIM1	1.20708	1.28638	1.4941

HGNC Symbol	ratioDiff_6Tc vs 100Tc	ratioDiff_5Tc vs 100Tc	ratioDiff_4Tc vs 100Tc
TBL3	1.23711	1.38175	1.49383
JUND	1.39854	1.31856	1.4348
PTBP1	1.15617	1.36786	1.43175
MRE11A	1.43326	1.30143	1.56588
HSPA5	1.23214	1.30682	1.43533
OAT	1.11385	1.20277	1.7458
TFRC	1.01142	1.1663	1.24182
SHMT1	1.92542	1.33317	1.52502
CLNS1A	1.24154	1.37863	1.39875
SEMA3C	1.42359	2.16307	0.60205
MCAM	1.09568	1.33053	1.38685
MAPKAPK5	1.4306	1.32714	1.30618
SIP1	1.33596	1.3053	1.21266
NF2	1.37248	1.30174	1.45042
SLC1A5	1.57681	2.00982	1.85443
PSMA2	1.17445	1.32753	1.37957
RAD51C	0.98008	1.0806	1.18319
CTSC	1.07321	1.0949	1.36775
HSPA8	1.34564	1.4386	1.63389
n.a.	0.50858	1.19812	0.99952
IGFBP2	1.04942	0.97923	1.20325
DARS	1.05074	1.34506	1.36797
UCHL3	1.1508	1.33321	1.50905
GTF3A	1.1458	1.42162	1.36544
RPL5	1.19306	1.35436	1.54653
AMD1	0.91694	1.35458	1.30986
HSPA1A	2.50251	2.02209	1.68169
SYNGR3	0.98368	1.03472	1.31079
NINJ1	0.90496	0.56941	1.04925
SNRPA1	1.36757	1.42166	1.37707
TAF9	1.16729	1.2921	1.36929
SYNCRIP	1.23111	1.70773	1.75101
n.a.	1.30608	1.3199	1.42706
ITGB3BP	1.23727	1.2678	1.58749
PTPRF	0.78533	1.44589	1.29964
CHEK1	1.28042	1.32372	1.37843
TCEB1	1.12161	1.37051	1.38793
n.a.	1.27772	1.42337	1.38203
VBP1	1.08205	1.15711	1.37953
BUB1B	1.28166	1.57021	1.43236
RACGAP1	1.25419	1.42432	1.59703
AK3	0.97056	3.3664	1.73792
HNRPF	1.2064	1.48182	1.5015
PDAP1	1.36813	1.10505	1.43392
SELE	1.17509	1.34232	1.29611
n.a.	1.22682	1.58391	1.72964
RCN1	0.63597	2.03976	1.55543
GLDC	1.06106	1.17037	1.20599
PMS1	0.88411	1.16837	1.72631
PFKP	1.04765	1.13303	1.15028
PDCD2	1.25076	1.29272	1.53306
MGST2	1.14382	1.24924	1.21992
NDUFB7	1.26941	1.17246	1.36696
G22P1	1.23504	1.37817	1.43209
n.a.	1.16331	1.28916	1.29282
PBEF1	1.26953	1.01908	0.85629
TBL2	1.34037	1.09588	1.5104

HGNC Symbol	ratioDiff_6Tc vs 100Tc	ratioDiff_5Tc vs 100Tc	ratioDiff_4Tc vs 100Tc
GCN5L2	1.18565	1.53618	1.29113
CDK2AP1	1.08947	1.28619	1.29295
NOL1	1.29501	1.16495	1.3197
SLC29A1	0.9107	0.95277	1.23615
BNIP1	2.07308	1.37236	1.52779
DBN1	0.89039	1.15516	1.16155
EIF4G1	1.19633	1.354	1.44219
B4GALT2	1.12376	1.23139	1.11688
TMEM5	1.01788	1.20934	1.2524
FVT1	0.15944	1.58378	1.24199
ETF1	1.41824	1.62946	1.78485
ATF4	1.0212	0.99316	1.15285
ILF3	1.23224	1.46661	1.4456
RAMP1	1.18455	0.61564	1.09466
n.a.	1.19947	1.30391	1.29219
ADCY3	0.79299	0.97611	1.12168
AFG3L2	1.14608	1.2803	1.29512
PRPS1	1.26991	1.04015	1.35957
OPRS1	0.85733	1.15606	1.0864
TOMM70A	1.51196	1.42919	1.9022
APRT	1.44246	1.38176	1.46593
FGFR4	1.09695	0.62692	1.13336
DEFA6	1.87951	0.81984	1.95287
ZNF9	2.00292	2.18833	7.24229
RAC3	0.19521	3.4411	2.48214
WNT10B	0.90817	4.32133	3.7414
NFRKB	1.39616	0.97651	1.60998
CDK5R2	0.31257	1.16259	0.68765
CYCS	0.81954	2.38292	1.82884
YES1	1.00476	0.93581	1.22672
DLEU1	1.17498	1.12858	1.32786
BNIP3	1.09549	1.0033	1.14375
RAD23A	1.1333	1.27838	1.39914
	1.3958	3.78709	1.72
UBE2G2	1.18656	1.37832	1.45728
KCNQ3	1.01398	0.63747	0.65028
MTA1	1.13924	1.0163	1.18657
LIG3	1.14915	0.99918	1.32903
ITGA2B	1.28758	1.89885	1.71598
TOMM34	0.90409	0.35709	2.44076
ITIH4	1.20227	1.2289	1.44091
POLD1	1.27841	1.23885	1.32148
IKBKAP	0.9328	1.18483	1.22793
ASNS	0.8199	0.87529	1.18092
MX1	0.81876	1.01753	1.3563
XRCC5	1.55747	1.89786	2.07611
XPO1	1.11758	1.31164	1.39555
RAD54L	1.68937	1.70003	1.422
PTHLH	0.93206	1.28298	0.26569
MSH2	1.22944	1.39876	1.67335
CDKL1	1.27422	2.59521	1.17348
ADA	1.29998	1.22812	1.37405
n.a.	1.0138	1.24452	1.05187
TGFB1	0.88889	7.10936	0.69789
NPTX2	1.71847	1.61177	0.35312
BAG1	1.17362	1.3072	1.19474
BAG1	1.17525	1.20341	1.10759

HGNC Symbol	ratioDiff_6Tc vs 100Tc	ratioDiff_5Tc vs 100Tc	ratioDiff_4Tc vs 100Tc
SHB	0.84765	0.88004	1.03833
EIF3S10	1.14591	1.37776	1.35358
HTATIP2	1.6758	1.15264	1.47362
CALCA	1.44599	1.57128	1.61023
C6orf108	1.27696	1.31296	1.43525
ACY1	1.15447	1.07613	1.42712
PASK	0.77175	0.6829	0.77769
CEBPZ	1.06497	1.19553	1.30525
RAP1A	0.67928	1.06945	0.95514
NID	1.80346	3.16872	3.41103
IDE	1.16389	1.12688	1.32239
HOXB7	1.19832	0.71134	1.0822
GUCY1B2	1.47788	1.40074	1.52368
SERPINA7	1.25204	1.1769	1.51905
FPRL2	1.25372	1.3291	1.28725
MTRR	1.04965	1.37959	1.2704
THRA	1.0731	1.22143	1.21715
POR	1.13954	1.33435	1.13064
YWHAH	1.17877	1.29924	1.48519
TRIM28	1.36011	1.46573	1.5112
DHX30	1.30156	1.35335	1.35254
CDK8	0.89522	0.94533	1.50464
CCNH	1.02629	1.17347	1.1388
RFK	1.14418	1.40914	1.46824
RABGGTB	1.13529	1.15813	1.16389
PLK4	1.1231	1.33374	1.25495
CYP4B1	0.81355	1.54551	0.94931
TP53BP2	1.35674	1.51305	1.13398
NVL	1.08326	1.34043	1.38316
ARF1	0.98633	1.28356	1.12594
PLK2	0.95277	0.77905	0.80503
GZMA	1.09549	1.41137	1.24976
NOLA2	1.24852	1.06095	1.02717
HMBS	1.46905	1.67248	1.5853
ITIH2	0.71147	1.28372	1.16288
SACS	1.06878	1.12275	0.9261
GABPA	1.11316	1.46483	1.59847
ETS2	0.98439	1.03957	1.09818
IL8RA	1.20766	1.13181	1.43267
API5	1.6649	3.10374	2.12926
n.a.	1.14312	1.07736	1.22184
ICT1	2.12424	1.23888	1.14807
DFFB	0.92897	1.05236	1.00404
USP7	0.99249	1.08675	1.10627
PAP	1.20722	1.20541	1.13253
BSG	0.84388	1.0299	1.1167
YIF1	1.27416	1.45378	1.37105
POLE	2.01802	1.19232	1.31779
	1.07274	2.59249	1.10129

HGNC Symbol	ratioDiff_3Tc vs 100Tc	ratioDiff_2Tc vs 100Tc	ratioDiff_1 5Tc vs 100Tc
MYC	13.11573	21.17833	26.06885
CACNA1G	5.55876	6.40089	6.68435
NME1	7.35152	9.80579	11.12337
ADCY2	3.06001	2.03685	2.34019
C4orf9	3.42652	3.20666	3.31588
FKBP5	5.90076	6.55599	9.51036
CRKL	2.59587	8.10613	3.98033
RFC5	12.10905	15.88817	19.18292
PPP2CA	6.42169	7.12388	9.79533
TIMM8A	5.78616	3.46901	6.37967
n.a.	8.91352	6.3907	6.05618
MAD2L1	12.3419	22.41183	20.32034
MRPL12	3.08798	3.63391	4.02403
NME1	6.1018	8.51046	9.64544
METTL1	4.33956	4.79779	5.62588
SLC7A5	3.67267	9.09594	7.41599
SRM	4.51071	5.83574	6.43193
IL1B	2.89179	2.4634	3.36876
PAICS	5.98648	7.71481	8.25106
TOMM40	2.9864	3.89912	4.73016
PYCR1	5.06488	7.28193	8.88317
UMPK	2.87093	3.44335	4.0815
LRP8	2.58755	4.07592	4.01285
DUSP14	7.28652	15.32848	3.63227
METAP1	2.85821	3.71819	3.63575
ABCE1	3.0779	4.42506	4.01333
PA2G4	3.49131	4.04725	5.29434
BOP1	2.99582	3.16191	4.37029
RANBP1	3.97853	4.58428	5.32856
CTPS	3.3416	4.06858	4.79479
TRAP1	4.46685	5.89092	7.08906
HSPD1	4.7571	5.97775	7.64331
PFAS	3.39264	4.42702	5.28414
TEAD4	3.26571	4.36685	5.07555
MIF	2.68197	3.08827	3.66679
VARS2	2.85023	3.34788	4.34955
CENTG1	3.99745	5.41579	6.99128
DSCR2	4.02502	5.271	5.78745
JAG2	3.42931	4.30959	5.33996
PRKAR1B	2.9178	3.08907	3.05459
n.a.	2.64887	2.71032	3.17837
MATK	2.99194	4.51007	4.31026
IARS	2.39723	3.47795	3.44154
GAL	4.60843	6.5576	8.84941
MCAM	2.63238	3.014	4.28346
CAD	2.91879	3.51196	4.39815
FH	3.00131	3.63388	4.24662
SRPK1	3.22641	4.39484	4.58202
NEFH	34.32732	32.40066	37.52651
NP	2.6348	3.0029	3.73352
AHCY	2.81402	4.13553	4.30424
POLD2	2.32129	2.95247	3.73194
C1QBP	3.19004	4.17922	4.65361
CAMKK2	3.54622	3.81196	4.38879
n.a.	3.06129	3.25807	4.04027
BYSL	2.69546	2.52688	3.25474
NUP155	2.39694	3.39124	3.28079

HGNC Symbol	ratioDiff_3Tc vs 100Tc	ratioDiff_2Tc vs 100Tc	ratioDiff_1 5Tc vs 100Tc
IFRD2	3.83553	5.45814	5.6542
MRPL3	3.14418	4.01065	4.63103
HSPE1	3.22456	4.92942	5.02204
HSPE1	3.3612	4.5916	4.91382
n.a.	2.50168	3.31217	3.59429
EBNA1BP2	3.04535	3.72904	4.5457
TNFRSF8	4.47339	5.67884	8.8153
PRDX4	3.62518	4.1845	5.20667
CSE1L	4.0741	4.30929	4.2079
RPP40	3.23948	8.15883	5.68718
n.a.	5.63691	3.91489	8.52168
HRMT1L2	2.6766	3.40082	3.91463
n.a.	2.43178	3.33003	3.54306
n.a.	2.97261	3.46612	4.529
MADH4	2.7561	3.38791	4.60386
IL9	2.71922	2.88726	3.52769
PDCD11	2.11052	2.63502	2.98456
HK2	2.97316	6.14039	3.06521
PWP2H	2.27695	2.85	3.03675
n.a.	4.23425	4.66391	6.60921
NOLC1	3.29637	4.73757	4.54123
NOLC1	2.96016	3.31189	4.08686
CCT2	2.6524	3.29523	3.48001
DTYMK	2.49677	2.8296	3.53333
HNRPAB	2.78865	3.43486	3.73266
FASN	4.31382	6.39053	7.2928
FASN	2.82912	4.37649	4.53848
NMB	2.34896	2.80413	4.20309
CHC1	3.25422	3.70893	3.931
	3.2359	4.66654	5.6421
KIAA0179	2.20729	3.09668	3.78402
NTHL1	2.69877	2.88481	3.73981
UNG	2.64743	3.89127	3.72097
KIAA0020	2.45173	3.0628	3.25393
n.a.	2.46973	2.85156	3.0262
n.a.	2.73111	3.04541	3.35436
POLE2	2.69124	2.39273	3.28753
MTHFD1	2.49816	2.8522	3.06417
NOL5A	2.45636	2.96397	3.42436
PRPS2	2.48554	3.20592	3.2613
RUVBL2	2.4332	2.85719	3.45679
GPI	2.3611	2.47657	3.45562
n.a.	2.54	2.97707	3.73295
NPM3	3.32762	4.42402	4.23353
n.a.	3.11147	4.04051	4.5615
CDC20	2.63075	2.78986	3.36151
n.a.	2.47137	3.33849	3.24681
PRKDC	2.42545	2.74548	3.03527
CKS2	2.35955	2.86347	2.92115
CSE1L	2.85022	3.37157	4.36284
EEF1E1	3.10271	4.3193	4.03704
HRMT1L2	2.445	3.22009	3.47098
n.a.	2.77605	2.98994	3.69024
TST	2.19737	2.40475	2.79054
DKC1	2.38085	2.77555	3.42876
RAN	2.73601	3.19216	2.82854
PDGFRA	2.38752	3.6968	3.39889

HGNC Symbol	ratioDiff_3Tc vs 100Tc	ratioDiff_2Tc vs 100Tc	ratioDiff_1 5Tc vs 100Tc
CDK4	5.21739	4.28043	7.14526
ALDH1B1	2.33893	2.34634	2.66675
SORD	3.05798	3.48671	4.01693
BDH	2.38999	2.54767	3.59211
GMPS	2.42142	2.92137	3.46375
GPR30	2.51901	2.87735	4.02997
PHB	2.70203	3.42971	3.9659
STRA13	2.93112	3.7031	4.18997
XPOT	2.96685	3.28927	4.04917
SMN1	2.09572	2.25422	2.61082
CHC1	2.77219	3.11053	3.4607
PLK1	2.41324	3.5006	3.7431
n.a.	3.30157	4.20236	3.71866
AK2	2.24136	2.60973	3.01149
n.a.	2.29635	3.10695	2.91121
MGST1	3.1245	2.9063	3.36254
CSDA	2.13307	2.36175	2.92288
n.a.	2.32364	2.47389	2.77128
ATP1B3	2.1113	2.69327	2.73718
BCS1L	2.26679	2.46232	3.02763
UNG	2.27898	3.01784	3.16144
PBP	2.1434	2.48968	3.13118
CDC6	2.45582	2.56985	3.21684
CDC7	2.64609	3.3473	3.2567
MTAP	2.01895	3.13985	2.60402
ADSL	2.00854	2.31834	2.87848
CDKN3	2.46837	3.03378	2.82948
VRK1	2.03379	2.25423	2.21444
WFDC2	2.08412	2.63314	2.71323
GSPT1	2.06898	2.38976	2.53225
SLC39A14	2.55303	3.8471	4.0475
n.a.	2.19733	2.88371	3.11043
RLN2	2.32583	2.16321	2.48651
BAG2	2.04647	2.38296	2.3735
HSD17B8	2.4016	2.4857	3.36852
UCHL3	2.06257	2.59132	2.60867
NME2	2.43789	2.61647	2.93229
MRPS12	2.01792	2.35097	2.70461
PCNA	2.23495	2.43077	2.57957
DPH2L2	2.21414	2.71201	3.30122
CCNB1	2.34069	2.82208	2.9398
MC1R	2.54872	3.06729	4.05467
SOD1	2.13094	2.63096	2.68426
ATP5G3	2.01797	2.29227	2.74529
CCT3	2.24354	2.37697	2.83264
RFC4	2.17779	2.62455	2.71957
CDC25A	2.11938	2.23875	2.78681
FRDA	2.36888	2.75345	2.99976
SNRPD1	2.09972	2.55053	2.64326
CHAF1A	2.05101	2.23695	2.32871
PRDX2	2.20327	2.40886	3.36235
BUB1	2.01412	2.44101	2.62062
CDC2	2.34019	2.88102	2.73744
POLR1C	2.37136	2.39968	2.66301
SLC19A1	6.18694	4.72295	3.01465
TOMM20	2.07764	2.56068	2.70897
MMP3	2.33182	2.67078	3.49384

HGNC Symbol	ratioDiff_3Tc vs 100Tc	ratioDiff_2Tc vs 100Tc	ratioDiff_1 5Tc vs 100Tc
UBE2C	2.36155	2.47949	2.96123
PTPN2	2.65996	3.06246	3.47277
RUVBL1	2.06368	2.50079	2.70317
TYMS	2.07742	2.27395	2.38322
DDX10	2.09698	2.59569	2.58514
TUFM	2.04731	2.17567	2.7339
AURKB	2.21238	2.4034	2.57223
RRS1	2.10372	2.80412	2.99634
GEMIN4	2.1499	2.40223	2.77992
PTMA	2.3608	2.69074	2.91844
CYP51A1	1.64078	2.21704	2.44069
ARHGEF5	1.71096	2.97458	3.12292
KIAA0690	1.82813	2.48757	2.74485
VDAC1	1.74526	2.44286	2.19877
DDX1	1.9286	2.1444	2.37764
SCAMP1	1.68105	2.00934	2.8272
DDX18	1.66147	2.25165	2.19743
PES1	1.94327	2.38792	2.72053
RANGAP1	1.79942	2.26594	2.12772
APEX1	1.9782	2.20126	2.7381
MYBL2	1.90873	2.5218	2.38788
USP10	1.9306	2.0833	2.44318
n.a.	1.74267	2.06561	2.38999
RPA3	1.94007	2.52789	2.10001
CXCL12	1.85852	2.09233	2.34589
n.a.	1.75947	2.09357	2.63819
MCM3	1.98581	2.39013	2.19818
GMNN	1.91369	2.30337	2.29317
HSPA9B	1.9939	2.15481	2.52409
TCERG1	1.88379	2.12908	2.20921
RNU3IP2	1.89929	2.4582	2.86836
SFRS7	1.83473	2.18597	2.14227
MSH6	1.99363	2.39288	2.48281
CENPF	1.89439	2.29573	2.24953
MXI1	1.80239	2.11941	2.135
AMD1	1.9196	2.43756	2.39397
ELK1	1.54908	2.02143	2.07359
ILF3	1.88431	2.13064	2.52537
TFDP1	1.70851	2.2382	2.17637
n.a.	1.87351	2.24748	2.40202
TOP2A	1.94057	2.15076	2.07898
EIF5A	1.77209	2.15931	2.26745
n.a.	1.98259	2.29706	2.25136
n.a.	1.81903	2.05254	2.47649
ATIC	1.95968	2.46525	2.47984
ATIC	1.89584	2.07723	2.27432
PEX5	1.99741	2.05921	2.32912
TAF4B	1.8123	2.13205	2.01349
HDGF	1.85283	2.0435	2.29815
HDGF	1.98856	2.22199	2.48221
ILF2	1.87134	2.02237	2.35109
CCNA2	1.96678	2.40726	2.10283
MDH2	1.90377	2.60622	2.64823
PEG10	1.88138	2.77629	2.21727
PPRC1	1.91826	2.39833	2.69448
SSRP1	1.98113	2.22046	2.58201
PTK9	1.74734	10.74686	15.67224

HGNC Symbol	**ratioDiff_3Tc vs 100Tc**	**ratioDiff_2Tc vs 100Tc**	**ratioDiff_1 5Tc vs 100Tc**
ACSL1	1.67209	2.49683	2.61338
PFKM	1.96933	2.38548	3.23589
HNRPDL	1.76196	2.0154	2.08819
RPIA	1.76398	2.44571	2.63509
SLC16A1	1.54498	2.56516	3.15358
KCNJ6	1.8489	2.08212	2.19253
SFRS2	1.76825	2.09721	2.11701
PRKCI	1.62721	2.30503	4.78829
POLR2H	1.96646	2.274	2.72492
ABCE1	1.55991	2.0614	2.30309
MELK	1.76092	2.21844	2.14613
DDX21	1.33709	2.72086	2.646
SSSCA1	1.61987	2.31451	2.24889
n.a.	1.74626	2.12788	2.38463
HSPCA	1.55843	2.16403	2.39837
DEAF1	1.69562	2.05664	2.25179
n.a.	1.92193	2.32045	2.81974
EIF1AX	1.7661	2.4927	2.33677
n.a.	1.73497	2.52681	2.49597
n.a.	1.62294	2.00053	2.05847
SF3A3	1.62036	1.98687	2.01857
n.a.	2.01046	1.88781	2.21733
AK2	1.66779	1.8936	2.11445
PLAUR	3.14161	1.97863	3.49915
SCARB1	1.54626	1.89872	2.23497
MCM2	1.75544	1.71356	2.16229
EXOSC7	1.74717	1.92946	2.18852
KHSRP	1.67406	1.91834	2.15423
NUDC	1.67434	1.85587	2.0756
CGRRF1	2.16563	1.85064	2.34343
APEX1	1.68873	1.76364	2.24981
GARS	1.8577	1.93443	2.27537
EIF3S9	1.76491	1.82618	2.30478
IMPDH1	1.58961	1.85123	2.05051
VEGF	4.73812	1.94291	2.5559
TFDP2	1.69612	1.836	2.10575
PRDX1	1.60717	1.89065	2.05707
SCO2	1.835	1.80502	2.46641
TUBG1	1.97191	1.87307	2.41932
MYCN	1.64245	1.65202	2.05377
ABL2	1.42487	1.54787	9.99615
SLC20A1	1.81764	1.82315	2.16346
CDKN2B	2.12224	1.42292	2.24799
n.a.	1.49995	1.93163	2.25665
FANCG	1.84558	1.92713	2.25021
PMPCA	1.39397	1.77646	2.08026
PSMC3	1.5638	1.74202	2.00101
MCM7	1.88727	1.77272	2.10953
ABCA3	2.04587	1.80847	2.21206
EIF4EBP1	1.44348	1.60906	2.20363
TNFRSF4	0.9756	1.92307	2.09305
SRP72	1.3648	1.61317	2.01192
ALG3	1.48196	1.66408	2.44095
CKS1B	1.57172	1.69886	2.0868
NSEP1	1.75454	1.93118	2.26607
FARSLA	1.85024	1.79068	2.20319
PRIM1	1.77856	1.75704	2.19618

HGNC Symbol	ratioDiff_3Tc vs 100Tc	ratioDiff_2Tc vs 100Tc	ratioDiff_1 5Tc vs 100Tc
TBL3	1.65976	1.7365	1.99443
JUND	1.58372	1.85818	1.9196
PTBP1	1.48562	2.42327	1.73328
MRE11A	1.65826	1.63339	1.75464
HSPA5	1.52169	1.50422	1.91511
OAT	1.67448	1.75015	1.74451
TFRC	1.36136	1.65318	1.62295
SHMT1	1.67296	1.87978	1.89917
CLNS1A	1.58962	1.88611	1.87735
SEMA3C	1.89269	2.38248	1.61418
MCAM	1.41471	1.97199	1.96786
MAPKAPK5	1.55913	1.66474	1.82121
SIP1	2.03701	2.2293	1.83333
NF2	1.63676	1.8572	1.9114
SLC1A5	1.74928	1.83156	1.8496
PSMA2	1.58956	1.82695	1.8689
RAD51C	1.33001	1.64797	1.76893
CTSC	1.61216	1.93882	1.7539
HSPA8	1.58901	2.04339	1.97461
n.a.	1.39744	1.70573	1.59459
IGFBP2	1.275	1.52863	1.9553
DARS	1.41342	1.97742	1.78804
UCHL3	1.63483	2.00625	1.89131
GTF3A	1.52701	1.73322	1.90108
RPL5	1.61301	2.06604	1.99476
AMD1	1.5203	1.96941	1.72426
HSPA1A	1.83462	2.01103	1.93227
SYNGR3	1.60589	1.96038	1.85005
NINJ1	0.7598	0.99127	1.72971
SNRPA1	1.55278	1.66008	1.96275
TAF9	1.481	1.65761	1.76281
SYNCRIP	1.91962	2.19583	1.99841
n.a.	1.60636	1.91587	1.90396
ITGB3BP	1.64182	2.14539	1.77688
PTPRF	1.42956	1.63305	1.75224
CHEK1	1.53422	2.10366	1.87561
TCEB1	1.556	1.776	1.85982
n.a.	1.43656	1.7346	1.73058
VBP1	1.56579	1.9559	1.87104
BUB1B	1.6049	1.9241	1.96255
RACGAP1	1.73364	2.05916	1.88894
AK3	2.06656	1.95104	1.69952
HNRPF	1.59736	1.81054	1.91604
PDAP1	1.66448	2.15136	1.85385
SELE	1.24623	1.68338	1.66527
n.a.	1.68295	1.93071	1.97424
RCN1	2.06009	2.16931	2.63858
GLDC	1.41125	1.31327	2.34409
PMS1	1.08559	1.89891	2.13631
PFKP	1.41933	1.62586	1.70069
PDCD2	1.47801	1.48647	1.70576
MGST2	1.16869	1.54234	1.50267
NDUFB7	1.4699	1.79464	1.81315
G22P1	1.53247	1.72329	1.95877
n.a.	1.51863	1.47004	1.7866
PBEF1	1.33303	1.15444	1.5802
TBL2	1.40932	1.67972	1.67829

HGNC Symbol	**ratioDiff_3Tc vs 100Tc**	**ratioDiff_2Tc vs 100Tc**	**ratioDiff_1 5Tc vs 100Tc**
GCN5L2	1.37692	1.62332	1.6067
CDK2AP1	1.35068	1.76676	1.67184
NOL1	1.55408	1.73149	1.71902
SLC29A1	1.47715	1.55412	1.48343
BNIP1	1.34045	1.82553	1.59496
DBN1	1.34257	1.71716	1.92058
EIF4G1	1.59704	1.73892	1.96695
B4GALT2	1.49336	1.92129	1.68492
TMEM5	1.3202	1.42458	1.56542
FVT1	1.35657	1.55874	1.49288
ETF1	1.76494	2.84583	2.38456
ATF4	1.23206	1.29648	1.62725
ILF3	1.569	1.92895	1.80783
RAMP1	1.54661	1.43014	1.44015
n.a.	1.5583	1.6439	1.88072
ADCY3	1.25143	1.56182	1.74507
AFG3L2	1.41154	1.53707	1.89924
PRPS1	1.14059	1.51571	1.54713
OPRS1	1.88948	1.83557	2.21701
TOMM70A	1.89897	1.9646	1.96088
APRT	1.54865	1.79082	1.95745
FGFR4	1.11376	1.0763	1.30802
DEFA6	1.20942	1.38198	2.16191
ZNF9	1.95854	2.63833	2.77646
RAC3	2.32464	1.88603	3.33046
WNT10B	2.21465	4.0642	4.88812
NFRKB	1.60198	1.54885	1.52483
CDK5R2	0.9715	1.06114	1.43417
CYCS	2.62178	3.84074	3.58463
YES1	1.18168	1.28812	1.53605
DLEU1	1.32147	1.62415	1.80471
BNIP3	1.27468	1.50986	1.66027
RAD23A	1.44565	1.60644	1.69668
	1.25844	2.04729	0.94385
UBE2G2	1.43482	1.76835	1.69219
KCNQ3	0.92554	1.09792	1.11777
MTA1	1.33323	1.58378	1.48892
LIG3	1.14078	1.14682	1.6073
ITGA2B	1.4994	1.65331	1.73939
TOMM34	1.50353	1.94252	1.59732
ITIH4	1.125	1.51867	1.82305
POLD1	1.5181	1.52941	1.68008
IKBKAP	1.29883	1.49896	1.27517
ASNS	1.12635	1.14946	1.50082
MX1	0.51808	1.13956	0.38581
XRCC5	2.09045	2.31348	2.18443
XPO1	1.44871	1.68418	1.59171
RAD54L	1.68088	1.62496	1.78545
PTHLH	0.43376	0.3154	0.05568
MSH2	1.90387	1.90799	1.93917
CDKL1	1.26031	1.55079	1.40044
ADA	1.35343	1.44438	1.62387
n.a.	1.12686	1.28207	1.40219
TGFB1	0.64508	0.81684	0.66545
NPTX2	0.62265	0.66252	0.1442
BAG1	1.33109	1.38447	1.48583
BAG1	1.17247	1.32243	1.44637

HGNC Symbol	**ratioDiff_3Tc vs 100Tc**	**ratioDiff_2Tc vs 100Tc**	**ratioDiff_1 5Tc vs 100Tc**
SHB	0.94802	1.37482	1.36243
EIF3S10	1.43497	1.59215	1.63039
HTATIP2	1.15159	1.49081	0.88688
CALCA	1.43684	2.51202	1.83745
C6orf108	1.4318	1.56574	1.61735
ACY1	1.49811	1.06198	1.57645
PASK	1.0524	1.0316	1.21096
CEBPZ	1.31128	1.45701	1.47952
RAP1A	0.88376	1.09314	1.1763
NID	2.40123	1.21164	1.80008
IDE	1.43872	1.7147	1.59449
HOXB7	1.01438	1.04476	0.78405
GUCY1B2	1.60775	1.56864	1.86421
SERPINA7	1.46628	1.67917	1.88827
FPRL2	1.23948	1.36196	1.3578
MTRR	1.11957	1.36195	1.29398
THRA	1.18024	1.16	1.46785
POR	1.17039	1.1875	1.73828
YWHAH	1.52887	1.80174	1.76687
TRIM28	1.49821	1.56013	1.80524
DHX30	1.31792	1.52042	1.69992
CDK8	1.49728	1.55073	1.62099
CCNH	1.26842	1.32238	1.41908
RFK	1.37716	1.87081	2.06224
RABGGTB	1.17809	1.52625	1.57306
PLK4	1.61233	1.72317	1.53458
CYP4B1	1.41241	0.25675	0.7211
TP53BP2	1.37046	1.64057	1.61474
NVL	1.28761	1.59927	1.6342
ARF1	1.25506	1.29396	1.51245
PLK2	0.63493	0.67669	0.5193
GZMA	2.01651	1.69236	1.79475
NOLA2	1.4335	1.41897	1.51016
HMBS	1.58312	1.69048	1.93167
ITIH2	1.00829	1.08656	1.40847
SACS	0.82328	0.95062	1.27284
GABPA	1.53504	1.89061	1.95039
ETS2	1.16747	1.41531	1.18718
IL8RA	1.22945	1.42727	1.64043
API5	2.17643	2.78404	2.7498
n.a.	1.19458	1.34948	1.43581
ICT1	1.43444	1.8585	1.83986
DFFB	1.07017	1.25286	1.28066
USP7	1.11755	1.33793	1.38624
PAP	1.16816	1.5484	1.58784
BSG	1.06042	1.20233	1.4945
YIF1	1.37672	1.38607	1.66112
POLE	1.60146	1.81813	1.98996
	1.44818	1.54321	1.95893

HGNC Symbol	**ratioDiff_1Tc vs 100Tc**	**ratioDiff_0 5Tc vs 100Tc**	**ratioDiff_0Tc vs 100Tc**
MYC	42.55956	61.70016	87.2543
CACNA1G	4.10357	6.3119	8.40158
NME1	12.65542	14.61954	17.96404
ADCY2	3.12449	2.66786	5.3241
C4orf9	3.37662	3.7349	4.01786
FKBP5	9.78958	11.42233	11.98342
CRKL	5.17794	6.20751	5.98053
RFC5	21.45423	18.44407	18.12116
PPP2CA	11.25789	16.51385	22.38685
TIMM8A	5.63313	5.12545	3.8733
n.a.	9.50067	7.22699	7.64863
MAD2L1	22.08802	22.70379	19.9753
MRPL12	4.05368	4.95686	4.80397
NME1	11.13922	12.14102	16.09313
METTL1	4.96488	6.3203	7.57916
SLC7A5	8.45513	11.33701	18.69516
SRM	7.76917	9.92205	10.99592
IL1B	3.33098	3.80349	4.04879
PAICS	10.14723	11.5871	12.46339
TOMM40	5.06835	5.95614	7.63457
PYCR1	10.54797	14.22591	20.6756
UMPK	3.74271	4.48048	4.79269
LRP8	5.07592	5.03899	5.91824
DUSP14	4.07593	4.50861	5.75267
METAP1	4.40334	4.12686	3.93035
ABCE1	4.64929	4.99496	6.79621
PA2G4	6.10337	7.34251	7.60621
BOP1	4.46313	5.69714	6.76932
RANBP1	6.1002	6.72988	7.87789
CTPS	4.88121	5.31886	5.92513
TRAP1	8.67284	10.7689	13.92644
HSPD1	8.50328	10.41076	11.85225
PFAS	5.90896	6.46556	6.19095
TEAD4	5.93397	7.63018	9.67222
MIF	3.78125	3.89994	5.11409
VARS2	4.3718	5.55623	6.38357
CENTG1	7.99525	9.57574	13.05877
DSCR2	6.87953	8.24313	9.64521
JAG2	6.39893	7.51493	9.51248
PRKAR1B	3.81095	4.63422	4.71128
n.a.	3.77528	4.29986	5.4231
MATK	6.17682	7.30694	7.93624
IARS	4.08365	5.12234	6.07415
GAL	9.25781	12.62613	16.02949
MCAM	5.43696	4.44095	7.88416
CAD	4.11547	5.68639	6.2572
FH	5.16085	5.88788	6.1659
SRPK1	5.88368	6.22625	7.96465
NEFH	51.35556	47.78841	37.6185
NP	4.53701	5.11245	6.1202
AHCY	5.45996	5.74862	7.26408
POLD2	3.66692	4.06559	5.12376
C1QBP	5.28119	6.08349	6.8464
CAMKK2	5.05363	5.58444	5.50539
n.a.	4.89528	5.33063	5.99164
BYSL	3.25353	3.75738	4.18224
NUP155	2.91755	3.16489	3.45813

HGNC Symbol	**ratioDiff_1Tc vs 100Tc**	**ratioDiff_0 5Tc vs 100Tc**	**ratioDiff_0Tc vs 100Tc**
IFRD2	6.97507	8.90679	10.31138
MRPL3	5.81345	6.35628	7.08892
HSPE1	6.45011	7.25866	8.54071
HSPE1	6.05208	7.05795	7.6957
n.a.	4.05807	4.39638	4.86893
EBNA1BP2	5.13769	5.37035	6.73213
TNFRSF8	12.17168	15.70198	24.75813
PRDX4	6.0683	7.10777	8.69138
CSE1L	5.98972	6.24911	7.8576
RPP40	5.12628	5.10119	7.10827
n.a.	5.6546	6.54545	6.72008
HRMT1L2	4.36018	6.13504	6.92114
n.a.	2.22142	3.79878	5.85442
n.a.	5.10289	6.2327	7.61093
MADH4	5.18027	5.7891	6.2482
IL9	3.79467	3.89917	4.04968
PDCD11	2.93079	3.62611	4.39651
HK2	4.56867	5.595	5.11866
PWP2H	3.37525	4.37841	4.55456
n.a.	7.74379	7.31666	8.54731
NOLC1	5.81309	6.48608	7.15331
NOLC1	4.23015	4.94352	6.29532
CCT2	4.34853	4.80487	5.34596
DTYMK	3.48797	3.98954	4.13029
HNRPAB	4.2107	4.86906	5.04736
FASN	9.42903	12.29211	15.74478
FASN	5.96045	7.82376	10.59142
NMB	3.08516	3.64827	3.45723
CHC1	4.6726	5.77466	5.71765
	6.69718	7.99568	8.69962
KIAA0179	4.0559	4.23454	7.16147
NTHL1	3.96675	4.62964	5.415
UNG	5.09676	5.90432	6.29802
KIAA0020	4.23861	4.55516	5.54856
n.a.	3.26672	3.37693	4.47474
n.a.	3.56795	4.08401	4.57245
POLE2	3.53942	3.65389	4.70149
MTHFD1	3.40318	3.77155	3.97735
NOL5A	4.0127	4.13728	5.35134
PRPS2	4.19954	4.61977	5.29812
RUVBL2	3.85889	4.08958	4.58245
GPI	3.39492	3.93178	4.57534
n.a.	3.75454	4.32384	4.30478
NPM3	5.63011	7.46509	8.41908
n.a.	5.93825	6.85478	8.48588
CDC20	3.22934	3.23128	3.48935
n.a.	4.05137	4.85003	5.1328
PRKDC	3.33136	3.05039	3.5464
CKS2	3.61249	3.42897	3.8564
CSE1L	4.2137	5.52823	6.58006
EEF1E1	5.05568	5.83235	6.66591
HRMT1L2	4.53008	5.29093	6.20834
n.a.	3.6842	4.13598	4.56806
TST	3.01959	3.76553	3.61984
DKC1	3.8259	4.19661	4.69489
RAN	3.45009	3.32415	3.5811
PDGFRA	7.00185	7.50938	12.48374

HGNC Symbol	**ratioDiff_1Tc vs 100Tc**	**ratioDiff_0 5Tc vs 100Tc**	**ratioDiff_0Tc vs 100Tc**
CDK4	3.14164	7.8463	10.85495
ALDH1B1	3.26482	3.60919	3.45183
SORD	4.42329	5.5685	6.53145
BDH	3.33788	3.31949	3.43358
GMPS	3.44961	3.61628	3.39589
GPR30	4.68597	6.03741	6.94378
PHB	4.27309	4.67398	4.78849
STRA13	4.56474	5.36788	5.97681
XPOT	4.89194	4.95985	6.10057
SMN1	2.84982	3.4874	3.97206
CHC1	4.20229	4.99297	4.87651
PLK1	4.37765	5.50917	4.90759
n.a.	4.67172	5.61973	6.78752
AK2	3.42662	3.81534	4.68601
n.a.	3.17558	3.36099	4.35299
MGST1	3.90251	4.525	6.11094
CSDA	3.02137	3.50232	4.20475
n.a.	3.23947	3.77981	4.96559
ATP1B3	3.07938	3.55716	3.82131
BCS1L	3.39876	4.11329	4.75064
UNG	3.94301	4.44875	6.20913
PBP	3.03254	3.52436	2.99671
CDC6	3.9416	4.41847	4.17811
CDC7	3.43513	3.83948	3.716
MTAP	3.59547	3.94082	4.02843
ADSL	3.19411	3.67234	3.90437
CDKN3	3.54552	3.80539	3.88604
VRK1	2.58006	3.02842	2.81075
WFDC2	3.59872	3.70886	4.66488
GSPT1	2.86741	3.11077	3.40794
SLC39A14	5.38773	5.98195	8.32828
n.a.	3.45094	4.3423	5.21027
RLN2	2.32137	2.95401	3.63672
BAG2	2.50986	2.74883	3.4578
HSD17B8	3.35422	4.45612	5.50266
UCHL3	3.22446	3.88522	3.86965
NME2	3.10485	3.64699	3.66958
MRPS12	2.72984	3.02598	3.26639
PCNA	2.8697	2.66505	3.01777
DPH2L2	3.49658	4.04596	4.858
CCNB1	3.34435	3.3341	3.49195
MC1R	4.61441	5.65785	6.88885
SOD1	3.23678	3.74546	4.08886
ATP5G3	3.19433	3.33559	3.22191
CCT3	2.90333	3.13124	3.43273
RFC4	3.3877	3.4775	4.07296
CDC25A	3.00332	3.30828	3.68558
FRDA	3.45462	3.79875	4.26683
SNRPD1	2.49215	3.07422	3.43912
CHAF1A	2.50939	2.77248	3.04709
PRDX2	3.29341	3.79516	4.42731
BUB1	2.92046	2.99785	2.88227
CDC2	3.08611	2.81643	2.11441
POLR1C	2.86722	2.97472	3.93541
SLC19A1	3.27889	3.72518	3.88466
TOMM20	3.13807	4.07067	4.80403
MMP3	3.39477	3.86957	4.60307

HGNC Symbol	**ratioDiff_1Tc vs 100Tc**	**ratioDiff_0 5Tc vs 100Tc**	**ratioDiff_0Tc vs 100Tc**
UBE2C	3.03537	3.04107	3.27422
PTPN2	4.28245	5.8698	7.90338
RUVBL1	3.4574	3.62206	4.4895
TYMS	2.65722	2.47974	2.61263
DDX10	3.11147	3.60279	4.32251
TUFM	3.02627	3.21677	4.08699
AURKB	2.58118	2.6182	3.10905
RRS1	3.58031	3.6395	4.33429
GEMIN4	2.83237	3.12387	3.60669
PTMA	3.19486	3.70007	3.46455
CYP51A1	3.29189	3.89596	5.39441
ARHGEF5	5.04372	7.33883	6.81309
KIAA0690	3.20898	3.73572	4.86181
VDAC1	2.94232	3.4234	3.8747
DDX1	2.90741	3.3595	3.31665
SCAMP1	2.24616	2.73019	2.78406
DDX18	2.86706	2.84874	3.38371
PES1	2.75486	3.40684	3.81137
RANGAP1	2.87308	2.86838	3.32081
APEX1	2.4864	2.67292	3.14228
MYBL2	3.039	3.46259	3.1865
USP10	2.68116	2.61077	2.77824
n.a.	2.58438	2.88128	3.13738
RPA3	2.4983	2.50235	2.98915
CXCL12	2.48943	2.71107	3.0859
n.a.	2.85736	3.18002	4.52962
MCM3	3.16556	4.71474	5.36383
GMNN	2.30297	2.54958	3.0563
HSPA9B	3.09991	3.06831	3.12303
TCERG1	2.44073	2.71768	2.65569
RNU3IP2	2.96337	3.97149	4.98986
SFRS7	2.51243	2.4568	2.60276
MSH6	2.95288	2.93276	3.6924
CENPF	2.27301	2.24101	2.62182
MXI1	2.42274	2.84671	2.77717
AMD1	3.12782	3.0286	3.29496
ELK1	2.57974	2.75663	3.21652
ILF3	2.58064	3.33287	3.5075
TFDP1	2.56869	2.3599	2.11254
n.a.	2.89697	2.68215	3.01261
TOP2A	2.64039	2.36501	2.01929
EIF5A	2.53638	2.25526	2.38186
n.a.	2.91693	3.61117	4.56836
n.a.	2.76538	3.03843	3.40013
ATIC	3.01641	3.27294	3.76506
ATIC	2.53944	2.46581	2.68238
PEX5	2.96819	2.93627	4.34525
TAF4B	2.58881	2.60088	2.76189
HDGF	2.44038	3.06291	3.57493
HDGF	2.79845	3.3779	3.3949
ILF2	2.4026	2.31204	2.53093
CCNA2	2.61863	2.17888	2.17448
MDH2	3.04362	3.67645	4.09346
PEG10	3.36856	4.51214	8.13611
PPRC1	3.13069	3.58351	4.16674
SSRP1	2.75375	3.18396	3.65571
PTK9	17.9661	40.6391	46.43332

HGNC Symbol	ratioDiff_1Tc vs 100Tc	ratioDiff_0 5Tc vs 100Tc	ratioDiff_0Tc vs 100Tc
ACSL1	3.82401	4.20253	5.11831
PFKM	3.33415	4.05675	5.36111
HNRPDL	2.40166	2.37392	2.90982
RPIA	3.10379	3.31655	4.24014
SLC16A1	2.395	5.41817	5.66308
KCNJ6	2.34355	2.47237	2.70192
SFRS2	2.37024	2.78461	2.87238
PRKCI	3.99947	4.17585	4.12576
POLR2H	2.6848	2.76369	3.78647
ABCE1	2.43505	2.39152	3.06277
MELK	2.2525	2.0913	2.42966
DDX21	2.14047	2.94047	4.46449
SSSCA1	2.47409	2.60138	2.9706
n.a.	2.76305	2.91814	3.68001
HSPCA	2.29792	2.15057	2.25279
DEAF1	2.65433	3.1304	3.97091
n.a.	3.25924	4.11289	5.74854
EIF1AX	3.16383	2.81899	3.62597
n.a.	2.80236	3.13596	4.09026
n.a.	2.4932	2.5794	2.75322
SF3A3	2.72055	2.73358	2.75006
n.a.	2.33998	2.60733	3.67897
AK2	2.07205	2.47743	2.32938
PLAUR	2.00149	5.077	4.13651
SCARB1	2.33704	3.13243	3.26626
MCM2	2.00686	2.33583	2.48666
EXOSC7	2.43804	2.81959	2.77967
KHSRP	2.46717	2.71192	2.87402
NUDC	2.08878	2.47941	2.71591
CGRRF1	2.46383	2.87671	3.04495
APEX1	2.31787	2.40803	2.87503
GARS	2.63679	2.90124	3.58124
EIF3S9	2.42211	2.61943	3.05344
IMPDH1	2.13935	2.35305	3.16127
VEGF	3.10277	3.34944	7.00747
TFDP2	2.44544	3.01612	3.38846
PRDX1	2.28505	2.38325	2.63213
SCO2	2.24647	2.2319	2.13269
TUBG1	2.49799	2.59029	3.21643
MYCN	2.27004	2.53736	3.14659
ABL2	2.97884	2.85068	3.75771
SLC20A1	2.10106	2.39641	2.43014
CDKN2B	2.42227	3.01018	3.26388
n.a.	2.34068	2.75513	3.03272
FANCG	2.24945	2.40791	2.62456
PMPCA	2.138	2.44032	2.81063
PSMC3	2.03595	2.28076	2.29805
MCM7	2.00869	2.29669	2.50078
ABCA3	2.28794	3.27194	4.05195
EIF4EBP1	2.24692	2.50195	3.17964
TNFRSF4	2.34863	2.95533	3.30479
SRP72	2.09652	2.28961	2.38668
ALG3	2.08552	2.32703	3.09045
CKS1B	2.37541	2.65577	2.87021
NSEP1	2.30786	2.18322	2.29475
FARSLA	2.13637	2.7354	2.38551
PRIM1	2.34305	2.49709	2.30926

HGNC Symbol	**ratioDiff_1Tc vs 100Tc**	**ratioDiff_0 5Tc vs 100Tc**	**ratioDiff_0Tc vs 100Tc**
TBL3	2.12114	2.22305	2.54996
JUND	2.19603	2.35626	2.45988
PTBP1	2.10288	2.23436	2.40669
MRE11A	2.10988	2.0012	2.26884
HSPA5	2.17778	2.17846	2.12109
OAT	2.2997	2.56202	2.56884
TFRC	2.00211	2.01432	2.32121
SHMT1	2.08243	2.59617	2.78876
CLNS1A	2.23441	2.25281	2.66778
SEMA3C	2.75925	3.05475	4.09492
MCAM	2.38139	2.52941	3.00442
MAPKAPK5	2.00687	2.25608	2.34269
SIP1	2.35874	2.45948	3.00766
NF2	2.20512	2.15203	2.29737
SLC1A5	2.26812	2.51159	3.81948
PSMA2	2.02182	2.21533	2.36574
RAD51C	2.01237	2.31669	2.06484
CTSC	2.09898	2.18691	2.75012
HSPA8	2.55568	2.37367	2.63081
n.a.	2.06934	2.29935	2.38391
IGFBP2	2.68317	3.70784	4.15456
DARS	2.04423	2.27549	2.80422
UCHL3	2.42562	2.54005	3.0887
GTF3A	2.03682	2.18373	2.45271
RPL5	2.07825	2.01389	2.49848
AMD1	2.54805	2.17837	2.71465
HSPA1A	2.23857	2.10131	2.47026
SYNGR3	2.7029	3.38976	4.36192
NINJ1	2.5549	3.35698	4.70439
SNRPA1	2.179	2.25245	2.48261
TAF9	2.08443	2.12874	2.13455
SYNCRIP	2.16904	2.69458	2.55817
n.a.	2.18487	2.5438	2.80921
ITGB3BP	2.15417	2.07467	2.65332
PTPRF	2.04696	3.07111	3.5114
CHEK1	2.19603	2.2159	2.04195
TCEB1	2.34188	2.45703	2.49718
n.a.	2.12772	2.00923	2.42507
VBP1	2.06351	2.2361	2.29782
BUB1B	2.47283	2.8594	3.10059
RACGAP1	2.14886	2.13781	2.26063
AK3	2.35488	3.01216	3.00224
HNRPF	2.00084	2.09886	2.2827
PDAP1	2.60091	2.68426	2.47501
SELE	1.76465	2.03393	2.03114
n.a.	1.99734	2.60169	2.5236
RCN1	0.17523	2.58736	3.12291
GLDC	1.91757	2.19872	2.47885
PMS1	1.54878	2.27122	2.15604
PFKP	1.92083	2.39259	2.33567
PDCD2	1.70822	2.03668	2.15808
MGST2	1.6855	2.06148	2.29762
NDUFB7	1.97	2.14669	2.30556
G22P1	1.99051	2.03141	2.30922
n.a.	1.84628	2.09751	2.47187
PBEF1	1.34258	2.03608	2.23494
TBL2	1.90188	2.1786	2.24235

HGNC Symbol	ratioDiff_1Tc vs 100Tc	ratioDiff_0 5Tc vs 100Tc	ratioDiff_0Tc vs 100Tc
GCN5L2	1.24358	2.29638	2.26522
CDK2AP1	1.92764	2.36413	2.75525
NOL1	1.98243	2.12644	2.73116
SLC29A1	1.87925	2.01848	2.20564
BNIP1	1.75553	2.24189	2.04478
DBN1	1.54869	2.4275	2.94763
EIF4G1	1.98744	2.36364	2.50655
B4GALT2	1.10763	2.49573	2.99692
TMEM5	1.77509	2.03239	2.23446
FVT1	1.66279	2.8837	3.88861
ETF1	1.48537	2.62282	3.42267
ATF4	1.66561	2.04373	2.37346
ILF3	1.76678	2.19128	2.5045
RAMP1	1.73581	2.44218	2.57713
n.a.	1.94067	2.19141	2.39246
ADCY3	1.8449	2.3599	3.01733
AFG3L2	1.93965	2.23644	2.53436
PRPS1	1.66392	2.00555	2.48746
OPRS1	1.58171	3.16209	4.05827
TOMM70A	1.85241	2.42402	3.42677
APRT	1.84727	2.25601	2.12414
FGFR4	1.59993	2.31677	3.26111
DEFA6	1.83428	2.90574	2.60167
ZNF9	1.62604	2.28333	3.00708
RAC3	0.25238	3.81293	5.49261
WNT10B	1.98001	4.53153	6.2122
NFRKB	1.7787	2.51335	2.62413
CDK5R2	1.63492	2.32141	2.51195
CYCS	0.547	4.24049	5.17051
YES1	1.97717	2.70757	3.14159
DLEU1	1.97516	2.12475	2.34238
BNIP3	1.92427	2.36297	2.97966
RAD23A	1.93086	2.08553	2.30461
	1.74536	2.1401	2.27126
UBE2G2	1.90597	1.84827	2.34154
KCNQ3	1.3443	1.07219	2.15838
MTA1	1.81367	1.87632	2.25746
LIG3	1.50686	1.89846	2.28307
ITGA2B	1.84054	1.99881	2.56326
TOMM34	1.34485	1.46227	2.00106
ITIH4	1.74286	1.69042	2.73182
POLD1	1.72163	1.85457	2.18547
IKBKAP	1.66509	1.59204	2.23281
ASNS	1.40134	1.64749	2.2332
MX1	0.98617	0.69956	3.82523
XRCC5	2.00243	1.93514	2.26803
XPO1	1.71726	1.75515	2.02546
RAD54L	1.92601	1.85774	2.0831
PTHLH	1.49946	0.5356	3.68779
MSH2	1.96053	1.98553	2.15761
CDKL1	1.82786	1.62387	2.12672
ADA	1.73706	1.9483	2.51644
n.a.	1.51007	1.6771	2.17437
TGFB1	0.96478	0.53068	26.38897
NPTX2	0.63812	0.61151	5.99783
BAG1	1.62322	1.59474	2.076
BAG1	1.49589	1.52093	2.02536

HGNC Symbol	ratioDiff_1Tc vs 100Tc	ratioDiff_0 5Tc vs 100Tc	ratioDiff_0Tc vs 100Tc
SHB	1.46152	1.933	2.008
EIF3S10	1.76727	1.8097	2.01006
HTATIP2	1.3001	1.25372	2.46993
CALCA	1.46495	1.85066	2.32848
C6orf108	1.71032	1.75957	2.0432
ACY1	1.43372	1.67146	2.09794
PASK	1.23392	1.76769	2.07185
CEBPZ	1.77124	1.73182	2.13946
RAP1A	1.44352	1.71952	2.14292
NID	1.2512	1.06807	3.42032
IDE	2.043	1.9388	2.34453
HOXB7	0.92105	0.63728	3.38063
GUCY1B2	1.66455	1.9234	2.31464
SERPINA7	1.87012	1.98896	2.59359
FPRL2	1.47086	1.52147	2.00635
MTRR	1.52986	1.67138	2.08267
THRA	1.45482	1.808	2.2475
POR	1.56192	1.93125	2.08338
YWHAH	1.88426	1.7047	2.00634
TRIM28	1.85181	1.94295	2.2735
DHX30	1.83512	1.81065	2.22894
CDK8	2.45068	1.93096	2.17855
CCNH	1.41922	1.62185	2.00283
RFK	2.02827	1.99729	2.60186
RABGGTB	1.64906	1.94136	2.04018
PLK4	1.76239	1.76554	2.62038
CYP4B1	0.72928	0.85251	2.77588
TP53BP2	1.52489	1.85311	2.4665
NVL	1.7623	1.92322	2.50029
ARF1	1.53188	1.72703	2.00703
PLK2	0.65117	0.64504	2.26671
GZMA	1.16987	1.1414	2.66388
NOLA2	1.56083	1.86499	2.51595
HMBS	2.10447	1.96718	2.59794
ITIH2	1.02004	0.4869	3.02975
SACS	1.33404	1.27125	2.2351
GABPA	1.89262	1.96747	2.23562
ETS2	1.48816	1.68684	2.05107
IL8RA	1.61113	1.76378	2.04316
API5	1.60795	1.96574	2.34659
n.a.	1.60917	1.78271	2.19883
ICT1	1.86327	1.99457	2.06577
DFFB	1.47759	1.73099	2.01046
USP7	1.63516	1.68333	2.09794
PAP	1.28859	1.75648	2.16521
BSG	1.72851	1.73983	2.44774
YIF1	1.69088	1.99934	2.26741
POLE	2.01623	1.84675	2.05241
	1.42589	1.92804	2.35549

HGNC Symbol	**Ex_100Tc**	**Ex_8Tc**	**Ex_6Tc**	**Ex_5Tc**	**Ex_4Tc**	**Ex_3Tc**
MYC	1.14494	2.72084	5.51345	7.63208	10.95632	15.01672
CACNA1G	0.00607	0.02938	0.04077	0.05626	0.02905	0.03373
NME1	0.62349	1.43929	2.34013	2.90831	3.57392	4.5836
ADCY2	0.00946	0.0342	0.02784	0.07716	0.02054	0.02895
C4orf9	0.02124	0.08426	0.045	0.04417	0.05143	0.07278
FKBP5	0.0188	0.04225	0.07879	0.0634	0.09091	0.11095
CRKL	0.00797	0.01968	0.01795	0.02388	0.03277	0.0207
RFC5	0.00365	0.01919	0.01376	0.02814	0.03454	0.04425
PPP2CA	0.01668	0.04509	0.04247	0.06434	0.07373	0.10709
TIMM8A	0.00967	0.03884	0.04555	0.04775	0.14922	0.05596
n.a.	0.00574	0.01295	0.02577	0.02039	0.03345	0.05116
MAD2L1	0.00188	0.01042	0.02928	0.02576	0.02751	0.02325
MRPL12	0.37371	0.56077	0.77596	0.83337	0.99352	1.15401
NME1	1.03202	1.95079	3.3667	3.81699	5.04469	6.29718
METTL1	0.03531	0.04793	0.07764	0.11283	0.13705	0.15323
SLC7A5	0.02887	0.04378	0.07786	0.07021	0.10571	0.10603
SRM	0.59308	0.93146	1.53687	1.95533	2.11241	2.67521
IL1B	0.19083	0.3106	0.39531	0.40171	0.44765	0.55184
PAICS	0.1931	0.30746	0.52878	0.65254	0.75528	1.15599
TOMM40	0.26834	0.44636	0.54747	0.73507	0.73118	0.80137
PYCR1	0.09818	0.18277	0.25753	0.31944	0.38002	0.49727
UMPK	0.17828	0.27512	0.37137	0.45008	0.4898	0.51183
LRP8	0.0241	0.01094	0.05411	0.10564	0.05556	0.06236
DUSP14	0.01001	0.00521	0.02611	0.05492	0.02652	0.07292
METAP1	0.02814	0.04556	0.0788	0.07314	0.09086	0.08043
ABCE1	0.03376	0.06294	0.0813	0.09458	0.08224	0.10391
PA2G4	2.27609	3.29638	4.99022	6.27142	7.11613	7.94653
BOP1	0.22512	0.33403	0.47873	0.54116	0.57053	0.67442
RANBP1	0.91393	1.44529	1.90911	2.46137	2.55222	3.6361
CTPS	0.07787	0.14722	0.16947	0.23075	0.23679	0.26021
TRAP1	0.33021	0.56462	0.9114	0.95538	1.1384	1.475
HSPD1	0.89231	1.39915	2.13138	2.76721	3.46373	4.24481
PFAS	0.07447	0.108	0.17163	0.2128	0.23305	0.25265
TEAD4	0.05043	0.07495	0.10684	0.12837	0.13349	0.16469
MIF	6.20475	9.80911	13.37389	12.47483	14.98075	16.64096
VARS2	0.32776	0.52619	0.67921	0.7469	0.79481	0.93419
CENTG1	0.47798	0.7797	0.98087	1.20231	1.40746	1.9107
DSCR2	0.24978	0.33627	0.48692	0.58554	0.70823	1.00537
JAG2	0.11819	0.14246	0.22425	0.2855	0.30794	0.40531
PRKAR1B	0.06411	0.07774	0.11695	0.19249	0.13819	0.18706
n.a.	0.02848	0.02838	0.04902	0.06015	0.07113	0.07544
MATK	0.04219	0.01546	0.07179	0.10016	0.10373	0.12623
IARS	0.67473	0.8146	0.99372	1.41678	1.37154	1.61748
GAL	0.05764	0.1112	0.11263	0.13695	0.21253	0.26563
MCAM	0.01156	0.02009	0.01801	0.02738	0.02515	0.03042
CAD	0.08989	0.11537	0.16438	0.21521	0.23491	0.26237
FH	0.67106	0.90287	1.0056	1.43407	1.55879	2.01406
SRPK1	0.19094	0.24095	0.34002	0.45412	0.49353	0.61605
NEFH	0.00196	0.02634	0.00351	0.1625	0.0449	0.06717
NP	0.21698	0.29686	0.37147	0.44869	0.4605	0.5717
AHCY	0.4101	0.54158	0.72434	0.87665	1.09071	1.15403
POLD2	0.0526	0.05972	0.08534	0.11983	0.13813	0.1221
C1QBP	1.19476	1.70364	2.35526	2.81015	3.1539	3.81133
CAMKK2	0.10386	0.15136	0.19077	0.2573	0.30934	0.36831
n.a.	0.07897	0.11468	0.131	0.24188	0.2344	0.24175
BYSL	0.09076	0.13802	0.1772	0.19625	0.20504	0.24464
NUP155	0.03857	0.02744	0.03072	0.09244	0.09189	0.09245

HGNC Symbol	Ex_100Tc	Ex_8Tc	Ex_6Tc	Ex_5Tc	Ex_4Tc	Ex_3Tc
IFRD2	0.12756	0.17517	0.24404	0.29537	0.42921	0.48926
MRPL3	0.20557	0.28678	0.30329	0.53156	0.55857	0.64635
HSPE1	1.63781	2.41191	3.2031	4.03558	4.60515	5.28121
HSPE1	1.67426	2.2026	3.07637	4.11197	4.85821	5.62752
n.a.	0.05356	0.05698	0.06008	0.10998	0.11278	0.13399
EBNA1BP2	0.55653	0.76963	0.99163	1.28679	1.42234	1.69483
TNFRSF8	0.01673	0.01415	0.0319	0.03517	0.05413	0.07485
PRDX4	0.35361	0.57011	0.68207	0.78549	0.90824	1.2819
CSE1L	0.10702	0.10764	0.16799	0.23711	0.27286	0.43601
RPP40	0.01754	0.02472	0.00826	0.05538	0.05141	0.05683
n.a.	0.00905	0.03827	0.0017	0.04505	0.0485	0.051
HRMT1L2	0.38234	0.52272	0.70103	0.82727	0.86441	1.02337
n.a.	0.02624	0.03069	0.04668	0.06422	0.05638	0.06381
n.a.	0.16794	0.15729	0.27174	0.35423	0.38166	0.49922
MADH4	0.13485	0.1751	0.23269	0.2921	0.35223	0.37166
IL9	0.42716	0.61657	0.85126	0.8768	0.91416	1.16154
PDCD11	0.13798	0.19542	0.21151	0.28612	0.28978	0.29121
HK2	0.01304	0.00168	0.01933	0.04509	0.03817	0.03876
PWP2H	0.18393	0.26146	0.28777	0.37297	0.37989	0.4188
n.a.	0.02779	0.05215	0.03905	0.11638	0.09963	0.11767
NOLC1	0.26072	0.37211	0.48101	0.5745	0.74024	0.85943
NOLC1	0.62782	0.99734	1.19315	1.42979	1.42208	1.85845
CCT2	2.43353	2.85904	3.68397	4.92438	5.43042	6.4547
DTYMK	0.24184	0.38786	0.45957	0.49938	0.52004	0.60382
HNRPAB	1.11177	1.58145	1.96094	2.42043	2.6421	3.10034
FASN	0.12985	0.18444	0.22067	0.36647	0.43991	0.56015
FASN	0.20909	0.34431	0.37885	0.42249	0.54651	0.59154
NMB	0.029	0.06269	0.04747	0.07798	0.0687	0.06812
CHC1	0.02175	0.03428	0.03752	0.04765	0.06105	0.07078
	0.0532	0.08223	0.06607	0.16105	0.1703	0.17215
KIAA0179	0.10126	0.09446	0.11186	0.1752	0.23248	0.22351
NTHL1	0.19759	0.27218	0.34325	0.35878	0.48383	0.53325
UNG	0.1111	0.12257	0.18103	0.21446	0.24322	0.29413
KIAA0020	0.57771	0.70518	0.8732	1.13228	1.18744	1.41639
n.a.	0.17974	0.2523	0.31659	0.34597	0.37724	0.44391
n.a.	0.28034	0.33137	0.49722	0.53298	0.63765	0.76564
POLE2	0.04097	0.04876	0.0674	0.0674	0.09221	0.11026
MTHFD1	0.50365	0.76074	0.76954	0.93093	1.09158	1.2582
NOL5A	0.65492	0.83479	1.02563	1.29937	1.4025	1.60872
PRPS2	0.39836	0.47162	0.58868	0.74527	0.81358	0.99014
RUVBL2	0.49898	0.6323	0.85521	0.93326	1.06465	1.21412
GPI	0.55173	0.68824	0.90332	0.99447	1.16317	1.30269
n.a.	0.44272	0.63342	0.83506	0.86109	0.96624	1.12451
NPM3	0.09108	0.13665	0.22275	0.17743	0.21375	0.30308
n.a.	0.08146	0.08426	0.14247	0.15775	0.1904	0.25346
CDC20	0.20049	0.27713	0.40351	0.39241	0.49209	0.52744
n.a.	0.13569	0.16154	0.18379	0.24523	0.29818	0.33534
PRKDC	0.02381	0.03185	0.04084	0.04677	0.05683	0.05775
CKS2	1.80037	1.76276	2.72813	2.96937	3.61872	4.24807
CSE1L	0.12485	0.14767	0.20606	0.22585	0.29604	0.35585
EEF1E1	0.08315	0.12681	0.16839	0.15695	0.20192	0.25799
HRMT1L2	0.47836	0.52977	0.72411	0.8595	1.00109	1.16959
n.a.	0.06957	0.12403	0.13413	0.11113	0.1698	0.19313
TST	0.04798	0.08111	0.10307	0.08049	0.09903	0.10543
DKC1	0.29098	0.35239	0.4892	0.55205	0.60176	0.69278
RAN	0.98569	1.36938	1.677	1.73954	2.21275	2.69686
PDGFRA	0.03783	0.04997	0.05511	0.06196	0.08098	0.09032

HGNC Symbol	**Ex_100Tc**	**Ex_8Tc**	**Ex_6Tc**	**Ex_5Tc**	**Ex_4Tc**	**Ex_3Tc**
CDK4	0.00445	0.01414	0.02387	0.00142	0.0242	0.02322
ALDH1B1	0.04048	0.05875	0.07738	0.07008	0.09382	0.09468
SORD	0.09745	0.13241	0.1999	0.18017	0.24083	0.298
BDH	0.08213	0.10416	0.09352	0.15097	0.1854	0.19629
GMPS	0.20718	0.25386	0.35901	0.39891	0.44805	0.50167
GPR30	0.14782	0.14445	0.235	0.22368	0.2984	0.37236
PHB	1.21131	1.44738	2.33034	2.37561	2.54409	3.273
STRA13	0.18582	0.32551	0.33059	0.36067	0.42585	0.54466
XPOT	0.14298	0.16212	0.26215	0.2352	0.34993	0.4242
SMN1	0.0841	0.10862	0.11418	0.11899	0.17546	0.17625
CHC1	0.3542	0.41133	0.59836	0.63713	0.77295	0.98191
PLK1	0.19023	0.20572	0.28532	0.3273	0.39665	0.45907
n.a.	0.03558	0.04319	0.07013	0.07242	0.0655	0.11747
AK2	0.62993	0.76633	0.95519	1.03435	1.09063	1.4119
n.a.	0.06003	0.06934	0.08938	0.0952	0.11612	0.13785
MGST1	0.09221	0.11708	0.12889	0.14993	0.17617	0.28811
CSDA	0.99187	1.17785	1.4786	1.5707	1.77027	2.11573
n.a.	0.13484	0.11324	0.1639	0.19154	0.21258	0.31332
ATP1B3	1.16721	1.37704	1.68907	2.10815	2.16425	2.46433
BCS1L	0.10495	0.121	0.16099	0.16313	0.18758	0.2379
UNG	0.09248	0.13337	0.13725	0.15604	0.17718	0.21076
PBP	0.54093	0.56499	0.93605	0.95527	1.04152	1.15943
CDC6	0.06507	0.08747	0.11341	0.10085	0.11515	0.1598
CDC7	0.0575	0.06781	0.09571	0.11628	0.10539	0.15215
MTAP	0.04326	0.02766	0.05673	0.09472	0.0847	0.08734
ADSL	1.4174	1.84175	1.99404	2.4638	2.42568	2.84691
CDKN3	0.39936	0.54619	0.65379	0.74177	0.78962	0.98577
VRK1	0.52524	0.55605	0.66497	0.86459	0.91363	1.06823
WFDC2	0.05956	0.05717	0.07518	0.09169	0.0959	0.12413
GSPT1	0.37069	0.47467	0.52939	0.57956	0.67086	0.76695
SLC39A14	0.09032	0.0833	0.12974	0.1609	0.16822	0.23059
n.a.	0.13982	0.19078	0.24444	0.23266	0.25702	0.30723
RLN2	0.05153	0.08816	0.07862	0.08449	0.08088	0.11985
BAG2	0.09834	0.09048	0.13213	0.13741	0.16019	0.20125
HSD17B8	0.06016	0.05006	0.1131	0.10165	0.10493	0.14448
UCHL3	0.62729	0.61884	0.80061	1.04594	1.06913	1.29383
NME2	7.55561	10.38378	12.64778	13.29127	14.58179	18.41978
MRPS12	0.32137	0.41112	0.51989	0.51661	0.62005	0.6485
PCNA	0.8066	1.02107	1.23744	1.41216	1.4529	1.80271
DPH2L2	0.07028	0.06583	0.1013	0.09406	0.1335	0.15561
CCNB1	0.85245	0.92052	1.23335	1.37378	1.62246	1.99532
MC1R	0.48549	0.4532	0.69749	0.95791	0.96435	1.23738
SOD1	2.5858	3.45486	3.7023	4.49667	4.68941	5.51018
ATP5G3	3.3077	4.20899	4.27423	5.60963	6.12595	6.67483
CCT3	1.72846	2.0646	2.79991	3.44075	3.40841	3.87786
RFC4	0.27426	0.35881	0.37662	0.48591	0.51809	0.59728
CDC25A	0.03912	0.04158	0.08498	0.06342	0.06112	0.08291
FRDA	0.25496	0.26757	0.39688	0.42322	0.49335	0.60397
SNRPD1	0.12746	0.14801	0.21029	0.27204	0.25391	0.26763
CHAF1A	0.11977	0.15836	0.19916	0.18424	0.19483	0.24565
PRDX2	0.82861	1.0668	1.30645	1.51599	1.5828	1.82565
BUB1	0.44618	0.46291	0.57289	0.70704	0.75849	0.89866
CDC2	0.70282	0.87813	1.16183	1.30499	1.39656	1.64473
POLR1C	0.18392	0.25254	0.30128	0.30304	0.35209	0.43614
SLC19A1	0.04916	0.00569	0.04112	0.05153	0.07274	0.30415
TOMM20	0.51946	0.64114	0.70457	0.82917	0.93901	1.07925
MMP3	0.04623	0.05491	0.08705	0.09128	0.09137	0.1078

HGNC Symbol	**Ex_100Tc**	**Ex_8Tc**	**Ex_6Tc**	**Ex_5Tc**	**Ex_4Tc**	**Ex_3Tc**
UBE2C	1.35685	1.68073	2.14081	2.37378	2.66406	3.20427
PTPN2	0.05123	0.07934	0.08731	0.09952	0.09626	0.13627
RUVBL1	0.3056	0.37941	0.47328	0.54928	0.58195	0.63066
TYMS	0.58175	0.75875	0.94859	0.99175	1.15885	1.20854
DDX10	0.24365	0.22511	0.3165	0.40521	0.41165	0.51093
TUFM	1.56785	2.07254	2.14171	2.68676	2.7756	3.20988
AURKB	0.32169	0.53301	0.56115	0.49698	0.56539	0.7117
RRS1	0.08735	0.06338	0.12137	0.13614	0.14353	0.18376
GEMIN4	0.2555	0.32168	0.4234	0.4994	0.48664	0.5493
PTMA	6.78421	9.25981	10.07721	11.49298	13.38787	16.01615
CYP51A1	0.13159	0.13805	0.14288	0.1814	0.18395	0.21591
ARHGEF5	0.01301	0.02177	0.01552	0.00389	0.01615	0.02226
KIAA0690	0.15442	0.14763	0.17722	0.23949	0.26635	0.2823
VDAC1	0.39322	0.39711	0.48106	0.5248	0.65884	0.68627
DDX1	0.96723	1.21099	1.2092	1.56729	1.56389	1.8654
SCAMP1	0.08669	0.04982	0.07383	0.11709	0.13411	0.14573
DDX18	0.43402	0.49942	0.51273	0.6524	0.66894	0.72111
PES1	0.40434	0.46262	0.59507	0.69203	0.69321	0.78574
RANGAP1	0.10006	0.10162	0.13747	0.14422	0.14854	0.18005
APEX1	0.1743	0.23255	0.26857	0.2912	0.32431	0.3448
MYBL2	0.19153	0.24814	0.26918	0.29164	0.31745	0.36558
USP10	0.09064	0.09243	0.05771	0.18437	0.15377	0.17499
n.a.	0.04877	0.03711	0.05672	0.0846	0.06836	0.08499
RPA3	0.20008	0.28308	0.3321	0.30926	0.36863	0.38817
CXCL12	0.04354	0.04356	0.06168	0.04836	0.07894	0.08092
n.a.	0.03933	0.03851	0.05566	0.03665	0.07557	0.0692
MCM3	0.22131	0.39617	0.24249	0.37917	0.35938	0.43948
GMNN	0.15097	0.15009	0.22639	0.2091	0.25006	0.28891
HSPA9B	0.87101	0.9069	1.23526	1.3119	1.47143	1.73671
TCERG1	0.18957	0.15319	0.2714	0.26835	0.29363	0.35711
RNU3IP2	0.19819	0.21141	0.27326	0.28772	0.33393	0.37642
SFRS7	1.02456	1.25452	1.39769	1.69077	1.75382	1.87979
MSH6	0.73302	0.84452	0.94861	1.11714	1.35018	1.46137
CENPF	0.32252	0.34947	0.43437	0.55535	0.55215	0.61098
MXI1	0.07378	0.09181	0.09691	0.0972	0.08826	0.13298
AMD1	0.2423	0.23681	0.3559	0.42642	0.4395	0.46512
ELK1	0.18848	0.18717	0.23669	0.23671	0.28941	0.29197
ILF3	0.3812	0.4695	0.48673	0.64706	0.55348	0.7183
TFDP1	0.2903	0.30143	0.38	0.34716	0.44893	0.49598
n.a.	0.21101	0.2126	0.30828	0.30269	0.34447	0.39533
TOP2A	0.19435	0.21933	0.25773	0.25915	0.33606	0.37715
EIF5A	0.29621	0.33319	0.42675	0.39059	0.47944	0.52491
n.a.	0.02757	0.02822	0.03701	0.04104	0.06982	0.05466
n.a.	0.28131	0.34735	0.35721	0.41436	0.44881	0.51171
ATIC	1.68325	1.89152	2.22084	2.8356	3.00291	3.29863
ATIC	0.78872	0.95959	1.05788	1.1388	1.26879	1.49529
PEX5	0.08866	0.09568	0.09127	0.12703	0.12801	0.17709
TAF4B	0.07043	0.0724	0.08995	0.05523	0.11239	0.12764
HDGF	0.36462	0.44614	0.51379	0.52403	0.55071	0.67558
HDGF	0.81301	1.04123	1.13866	1.38824	1.28702	1.61672
ILF2	1.38592	1.67342	1.9281	2.15145	2.16057	2.59353
CCNA2	0.12282	0.14654	0.20375	0.16241	0.20873	0.24156
MDH2	0.64929	0.79251	0.92431	1.12829	1.13097	1.2361
PEG10	0.02075	0.03008	0.05109	0.04636	0.0354	0.03904
PPRC1	0.07047	0.06655	0.09263	0.10562	0.1226	0.13518
SSRP1	0.72021	0.8971	0.97503	1.07707	1.26108	1.42683
PTK9	0.00151	0.00203	0.00118	0.00177	0.00295	0.00264

HGNC Symbol	**Ex_100Tc**	**Ex_8Tc**	**Ex_6Tc**	**Ex_5Tc**	**Ex_4Tc**	**Ex_3Tc**
ACSL1	0.16541	0.15166	0.17461	0.23126	0.22849	0.27658
PFKM	0.23965	0.30738	0.36714	0.44435	0.44154	0.47195
HNRPDL	0.38179	0.39766	0.4517	0.52815	0.54946	0.6727
RPIA	0.17969	0.16909	0.21038	0.2724	0.32226	0.31697
SLC16A1	0.01258	0.0052	0.01877	0.00825	0.02344	0.01943
KCNJ6	0.44605	0.57032	0.64367	0.67001	0.76323	0.8247
SFRS2	4.06265	4.17249	4.51995	5.52168	5.89467	7.18378
PRKCI	0.03793	0.03212	0.05032	0.04552	0.05732	0.06172
POLR2H	0.25996	0.34345	0.43898	0.44009	0.45822	0.5112
ABCE1	0.04365	0.02997	0.04205	0.06384	0.12019	0.06809
MELK	0.07897	0.10064	0.09106	0.10175	0.12393	0.13906
DDX21	0.04435	0.03282	0.07481	0.06756	0.14962	0.0593
SSSCA1	0.32994	0.37188	0.4429	0.48868	0.52068	0.53446
n.a.	0.39139	0.47498	0.51744	0.57769	0.64175	0.68347
HSPCA	0.34543	0.33887	0.53216	0.48753	0.7007	0.53833
DEAF1	0.27876	0.29724	0.34559	0.39591	0.4384	0.47267
n.a.	0.15422	0.1555	0.18537	0.26423	0.25285	0.2964
EIF1AX	0.05823	0.04822	0.08311	0.09002	0.12483	0.10284
n.a.	2.16861	2.63815	2.99197	3.3629	3.6305	3.76247
n.a.	0.11253	0.12339	0.13379	0.13556	0.1509	0.18263
SF3A3	0.48299	0.50785	0.64764	0.6047	0.68941	0.78262
n.a.	0.01769	0.02525	0.03465	0.03349	0.02706	0.03557
AK2	0.22594	0.2029	0.23451	0.30261	0.35811	0.37682
PLAUR	0.02058	0.02105	0.04775	0.10205	0.08882	0.06467
SCARB1	0.29118	0.22465	0.39207	0.43555	0.42046	0.45024
MCM2	0.95433	1.18717	1.35289	1.52955	1.51103	1.67527
EXOSC7	0.20215	0.24581	0.30236	0.28921	0.31601	0.35319
KHSRP	2.39112	2.46335	2.84733	3.45164	3.66491	4.00287
NUDC	0.72867	0.92336	1.04643	1.0801	1.07674	1.22004
CGRRF1	0.21023	0.21271	0.28372	0.37179	0.32569	0.45528
APEX1	0.39394	0.43275	0.53017	0.60873	0.64374	0.66526
GARS	1.05699	1.26298	1.26319	1.49055	1.53044	1.96357
EIF3S9	1.19013	1.44633	1.65457	1.8181	1.94003	2.10047
IMPDH1	0.18156	0.21177	0.22634	0.27213	0.26281	0.28861
VEGF	0.00953	0.01785	0.00982	0.00918	0.0149	0.04514
TFDP2	0.09494	0.1053	0.09638	0.10033	0.15867	0.16103
PRDX1	4.71743	4.96304	5.98365	6.65052	7.27766	7.5817
SCO2	0.21479	0.23957	0.37451	0.34625	0.42403	0.39414
TUBG1	0.10715	0.12251	0.1324	0.17265	0.19354	0.21129
MYCN	0.07736	0.08694	0.10984	0.10834	0.12966	0.12706
ABL2	0.0213	0.03045	0.02046	0.02581	0.02656	0.03035
SLC20A1	0.31071	0.35455	0.45075	0.62141	0.50668	0.56476
CDKN2B	0.01813	0.02984	0.04801	0.03193	0.03226	0.03848
n.a.	0.38294	0.4242	0.46436	0.6373	0.60362	0.57439
FANCG	0.21066	0.2847	0.30442	0.31181	0.34771	0.38879
PMPCA	0.96683	1.08602	1.15648	1.44322	1.25674	1.34773
PSMC3	0.51492	0.68422	0.71401	0.6735	0.78355	0.80523
MCM7	1.3928	2.07175	2.04609	2.18716	2.23329	2.62859
ABCA3	0.07064	0.06987	0.08227	0.11617	0.10355	0.14452
EIF4EBP1	0.42807	0.49271	0.54044	0.56871	0.57	0.61791
TNFRSF4	0.02418	0.03075	0.03178	0.02774	0.03102	0.02359
SRP72	0.53034	0.53248	0.68798	0.70946	0.84177	0.72381
ALG3	0.13167	0.11852	0.16198	0.16048	0.1748	0.19513
CKS1B	0.09816	0.10628	0.12768	0.15319	0.15184	0.15428
NSEP1	3.95051	3.98514	5.37267	5.63018	6.16381	6.93133
FARSLA	0.33628	0.37924	0.44664	0.44722	0.506	0.6222
PRIM1	0.1101	0.11122	0.1329	0.14163	0.1645	0.19582

HGNC Symbol	Ex_100Tc	Ex_8Tc	Ex_6Tc	Ex_5Tc	Ex_4Tc	Ex_3Tc
TBL3	0.48851	0.50596	0.60434	0.675	0.72975	0.81081
JUND	0.25807	0.33436	0.36092	0.34028	0.37028	0.40871
PTBP1	0.4095	0.46081	0.47345	0.56014	0.5863	0.60836
MRE11A	0.15035	0.1686	0.21549	0.19567	0.23543	0.24932
HSPA5	0.75249	0.84951	0.92717	0.98337	1.08007	1.14506
OAT	0.1011	0.11118	0.11261	0.1216	0.1765	0.16929
TFRC	1.12985	1.17963	1.14275	1.31774	1.40307	1.53813
SHMT1	0.04076	0.04125	0.07848	0.05434	0.06216	0.06819
CLNS1A	1.56246	1.84368	1.93986	2.15405	2.18549	2.48371
SEMA3C	0.01354	0.01899	0.01927	0.02928	0.00815	0.02562
MCAM	0.06783	0.06671	0.07432	0.09025	0.09407	0.09596
MAPKAPK5	0.40885	0.48439	0.5849	0.5426	0.53403	0.63745
SIP1	0.04566	0.04862	0.061	0.0596	0.05537	0.09301
NF2	0.09853	0.11411	0.13523	0.12826	0.14291	0.16127
SLC1A5	0.0621	0.0916	0.09792	0.12481	0.11516	0.10863
PSMA2	1.22018	1.45143	1.43304	1.61982	1.68332	1.93955
RAD51C	0.49556	0.53203	0.48569	0.5355	0.58634	0.6591
CTSC	0.10053	0.09636	0.10789	0.11007	0.1375	0.16207
HSPA8	2.32214	2.51969	3.12476	3.34063	3.79412	3.6899
n.a.	0.04139	0.02115	0.02105	0.04959	0.04137	0.05784
IGFBP2	0.54367	0.57135	0.57054	0.53238	0.65417	0.69318
DARS	0.23787	0.25718	0.24994	0.31995	0.3254	0.33621
UCHL3	0.40776	0.41674	0.46925	0.54363	0.61533	0.66662
GTF3A	1.70377	1.65382	1.95218	2.42211	2.3264	2.60168
RPL5	9.28582	10.48347	11.07853	12.57631	14.36083	14.9781
AMD1	0.10198	0.07544	0.09351	0.13814	0.13358	0.15504
HSPA1A	0.02171	0.04854	0.05433	0.0439	0.03651	0.03983
SYNGR3	0.1103	0.09921	0.1085	0.11413	0.14458	0.17713
NINJ1	0.02294	0.00553	0.02076	0.01306	0.02407	0.01743
SNRPA1	0.99392	1.0957	1.35926	1.41302	1.3687	1.54334
TAF9	0.79486	0.89246	0.92783	1.02704	1.08839	1.17719
SYNCRIP	0.32768	0.43255	0.40341	0.55959	0.57377	0.62902
n.a.	0.31747	0.38994	0.41464	0.41903	0.45305	0.50997
ITGB3BP	0.14705	0.1634	0.18194	0.18643	0.23344	0.24143
PTPRF	0.04472	0.0479	0.03512	0.06466	0.05812	0.06393
CHEK1	0.08152	0.08298	0.10438	0.10791	0.11237	0.12507
TCEB1	1.34027	1.40933	1.50326	1.83685	1.8602	2.08546
n.a.	0.30113	0.27245	0.38476	0.42862	0.41617	0.43259
VBP1	0.34198	0.31257	0.37004	0.39571	0.47177	0.53547
BUB1B	0.10896	0.12627	0.13965	0.17109	0.15607	0.17487
RACGAP1	0.24069	0.21418	0.30187	0.34282	0.38439	0.41727
AK3	0.03125	0.05289	0.03033	0.1052	0.05431	0.06458
HNRPF	2.56957	3.16554	3.09992	3.80763	3.8582	4.10454
PDAP1	0.10366	0.1073	0.14182	0.11455	0.14864	0.17254
SELE	0.07899	0.10097	0.09282	0.10603	0.10238	0.09844
n.a.	0.06018	0.06911	0.07383	0.09532	0.10409	0.10128
RCN1	0.01328	0.00308	0.00844	0.02708	0.02065	0.02735
GLDC	0.06879	0.03697	0.07299	0.08051	0.08296	0.09708
PMS1	0.02839	0.03039	0.0251	0.03317	0.04901	0.03082
PFKP	0.27196	0.24657	0.28492	0.30814	0.31283	0.386
PDCD2	0.13822	0.14414	0.17288	0.17868	0.2119	0.20429
MGST2	0.28792	0.36902	0.32933	0.35968	0.35124	0.33649
NDUFB7	0.95357	1.11146	1.21047	1.11802	1.30349	1.40165
G22P1	0.927	1.12744	1.14488	1.27756	1.32755	1.4206
n.a.	0.21279	0.2809	0.24754	0.27432	0.2751	0.32315
PBEF1	0.03354	0.02307	0.04258	0.03418	0.02872	0.04471
TBL2	0.09804	0.09615	0.13141	0.10744	0.14808	0.13817

HGNC Symbol	**Ex_100Tc**	**Ex_8Tc**	**Ex_6Tc**	**Ex_5Tc**	**Ex_4Tc**	**Ex_3Tc**
GCN5L2	0.08182	0.06675	0.09701	0.12569	0.10564	0.11266
CDK2AP1	0.47154	0.57341	0.51373	0.60649	0.60968	0.6369
NOL1	0.23735	0.27966	0.30737	0.2765	0.31323	0.36886
SLC29A1	0.34088	0.35329	0.31044	0.32478	0.42138	0.50353
BNIP1	0.03886	0.05899	0.08056	0.05333	0.05937	0.05209
DBN1	0.09242	0.08988	0.08229	0.10676	0.10735	0.12408
EIF4G1	0.33189	0.3699	0.39705	0.44938	0.47865	0.53004
B4GALT2	0.04218	0.02359	0.0474	0.05194	0.04711	0.06299
TMEM5	0.34116	0.29113	0.34726	0.41258	0.42727	0.4504
FVT1	0.01519	0.00335	0.00242	0.02405	0.01886	0.0206
ETF1	0.04067	0.03906	0.05768	0.06627	0.07259	0.07178
ATF4	1.88943	1.99796	1.92948	1.87651	2.17823	2.32789
ILF3	0.22464	0.26282	0.27681	0.32946	0.32474	0.35246
RAMP1	0.08388	0.11987	0.09936	0.05164	0.09182	0.12973
n.a.	0.3993	0.43387	0.47895	0.52065	0.51597	0.62223
ADCY3	0.22559	0.13985	0.17889	0.2202	0.25304	0.28231
AFG3L2	0.44324	0.49942	0.50799	0.56748	0.57405	0.62565
PRPS1	0.06302	0.07125	0.08003	0.06555	0.08568	0.07188
OPRS1	0.02986	0.0113	0.0256	0.03452	0.03244	0.05642
TOMM70A	0.06186	0.07491	0.09353	0.08841	0.11767	0.11747
APRT	1.00542	1.30054	1.45028	1.38925	1.47388	1.55704
FGFR4	0.02857	0.01999	0.03134	0.01791	0.03238	0.03182
DEFA6	0.02631	0.03105	0.04945	0.02157	0.05138	0.03182
ZNF9	0.048	0.07908	0.09614	0.10504	0.34763	0.09401
RAC3	0.01003	0.00121	0.00196	0.03452	0.0249	0.02332
WNT10B	0.01066	0.03253	0.00968	0.04605	0.03987	0.0236
NFRKB	0.03746	0.04885	0.0523	0.03658	0.06031	0.06001
CDK5R2	0.01863	0.02181	0.00582	0.02166	0.01281	0.0181
CYCS	0.01218	0.00169	0.00998	0.02903	0.02228	0.03194
YES1	0.11124	0.11174	0.11177	0.1041	0.13646	0.13145
DLEU1	0.18316	0.19746	0.21521	0.20671	0.24321	0.24204
BNIP3	0.43367	0.41211	0.47508	0.4351	0.49601	0.55279
RAD23A	0.67809	0.76187	0.76848	0.86686	0.94874	0.98028
	0.01616	0.00672	0.02256	0.06121	0.0278	0.02034
UBE2G2	0.29203	0.3657	0.34651	0.40251	0.42557	0.41901
KCNQ3	0.02216	0.01863	0.02247	0.01413	0.01441	0.02051
MTA1	0.2546	0.28328	0.29005	0.25875	0.3021	0.33944
LIG3	0.07288	0.09509	0.08375	0.07282	0.09686	0.08314
ITGA2B	0.02521	0.03456	0.03246	0.04787	0.04326	0.0378
TOMM34	0.02836	0.03311	0.02564	0.01013	0.06922	0.04264
ITIH4	0.0616	0.06368	0.07406	0.0757	0.08876	0.0693
POLD1	0.41801	0.508	0.53439	0.51785	0.55239	0.63458
IKBKAP	0.13526	0.14621	0.12617	0.16026	0.16609	0.17568
ASNS	0.06102	0.04786	0.05003	0.05341	0.07206	0.06873
MX1	0.01523	0.01857	0.01247	0.01549	0.02065	0.00789
XRCC5	0.04533	0.07403	0.0706	0.08603	0.09411	0.09476
XPO1	0.56709	0.61779	0.63377	0.74382	0.7914	0.82155
RAD54L	0.06474	0.08469	0.10937	0.11006	0.09206	0.10882
PTHLH	0.02767	0.0162	0.02579	0.0355	0.00735	0.012
MSH2	0.21356	0.25043	0.26256	0.29872	0.35736	0.40659
CDKL1	0.05966	0.05407	0.07602	0.15483	0.07001	0.07519
ADA	0.14931	0.16258	0.1941	0.18337	0.20516	0.20208
n.a.	0.26816	0.29025	0.27186	0.33373	0.28207	0.30218
TGFB1	0.00152	0.0011	0.00135	0.01083	0.00106	0.00098
NPTX2	0.01218	0.00511	0.02093	0.01963	0.0043	0.00758
BAG1	0.39355	0.50764	0.46188	0.51445	0.47019	0.52385
BAG1	0.55042	0.63504	0.64688	0.66238	0.60964	0.64535

HGNC Symbol	**Ex_100Tc**	**Ex_8Tc**	**Ex_6Tc**	**Ex_5Tc**	**Ex_4Tc**	**Ex_3Tc**
SHB	0.10253	0.08904	0.08691	0.09023	0.10646	0.0972
EIF3S10	0.32007	0.29646	0.36677	0.44098	0.43324	0.45929
HTATIP2	0.01919	0.028	0.03216	0.02212	0.02828	0.0221
CALCA	0.02953	0.0335	0.0427	0.0464	0.04755	0.04243
C6orf108	1.0813	1.28889	1.38078	1.4197	1.55194	1.5482
ACY1	0.09536	0.14241	0.11009	0.10262	0.13609	0.14286
PASK	0.03702	0.02916	0.02857	0.02528	0.02879	0.03896
CEBPZ	0.35846	0.33932	0.38175	0.42855	0.46788	0.47004
RAP1A	0.0671	0.0511	0.04558	0.07176	0.06409	0.0593
NID	0.01184	0.01485	0.02136	0.03753	0.0404	0.02844
IDE	0.13186	0.13929	0.15347	0.14859	0.17437	0.18971
HOXB7	0.03686	0.04668	0.04417	0.02622	0.03989	0.03739
GUCY1B2	0.16724	0.20338	0.24716	0.23426	0.25482	0.26888
SERPINA7	0.06614	0.05808	0.08281	0.07784	0.10047	0.09698
FPRL2	0.04564	0.05223	0.05722	0.06066	0.05875	0.05657
MTRR	0.15991	0.14022	0.16785	0.22061	0.20315	0.17903
THRA	0.20562	0.20507	0.22065	0.25115	0.25027	0.24268
POR	0.15723	0.1794	0.17917	0.2098	0.17777	0.18402
YWHAH	0.6024	0.61589	0.71009	0.78266	0.89468	0.92099
TRIM28	1.3807	1.87402	1.87791	2.02374	2.08652	2.06858
DHX30	0.50746	0.53975	0.66049	0.68677	0.68636	0.66879
CDK8	0.05707	0.03231	0.05109	0.05395	0.08587	0.08545
CCNH	0.21571	0.22923	0.22138	0.25313	0.24565	0.27361
RFK	0.07005	0.08681	0.08015	0.09871	0.10285	0.09647
RABGGTB	0.36684	0.42855	0.41647	0.42485	0.42696	0.43217
PLK4	0.05711	0.06566	0.06414	0.07617	0.07167	0.09208
CYP4B1	0.01818	0.02212	0.01479	0.0281	0.01726	0.02568
TP53BP2	0.03717	0.10155	0.05043	0.05624	0.04215	0.05094
NVL	0.55836	0.51672	0.60485	0.74844	0.7723	0.71895
ARF1	2.00879	2.18815	1.98132	2.5784	2.26177	2.52116
PLK2	0.10776	0.09893	0.10267	0.08395	0.08675	0.06842
GZMA	0.02178	0.03853	0.02386	0.03074	0.02722	0.04392
NOLA2	0.08466	0.28532	0.1057	0.08982	0.08696	0.12136
HMBS	0.14167	0.17194	0.20812	0.23694	0.22459	0.22428
ITIH2	0.02044	0.01754	0.01454	0.02624	0.02377	0.02061
SACS	0.0567	0.01686	0.0606	0.06366	0.05251	0.04668
GABPA	0.07962	0.09354	0.08863	0.11663	0.12727	0.12222
ETS2	0.07303	0.05037	0.07189	0.07592	0.0802	0.08526
IL8RA	0.09453	0.09742	0.11416	0.10699	0.13543	0.11622
API5	0.02862	0.02842	0.04765	0.08883	0.06094	0.06229
n.a.	0.40678	0.42398	0.465	0.43825	0.49702	0.48593
ICT1	0.16573	0.14977	0.35205	0.20532	0.19027	0.23773
DFFB	0.15107	0.14199	0.14034	0.15898	0.15168	0.16167
USP7	0.36369	0.36912	0.36096	0.39524	0.40234	0.40644
PAP	0.10496	0.10761	0.12671	0.12652	0.11887	0.12261
BSG	0.12811	0.1104	0.10811	0.13194	0.14306	0.13585
YIF1	0.36154	0.45125	0.46066	0.5256	0.49569	0.49774
POLE	0.07269	0.07966	0.14669	0.08667	0.09579	0.11641
	0.02557	0.00917	0.02743	0.06629	0.02816	0.03703

HGNC Symbol	Ex_2Tc	Ex_1 5Tc	Ex_1Tc	Ex_0 5Tc	Ex_0Tc
MYC	24.24792	29.84727	48.72814	70.64298	99.90093
CACNA1G	0.03884	0.04056	0.0249	0.0383	0.05098
NME1	6.11381	6.93531	7.89053	9.11514	11.2004
ADCY2	0.01927	0.02214	0.02956	0.02524	0.05037
C4orf9	0.06811	0.07043	0.07172	0.07933	0.08534
FKBP5	0.12327	0.17882	0.18407	0.21477	0.22532
CRKL	0.06464	0.03174	0.04129	0.0495	0.04769
RFC5	0.05806	0.0701	0.0784	0.0674	0.06622
PPP2CA	0.1188	0.16335	0.18774	0.27539	0.37333
TIMM8A	0.03355	0.0617	0.05448	0.04957	0.03746
n.a.	0.03668	0.03476	0.05453	0.04148	0.0439
MAD2L1	0.04222	0.03828	0.04161	0.04277	0.03763
MRPL12	1.35803	1.50382	1.5149	1.85243	1.79529
NME1	8.78296	9.95429	11.4959	12.52977	16.60843
METTL1	0.16941	0.19865	0.17531	0.22317	0.26762
SLC7A5	0.2626	0.2141	0.2441	0.3273	0.53973
SRM	3.46106	3.81465	4.60774	5.88457	6.52146
IL1B	0.47009	0.64286	0.63565	0.72582	0.77263
PAICS	1.48973	1.59328	1.95943	2.23747	2.40668
TOMM40	1.04629	1.26929	1.36004	1.59827	2.04866
PYCR1	0.71494	0.87215	1.0356	1.3967	2.02993
UMPK	0.61388	0.72765	0.66725	0.79878	0.85444
LRP8	0.09823	0.09671	0.12233	0.12144	0.14263
DUSP14	0.1534	0.03635	0.04079	0.04512	0.05757
METAP1	0.10463	0.10231	0.12391	0.11613	0.1106
ABCE1	0.14939	0.13549	0.15696	0.16863	0.22944
PA2G4	9.2119	12.0504	13.89182	16.71221	17.31241
BOP1	0.71181	0.98384	1.00474	1.28254	1.52391
RANBP1	4.18971	4.86993	5.57516	6.15064	7.19984
CTPS	0.31682	0.37337	0.3801	0.41418	0.46139
TRAP1	1.94524	2.34088	2.86386	3.556	4.59865
HSPD1	5.33401	6.8202	7.58756	9.28963	10.57588
PFAS	0.32968	0.39351	0.44004	0.48149	0.46104
TEAD4	0.22022	0.25596	0.29925	0.38479	0.48777
MIF	19.16197	22.75153	23.46172	24.19818	31.73168
VARS2	1.0973	1.42561	1.4329	1.82111	2.09228
CENTG1	2.58864	3.34169	3.82157	4.57701	6.24183
DSCR2	1.31659	1.44559	1.71837	2.05897	2.40918
JAG2	0.50935	0.63113	0.75629	0.88819	1.12428
PRKAR1B	0.19804	0.19583	0.24432	0.2971	0.30204
n.a.	0.07719	0.09052	0.10752	0.12246	0.15445
MATK	0.19028	0.18185	0.2606	0.30828	0.33483
IARS	2.34668	2.32211	2.75536	3.4562	4.09841
GAL	0.37798	0.51008	0.53362	0.72777	0.92394
MCAM	0.03483	0.0495	0.06283	0.05132	0.09111
CAD	0.31569	0.39535	0.36994	0.51115	0.56246
FH	2.43855	2.84974	3.46324	3.95112	4.13769
SRPK1	0.83915	0.87489	1.12343	1.18884	1.52077
NEFH	0.0634	0.07343	0.10049	0.09351	0.07361
NP	0.65157	0.8101	0.98444	1.1093	1.32796
AHCY	1.69598	1.76517	2.23913	2.35751	2.979
POLD2	0.1553	0.1963	0.19288	0.21385	0.26951
C1QBP	4.99316	5.55995	6.30976	7.26831	8.1798
CAMKK2	0.39591	0.45582	0.52487	0.58	0.57179
n.a.	0.25729	0.31906	0.38658	0.42096	0.47316
BYSL	0.22934	0.2954	0.29529	0.34102	0.37958
NUP155	0.1308	0.12654	0.11253	0.12207	0.13338

HGNC Symbol	**Ex_2Tc**	**Ex_1 5Tc**	**Ex_1Tc**	**Ex_0 5Tc**	**Ex_0Tc**
IFRD2	0.69624	0.72125	0.88974	1.13615	1.31532
MRPL3	0.82447	0.952	1.19507	1.30666	1.45727
HSPE1	8.07346	8.22515	10.56405	11.8883	13.98806
HSPE1	7.68753	8.22701	10.13275	11.81685	12.8846
n.a.	0.1774	0.19251	0.21735	0.23547	0.26078
EBNA1BP2	2.07532	2.52982	2.85928	2.98876	3.74663
TNFRSF8	0.09502	0.1475	0.20366	0.26273	0.41426
PRDX4	1.47968	1.84113	2.14581	2.51338	3.07336
CSE1L	0.46118	0.45033	0.64102	0.66878	0.84092
RPP40	0.14313	0.09977	0.08993	0.08949	0.1247
n.a.	0.03542	0.0771	0.05116	0.05922	0.0608
HRMT1L2	1.30027	1.49672	1.66707	2.34567	2.64623
n.a.	0.08738	0.09297	0.05829	0.09968	0.15362
n.a.	0.5821	0.7606	0.85698	1.04672	1.27818
MADH4	0.45686	0.62083	0.69856	0.78066	0.84257
IL9	1.23332	1.50689	1.62093	1.66557	1.72986
PDCD11	0.36358	0.41181	0.40439	0.50033	0.60663
HK2	0.08005	0.03996	0.05956	0.07294	0.06673
PWP2H	0.5242	0.55855	0.62081	0.80532	0.83772
n.a.	0.12961	0.18367	0.2152	0.20333	0.23753
NOLC1	1.23518	1.18399	1.51559	1.69105	1.86501
NOLC1	2.07927	2.56581	2.65577	3.10364	3.95233
CCT2	8.01904	8.46872	10.58227	11.69279	13.00955
DTYMK	0.68431	0.8545	0.84353	0.96483	0.99887
HNRPAB	3.81878	4.14986	4.68133	5.41328	5.6115
FASN	0.82981	0.94697	1.22436	1.59613	2.04446
FASN	0.91508	0.94895	1.24627	1.63587	2.21456
NMB	0.08132	0.12189	0.08947	0.1058	0.10026
CHC1	0.08067	0.0855	0.10163	0.1256	0.12436
	0.24826	0.30016	0.35629	0.42537	0.46282
KIAA0179	0.31357	0.38317	0.4107	0.42879	0.72517
NTHL1	0.57001	0.73895	0.78379	0.91477	1.06995
UNG	0.43232	0.4134	0.56625	0.65597	0.69971
KIAA0020	1.76941	1.87983	2.44869	2.63156	3.20546
n.a.	0.51254	0.54393	0.58716	0.60697	0.80429
n.a.	0.85375	0.94036	1.00024	1.14491	1.28184
POLE2	0.09803	0.13469	0.14501	0.1497	0.19262
MTHFD1	1.43651	1.54327	1.71401	1.89954	2.00319
NOL5A	1.94116	2.24268	2.628	2.70959	3.5047
PRPS2	1.27711	1.29917	1.67293	1.84033	2.11056
RUVBL2	1.42568	1.72487	1.92551	2.04062	2.28655
GPI	1.3664	1.90657	1.87308	2.16928	2.52435
n.a.	1.31801	1.65265	1.66221	1.91425	1.90581
NPM3	0.40294	0.38559	0.51279	0.67992	0.76681
n.a.	0.32914	0.37158	0.48373	0.55839	0.69126
CDC20	0.55934	0.67395	0.64745	0.64784	0.69958
n.a.	0.453	0.44056	0.54973	0.6581	0.69647
PRKDC	0.06537	0.07227	0.07932	0.07263	0.08444
CKS2	5.1553	5.25915	6.50381	6.17341	6.94295
CSE1L	0.42094	0.5447	0.52608	0.6902	0.82152
EEF1E1	0.35915	0.33568	0.42038	0.48496	0.55427
HRMT1L2	1.54036	1.66038	2.16701	2.53097	2.96982
n.a.	0.20801	0.25673	0.25631	0.28774	0.3178
TST	0.11538	0.13389	0.14488	0.18067	0.17368
DKC1	0.80763	0.9977	1.11326	1.22113	1.36612
RAN	3.14648	2.78806	3.40072	3.27658	3.52985
PDGFRA	0.13985	0.12858	0.26488	0.28408	0.47226

HGNC Symbol	Ex_2Tc	Ex_1 5Tc	Ex_1Tc	Ex_0 5Tc	Ex_0Tc
CDK4	0.01905	0.0318	0.01398	0.03492	0.04831
ALDH1B1	0.09498	0.10795	0.13216	0.1461	0.13973
SORD	0.33978	0.39145	0.43105	0.54265	0.63649
BDH	0.20924	0.29502	0.27414	0.27263	0.282
GMPS	0.60525	0.71762	0.71469	0.74922	0.70356
GPR30	0.42533	0.59571	0.69268	0.89245	1.02643
PHB	4.15444	4.80394	5.17604	5.66164	5.80035
STRA13	0.68811	0.77858	0.84822	0.99746	1.11061
XPOT	0.4703	0.57895	0.69945	0.70916	0.87226
SMN1	0.18958	0.21957	0.23967	0.29329	0.33405
CHC1	1.10175	1.22578	1.48845	1.76851	1.72726
PLK1	0.66592	0.71205	0.83276	1.04801	0.93357
n.a.	0.14952	0.13231	0.16622	0.19995	0.2415
AK2	1.64395	1.89703	2.15853	2.4034	2.95186
n.a.	0.18651	0.17476	0.19063	0.20176	0.26131
MGST1	0.26799	0.31006	0.35985	0.41725	0.56349
CSDA	2.34255	2.89912	2.99681	3.47385	4.17057
n.a.	0.33358	0.37368	0.43681	0.50967	0.66956
ATP1B3	3.14361	3.19486	3.59428	4.15195	4.46027
BCS1L	0.25842	0.31775	0.3567	0.43169	0.49858
UNG	0.27909	0.29237	0.36465	0.41142	0.57422
PBP	1.34674	1.69375	1.64039	1.90643	1.62101
CDC6	0.16722	0.20932	0.25648	0.28751	0.27187
CDC7	0.19247	0.18726	0.19752	0.22077	0.21367
MTAP	0.13583	0.11265	0.15554	0.17048	0.17427
ADSL	3.28601	4.07996	4.52733	5.20518	5.53405
CDKN3	1.21157	1.12998	1.41594	1.51972	1.55193
VRK1	1.18401	1.16311	1.35515	1.59065	1.47632
WFDC2	0.15683	0.1616	0.21434	0.2209	0.27784
GSPT1	0.88586	0.93868	1.06292	1.15313	1.26329
SLC39A14	0.34747	0.36557	0.48662	0.54029	0.75221
n.a.	0.4032	0.4349	0.48251	0.60714	0.7285
RLN2	0.11147	0.12813	0.11962	0.15222	0.1874
BAG2	0.23434	0.23341	0.24682	0.27032	0.34004
HSD17B8	0.14954	0.20265	0.20179	0.26808	0.33104
UCHL3	1.62551	1.63639	2.02267	2.43716	2.42739
NME2	19.76906	22.15522	23.45902	27.55526	27.72588
MRPS12	0.75553	0.86918	0.87729	0.97246	1.04972
PCNA	1.96066	2.08068	2.3147	2.14963	2.43413
DPH2L2	0.1906	0.23201	0.24574	0.28435	0.34142
CCNB1	2.40568	2.50603	2.85089	2.84215	2.97671
MC1R	1.48914	1.9685	2.24025	2.74683	3.34447
SOD1	6.80314	6.94095	8.36967	9.68501	10.57298
ATP5G3	7.58213	9.08059	10.56587	11.03314	10.65712
CCT3	4.1085	4.8961	5.01829	5.41222	5.93334
RFC4	0.71981	0.74587	0.92911	0.95374	1.11705
CDC25A	0.08758	0.10902	0.11749	0.12942	0.14418
FRDA	0.70202	0.76482	0.88079	0.96853	1.08787
SNRPD1	0.32509	0.33691	0.31765	0.39184	0.43835
CHAF1A	0.26792	0.27891	0.30055	0.33206	0.36495
PRDX2	1.99601	2.78608	2.72895	3.14471	3.66851
BUB1	1.08913	1.16927	1.30305	1.33758	1.28601
CDC2	2.02484	1.92393	2.16898	1.97944	1.48605
POLR1C	0.44135	0.48978	0.52734	0.54711	0.7238
SLC19A1	0.23218	0.1482	0.16119	0.18313	0.19097
TOMM20	1.33017	1.4072	1.6301	2.11455	2.4955
MMP3	0.12347	0.16152	0.15694	0.17889	0.2128

HGNC Symbol	Ex_2Tc	Ex_1 5Tc	Ex_1Tc	Ex_0 5Tc	Ex_0Tc
UBE2C	3.36429	4.01794	4.11854	4.12627	4.44263
PTPN2	0.15689	0.17791	0.21939	0.30071	0.40489
RUVBL1	0.76424	0.82609	1.05658	1.1069	1.37199
TYMS	1.32287	1.38644	1.54584	1.44259	1.5199
DDX10	0.63244	0.62987	0.75811	0.87782	1.05318
TUFM	3.41112	4.28634	4.74474	5.04342	6.40778
AURKB	0.77315	0.82746	0.83034	0.84225	1.00015
RRS1	0.24494	0.26173	0.31274	0.31791	0.3786
GEMIN4	0.61377	0.71027	0.72367	0.79815	0.92151
PTMA	18.25454	19.79934	21.6746	25.10207	23.50425
CYP51A1	0.29174	0.32117	0.43318	0.51267	0.70985
ARHGEF5	0.0387	0.04063	0.06562	0.09548	0.08864
KIAA0690	0.38413	0.42386	0.49553	0.57687	0.75076
VDAC1	0.96058	0.8646	1.15698	1.34615	1.52361
DDX1	2.07413	2.29972	2.81213	3.24941	3.20796
SCAMP1	0.17419	0.24509	0.19472	0.23668	0.24135
DDX18	0.97726	0.95373	1.24436	1.23641	1.4686
PES1	0.96553	1.10002	1.1139	1.37752	1.54109
RANGAP1	0.22673	0.2129	0.28748	0.28701	0.33228
APEX1	0.38368	0.47725	0.43338	0.46589	0.5477
MYBL2	0.483	0.45735	0.58206	0.66319	0.61031
USP10	0.18883	0.22145	0.24302	0.23664	0.25182
n.a.	0.10074	0.11656	0.12604	0.14052	0.15301
RPA3	0.50578	0.42017	0.49986	0.50067	0.59807
CXCL12	0.0911	0.10214	0.10839	0.11804	0.13436
n.a.	0.08234	0.10376	0.11238	0.12507	0.17815
MCM3	0.52896	0.48648	0.70057	1.04342	1.18707
GMNN	0.34774	0.3462	0.34768	0.38491	0.46141
HSPA9B	1.87686	2.19851	2.70005	2.67253	2.72019
TCERG1	0.40361	0.4188	0.46269	0.51519	0.50344
RNU3IP2	0.48719	0.56848	0.58731	0.78711	0.98894
SFRS7	2.23966	2.19488	2.57414	2.51714	2.66668
MSH6	1.75403	1.81995	2.16452	2.14977	2.7066
CENPF	0.74042	0.72552	0.73309	0.72277	0.84559
MXI1	0.15637	0.15752	0.17875	0.21003	0.2049
AMD1	0.59062	0.58006	0.75787	0.73383	0.79837
ELK1	0.381	0.39083	0.48623	0.51957	0.60625
ILF3	0.8122	0.96267	0.98374	1.27049	1.33706
TFDP1	0.64975	0.6318	0.74569	0.68508	0.61327
n.a.	0.47424	0.50685	0.61129	0.56596	0.63569
TOP2A	0.418	0.40405	0.51316	0.45964	0.39245
EIF5A	0.63961	0.67164	0.7513	0.66803	0.70553
n.a.	0.06333	0.06207	0.08042	0.09956	0.12595
n.a.	0.5774	0.69666	0.77793	0.85474	0.95649
ATIC	4.14963	4.17419	5.07737	5.50918	6.33753
ATIC	1.63835	1.7938	2.00291	1.94483	2.11565
PEX5	0.18257	0.2065	0.26316	0.26033	0.38525
TAF4B	0.15016	0.14181	0.18233	0.18318	0.19452
HDGF	0.7451	0.83795	0.88981	1.1168	1.30349
HDGF	1.8065	2.01806	2.27517	2.74627	2.76009
ILF2	2.80284	3.25842	3.32981	3.2043	3.50766
CCNA2	0.29566	0.25827	0.32162	0.26761	0.26707
MDH2	1.69219	1.71947	1.97619	2.38708	2.65784
PEG10	0.05761	0.04601	0.0699	0.09363	0.16883
PPRC1	0.16901	0.18988	0.22062	0.25253	0.29363
SSRP1	1.5992	1.85959	1.98328	2.29312	2.63288
PTK9	0.01621	0.02364	0.0271	0.0613	0.07004

HGNC Symbol	**Ex_2Tc**	**Ex_1 5Tc**	**Ex_1Tc**	**Ex_0 5Tc**	**Ex_0Tc**
ACSL1	0.413	0.43228	0.63253	0.69514	0.84662
PFKM	0.57168	0.77548	0.79903	0.9722	1.28479
HNRPDL	0.76946	0.79725	0.91693	0.90634	1.11094
RPIA	0.43947	0.4735	0.55772	0.59595	0.76191
SLC16A1	0.03226	0.03966	0.03012	0.06814	0.07122
KCNJ6	0.92873	0.97798	1.04534	1.1028	1.20519
SFRS2	8.52023	8.60066	9.62945	11.31289	11.66946
PRKCI	0.08743	0.18162	0.1517	0.15839	0.15649
POLR2H	0.59115	0.70837	0.69794	0.71845	0.98433
ABCE1	0.08998	0.10053	0.10629	0.10439	0.13369
MELK	0.17519	0.16948	0.17788	0.16515	0.19187
DDX21	0.12067	0.11735	0.09493	0.13041	0.198
SSSCA1	0.76365	0.742	0.8163	0.8583	0.98012
n.a.	0.83283	0.93332	1.08143	1.14213	1.44032
HSPCA	0.74752	0.82847	0.79377	0.74287	0.77818
DEAF1	0.57331	0.62771	0.73992	0.87263	1.10693
n.a.	0.35786	0.43486	0.50264	0.63429	0.88654
EIF1AX	0.14515	0.13607	0.18423	0.16415	0.21114
n.a.	5.47967	5.41279	6.07723	6.80067	8.87019
n.a.	0.22512	0.23164	0.28056	0.29026	0.30982
SF3A3	0.95964	0.97495	1.314	1.32029	1.32825
n.a.	0.0334	0.03923	0.0414	0.04613	0.06509
AK2	0.42784	0.47774	0.46816	0.55975	0.5263
PLAUR	0.04073	0.07203	0.0412	0.10451	0.08515
SCARB1	0.55287	0.65078	0.6805	0.9121	0.95107
MCM2	1.6353	2.06354	1.91521	2.22915	2.37309
EXOSC7	0.39004	0.44241	0.49285	0.56998	0.56191
KHSRP	4.58697	5.15101	5.89931	6.48452	6.87213
NUDC	1.35232	1.51243	1.52203	1.80667	1.979
CGRRF1	0.38906	0.49266	0.51797	0.60477	0.64014
APEX1	0.69477	0.88629	0.9131	0.94862	1.13259
GARS	2.04467	2.40504	2.78706	3.06658	3.78534
EIF3S9	2.17339	2.74299	2.88262	3.11746	3.63399
IMPDH1	0.33611	0.37229	0.38842	0.42722	0.57396
VEGF	0.01851	0.02435	0.02956	0.03191	0.06676
TFDP2	0.17431	0.19992	0.23217	0.28635	0.3217
PRDX1	8.919	9.7041	10.77956	11.24282	12.41687
SCO2	0.3877	0.52976	0.48252	0.47939	0.45808
TUBG1	0.2007	0.25923	0.26766	0.27755	0.34464
MYCN	0.1278	0.15888	0.17561	0.19629	0.24342
ABL2	0.03297	0.21292	0.06345	0.06072	0.08004
SLC20A1	0.56647	0.67221	0.65282	0.74459	0.75507
CDKN2B	0.0258	0.04076	0.04392	0.05458	0.05918
n.a.	0.7397	0.86416	0.89634	1.05505	1.16135
FANCG	0.40597	0.47403	0.47387	0.50725	0.55289
PMPCA	1.71753	2.01126	2.06708	2.35937	2.7174
PSMC3	0.897	1.03036	1.04835	1.17441	1.18331
MCM7	2.46905	2.93816	2.7977	3.19883	3.48309
ABCA3	0.12775	0.15626	0.16162	0.23113	0.28623
EIF4EBP1	0.68879	0.94331	0.96184	1.07101	1.36111
TNFRSF4	0.0465	0.05061	0.05679	0.07146	0.07991
SRP72	0.85553	1.067	1.11187	1.21427	1.26575
ALG3	0.21911	0.3214	0.2746	0.3064	0.40692
CKS1B	0.16676	0.20484	0.23317	0.26069	0.28174
NSEP1	7.62913	8.95213	9.11721	8.62483	9.06543
FARSLA	0.60217	0.74089	0.71842	0.91986	0.8022
PRIM1	0.19345	0.2418	0.25797	0.27493	0.25425

HGNC Symbol	**Ex_2Tc**	**Ex_1 5Tc**	**Ex_1Tc**	**Ex_0 5Tc**	**Ex_0Tc**
TBL3	0.8483	0.9743	1.0362	1.08598	1.24568
JUND	0.47954	0.49539	0.56673	0.60808	0.63482
PTBP1	0.99233	0.70978	0.86113	0.91497	0.98554
MRE11A	0.24558	0.26381	0.31722	0.30088	0.34112
HSPA5	1.13191	1.4411	1.63876	1.63927	1.5961
OAT	0.17694	0.17637	0.2325	0.25902	0.25971
TFRC	1.86784	1.83369	2.26208	2.27588	2.62262
SHMT1	0.07662	0.07741	0.08488	0.10582	0.11367
CLNS1A	2.94697	2.93329	3.49117	3.51993	4.1683
SEMA3C	0.03225	0.02185	0.03735	0.04135	0.05543
MCAM	0.13376	0.13348	0.16153	0.17157	0.20379
MAPKAPK5	0.68063	0.7446	0.82051	0.9224	0.95781
SIP1	0.10179	0.08371	0.1077	0.1123	0.13733
NF2	0.18299	0.18833	0.21727	0.21204	0.22636
SLC1A5	0.11374	0.11486	0.14085	0.15597	0.23719
PSMA2	2.22921	2.28039	2.46698	2.7031	2.88663
RAD51C	0.81667	0.87661	0.99725	1.14806	1.02325
CTSC	0.19491	0.17632	0.21101	0.21985	0.27647
HSPA8	4.74504	4.58531	5.93465	5.512	6.10911
n.a.	0.0706	0.066	0.08565	0.09517	0.09867
IGFBP2	0.83107	1.06304	1.45876	2.01584	2.25871
DARS	0.47037	0.42532	0.48626	0.54127	0.66704
UCHL3	0.81807	0.7712	0.98907	1.03573	1.25945
GTF3A	2.95301	3.239	3.47028	3.72058	4.17885
RPL5	19.18486	18.52295	19.29822	18.70064	23.20047
AMD1	0.20084	0.17584	0.25985	0.22215	0.27684
HSPA1A	0.04366	0.04195	0.0486	0.04562	0.05363
SYNGR3	0.21623	0.20406	0.29813	0.37389	0.48112
NINJ1	0.02274	0.03968	0.05861	0.07701	0.10792
SNRPA1	1.64999	1.95082	2.16575	2.23876	2.46752
TAF9	1.31757	1.40119	1.65683	1.69205	1.69667
SYNCRIP	0.71953	0.65484	0.71075	0.88296	0.83826
n.a.	0.60823	0.60445	0.69363	0.80758	0.89184
ITGB3BP	0.31548	0.26129	0.31677	0.30508	0.39017
PTPRF	0.07303	0.07836	0.09154	0.13734	0.15703
CHEK1	0.17149	0.1529	0.17902	0.18064	0.16646
TCEB1	2.38032	2.49266	3.13875	3.29309	3.34689
n.a.	0.52234	0.52113	0.64072	0.60504	0.73026
VBP1	0.66888	0.63986	0.70568	0.7647	0.78581
BUB1B	0.20965	0.21384	0.26944	0.31156	0.33784
RACGAP1	0.49562	0.45465	0.51721	0.51455	0.54411
AK3	0.06097	0.05311	0.07359	0.09413	0.09382
HNRPF	4.6523	4.92339	5.14131	5.39316	5.86556
PDAP1	0.22301	0.19217	0.26961	0.27825	0.25656
SELE	0.13297	0.13154	0.13939	0.16066	0.16044
n.a.	0.11619	0.11881	0.1202	0.15657	0.15187
RCN1	0.0288	0.03503	0.00233	0.03435	0.04146
GLDC	0.09034	0.16125	0.13191	0.15125	0.17052
PMS1	0.05391	0.06065	0.04397	0.06448	0.06121
PFKP	0.44217	0.46252	0.52239	0.65069	0.63521
PDCD2	0.20546	0.23577	0.23611	0.28151	0.29829
MGST2	0.44407	0.43265	0.48529	0.59354	0.66153
NDUFB7	1.71131	1.72897	1.87853	2.04702	2.19851
G22P1	1.59749	1.81578	1.8452	1.88312	2.14065
n.a.	0.31281	0.38017	0.39287	0.44633	0.52599
PBEF1	0.03872	0.053	0.04503	0.06829	0.07496
TBL2	0.16468	0.16454	0.18646	0.21359	0.21984

HGNC Symbol	Ex_2Tc	Ex_1 5Tc	Ex_1Tc	Ex_0 5Tc	Ex_0Tc
GCN5L2	0.13282	0.13146	0.10175	0.18789	0.18534
CDK2AP1	0.8331	0.78834	0.90896	1.11478	1.29921
NOL1	0.41097	0.40801	0.47053	0.50471	0.64824
SLC29A1	0.52977	0.50567	0.6406	0.68806	0.75186
BNIP1	0.07094	0.06198	0.06822	0.08712	0.07946
DBN1	0.1587	0.1775	0.14313	0.22435	0.27242
EIF4G1	0.57713	0.65281	0.65961	0.78447	0.8319
B4GALT2	0.08104	0.07107	0.04672	0.10527	0.12641
TMEM5	0.48601	0.53406	0.60559	0.69337	0.76231
FVT1	0.02367	0.02267	0.02525	0.04379	0.05905
ETF1	0.11574	0.09698	0.06041	0.10667	0.1392
ATF4	2.4496	3.07457	3.14706	3.86149	4.48449
ILF3	0.43332	0.40611	0.39689	0.49225	0.56261
RAMP1	0.11996	0.1208	0.1456	0.20485	0.21617
n.a.	0.65641	0.75097	0.77491	0.87503	0.95531
ADCY3	0.35233	0.39367	0.41619	0.53237	0.68068
AFG3L2	0.68129	0.84182	0.85973	0.99128	1.12333
PRPS1	0.09552	0.0975	0.10486	0.12639	0.15676
OPRS1	0.05481	0.0662	0.04723	0.09442	0.12118
TOMM70A	0.12153	0.1213	0.11459	0.14995	0.21198
APRT	1.80053	1.96806	1.85728	2.26824	2.13565
FGFR4	0.03075	0.03737	0.04571	0.06619	0.09317
DEFA6	0.03636	0.05688	0.04826	0.07645	0.06845
ZNF9	0.12664	0.13327	0.07805	0.1096	0.14434
RAC3	0.01892	0.03341	0.00253	0.03825	0.0551
WNT10B	0.04331	0.05209	0.0211	0.04829	0.0662
NFRKB	0.05802	0.05712	0.06663	0.09415	0.0983
CDK5R2	0.01977	0.02672	0.03046	0.04325	0.0468
CYCS	0.04679	0.04367	0.00666	0.05166	0.06299
YES1	0.14329	0.17087	0.21994	0.30119	0.34947
DLEU1	0.29748	0.33055	0.36177	0.38917	0.42903
BNIP3	0.65478	0.72001	0.8345	1.02475	1.29219
RAD23A	1.08931	1.1505	1.3093	1.41418	1.56273
	0.03309	0.01526	0.02821	0.03459	0.03671
UBE2G2	0.51641	0.49417	0.5566	0.53975	0.6838
KCNQ3	0.02433	0.02477	0.02979	0.02376	0.04783
MTA1	0.40323	0.37908	0.46176	0.47771	0.57475
LIG3	0.08358	0.11714	0.10982	0.13836	0.16639
ITGA2B	0.04168	0.04385	0.0464	0.05039	0.06462
TOMM34	0.05509	0.0453	0.03814	0.04147	0.05675
ITIH4	0.09355	0.1123	0.10736	0.10413	0.16828
POLD1	0.63931	0.70229	0.71966	0.77523	0.91355
IKBKAP	0.20275	0.17248	0.22522	0.21534	0.30201
ASNS	0.07014	0.09158	0.08551	0.10053	0.13627
MX1	0.01735	0.00587	0.01501	0.01065	0.05824
XRCC5	0.10487	0.09902	0.09077	0.08772	0.10281
XPO1	0.95508	0.90264	0.97384	0.99533	1.14862
RAD54L	0.1052	0.11559	0.12469	0.12027	0.13486
PTHLH	0.00873	0.00154	0.04149	0.01482	0.10204
MSH2	0.40747	0.41413	0.41869	0.42403	0.46078
CDKL1	0.09252	0.08355	0.10905	0.09688	0.12688
ADA	0.21566	0.24246	0.25936	0.2909	0.37573
n.a.	0.3438	0.37601	0.40494	0.44973	0.58308
TGFB1	0.00124	0.00101	0.00147	0.00081	0.04021
NPTX2	0.00807	0.00176	0.00777	0.00745	0.07305
BAG1	0.54486	0.58475	0.63882	0.62761	0.81701
BAG1	0.72789	0.79611	0.82337	0.83715	1.1148

HGNC Symbol	Ex_2Tc	Ex_1 5Tc	Ex_1Tc	Ex_0 5Tc	Ex_0Tc
SHB	0.14096	0.13969	0.14985	0.19819	0.20588
EIF3S10	0.5096	0.52184	0.56565	0.57923	0.64336
HTATIP2	0.02861	0.01702	0.02495	0.02406	0.0474
CALCA	0.07418	0.05426	0.04326	0.05465	0.06876
C6orf108	1.69303	1.74884	1.84937	1.90262	2.20931
ACY1	0.10127	0.15033	0.13672	0.15939	0.20006
PASK	0.03819	0.04483	0.04568	0.06544	0.0767
CEBPZ	0.52228	0.53035	0.63492	0.62079	0.76691
RAP1A	0.07335	0.07893	0.09686	0.11538	0.14379
NID	0.01435	0.02132	0.01482	0.01265	0.04051
IDE	0.2261	0.21025	0.26939	0.25565	0.30915
HOXB7	0.03851	0.0289	0.03395	0.02349	0.12461
GUCY1B2	0.26234	0.31177	0.27838	0.32167	0.3871
SERPINA7	0.11106	0.12489	0.12369	0.13155	0.17154
FPRL2	0.06216	0.06197	0.06713	0.06944	0.09157
MTRR	0.21779	0.20692	0.24464	0.26727	0.33304
THRA	0.23852	0.30182	0.29914	0.37176	0.46213
POR	0.18671	0.27331	0.24558	0.30365	0.32757
YWHAH	1.08537	1.06436	1.13508	1.02691	1.20862
TRIM28	2.15407	2.49249	2.55679	2.68263	3.13902
DHX30	0.77155	0.86264	0.93125	0.91883	1.1311
CDK8	0.0885	0.09251	0.13986	0.1102	0.12433
CCNH	0.28525	0.30611	0.30614	0.34985	0.43203
RFK	0.13105	0.14446	0.14208	0.13991	0.18226
RABGGTB	0.55989	0.57706	0.60494	0.71217	0.74842
PLK4	0.09841	0.08764	0.10065	0.10083	0.14965
CYP4B1	0.00467	0.01311	0.01326	0.0155	0.05047
TP53BP2	0.06098	0.06002	0.05668	0.06888	0.09168
NVL	0.89297	0.91247	0.984	1.07385	1.39606
ARF1	2.59929	3.0382	3.07722	3.46924	4.0317
PLK2	0.07292	0.05596	0.07017	0.06951	0.24426
GZMA	0.03686	0.03909	0.02548	0.02486	0.05802
NOLA2	0.12013	0.12785	0.13214	0.15789	0.213
HMBS	0.23949	0.27366	0.29814	0.27869	0.36805
ITIH2	0.02221	0.02879	0.02085	0.00995	0.06193
SACS	0.0539	0.07217	0.07564	0.07208	0.12673
GABPA	0.15053	0.15529	0.15069	0.15665	0.178
ETS2	0.10336	0.0867	0.10868	0.12319	0.14979
IL8RA	0.13492	0.15507	0.1523	0.16673	0.19314
API5	0.07968	0.0787	0.04602	0.05626	0.06716
n.a.	0.54894	0.58406	0.65458	0.72517	0.89444
ICT1	0.30801	0.30492	0.3088	0.33056	0.34236
DFFB	0.18927	0.19347	0.22322	0.2615	0.30372
USP7	0.48659	0.50416	0.59469	0.61221	0.763
PAP	0.16252	0.16666	0.13525	0.18436	0.22726
BSG	0.15403	0.19146	0.22144	0.22289	0.31358
YIF1	0.50112	0.60056	0.61132	0.72284	0.81976
POLE	0.13216	0.14465	0.14656	0.13424	0.14919
	0.03946	0.05009	0.03646	0.0493	0.06023

HGNC Symbol	signDiff _8Tc vs 100Tc	signDiff_6Tc vs 100Tc	signDiff_5Tc vs 100Tc
MYC	+	+	+
CACNA1G	+	+	+
NME1	+	+	+
ADCY2	+	+	+
C4orf9	+	+	+
FKBP5	+	+	+
CRKL	=	=	+
RFC5	+	=	+
PPP2CA	+	+	+
TIMM8A	+	+	+
n.a.	=	+	+
MAD2L1	=	+	+
MRPL12	=	+	+
NME1	=	+	+
METTL1	=	+	+
SLC7A5	=	+	+
SRM	=	+	+
IL1B	=	+	+
PAICS	=	+	+
TOMM40	=	+	+
PYCR1	=	+	+
UMPK	=	+	+
LRP8	=	+	+
DUSP14	=	+	+
METAP1	=	+	+
ABCE1	=	+	+
PA2G4	=	+	+
BOP1	=	+	+
RANBP1	=	+	+
CTPS	=	+	+
TRAP1	=	+	+
HSPD1	=	+	+
PFAS	=	+	+
TEAD4	=	+	+
MIF	=	+	+
VARS2	=	+	+
CENTG1	=	+	+
DSCR2	=	=	+
JAG2	=	=	+
PRKAR1B	=	=	+
n.a.	=	=	+
MATK	-	=	+
IARS	=	=	+
GAL	=	=	+
MCAM	=	=	+
CAD	=	=	+
FH	=	=	+
SRPK1	=	=	+
NEFH	+	=	+
NP	=	=	+
AHCY	=	=	+
POLD2	=	=	+
C1QBP	=	=	+
CAMKK2	=	=	+
n.a.	=	=	+
BYSL	=	=	+
NUP155	=	=	+

HGNC Symbol	signDiff _8Tc vs 100Tc	signDiff_6Tc vs 100Tc	signDiff_5Tc vs 100Tc
IFRD2	=	=	+
MRPL3	=	=	+
HSPE1	=	=	+
HSPE1	=	=	+
n.a.	=	=	+
EBNA1BP2	=	=	+
TNFRSF8	=	=	+
PRDX4	=	=	+
CSE1L	=	=	+
RPP40	=	=	+
n.a.	+	=	+
HRMT1L2	=	=	+
n.a.	=	=	+
n.a.	=	=	+
MADH4	=	=	+
IL9	=	+	+
PDCD11	=	=	+
HK2	=	=	+
PWP2H	=	=	+
n.a.	=	=	+
NOLC1	=	=	+
NOLC1	=	=	+
CCT2	=	=	+
DTYMK	=	=	+
HNRPAB	=	=	+
FASN	=	=	+
FASN	=	=	+
NMB	+	=	+
CHC1	=	=	+
	=	=	+
KIAA0179	=	=	=
NTHL1	=	=	=
UNG	=	=	=
KIAA0020	=	=	=
n.a.	=	=	=
n.a.	=	=	=
POLE2	=	=	=
MTHFD1	=	=	=
NOL5A	=	=	+
PRPS2	=	=	=
RUVBL2	=	=	=
GPI	=	=	=
n.a.	=	=	=
NPM3	=	+	=
n.a.	=	=	=
CDC20	=	+	=
n.a.	=	=	=
PRKDC	=	=	=
CKS2	=	=	=
CSE1L	=	=	=
EEF1E1	=	+	=
HRMT1L2	=	=	=
n.a.	=	=	=
TST	=	+	=
DKC1	=	=	=
RAN	=	=	=
PDGFRA	=	=	=

HGNC Symbol	signDiff _8Tc vs 100Tc	signDiff_6Tc vs 100Tc	signDiff_5Tc vs 100Tc
CDK4	=	+	=
ALDH1B1	=	=	=
SORD	=	+	=
BDH	=	=	=
GMPS	=	=	=
GPR30	=	=	=
PHB	=	=	=
STRA13	=	=	=
XPOT	=	=	=
SMN1	=	=	=
CHC1	=	=	=
PLK1	=	=	=
n.a.	=	=	+
AK2	=	=	=
n.a.	=	=	=
MGST1	=	=	=
CSDA	=	=	=
n.a.	=	=	=
ATP1B3	=	=	=
BCS1L	=	=	=
UNG	=	=	=
PBP	=	=	=
CDC6	=	=	=
CDC7	=	=	+
MTAP	=	=	+
ADSL	=	=	=
CDKN3	=	=	=
VRK1	=	=	=
WFDC2	=	=	=
GSPT1	=	=	=
SLC39A14	=	=	=
n.a.	=	=	=
RLN2	=	=	=
BAG2	=	=	=
HSD17B8	=	=	=
UCHL3	=	=	=
NME2	=	=	=
MRPS12	=	=	=
PCNA	=	=	=
DPH2L2	=	=	=
CCNB1	=	=	=
MC1R	=	=	=
SOD1	=	=	=
ATP5G3	=	=	=
CCT3	=	=	+
RFC4	=	=	=
CDC25A	=	+	=
FRDA	=	=	=
SNRPD1	=	=	+
CHAF1A	=	=	=
PRDX2	=	=	=
BUB1	=	=	=
CDC2	=	=	=
POLR1C	=	=	=
SLC19A1	-	=	=
TOMM20	=	=	=
MMP3	=	=	=

HGNC Symbol	signDiff _8Tc vs 100Tc	signDiff_6Tc vs 100Tc	signDiff_5Tc vs 100Tc
UBE2C	=	=	=
PTPN2	=	=	=
RUVBL1	=	=	=
TYMS	=	=	=
DDX10	=	=	=
TUFM	=	=	=
AURKB	=	=	=
RRS1	=	=	=
GEMIN4	=	=	=
PTMA	=	=	=
CYP51A1	=	=	=
ARHGEF5	=	=	=
KIAA0690	=	=	=
VDAC1	=	=	=
DDX1	=	=	=
SCAMP1	=	=	=
DDX18	=	=	=
PES1	=	=	=
RANGAP1	=	=	=
APEX1	=	=	=
MYBL2	=	=	=
USP10	=	=	+
n.a.	=	=	=
RPA3	=	=	=
CXCL12	=	=	=
n.a.	=	=	=
MCM3	=	=	=
GMNN	=	=	=
HSPA9B	=	=	=
TCERG1	=	=	=
RNU3IP2	=	=	=
SFRS7	=	=	=
MSH6	=	=	=
CENPF	=	=	=
MXI1	=	=	=
AMD1	=	=	=
ELK1	=	=	=
ILF3	=	=	=
TFDP1	=	=	=
n.a.	=	=	=
TOP2A	=	=	=
EIF5A	=	=	=
n.a.	=	=	=
n.a.	=	=	=
ATIC	=	=	=
ATIC	=	=	=
PEX5	=	=	=
TAF4B	=	=	=
HDGF	=	=	=
HDGF	=	=	=
ILF2	=	=	=
CCNA2	=	=	=
MDH2	=	=	=
PEG10	=	+	+
PPRC1	=	=	=
SSRP1	=	=	=
PTK9	=	=	=

HGNC Symbol	signDiff _8Tc vs 100Tc	signDiff_6Tc vs 100Tc	signDiff_5Tc vs 100Tc
ACSL1	=	=	=
PFKM	=	=	=
HNRPDL	=	=	=
RPIA	=	=	=
SLC16A1	=	=	=
KCNJ6	=	=	=
SFRS2	=	=	=
PRKCI	=	=	=
POLR2H	=	=	=
ABCE1	=	=	=
MELK	=	=	=
DDX21	=	=	=
SSSCA1	=	=	=
n.a.	=	=	=
HSPCA	=	=	=
DEAF1	=	=	=
n.a.	=	=	=
EIF1AX	=	=	=
n.a.	=	=	=
n.a.	=	=	=
SF3A3	=	=	=
n.a.	=	=	=
AK2	=	=	=
PLAUR	=	+	+
SCARB1	=	=	=
MCM2	=	=	=
EXOSC7	=	=	=
KHSRP	=	=	=
NUDC	=	=	=
CGRRF1	=	=	=
APEX1	=	=	=
GARS	=	=	=
EIF3S9	=	=	=
IMPDH1	=	=	=
VEGF	=	=	=
TFDP2	=	=	=
PRDX1	=	=	=
SCO2	=	=	=
TUBG1	=	=	=
MYCN	=	=	=
ABL2	=	=	=
SLC20A1	=	=	+
CDKN2B	=	+	=
n.a.	=	=	=
FANCG	=	=	=
PMPCA	=	=	=
PSMC3	=	=	=
MCM7	=	=	=
ABCA3	=	=	=
EIF4EBP1	=	=	=
TNFRSF4	=	=	=
SRP72	=	=	=
ALG3	=	=	=
CKS1B	=	=	=
NSEP1	=	=	=
FARSLA	=	=	=
PRIM1	=	=	=

HGNC Symbol	**signDiff _8Tc vs 100Tc**	**signDiff_6Tc vs 100Tc**	**signDiff_5Tc vs 100Tc**
TBL3	=	=	=
JUND	=	=	=
PTBP1	=	=	=
MRE11A	=	=	=
HSPA5	=	=	=
OAT	=	=	=
TFRC	=	=	=
SHMT1	=	=	=
CLNS1A	=	=	=
SEMA3C	=	=	+
MCAM	=	=	=
MAPKAPK5	=	=	=
SIP1	=	=	=
NF2	=	=	=
SLC1A5	=	=	+
PSMA2	=	=	=
RAD51C	=	=	=
CTSC	=	=	=
HSPA8	=	=	=
n.a.	=	=	=
IGFBP2	=	=	=
DARS	=	=	=
UCHL3	=	=	=
GTF3A	=	=	=
RPL5	=	=	=
AMD1	=	=	=
HSPA1A	+	+	+
SYNGR3	=	=	=
NINJ1	-	=	=
SNRPA1	=	=	=
TAF9	=	=	=
SYNCRIP	=	=	=
n.a.	=	=	=
ITGB3BP	=	=	=
PTPRF	=	=	=
CHEK1	=	=	=
TCEB1	=	=	=
n.a.	=	=	=
VBP1	=	=	=
BUB1B	=	=	=
RACGAP1	=	=	=
AK3	=	=	+
HNRPF	=	=	=
PDAP1	=	=	=
SELE	=	=	=
n.a.	=	=	=
RCN1	=	=	+
GLDC	=	=	=
PMS1	=	=	=
PFKP	=	=	=
PDCD2	=	=	=
MGST2	=	=	=
NDUFB7	=	=	=
G22P1	=	=	=
n.a.	=	=	=
PBEF1	=	=	=
TBL2	=	=	=

HGNC Symbol	**signDiff _8Tc vs 100Tc**	**signDiff_6Tc vs 100Tc**	**signDiff_5Tc vs 100Tc**
GCN5L2	=	=	=
CDK2AP1	=	=	=
NOL1	=	=	=
SLC29A1	=	=	=
BNIP1	=	+	=
DBN1	=	=	=
EIF4G1	=	=	=
B4GALT2	=	=	=
TMEM5	=	=	=
FVT1	=	=	=
ETF1	=	=	=
ATF4	=	=	=
ILF3	=	=	=
RAMP1	=	=	=
n.a.	=	=	=
ADCY3	=	=	=
AFG3L2	=	=	=
PRPS1	=	=	=
OPRS1	-	=	=
TOMM70A	=	=	=
APRT	=	=	=
FGFR4	=	=	=
DEFA6	=	=	=
ZNF9	=	+	+
RAC3	=	=	+
WNT10B	=	=	+
NFRKB	=	=	=
CDK5R2	=	-	=
CYCS	=	=	+
YES1	=	=	=
DLEU1	=	=	=
BNIP3	=	=	=
RAD23A	=	=	=
	=	=	+
UBE2G2	=	=	=
KCNQ3	=	=	=
MTA1	=	=	=
LIG3	=	=	=
ITGA2B	=	=	=
TOMM34	=	=	-
ITIH4	=	=	=
POLD1	=	=	=
IKBKAP	=	=	=
ASNS	=	=	=
MX1	=	=	=
XRCC5	=	=	=
XPO1	=	=	=
RAD54L	=	=	=
PTHLH	=	=	=
MSH2	=	=	=
CDKL1	=	=	+
ADA	=	=	=
n.a.	=	=	=
TGFB1	=	=	=
NPTX2	=	=	=
BAG1	=	=	=
BAG1	=	=	=

HGNC Symbol	signDiff _8Tc vs 100Tc	signDiff_6Tc vs 100Tc	signDiff_5Tc vs 100Tc
SHB	=	=	=
EIF3S10	=	=	=
HTATIP2	=	=	=
CALCA	=	=	=
C6orf108	=	=	=
ACY1	=	=	=
PASK	=	=	=
CEBPZ	=	=	=
RAP1A	=	=	=
NID	=	=	+
IDE	=	=	=
HOXB7	=	=	=
GUCY1B2	=	=	=
SERPINA7	=	=	=
FPRL2	=	=	=
MTRR	=	=	=
THRA	=	=	=
POR	=	=	=
YWHAH	=	=	=
TRIM28	=	=	=
DHX30	=	=	=
CDK8	=	=	=
CCNH	=	=	=
RFK	=	=	=
RABGGTB	=	=	=
PLK4	=	=	=
CYP4B1	=	=	=
TP53BP2	+	=	=
NVL	=	=	=
ARF1	=	=	=
PLK2	=	=	=
GZMA	=	=	=
NOLA2	+	=	=
HMBS	=	=	=
ITIH2	=	=	=
SACS	-	=	=
GABPA	=	=	=
ETS2	=	=	=
IL8RA	=	=	=
API5	=	=	+
n.a.	=	=	=
ICT1	=	+	=
DFFB	=	=	=
USP7	=	=	=
PAP	=	=	=
BSG	=	=	=
YIF1	=	=	=
POLE	=	+	=
	-	=	+

HGNC Symbol	signDiff_4Tc vs 100Tc	signDiff_3Tc vs 100Tc	signDiff_2Tc vs 100Tc
MYC	+	+	+
CACNA1G	+	+	+
NME1	+	+	+
ADCY2	=	+	=
C4orf9	+	+	+
FKBP5	+	+	+
CRKL	+	+	+
RFC5	+	+	+
PPP2CA	+	+	+
TIMM8A	+	+	+
n.a.	+	+	+
MAD2L1	+	+	+
MRPL12	+	+	+
NME1	+	+	+
METTL1	+	+	+
SLC7A5	+	+	+
SRM	+	+	+
IL1B	+	+	+
PAICS	+	+	+
TOMM40	+	+	+
PYCR1	+	+	+
UMPK	+	+	+
LRP8	+	+	+
DUSP14	+	+	+
METAP1	+	+	+
ABCE1	+	+	+
PA2G4	+	+	+
BOP1	+	+	+
RANBP1	+	+	+
CTPS	+	+	+
TRAP1	+	+	+
HSPD1	+	+	+
PFAS	+	+	+
TEAD4	+	+	+
MIF	+	+	+
VARS2	+	+	+
CENTG1	+	+	+
DSCR2	+	+	+
JAG2	+	+	+
PRKAR1B	+	+	+
n.a.	+	+	+
MATK	+	+	+
IARS	+	+	+
GAL	+	+	+
MCAM	+	+	+
CAD	+	+	+
FH	+	+	+
SRPK1	+	+	+
NEFH	+	+	+
NP	+	+	+
AHCY	+	+	+
POLD2	+	+	+
C1QBP	+	+	+
CAMKK2	+	+	+
n.a.	+	+	+
BYSL	+	+	+
NUP155	+	+	+

HGNC Symbol	**signDiff_4Tc vs 100Tc**	**signDiff_3Tc vs 100Tc**	**signDiff_2Tc vs 100Tc**
IFRD2	+	+	+
MRPL3	+	+	+
HSPE1	+	+	+
HSPE1	+	+	+
n.a.	+	+	+
EBNA1BP2	+	+	+
TNFRSF8	+	+	+
PRDX4	+	+	+
CSE1L	+	+	+
RPP40	+	+	+
n.a.	+	+	+
HRMT1L2	+	+	+
n.a.	+	+	+
n.a.	+	+	+
MADH4	+	+	+
IL9	+	+	+
PDCD11	+	+	+
HK2	+	+	+
PWP2H	+	+	+
n.a.	+	+	+
NOLC1	+	+	+
NOLC1	+	+	+
CCT2	+	+	+
DTYMK	+	+	+
HNRPAB	+	+	+
FASN	+	+	+
FASN	+	+	+
NMB	+	+	+
CHC1	+	+	+
	+	+	+
KIAA0179	+	+	+
NTHL1	+	+	+
UNG	+	+	+
KIAA0020	+	+	+
n.a.	+	+	+
n.a.	+	+	+
POLE2	+	+	+
MTHFD1	+	+	+
NOL5A	+	+	+
PRPS2	+	+	+
RUVBL2	+	+	+
GPI	+	+	+
n.a.	+	+	+
NPM3	+	+	+
n.a.	+	+	+
CDC20	+	+	+
n.a.	+	+	+
PRKDC	+	+	+
CKS2	+	+	+
CSE1L	+	+	+
EEF1E1	+	+	+
HRMT1L2	+	+	+
n.a.	+	+	+
TST	+	+	+
DKC1	+	+	+
RAN	+	+	+
PDGFRA	+	+	+

HGNC Symbol	signDiff_4Tc vs 100Tc	signDiff_3Tc vs 100Tc	signDiff_2Tc vs 100Tc
CDK4	+	+	+
ALDH1B1	+	+	+
SORD	+	+	+
BDH	+	+	+
GMPS	+	+	+
GPR30	+	+	+
PHB	+	+	+
STRA13	+	+	+
XPOT	+	+	+
SMN1	+	+	+
CHC1	+	+	+
PLK1	+	+	+
n.a.	=	+	+
AK2	=	+	+
n.a.	=	+	+
MGST1	=	+	+
CSDA	=	+	+
n.a.	=	+	+
ATP1B3	=	+	+
BCS1L	=	+	+
UNG	=	+	+
PBP	=	+	+
CDC6	=	+	+
CDC7	=	+	+
MTAP	=	+	+
ADSL	=	+	+
CDKN3	=	+	+
VRK1	=	+	+
WFDC2	=	+	+
GSPT1	=	+	+
SLC39A14	=	+	+
n.a.	=	+	+
RLN2	=	+	+
BAG2	=	+	+
HSD17B8	=	+	+
UCHL3	=	+	+
NME2	=	+	+
MRPS12	=	+	+
PCNA	=	+	+
DPH2L2	=	+	+
CCNB1	=	+	+
MC1R	+	+	+
SOD1	=	+	+
ATP5G3	=	+	+
CCT3	=	+	+
RFC4	=	+	+
CDC25A	=	+	+
FRDA	=	+	+
SNRPD1	+	+	+
CHAF1A	=	+	+
PRDX2	=	+	+
BUB1	=	+	+
CDC2	+	+	+
POLR1C	=	+	+
SLC19A1	=	+	+
TOMM20	=	+	+
MMP3	=	+	+

HGNC Symbol	**signDiff_4Tc vs 100Tc**	**signDiff_3Tc vs 100Tc**	**signDiff_2Tc vs 100Tc**
UBE2C	=	+	+
PTPN2	=	+	+
RUVBL1	=	+	+
TYMS	+	+	+
DDX10	=	+	+
TUFM	=	+	+
AURKB	=	+	+
RRS1	=	+	+
GEMIN4	=	+	+
PTMA	=	+	+
CYP51A1	=	=	+
ARHGEF5	=	=	+
KIAA0690	=	=	+
VDAC1	=	=	+
DDX1	=	=	+
SCAMP1	=	=	+
DDX18	=	=	+
PES1	=	=	+
RANGAP1	=	=	+
APEX1	=	=	+
MYBL2	=	=	+
USP10	=	=	+
n.a.	=	=	+
RPA3	=	=	+
CXCL12	=	=	+
n.a.	=	=	+
MCM3	=	+	+
GMNN	=	=	+
HSPA9B	=	+	+
TCERG1	=	=	+
RNU3IP2	=	=	+
SFRS7	=	=	+
MSH6	=	+	+
CENPF	=	=	+
MXI1	=	=	+
AMD1	=	=	+
ELK1	=	=	+
ILF3	=	=	+
TFDP1	=	=	+
n.a.	=	=	+
TOP2A	=	=	+
EIF5A	=	=	+
n.a.	+	+	+
n.a.	=	=	+
ATIC	=	=	+
ATIC	=	=	+
PEX5	=	+	+
TAF4B	=	=	+
HDGF	=	=	+
HDGF	=	+	+
ILF2	=	=	+
CCNA2	=	=	+
MDH2	=	=	+
PEG10	=	=	+
PPRC1	=	=	+
SSRP1	=	+	+
PTK9	=	=	+

HGNC Symbol	signDiff_4Tc vs 100Tc	signDiff_3Tc vs 100Tc	signDiff_2Tc vs 100Tc
ACSL1	=	=	+
PFKM	=	=	+
HNRPDL	=	=	+
RPIA	=	=	+
SLC16A1	=	=	+
KCNJ6	=	=	+
SFRS2	=	=	+
PRKCI	=	=	+
POLR2H	=	=	+
ABCE1	+	=	+
MELK	=	=	+
DDX21	+	=	+
SSSCA1	=	=	+
n.a.	=	=	+
HSPCA	+	=	+
DEAF1	=	=	+
n.a.	=	=	+
EIF1AX	+	=	+
n.a.	=	=	+
n.a.	=	=	+
SF3A3	=	=	+
n.a.	=	+	=
AK2	=	=	=
PLAUR	+	+	=
SCARB1	=	=	=
MCM2	=	=	=
EXOSC7	=	=	=
KHSRP	=	=	=
NUDC	=	=	=
CGRRF1	=	+	=
APEX1	=	=	=
GARS	=	=	=
EIF3S9	=	=	=
IMPDH1	=	=	=
VEGF	=	+	=
TFDP2	=	=	=
PRDX1	=	=	=
SCO2	=	=	=
TUBG1	=	=	=
MYCN	=	=	=
ABL2	=	=	=
SLC20A1	=	=	=
CDKN2B	=	+	=
n.a.	=	=	=
FANCG	=	=	=
PMPCA	=	=	=
PSMC3	=	=	=
MCM7	=	=	=
ABCA3	=	+	=
EIF4EBP1	=	=	=
TNFRSF4	=	=	=
SRP72	=	=	=
ALG3	=	=	=
CKS1B	=	=	=
NSEP1	=	=	=
FARSLA	=	=	=
PRIM1	=	=	=

HGNC Symbol	**signDiff_4Tc vs 100Tc**	**signDiff_3Tc vs 100Tc**	**signDiff_2Tc vs 100Tc**
TBL3	=	=	=
JUND	=	=	=
PTBP1	=	=	+
MRE11A	=	=	=
HSPA5	=	=	=
OAT	=	=	=
TFRC	=	=	=
SHMT1	=	=	=
CLNS1A	=	=	=
SEMA3C	=	=	+
MCAM	=	=	=
MAPKAPK5	=	=	=
SIP1	=	+	+
NF2	=	=	=
SLC1A5	=	=	=
PSMA2	=	=	=
RAD51C	=	=	=
CTSC	=	=	=
HSPA8	=	=	+
n.a.	=	=	=
IGFBP2	=	=	=
DARS	=	=	=
UCHL3	=	=	+
GTF3A	=	=	=
RPL5	=	=	+
AMD1	=	=	=
HSPA1A	=	=	+
SYNGR3	=	=	=
NINJ1	=	=	=
SNRPA1	=	=	=
TAF9	=	=	=
SYNCRIP	=	=	+
n.a.	=	=	=
ITGB3BP	=	=	+
PTPRF	=	=	=
CHEK1	=	=	+
TCEB1	=	=	=
n.a.	=	=	=
VBP1	=	=	=
BUB1B	=	=	=
RACGAP1	=	=	+
AK3	=	+	=
HNRPF	=	=	=
PDAP1	=	=	+
SELE	=	=	=
n.a.	=	=	=
RCN1	=	+	+
GLDC	=	=	=
PMS1	=	=	=
PFKP	=	=	=
PDCD2	=	=	=
MGST2	=	=	=
NDUFB7	=	=	=
G22P1	=	=	=
n.a.	=	=	=
PBEF1	=	=	=
TBL2	=	=	=

HGNC Symbol	signDiff_4Tc vs 100Tc	signDiff_3Tc vs 100Tc	signDiff_2Tc vs 100Tc
GCN5L2	=	=	=
CDK2AP1	=	=	=
NOL1	=	=	=
SLC29A1	=	=	=
BNIP1	=	=	=
DBN1	=	=	=
EIF4G1	=	=	=
B4GALT2	=	=	=
TMEM5	=	=	=
FVT1	=	=	=
ETF1	=	=	+
ATF4	=	=	=
ILF3	=	=	=
RAMP1	=	=	=
n.a.	=	=	=
ADCY3	=	=	=
AFG3L2	=	=	=
PRPS1	=	=	=
OPRS1	=	=	=
TOMM70A	=	=	=
APRT	=	=	=
FGFR4	=	=	=
DEFA6	=	=	=
ZNF9	+	=	+
RAC3	+	+	=
WNT10B	+	=	+
NFRKB	=	=	=
CDK5R2	=	=	=
CYCS	=	+	+
YES1	=	=	=
DLEU1	=	=	=
BNIP3	=	=	=
RAD23A	=	=	=
	=	=	+
UBE2G2	=	=	=
KCNQ3	=	=	=
MTA1	=	=	=
LIG3	=	=	=
ITGA2B	=	=	=
TOMM34	+	=	=
ITIH4	=	=	=
POLD1	=	=	=
IKBKAP	=	=	=
ASNS	=	=	=
MX1	=	=	=
XRCC5	+	+	+
XPO1	=	=	=
RAD54L	=	=	=
PTHLH	-	-	-
MSH2	=	=	=
CDKL1	=	=	=
ADA	=	=	=
n.a.	=	=	=
TGFB1	=	=	=
NPTX2	=	=	=
BAG1	=	=	=
BAG1	=	=	=

HGNC Symbol	signDiff_4Tc vs 100Tc	signDiff_3Tc vs 100Tc	signDiff_2Tc vs 100Tc
SHB	=	=	=
EIF3S10	=	=	=
HTATIP2	=	=	=
CALCA	=	=	+
C6orf108	=	=	=
ACY1	=	=	=
PASK	=	=	=
CEBPZ	=	=	=
RAP1A	=	=	=
NID	+	+	=
IDE	=	=	=
HOXB7	=	=	=
GUCY1B2	=	=	=
SERPINA7	=	=	=
FPRL2	=	=	=
MTRR	=	=	=
THRA	=	=	=
POR	=	=	=
YWHAH	=	=	=
TRIM28	=	=	=
DHX30	=	=	=
CDK8	=	=	=
CCNH	=	=	=
RFK	=	=	=
RABGGTB	=	=	=
PLK4	=	=	=
CYP4B1	=	=	-
TP53BP2	=	=	=
NVL	=	=	=
ARF1	=	=	=
PLK2	=	=	=
GZMA	=	+	=
NOLA2	=	=	=
HMBS	=	=	=
ITIH2	=	=	=
SACS	=	=	=
GABPA	=	=	=
ETS2	=	=	=
IL8RA	=	=	=
API5	+	+	+
n.a.	=	=	=
ICT1	=	=	=
DFFB	=	=	=
USP7	=	=	=
PAP	=	=	=
BSG	=	=	=
YIF1	=	=	=
POLE	=	=	=
	=	=	=

HGNC Symbol	**signDiff_1 5Tc vs 100Tc**	**signDiff_1Tc vs 100Tc**	**signDiff_0 5Tc vs 100Tc**
MYC	+	+	+
CACNA1G	+	+	+
NME1	+	+	+
ADCY2	+	+	+
C4orf9	+	+	+
FKBP5	+	+	+
CRKL	+	+	+
RFC5	+	+	+
PPP2CA	+	+	+
TIMM8A	+	+	+
n.a.	+	+	+
MAD2L1	+	+	+
MRPL12	+	+	+
NME1	+	+	+
METTL1	+	+	+
SLC7A5	+	+	+
SRM	+	+	+
IL1B	+	+	+
PAICS	+	+	+
TOMM40	+	+	+
PYCR1	+	+	+
UMPK	+	+	+
LRP8	+	+	+
DUSP14	+	+	+
METAP1	+	+	+
ABCE1	+	+	+
PA2G4	+	+	+
BOP1	+	+	+
RANBP1	+	+	+
CTPS	+	+	+
TRAP1	+	+	+
HSPD1	+	+	+
PFAS	+	+	+
TEAD4	+	+	+
MIF	+	+	+
VARS2	+	+	+
CENTG1	+	+	+
DSCR2	+	+	+
JAG2	+	+	+
PRKAR1B	+	+	+
n.a.	+	+	+
MATK	+	+	+
IARS	+	+	+
GAL	+	+	+
MCAM	+	+	+
CAD	+	+	+
FH	+	+	+
SRPK1	+	+	+
NEFH	+	+	+
NP	+	+	+
AHCY	+	+	+
POLD2	+	+	+
C1QBP	+	+	+
CAMKK2	+	+	+
n.a.	+	+	+
BYSL	+	+	+
NUP155	+	+	+

HGNC Symbol	signDiff_1 5Tc vs 100Tc	signDiff_1Tc vs 100Tc	signDiff_0 5Tc vs 100Tc
IFRD2	+	+	+
MRPL3	+	+	+
HSPE1	+	+	+
HSPE1	+	+	+
n.a.	+	+	+
EBNA1BP2	+	+	+
TNFRSF8	+	+	+
PRDX4	+	+	+
CSE1L	+	+	+
RPP40	+	+	+
n.a.	+	+	+
HRMT1L2	+	+	+
n.a.	+	+	+
n.a.	+	+	+
MADH4	+	+	+
IL9	+	+	+
PDCD11	+	+	+
HK2	+	+	+
PWP2H	+	+	+
n.a.	+	+	+
NOLC1	+	+	+
NOLC1	+	+	+
CCT2	+	+	+
DTYMK	+	+	+
HNRPAB	+	+	+
FASN	+	+	+
FASN	+	+	+
NMB	+	+	+
CHC1	+	+	+
	+	+	+
KIAA0179	+	+	+
NTHL1	+	+	+
UNG	+	+	+
KIAA0020	+	+	+
n.a.	+	+	+
n.a.	+	+	+
POLE2	+	+	+
MTHFD1	+	+	+
NOL5A	+	+	+
PRPS2	+	+	+
RUVBL2	+	+	+
GPI	+	+	+
n.a.	+	+	+
NPM3	+	+	+
n.a.	+	+	+
CDC20	+	+	+
n.a.	+	+	+
PRKDC	+	+	+
CKS2	+	+	+
CSE1L	+	+	+
EEF1E1	+	+	+
HRMT1L2	+	+	+
n.a.	+	+	+
TST	+	+	+
DKC1	+	+	+
RAN	+	+	+
PDGFRA	+	+	+

HGNC Symbol	**signDiff_1 5Tc vs 100Tc**	**signDiff_1Tc vs 100Tc**	**signDiff_0 5Tc vs 100Tc**
CDK4	+	=	+
ALDH1B1	+	+	+
SORD	+	+	+
BDH	+	+	+
GMPS	+	+	+
GPR30	+	+	+
PHB	+	+	+
STRA13	+	+	+
XPOT	+	+	+
SMN1	+	+	+
CHC1	+	+	+
PLK1	+	+	+
n.a.	+	+	+
AK2	+	+	+
n.a.	+	+	+
MGST1	+	+	+
CSDA	+	+	+
n.a.	+	+	+
ATP1B3	+	+	+
BCS1L	+	+	+
UNG	+	+	+
PBP	+	+	+
CDC6	+	+	+
CDC7	+	+	+
MTAP	+	+	+
ADSL	+	+	+
CDKN3	+	+	+
VRK1	+	+	+
WFDC2	+	+	+
GSPT1	+	+	+
SLC39A14	+	+	+
n.a.	+	+	+
RLN2	+	+	+
BAG2	+	+	+
HSD17B8	+	+	+
UCHL3	+	+	+
NME2	+	+	+
MRPS12	+	+	+
PCNA	+	+	+
DPH2L2	+	+	+
CCNB1	+	+	+
MC1R	+	+	+
SOD1	+	+	+
ATP5G3	+	+	+
CCT3	+	+	+
RFC4	+	+	+
CDC25A	+	+	+
FRDA	+	+	+
SNRPD1	+	+	+
CHAF1A	+	+	+
PRDX2	+	+	+
BUB1	+	+	+
CDC2	+	+	+
POLR1C	+	+	+
SLC19A1	+	+	+
TOMM20	+	+	+
MMP3	+	+	+

HGNC Symbol	signDiff_1 5Tc vs 100Tc	signDiff_1Tc vs 100Tc	signDiff_0 5Tc vs 100Tc
UBE2C	+	+	+
PTPN2	+	+	+
RUVBL1	+	+	+
TYMS	+	+	+
DDX10	+	+	+
TUFM	+	+	+
AURKB	+	+	+
RRS1	+	+	+
GEMIN4	+	+	+
PTMA	+	+	+
CYP51A1	+	+	+
ARHGEF5	+	+	+
KIAA0690	+	+	+
VDAC1	+	+	+
DDX1	+	+	+
SCAMP1	+	+	+
DDX18	+	+	+
PES1	+	+	+
RANGAP1	+	+	+
APEX1	+	+	+
MYBL2	+	+	+
USP10	+	+	+
n.a.	+	+	+
RPA3	+	+	+
CXCL12	+	+	+
n.a.	+	+	+
MCM3	+	+	+
GMNN	+	+	+
HSPA9B	+	+	+
TCERG1	+	+	+
RNU3IP2	+	+	+
SFRS7	+	+	+
MSH6	+	+	+
CENPF	+	+	+
MXI1	+	+	+
AMD1	+	+	+
ELK1	+	+	+
ILF3	+	+	+
TFDP1	+	+	+
n.a.	+	+	+
TOP2A	+	+	+
EIF5A	+	+	+
n.a.	+	+	+
n.a.	+	+	+
ATIC	+	+	+
ATIC	+	+	+
PEX5	+	+	+
TAF4B	+	+	+
HDGF	+	+	+
HDGF	+	+	+
ILF2	+	+	+
CCNA2	+	+	+
MDH2	+	+	+
PEG10	+	+	+
PPRC1	+	+	+
SSRP1	+	+	+
PTK9	+	+	+

HGNC Symbol	signDiff_1 5Tc vs 100Tc	signDiff_1Tc vs 100Tc	signDiff_0 5Tc vs 100Tc
ACSL1	+	+	+
PFKM	+	+	+
HNRPDL	+	+	+
RPIA	+	+	+
SLC16A1	+	+	+
KCNJ6	+	+	+
SFRS2	+	+	+
PRKCI	+	+	+
POLR2H	+	+	+
ABCE1	+	+	+
MELK	+	+	+
DDX21	+	+	+
SSSCA1	+	+	+
n.a.	+	+	+
HSPCA	+	+	+
DEAF1	+	+	+
n.a.	+	+	+
EIF1AX	+	+	+
n.a.	+	+	+
n.a.	+	+	+
SF3A3	+	+	+
n.a.	+	+	+
AK2	+	+	+
PLAUR	+	=	+
SCARB1	+	+	+
MCM2	+	+	+
EXOSC7	+	+	+
KHSRP	+	+	+
NUDC	+	+	+
CGRRF1	+	+	+
APEX1	+	+	+
GARS	+	+	+
EIF3S9	+	+	+
IMPDH1	+	+	+
VEGF	+	+	+
TFDP2	+	+	+
PRDX1	+	+	+
SCO2	+	+	+
TUBG1	+	+	+
MYCN	+	+	+
ABL2	+	+	+
SLC20A1	+	+	+
CDKN2B	+	+	+
n.a.	+	+	+
FANCG	+	+	+
PMPCA	+	+	+
PSMC3	+	+	+
MCM7	+	+	+
ABCA3	+	+	+
EIF4EBP1	+	+	+
TNFRSF4	+	+	+
SRP72	+	+	+
ALG3	+	+	+
CKS1B	+	+	+
NSEP1	+	+	+
FARSLA	+	+	+
PRIM1	+	+	+

HGNC Symbol	**signDiff_1 5Tc vs 100Tc**	**signDiff_1Tc vs 100Tc**	**signDiff_0 5Tc vs 100Tc**
TBL3	+	+	+
JUND	=	+	+
PTBP1	=	+	+
MRE11A	=	+	+
HSPA5	=	+	+
OAT	=	+	+
TFRC	=	+	+
SHMT1	=	+	+
CLNS1A	=	+	+
SEMA3C	=	+	+
MCAM	=	+	+
MAPKAPK5	=	+	+
SIP1	=	+	+
NF2	=	+	+
SLC1A5	=	+	+
PSMA2	=	+	+
RAD51C	=	+	+
CTSC	=	+	+
HSPA8	=	+	+
n.a.	=	+	+
IGFBP2	=	+	+
DARS	=	+	+
UCHL3	=	+	+
GTF3A	=	+	+
RPL5	+	+	+
AMD1	=	+	+
HSPA1A	=	+	+
SYNGR3	=	+	+
NINJ1	=	+	+
SNRPA1	=	+	+
TAF9	=	+	+
SYNCRIP	+	+	+
n.a.	=	+	+
ITGB3BP	=	+	+
PTPRF	=	+	+
CHEK1	=	+	+
TCEB1	=	+	+
n.a.	=	+	+
VBP1	=	+	+
BUB1B	=	+	+
RACGAP1	=	+	+
AK3	=	+	+
HNRPF	=	+	+
PDAP1	=	+	+
SELE	=	=	+
n.a.	=	+	+
RCN1	+	=	+
GLDC	+	=	+
PMS1	+	=	+
PFKP	=	=	+
PDCD2	=	=	+
MGST2	=	=	+
NDUFB7	=	=	+
G22P1	=	+	+
n.a.	=	=	+
PBEF1	=	=	+
TBL2	=	=	+

HGNC Symbol	**signDiff_1 5Tc vs 100Tc**	**signDiff_1Tc vs 100Tc**	**signDiff_0 5Tc vs 100Tc**
GCN5L2	=	=	+
CDK2AP1	=	=	+
NOL1	=	+	+
SLC29A1	=	=	+
BNIP1	=	=	+
DBN1	=	=	+
EIF4G1	=	+	+
B4GALT2	=	=	+
TMEM5	=	=	+
FVT1	=	=	+
ETF1	+	=	+
ATF4	=	=	+
ILF3	=	=	+
RAMP1	=	=	+
n.a.	=	=	+
ADCY3	=	=	+
AFG3L2	=	=	+
PRPS1	=	=	+
OPRS1	+	=	+
TOMM70A	=	=	+
APRT	=	=	+
FGFR4	=	=	+
DEFA6	+	=	+
ZNF9	+	=	+
RAC3	+	=	+
WNT10B	+	=	+
NFRKB	=	=	+
CDK5R2	=	=	+
CYCS	+	=	+
YES1	=	=	+
DLEU1	=	=	+
BNIP3	=	=	+
RAD23A	=	=	+
	=	=	+
UBE2G2	=	=	=
KCNQ3	=	=	=
MTA1	=	=	=
LIG3	=	=	=
ITGA2B	=	=	+
TOMM34	=	=	=
ITIH4	=	=	=
POLD1	=	=	=
IKBKAP	=	=	=
ASNS	=	=	=
MX1	=	=	=
XRCC5	+	+	=
XPO1	=	=	=
RAD54L	=	=	=
PTHLH	-	=	=
MSH2	=	=	+
CDKL1	=	=	=
ADA	=	=	=
n.a.	=	=	=
TGFB1	=	=	=
NPTX2	=	=	=
BAG1	=	=	=
BAG1	=	=	=

HGNC Symbol	signDiff_1 5Tc vs 100Tc	signDiff_1Tc vs 100Tc	signDiff_0 5Tc vs 100Tc
SHB	=	=	=
EIF3S10	=	=	=
HTATIP2	=	=	=
CALCA	=	=	=
C6orf108	=	=	=
ACY1	=	=	=
PASK	=	=	=
CEBPZ	=	=	=
RAP1A	=	=	=
NID	=	=	=
IDE	=	+	=
HOXB7	=	=	=
GUCY1B2	=	=	=
SERPINA7	=	=	+
FPRL2	=	=	=
MTRR	=	=	=
THRA	=	=	=
POR	=	=	=
YWHAH	=	=	=
TRIM28	=	=	=
DHX30	=	=	=
CDK8	=	+	=
CCNH	=	=	=
RFK	+	+	+
RABGGTB	=	=	=
PLK4	=	=	=
CYP4B1	=	=	=
TP53BP2	=	=	=
NVL	=	=	=
ARF1	=	=	=
PLK2	=	=	=
GZMA	=	=	=
NOLA2	=	=	=
HMBS	=	+	=
ITIH2	=	=	=
SACS	=	=	=
GABPA	=	=	=
ETS2	=	=	=
IL8RA	=	=	=
API5	+	=	=
n.a.	=	=	=
ICT1	=	=	+
DFFB	=	=	=
USP7	=	=	=
PAP	=	=	=
BSG	=	=	=
YIF1	=	=	+
POLE	+	+	=
	=	=	=

HGNC Symbol	**signDiff_0Tc vs 100Tc**	**signEx_100Tc**	**signEx_8Tc**	**signEx_6Tc**	**signEx_5Tc**
MYC	+	+	+	+	+
CACNA1G	+	-	-	-	+
NME1	+	+	+	+	+
ADCY2	+	-	-	-	+
C4orf9	+	-	+	-	-
FKBP5	+	-	+	+	+
CRKL	+	-	-	-	-
RFC5	+	-	-	-	-
PPP2CA	+	-	+	-	+
TIMM8A	+	-	-	-	+
n.a.	+	-	-	-	-
MAD2L1	+	-	-	-	-
MRPL12	+	+	+	+	+
NME1	+	+	+	+	+
METTL1	+	-	+	+	+
SLC7A5	+	-	+	+	+
SRM	+	+	+	+	+
IL1B	+	+	+	+	+
PAICS	+	+	+	+	+
TOMM40	+	+	+	+	+
PYCR1	+	+	+	+	+
UMPK	+	+	+	+	+
LRP8	+	-	-	+	+
DUSP14	+	-	-	-	+
METAP1	+	-	+	+	+
ABCE1	+	-	+	+	+
PA2G4	+	+	+	+	+
BOP1	+	+	+	+	+
RANBP1	+	+	+	+	+
CTPS	+	+	+	+	+
TRAP1	+	+	+	+	+
HSPD1	+	+	+	+	+
PFAS	+	+	+	+	+
TEAD4	+	-	+	+	+
MIF	+	+	+	+	+
VARS2	+	+	+	+	+
CENTG1	+	+	+	+	+
DSCR2	+	+	+	+	+
JAG2	+	+	+	+	+
PRKAR1B	+	+	+	+	+
n.a.	+	-	-	+	+
MATK	+	-	-	+	+
IARS	+	+	+	+	+
GAL	+	+	+	+	+
MCAM	+	-	-	-	-
CAD	+	+	+	+	+
FH	+	+	+	+	+
SRPK1	+	+	+	+	+
NEFH	+	-	-	-	+
NP	+	+	+	+	+
AHCY	+	+	+	+	+
POLD2	+	+	+	+	+
C1QBP	+	+	+	+	+
CAMKK2	+	+	+	+	+
n.a.	+	+	+	+	+
BYSL	+	+	+	+	+
NUP155	+	-	-	-	+

HGNC Symbol	signDiff_0Tc vs 100Tc	signEx_100Tc	signEx_8Tc	signEx_6Tc	signEx_5Tc
IFRD2	+	+	+	+	+
MRPL3	+	+	+	+	+
HSPE1	+	+	+	+	+
HSPE1	+	+	+	+	+
n.a.	+	+	+	+	+
EBNA1BP2	+	+	+	+	+
TNFRSF8	+	-	-	-	-
PRDX4	+	+	+	+	+
CSE1L	+	+	+	+	+
RPP40	+	-	-	-	+
n.a.	+	-	-	-	-
HRMT1L2	+	+	+	+	+
n.a.	+	-	-	+	+
n.a.	+	+	+	+	+
MADH4	+	+	+	+	+
IL9	+	+	+	+	+
PDCD11	+	+	+	+	+
HK2	+	-	-	-	-
PWP2H	+	+	+	+	+
n.a.	+	-	+	-	+
NOLC1	+	+	+	+	+
NOLC1	+	+	+	+	+
CCT2	+	+	+	+	+
DTYMK	+	+	+	+	+
HNRPAB	+	+	+	+	+
FASN	+	+	+	+	+
FASN	+	+	+	+	+
NMB	+	-	+	+	+
CHC1	+	-	-	-	+
	+	+	+	+	+
KIAA0179	+	+	+	+	+
NTHL1	+	+	+	+	+
UNG	+	+	+	+	+
KIAA0020	+	+	+	+	+
n.a.	+	+	+	+	+
n.a.	+	+	+	+	+
POLE2	+	-	+	+	+
MTHFD1	+	+	+	+	+
NOL5A	+	+	+	+	+
PRPS2	+	+	+	+	+
RUVBL2	+	+	+	+	+
GPI	+	+	+	+	+
n.a.	+	+	+	+	+
NPM3	+	+	+	+	+
n.a.	+	+	+	+	+
CDC20	+	+	+	+	+
n.a.	+	+	+	+	+
PRKDC	+	-	-	-	+
CKS2	+	+	+	+	+
CSE1L	+	+	+	+	+
EEF1E1	+	+	+	+	+
HRMT1L2	+	+	+	+	+
n.a.	+	+	+	+	+
TST	+	-	+	+	+
DKC1	+	+	+	+	+
RAN	+	+	+	+	+
PDGFRA	+	-	+	+	+

HGNC Symbol	signDiff_0Tc vs 100Tc	signEx_100Tc	signEx_8Tc	signEx_6Tc	signEx_5Tc
CDK4	+	-	-	-	-
ALDH1B1	+	-	+	+	+
SORD	+	+	+	+	+
BDH	+	+	+	+	+
GMPS	+	+	+	+	+
GPR30	+	+	+	+	+
PHB	+	+	+	+	+
STRA13	+	+	+	+	+
XPOT	+	+	+	+	+
SMN1	+	+	+	+	+
CHC1	+	+	+	+	+
PLK1	+	+	+	+	+
n.a.	+	-	+	+	+
AK2	+	+	+	+	+
n.a.	+	+	+	+	+
MGST1	+	+	+	+	+
CSDA	+	+	+	+	+
n.a.	+	+	+	+	+
ATP1B3	+	+	+	+	+
BCS1L	+	+	+	+	+
UNG	+	+	+	+	+
PBP	+	+	+	+	+
CDC6	+	+	+	+	+
CDC7	+	+	+	+	+
MTAP	+	-	-	+	+
ADSL	+	+	+	+	+
CDKN3	+	+	+	+	+
VRK1	+	+	+	+	+
WFDC2	+	+	+	+	+
GSPT1	+	+	+	+	+
SLC39A14	+	+	+	+	+
n.a.	+	+	+	+	+
RLN2	+	+	+	+	+
BAG2	+	+	+	+	+
HSD17B8	+	+	+	+	+
UCHL3	+	+	+	+	+
NME2	+	+	+	+	+
MRPS12	+	+	+	+	+
PCNA	+	+	+	+	+
DPH2L2	+	+	+	+	+
CCNB1	+	+	+	+	+
MC1R	+	+	+	+	+
SOD1	+	+	+	+	+
ATP5G3	+	+	+	+	+
CCT3	+	+	+	+	+
RFC4	+	+	+	+	+
CDC25A	+	-	+	+	+
FRDA	+	+	+	+	+
SNRPD1	+	+	+	+	+
CHAF1A	+	+	+	+	+
PRDX2	+	+	+	+	+
BUB1	+	+	+	+	+
CDC2	+	+	+	+	+
POLR1C	+	+	+	+	+
SLC19A1	+	-	-	-	+
TOMM20	+	+	+	+	+
MMP3	+	-	+	+	+

HGNC Symbol	signDiff_0Tc vs 100Tc	signEx_100Tc	signEx_8Tc	signEx_6Tc	signEx_5Tc
UBE2C	+	+	+	+	+
PTPN2	+	+	+	+	+
RUVBL1	+	+	+	+	+
TYMS	+	+	+	+	+
DDX10	+	+	+	+	+
TUFM	+	+	+	+	+
AURKB	+	+	+	+	+
RRS1	+	+	+	+	+
GEMIN4	+	+	+	+	+
PTMA	+	+	+	+	+
CYP51A1	+	+	+	+	+
ARHGEF5	+	-	-	-	-
KIAA0690	+	+	+	+	+
VDAC1	+	+	+	+	+
DDX1	+	+	+	+	+
SCAMP1	+	+	+	+	+
DDX18	+	+	+	+	+
PES1	+	+	+	+	+
RANGAP1	+	+	+	+	+
APEX1	+	+	+	+	+
MYBL2	+	+	+	+	+
USP10	+	+	+	+	+
n.a.	+	-	-	+	+
RPA3	+	+	+	+	+
CXCL12	+	-	+	+	+
n.a.	+	-	-	+	-
MCM3	+	+	+	+	+
GMNN	+	+	+	+	+
HSPA9B	+	+	+	+	+
TCERG1	+	+	+	+	+
RNU3IP2	+	+	+	+	+
SFRS7	+	+	+	+	+
MSH6	+	+	+	+	+
CENPF	+	+	+	+	+
MXI1	+	+	+	+	+
AMD1	+	+	+	+	+
ELK1	+	+	+	+	+
ILF3	+	+	+	+	+
TFDP1	+	+	+	+	+
n.a.	+	+	+	+	+
TOP2A	+	+	+	+	+
EIF5A	+	+	+	+	+
n.a.	+	-	-	-	-
n.a.	+	+	+	+	+
ATIC	+	+	+	+	+
ATIC	+	+	+	+	+
PEX5	+	+	+	+	+
TAF4B	+	+	+	+	+
HDGF	+	+	+	+	+
HDGF	+	+	+	+	+
ILF2	+	+	+	+	+
CCNA2	+	+	+	+	+
MDH2	+	+	+	+	+
PEG10	+	-	-	+	+
PPRC1	+	+	+	+	+
SSRP1	+	+	+	+	+
PTK9	+	-	-	-	-

HGNC Symbol	signDiff_0Tc vs 100Tc	signEx_100Tc	signEx_8Tc	signEx_6Tc	signEx_5Tc
ACSL1	+	+	+	+	+
PFKM	+	+	+	+	+
HNRPDL	+	+	+	+	+
RPIA	+	+	+	+	+
SLC16A1	+	-	-	-	-
KCNJ6	+	+	+	+	+
SFRS2	+	+	+	+	+
PRKCI	+	-	-	+	-
POLR2H	+	+	+	+	+
ABCE1	+	-	-	-	+
MELK	+	+	+	+	+
DDX21	+	-	-	+	+
SSSCA1	+	+	+	+	+
n.a.	+	+	+	+	+
HSPCA	+	+	+	+	+
DEAF1	+	+	+	+	+
n.a.	+	+	+	+	+
EIF1AX	+	+	+	+	+
n.a.	+	+	+	+	+
n.a.	+	+	+	+	+
SF3A3	+	+	+	+	+
n.a.	+	-	-	-	-
AK2	+	+	+	+	+
PLAUR	+	-	-	+	+
SCARB1	+	+	+	+	+
MCM2	+	+	+	+	+
EXOSC7	+	+	+	+	+
KHSRP	+	+	+	+	+
NUDC	+	+	+	+	+
CGRRF1	+	+	+	+	+
APEX1	+	+	+	+	+
GARS	+	+	+	+	+
EIF3S9	+	+	+	+	+
IMPDH1	+	+	+	+	+
VEGF	+	-	-	-	-
TFDP2	+	+	+	+	+
PRDX1	+	+	+	+	+
SCO2	+	+	+	+	+
TUBG1	+	+	+	+	+
MYCN	+	+	+	+	+
ABL2	+	-	-	-	-
SLC20A1	+	+	+	+	+
CDKN2B	+	-	-	+	-
n.a.	+	+	+	+	+
FANCG	+	+	+	+	+
PMPCA	+	+	+	+	+
PSMC3	+	+	+	+	+
MCM7	+	+	+	+	+
ABCA3	+	+	+	+	+
EIF4EBP1	+	+	+	+	+
TNFRSF4	+	-	-	-	-
SRP72	+	+	+	+	+
ALG3	+	+	+	+	+
CKS1B	+	+	+	+	+
NSEP1	+	+	+	+	+
FARSLA	+	+	+	+	+
PRIM1	+	+	+	+	+

HGNC Symbol	signDiff_0Tc vs 100Tc	signEx_100Tc	signEx_8Tc	signEx_6Tc	signEx_5Tc
TBL3	+	+	+	+	+
JUND	+	+	+	+	+
PTBP1	+	+	+	+	+
MRE11A	+	+	+	+	+
HSPA5	+	+	+	+	+
OAT	+	+	+	+	+
TFRC	+	+	+	+	+
SHMT1	+	-	-	+	+
CLNS1A	+	+	+	+	+
SEMA3C	+	-	-	-	-
MCAM	+	+	+	+	+
MAPKAPK5	+	+	+	+	+
SIP1	+	-	+	+	+
NF2	+	+	+	+	+
SLC1A5	+	+	+	+	+
PSMA2	+	+	+	+	+
RAD51C	+	+	+	+	+
CTSC	+	+	+	+	+
HSPA8	+	+	+	+	+
n.a.	+	-	-	-	+
IGFBP2	+	+	+	+	+
DARS	+	+	+	+	+
UCHL3	+	+	+	+	+
GTF3A	+	+	+	+	+
RPL5	+	+	+	+	+
AMD1	+	+	+	+	+
HSPA1A	+	-	+	+	-
SYNGR3	+	+	+	+	+
NINJ1	+	-	-	-	-
SNRPA1	+	+	+	+	+
TAF9	+	+	+	+	+
SYNCRIP	+	+	+	+	+
n.a.	+	+	+	+	+
ITGB3BP	+	+	+	+	+
PTPRF	+	-	+	-	+
CHEK1	+	+	+	+	+
TCEB1	+	+	+	+	+
n.a.	+	+	+	+	+
VBP1	+	+	+	+	+
BUB1B	+	+	+	+	+
RACGAP1	+	+	+	+	+
AK3	+	-	+	-	+
HNRPF	+	+	+	+	+
PDAP1	+	+	+	+	+
SELE	+	+	+	+	+
n.a.	+	+	+	+	+
RCN1	+	-	-	-	-
GLDC	+	+	-	+	+
PMS1	+	-	-	-	-
PFKP	+	+	+	+	+
PDCD2	+	+	+	+	+
MGST2	+	+	+	+	+
NDUFB7	+	+	+	+	+
G22P1	+	+	+	+	+
n.a.	+	+	+	+	+
PBEF1	+	-	-	-	-
TBL2	+	+	+	+	+

HGNC Symbol	signDiff_0Tc vs 100Tc	signEx_100Tc	signEx_8Tc	signEx_6Tc	signEx_5Tc
GCN5L2	+	+	+	+	+
CDK2AP1	+	+	+	+	+
NOL1	+	+	+	+	+
SLC29A1	+	+	+	+	+
BNIP1	+	-	+	+	+
DBN1	+	+	+	+	+
EIF4G1	+	+	+	+	+
B4GALT2	+	-	-	+	+
TMEM5	+	+	+	+	+
FVT1	+	-	-	-	-
ETF1	+	-	-	+	+
ATF4	+	+	+	+	+
ILF3	+	+	+	+	+
RAMP1	+	+	+	+	+
n.a.	+	+	+	+	+
ADCY3	+	+	+	+	+
AFG3L2	+	+	+	+	+
PRPS1	+	+	+	+	+
OPRS1	+	-	-	-	-
TOMM70A	+	+	+	+	+
APRT	+	+	+	+	+
FGFR4	+	-	-	-	-
DEFA6	+	-	-	+	-
ZNF9	+	-	+	+	+
RAC3	+	-	-	-	-
WNT10B	+	-	-	-	+
NFRKB	+	-	+	+	-
CDK5R2	+	-	-	-	-
CYCS	+	-	-	-	-
YES1	+	+	+	+	+
DLEU1	+	+	+	+	+
BNIP3	+	+	+	+	+
RAD23A	+	+	+	+	+
	+	-	-	-	+
UBE2G2	+	+	+	+	+
KCNQ3	+	-	-	-	-
MTA1	+	+	+	+	+
LIG3	+	+	+	+	+
ITGA2B	+	-	-	-	+
TOMM34	+	-	-	-	-
ITIH4	+	+	+	+	+
POLD1	+	+	+	+	+
IKBKAP	+	+	+	+	+
ASNS	+	+	+	+	+
MX1	+	-	-	-	-
XRCC5	+	-	+	+	+
XPO1	+	+	+	+	+
RAD54L	+	+	+	+	+
PTHLH	+	-	-	-	-
MSH2	+	+	+	+	+
CDKL1	+	+	+	+	+
ADA	+	+	+	+	+
n.a.	+	+	+	+	+
TGFB1	+	-	-	-	-
NPTX2	+	-	-	-	-
BAG1	+	+	+	+	+
BAG1	+	+	+	+	+

HGNC Symbol	signDiff_0Tc vs 100Tc	signEx_100Tc	signEx_8Tc	signEx_6Tc	signEx_5Tc
SHB	+	+	+	+	+
EIF3S10	+	+	+	+	+
HTATIP2	+	-	-	-	-
CALCA	+	-	-	-	+
C6orf108	+	+	+	+	+
ACY1	+	+	+	+	+
PASK	+	-	-	-	-
CEBPZ	+	+	+	+	+
RAP1A	+	+	+	-	+
NID	+	-	-	-	-
IDE	+	+	+	+	+
HOXB7	+	-	+	-	-
GUCY1B2	+	+	+	+	+
SERPINA7	+	+	+	+	+
FPRL2	+	-	+	+	+
MTRR	+	+	+	+	+
THRA	+	+	+	+	+
POR	+	+	+	+	+
YWHAH	+	+	+	+	+
TRIM28	+	+	+	+	+
DHX30	+	+	+	+	+
CDK8	+	+	-	+	+
CCNH	+	+	+	+	+
RFK	+	+	+	+	+
RABGGTB	+	+	+	+	+
PLK4	+	+	+	+	+
CYP4B1	+	-	-	-	-
TP53BP2	+	-	+	+	+
NVL	+	+	+	+	+
ARF1	+	+	+	+	+
PLK2	+	+	+	+	+
GZMA	+	-	-	-	-
NOLA2	+	+	+	+	+
HMBS	+	+	+	+	+
ITIH2	+	-	-	-	-
SACS	+	+	-	+	+
GABPA	+	+	+	+	+
ETS2	+	+	+	+	+
IL8RA	+	+	+	+	+
API5	+	-	-	+	+
n.a.	+	+	+	+	+
ICT1	+	+	+	+	+
DFFB	+	+	+	+	+
USP7	+	+	+	+	+
PAP	+	+	+	+	+
BSG	+	+	+	+	+
YIF1	+	+	+	+	+
POLE	+	+	+	+	+
	+	-	-	-	+

HGNC Symbol	**signEx_4Tc**	**signEx_3Tc**	**signEx_2Tc**	**signEx_1 5Tc**	**signEx_1Tc**
MYC	+	+	+	+	+
CACNA1G	-	-	-	+	-
NME1	+	+	+	+	+
ADCY2	-	-	-	-	-
C4orf9	+	+	+	+	+
FKBP5	+	+	+	+	+
CRKL	-	-	+	-	+
RFC5	-	+	+	+	+
PPP2CA	+	+	+	+	+
TIMM8A	+	+	-	+	+
n.a.	-	+	-	-	+
MAD2L1	-	-	+	+	+
MRPL12	+	+	+	+	+
NME1	+	+	+	+	+
METTL1	+	+	+	+	+
SLC7A5	+	+	+	+	+
SRM	+	+	+	+	+
IL1B	+	+	+	+	+
PAICS	+	+	+	+	+
TOMM40	+	+	+	+	+
PYCR1	+	+	+	+	+
UMPK	+	+	+	+	+
LRP8	+	+	+	+	+
DUSP14	-	+	+	-	+
METAP1	+	+	+	+	+
ABCE1	+	+	+	+	+
PA2G4	+	+	+	+	+
BOP1	+	+	+	+	+
RANBP1	+	+	+	+	+
CTPS	+	+	+	+	+
TRAP1	+	+	+	+	+
HSPD1	+	+	+	+	+
PFAS	+	+	+	+	+
TEAD4	+	+	+	+	+
MIF	+	+	+	+	+
VARS2	+	+	+	+	+
CENTG1	+	+	+	+	+
DSCR2	+	+	+	+	+
JAG2	+	+	+	+	+
PRKAR1B	+	+	+	+	+
n.a.	+	+	+	+	+
MATK	+	+	+	+	+
IARS	+	+	+	+	+
GAL	+	+	+	+	+
MCAM	-	-	-	+	+
CAD	+	+	+	+	+
FH	+	+	+	+	+
SRPK1	+	+	+	+	+
NEFH	+	+	+	+	+
NP	+	+	+	+	+
AHCY	+	+	+	+	+
POLD2	+	+	+	+	+
C1QBP	+	+	+	+	+
CAMKK2	+	+	+	+	+
n.a.	+	+	+	+	+
BYSL	+	+	+	+	+
NUP155	+	+	+	+	+

HGNC Symbol	**signEx_4Tc**	**signEx_3Tc**	**signEx_2Tc**	**signEx_1 5Tc**	**signEx_1Tc**
IFRD2	+	+	+	+	+
MRPL3	+	+	+	+	+
HSPE1	+	+	+	+	+
HSPE1	+	+	+	+	+
n.a.	+	+	+	+	+
EBNA1BP2	+	+	+	+	+
TNFRSF8	+	+	+	+	+
PRDX4	+	+	+	+	+
CSE1L	+	+	+	+	+
RPP40	+	+	+	+	+
n.a.	+	+	-	+	+
HRMT1L2	+	+	+	+	+
n.a.	+	+	+	+	+
n.a.	+	+	+	+	+
MADH4	+	+	+	+	+
IL9	+	+	+	+	+
PDCD11	+	+	+	+	+
HK2	-	-	+	+	+
PWP2H	+	+	+	+	+
n.a.	+	+	+	+	+
NOLC1	+	+	+	+	+
NOLC1	+	+	+	+	+
CCT2	+	+	+	+	+
DTYMK	+	+	+	+	+
HNRPAB	+	+	+	+	+
FASN	+	+	+	+	+
FASN	+	+	+	+	+
NMB	+	+	+	+	+
CHC1	+	+	+	+	+
	+	+	+	+	+
KIAA0179	+	+	+	+	+
NTHL1	+	+	+	+	+
UNG	+	+	+	+	+
KIAA0020	+	+	+	+	+
n.a.	+	+	+	+	+
n.a.	+	+	+	+	+
POLE2	+	+	+	+	+
MTHFD1	+	+	+	+	+
NOL5A	+	+	+	+	+
PRPS2	+	+	+	+	+
RUVBL2	+	+	+	+	+
GPI	+	+	+	+	+
n.a.	+	+	+	+	+
NPM3	+	+	+	+	+
n.a.	+	+	+	+	+
CDC20	+	+	+	+	+
n.a.	+	+	+	+	+
PRKDC	+	+	+	+	+
CKS2	+	+	+	+	+
CSE1L	+	+	+	+	+
EEF1E1	+	+	+	+	+
HRMT1L2	+	+	+	+	+
n.a.	+	+	+	+	+
TST	+	+	+	+	+
DKC1	+	+	+	+	+
RAN	+	+	+	+	+
PDGFRA	+	+	+	+	+

HGNC Symbol	signEx_4Tc	signEx_3Tc	signEx_2Tc	signEx_1 5Tc	signEx_1Tc
CDK4	-	-	-	-	-
ALDH1B1	+	+	+	+	+
SORD	+	+	+	+	+
BDH	+	+	+	+	+
GMPS	+	+	+	+	+
GPR30	+	+	+	+	+
PHB	+	+	+	+	+
STRA13	+	+	+	+	+
XPOT	+	+	+	+	+
SMN1	+	+	+	+	+
CHC1	+	+	+	+	+
PLK1	+	+	+	+	+
n.a.	+	+	+	+	+
AK2	+	+	+	+	+
n.a.	+	+	+	+	+
MGST1	+	+	+	+	+
CSDA	+	+	+	+	+
n.a.	+	+	+	+	+
ATP1B3	+	+	+	+	+
BCS1L	+	+	+	+	+
UNG	+	+	+	+	+
PBP	+	+	+	+	+
CDC6	+	+	+	+	+
CDC7	+	+	+	+	+
MTAP	+	+	+	+	+
ADSL	+	+	+	+	+
CDKN3	+	+	+	+	+
VRK1	+	+	+	+	+
WFDC2	+	+	+	+	+
GSPT1	+	+	+	+	+
SLC39A14	+	+	+	+	+
n.a.	+	+	+	+	+
RLN2	+	+	+	+	+
BAG2	+	+	+	+	+
HSD17B8	+	+	+	+	+
UCHL3	+	+	+	+	+
NME2	+	+	+	+	+
MRPS12	+	+	+	+	+
PCNA	+	+	+	+	+
DPH2L2	+	+	+	+	+
CCNB1	+	+	+	+	+
MC1R	+	+	+	+	+
SOD1	+	+	+	+	+
ATP5G3	+	+	+	+	+
CCT3	+	+	+	+	+
RFC4	+	+	+	+	+
CDC25A	+	+	+	+	+
FRDA	+	+	+	+	+
SNRPD1	+	+	+	+	+
CHAF1A	+	+	+	+	+
PRDX2	+	+	+	+	+
BUB1	+	+	+	+	+
CDC2	+	+	+	+	+
POLR1C	+	+	+	+	+
SLC19A1	+	+	+	+	+
TOMM20	+	+	+	+	+
MMP3	+	+	+	+	+

HGNC Symbol	**signEx_4Tc**	**signEx_3Tc**	**signEx_2Tc**	**signEx_1 5Tc**	**signEx_1Tc**
UBE2C	+	+	+	+	+
PTPN2	+	+	+	+	+
RUVBL1	+	+	+	+	+
TYMS	+	+	+	+	+
DDX10	+	+	+	+	+
TUFM	+	+	+	+	+
AURKB	+	+	+	+	+
RRS1	+	+	+	+	+
GEMIN4	+	+	+	+	+
PTMA	+	+	+	+	+
CYP51A1	+	+	+	+	+
ARHGEF5	-	-	-	+	+
KIAA0690	+	+	+	+	+
VDAC1	+	+	+	+	+
DDX1	+	+	+	+	+
SCAMP1	+	+	+	+	+
DDX18	+	+	+	+	+
PES1	+	+	+	+	+
RANGAP1	+	+	+	+	+
APEX1	+	+	+	+	+
MYBL2	+	+	+	+	+
USP10	+	+	+	+	+
n.a.	+	+	+	+	+
RPA3	+	+	+	+	+
CXCL12	+	+	+	+	+
n.a.	+	+	+	+	+
MCM3	+	+	+	+	+
GMNN	+	+	+	+	+
HSPA9B	+	+	+	+	+
TCERG1	+	+	+	+	+
RNU3IP2	+	+	+	+	+
SFRS7	+	+	+	+	+
MSH6	+	+	+	+	+
CENPF	+	+	+	+	+
MXI1	+	+	+	+	+
AMD1	+	+	+	+	+
ELK1	+	+	+	+	+
ILF3	+	+	+	+	+
TFDP1	+	+	+	+	+
n.a.	+	+	+	+	+
TOP2A	+	+	+	+	+
EIF5A	+	+	+	+	+
n.a.	+	+	+	+	+
n.a.	+	+	+	+	+
ATIC	+	+	+	+	+
ATIC	+	+	+	+	+
PEX5	+	+	+	+	+
TAF4B	+	+	+	+	+
HDGF	+	+	+	+	+
HDGF	+	+	+	+	+
ILF2	+	+	+	+	+
CCNA2	+	+	+	+	+
MDH2	+	+	+	+	+
PEG10	-	+	+	+	+
PPRC1	+	+	+	+	+
SSRP1	+	+	+	+	+
PTK9	-	-	-	-	-

HGNC Symbol	signEx_4Tc	signEx_3Tc	signEx_2Tc	signEx_1 5Tc	signEx_1Tc
ACSL1	+	+	+	+	+
PFKM	+	+	+	+	+
HNRPDL	+	+	+	+	+
RPIA	+	+	+	+	+
SLC16A1	-	-	-	+	-
KCNJ6	+	+	+	+	+
SFRS2	+	+	+	+	+
PRKCI	+	+	+	+	+
POLR2H	+	+	+	+	+
ABCE1	+	+	+	+	+
MELK	+	+	+	+	+
DDX21	+	+	+	+	+
SSSCA1	+	+	+	+	+
n.a.	+	+	+	+	+
HSPCA	+	+	+	+	+
DEAF1	+	+	+	+	+
n.a.	+	+	+	+	+
EIF1AX	+	+	+	+	+
n.a.	+	+	+	+	+
n.a.	+	+	+	+	+
SF3A3	+	+	+	+	+
n.a.	-	-	-	+	+
AK2	+	+	+	+	+
PLAUR	+	+	+	+	+
SCARB1	+	+	+	+	+
MCM2	+	+	+	+	+
EXOSC7	+	+	+	+	+
KHSRP	+	+	+	+	+
NUDC	+	+	+	+	+
CGRRF1	+	+	+	+	+
APEX1	+	+	+	+	+
GARS	+	+	+	+	+
EIF3S9	+	+	+	+	+
IMPDH1	+	+	+	+	+
VEGF	-	+	-	-	-
TFDP2	+	+	+	+	+
PRDX1	+	+	+	+	+
SCO2	+	+	+	+	+
TUBG1	+	+	+	+	+
MYCN	+	+	+	+	+
ABL2	-	-	-	+	+
SLC20A1	+	+	+	+	+
CDKN2B	-	-	-	+	+
n.a.	+	+	+	+	+
FANCG	+	+	+	+	+
PMPCA	+	+	+	+	+
PSMC3	+	+	+	+	+
MCM7	+	+	+	+	+
ABCA3	+	+	+	+	+
EIF4EBP1	+	+	+	+	+
TNFRSF4	-	-	+	+	+
SRP72	+	+	+	+	+
ALG3	+	+	+	+	+
CKS1B	+	+	+	+	+
NSEP1	+	+	+	+	+
FARSLA	+	+	+	+	+
PRIM1	+	+	+	+	+

HGNC Symbol	signEx_4Tc	signEx_3Tc	signEx_2Tc	signEx_1 5Tc	signEx_1Tc
TBL3	+	+	+	+	+
JUND	+	+	+	+	+
PTBP1	+	+	+	+	+
MRE11A	+	+	+	+	+
HSPA5	+	+	+	+	+
OAT	+	+	+	+	+
TFRC	+	+	+	+	+
SHMT1	+	+	+	+	+
CLNS1A	+	+	+	+	+
SEMA3C	-	-	-	-	-
MCAM	+	+	+	+	+
MAPKAPK5	+	+	+	+	+
SIP1	+	+	+	+	+
NF2	+	+	+	+	+
SLC1A5	+	+	+	+	+
PSMA2	+	+	+	+	+
RAD51C	+	+	+	+	+
CTSC	+	+	+	+	+
HSPA8	+	+	+	+	+
n.a.	+	+	+	+	+
IGFBP2	+	+	+	+	+
DARS	+	+	+	+	+
UCHL3	+	+	+	+	+
GTF3A	+	+	+	+	+
RPL5	+	+	+	+	+
AMD1	+	+	+	+	+
HSPA1A	-	+	+	+	+
SYNGR3	+	+	+	+	+
NINJ1	-	-	-	+	+
SNRPA1	+	+	+	+	+
TAF9	+	+	+	+	+
SYNCRIP	+	+	+	+	+
n.a.	+	+	+	+	+
ITGB3BP	+	+	+	+	+
PTPRF	+	+	+	+	+
CHEK1	+	+	+	+	+
TCEB1	+	+	+	+	+
n.a.	+	+	+	+	+
VBP1	+	+	+	+	+
BUB1B	+	+	+	+	+
RACGAP1	+	+	+	+	+
AK3	+	+	+	+	+
HNRPF	+	+	+	+	+
PDAP1	+	+	+	+	+
SELE	+	+	+	+	+
n.a.	+	+	+	+	+
RCN1	-	-	-	-	-
GLDC	+	+	+	+	+
PMS1	+	-	+	+	+
PFKP	+	+	+	+	+
PDCD2	+	+	+	+	+
MGST2	+	+	+	+	+
NDUFB7	+	+	+	+	+
G22P1	+	+	+	+	+
n.a.	+	+	+	+	+
PBEF1	-	+	-	+	+
TBL2	+	+	+	+	+

HGNC Symbol	signEx_4Tc	signEx_3Tc	signEx_2Tc	signEx_1 5Tc	signEx_1Tc
GCN5L2	+	+	+	+	+
CDK2AP1	+	+	+	+	+
NOL1	+	+	+	+	+
SLC29A1	+	+	+	+	+
BNIP1	+	+	+	+	+
DBN1	+	+	+	+	+
EIF4G1	+	+	+	+	+
B4GALT2	+	+	+	+	+
TMEM5	+	+	+	+	+
FVT1	-	-	-	-	-
ETF1	+	+	+	+	+
ATF4	+	+	+	+	+
ILF3	+	+	+	+	+
RAMP1	+	+	+	+	+
n.a.	+	+	+	+	+
ADCY3	+	+	+	+	+
AFG3L2	+	+	+	+	+
PRPS1	+	+	+	+	+
OPRS1	-	+	+	+	+
TOMM70A	+	+	+	+	+
APRT	+	+	+	+	+
FGFR4	-	-	-	+	+
DEFA6	+	-	-	+	+
ZNF9	+	+	+	+	+
RAC3	-	-	-	-	-
WNT10B	+	-	+	+	-
NFRKB	+	+	+	+	+
CDK5R2	-	-	-	-	-
CYCS	-	-	+	+	-
YES1	+	+	+	+	+
DLEU1	+	+	+	+	+
BNIP3	+	+	+	+	+
RAD23A	+	+	+	+	+
	-	-	-	-	-
UBE2G2	+	+	+	+	+
KCNQ3	-	-	-	-	-
MTA1	+	+	+	+	+
LIG3	+	+	+	+	+
ITGA2B	+	-	+	+	+
TOMM34	+	+	+	+	-
ITIH4	+	+	+	+	+
POLD1	+	+	+	+	+
IKBKAP	+	+	+	+	+
ASNS	+	+	+	+	+
MX1	-	-	-	-	-
XRCC5	+	+	+	+	+
XPO1	+	+	+	+	+
RAD54L	+	+	+	+	+
PTHLH	-	-	-	-	+
MSH2	+	+	+	+	+
CDKL1	+	+	+	+	+
ADA	+	+	+	+	+
n.a.	+	+	+	+	+
TGFB1	-	-	-	-	-
NPTX2	-	-	-	-	-
BAG1	+	+	+	+	+
BAG1	+	+	+	+	+

HGNC Symbol	**signEx_4Tc**	**signEx_3Tc**	**signEx_2Tc**	**signEx_1 5Tc**	**signEx_1Tc**
SHB	+	+	+	+	+
EIF3S10	+	+	+	+	+
HTATIP2	-	-	-	-	-
CALCA	+	+	+	+	+
C6orf108	+	+	+	+	+
ACY1	+	+	+	+	+
PASK	-	+	-	+	+
CEBPZ	+	+	+	+	+
RAP1A	+	+	+	+	+
NID	+	-	-	-	-
IDE	+	+	+	+	+
HOXB7	+	-	-	-	-
GUCY1B2	+	+	+	+	+
SERPINA7	+	+	+	+	+
FPRL2	+	+	+	+	+
MTRR	+	+	+	+	+
THRA	+	+	+	+	+
POR	+	+	+	+	+
YWHAH	+	+	+	+	+
TRIM28	+	+	+	+	+
DHX30	+	+	+	+	+
CDK8	+	+	+	+	+
CCNH	+	+	+	+	+
RFK	+	+	+	+	+
RABGGTB	+	+	+	+	+
PLK4	+	+	+	+	+
CYP4B1	-	-	-	-	-
TP53BP2	+	+	+	+	+
NVL	+	+	+	+	+
ARF1	+	+	+	+	+
PLK2	+	+	+	+	+
GZMA	-	+	-	+	-
NOLA2	+	+	+	+	+
HMBS	+	+	+	+	+
ITIH2	-	-	-	-	-
SACS	+	+	+	+	+
GABPA	+	+	+	+	+
ETS2	+	+	+	+	+
IL8RA	+	+	+	+	+
API5	+	+	+	+	+
n.a.	+	+	+	+	+
ICT1	+	+	+	+	+
DFFB	+	+	+	+	+
USP7	+	+	+	+	+
PAP	+	+	+	+	+
BSG	+	+	+	+	+
YIF1	+	+	+	+	+
POLE	+	+	+	+	+
	-	-	+	+	-

HGNC Symbol	**signEx_0 5Tc**	**signEx_0Tc**
MYC	+	+
CACNA1G	+	+
NME1	+	+
ADCY2	-	+
C4orf9	+	+
FKBP5	+	+
CRKL	+	+
RFC5	+	+
PPP2CA	+	+
TIMM8A	+	+
n.a.	+	+
MAD2L1	+	+
MRPL12	+	+
NME1	+	+
METTL1	+	+
SLC7A5	+	+
SRM	+	+
IL1B	+	+
PAICS	+	+
TOMM40	+	+
PYCR1	+	+
UMPK	+	+
LRP8	+	+
DUSP14	+	+
METAP1	+	+
ABCE1	+	+
PA2G4	+	+
BOP1	+	+
RANBP1	+	+
CTPS	+	+
TRAP1	+	+
HSPD1	+	+
PFAS	+	+
TEAD4	+	+
MIF	+	+
VARS2	+	+
CENTG1	+	+
DSCR2	+	+
JAG2	+	+
PRKAR1B	+	+
n.a.	+	+
MATK	+	+
IARS	+	+
GAL	+	+
MCAM	+	+
CAD	+	+
FH	+	+
SRPK1	+	+
NEFH	+	+
NP	+	+
AHCY	+	+
POLD2	+	+
C1QBP	+	+
CAMKK2	+	+
n.a.	+	+
BYSL	+	+
NUP155	+	+

HGNC Symbol	**signEx_0 5Tc**	**signEx_0Tc**
IFRD2	+	+
MRPL3	+	+
HSPE1	+	+
HSPE1	+	+
n.a.	+	+
EBNA1BP2	+	+
TNFRSF8	+	+
PRDX4	+	+
CSE1L	+	+
RPP40	+	+
n.a.	+	+
HRMT1L2	+	+
n.a.	+	+
n.a.	+	+
MADH4	+	+
IL9	+	+
PDCD11	+	+
HK2	+	+
PWP2H	+	+
n.a.	+	+
NOLC1	+	+
NOLC1	+	+
CCT2	+	+
DTYMK	+	+
HNRPAB	+	+
FASN	+	+
FASN	+	+
NMB	+	+
CHC1	+	+
	+	+
KIAA0179	+	+
NTHL1	+	+
UNG	+	+
KIAA0020	+	+
n.a.	+	+
n.a.	+	+
POLE2	+	+
MTHFD1	+	+
NOL5A	+	+
PRPS2	+	+
RUVBL2	+	+
GPI	+	+
n.a.	+	+
NPM3	+	+
n.a.	+	+
CDC20	+	+
n.a.	+	+
PRKDC	+	+
CKS2	+	+
CSE1L	+	+
EEF1E1	+	+
HRMT1L2	+	+
n.a.	+	+
TST	+	+
DKC1	+	+
RAN	+	+
PDGFRA	+	+

HGNC Symbol	**signEx_0 5Tc**	**signEx_0Tc**
CDK4	+	+
ALDH1B1	+	+
SORD	+	+
BDH	+	+
GMPS	+	+
GPR30	+	+
PHB	+	+
STRA13	+	+
XPOT	+	+
SMN1	+	+
CHC1	+	+
PLK1	+	+
n.a.	+	+
AK2	+	+
n.a.	+	+
MGST1	+	+
CSDA	+	+
n.a.	+	+
ATP1B3	+	+
BCS1L	+	+
UNG	+	+
PBP	+	+
CDC6	+	+
CDC7	+	+
MTAP	+	+
ADSL	+	+
CDKN3	+	+
VRK1	+	+
WFDC2	+	+
GSPT1	+	+
SLC39A14	+	+
n.a.	+	+
RLN2	+	+
BAG2	+	+
HSD17B8	+	+
UCHL3	+	+
NME2	+	+
MRPS12	+	+
PCNA	+	+
DPH2L2	+	+
CCNB1	+	+
MC1R	+	+
SOD1	+	+
ATP5G3	+	+
CCT3	+	+
RFC4	+	+
CDC25A	+	+
FRDA	+	+
SNRPD1	+	+
CHAF1A	+	+
PRDX2	+	+
BUB1	+	+
CDC2	+	+
POLR1C	+	+
SLC19A1	+	+
TOMM20	+	+
MMP3	+	+

HGNC Symbol	**signEx_0 5Tc**	**signEx_0Tc**
UBE2C	+	+
PTPN2	+	+
RUVBL1	+	+
TYMS	+	+
DDX10	+	+
TUFM	+	+
AURKB	+	+
RRS1	+	+
GEMIN4	+	+
PTMA	+	+
CYP51A1	+	+
ARHGEF5	+	+
KIAA0690	+	+
VDAC1	+	+
DDX1	+	+
SCAMP1	+	+
DDX18	+	+
PES1	+	+
RANGAP1	+	+
APEX1	+	+
MYBL2	+	+
USP10	+	+
n.a.	+	+
RPA3	+	+
CXCL12	+	+
n.a.	+	+
MCM3	+	+
GMNN	+	+
HSPA9B	+	+
TCERG1	+	+
RNU3IP2	+	+
SFRS7	+	+
MSH6	+	+
CENPF	+	+
MXI1	+	+
AMD1	+	+
ELK1	+	+
ILF3	+	+
TFDP1	+	+
n.a.	+	+
TOP2A	+	+
EIF5A	+	+
n.a.	+	+
n.a.	+	+
ATIC	+	+
ATIC	+	+
PEX5	+	+
TAF4B	+	+
HDGF	+	+
HDGF	+	+
ILF2	+	+
CCNA2	+	+
MDH2	+	+
PEG10	+	+
PPRC1	+	+
SSRP1	+	+
PTK9	+	+

HGNC Symbol	**signEx_0 5Tc**	**signEx_0Tc**
ACSL1	+	+
PFKM	+	+
HNRPDL	+	+
RPIA	+	+
SLC16A1	+	+
KCNJ6	+	+
SFRS2	+	+
PRKCI	+	+
POLR2H	+	+
ABCE1	+	+
MELK	+	+
DDX21	+	+
SSSCA1	+	+
n.a.	+	+
HSPCA	+	+
DEAF1	+	+
n.a.	+	+
EIF1AX	+	+
n.a.	+	+
n.a.	+	+
SF3A3	+	+
n.a.	+	+
AK2	+	+
PLAUR	+	+
SCARB1	+	+
MCM2	+	+
EXOSC7	+	+
KHSRP	+	+
NUDC	+	+
CGRRF1	+	+
APEX1	+	+
GARS	+	+
EIF3S9	+	+
IMPDH1	+	+
VEGF	-	+
TFDP2	+	+
PRDX1	+	+
SCO2	+	+
TUBG1	+	+
MYCN	+	+
ABL2	+	+
SLC20A1	+	+
CDKN2B	+	+
n.a.	+	+
FANCG	+	+
PMPCA	+	+
PSMC3	+	+
MCM7	+	+
ABCA3	+	+
EIF4EBP1	+	+
TNFRSF4	+	+
SRP72	+	+
ALG3	+	+
CKS1B	+	+
NSEP1	+	+
FARSLA	+	+
PRIM1	+	+

HGNC Symbol	**signEx_0 5Tc**	**signEx_0Tc**
TBL3	+	+
JUND	+	+
PTBP1	+	+
MRE11A	+	+
HSPA5	+	+
OAT	+	+
TFRC	+	+
SHMT1	+	+
CLNS1A	+	+
SEMA3C	+	+
MCAM	+	+
MAPKAPK5	+	+
SIP1	+	+
NF2	+	+
SLC1A5	+	+
PSMA2	+	+
RAD51C	+	+
CTSC	+	+
HSPA8	+	+
n.a.	+	+
IGFBP2	+	+
DARS	+	+
UCHL3	+	+
GTF3A	+	+
RPL5	+	+
AMD1	+	+
HSPA1A	+	+
SYNGR3	+	+
NINJ1	+	+
SNRPA1	+	+
TAF9	+	+
SYNCRIP	+	+
n.a.	+	+
ITGB3BP	+	+
PTPRF	+	+
CHEK1	+	+
TCEB1	+	+
n.a.	+	+
VBP1	+	+
BUB1B	+	+
RACGAP1	+	+
AK3	+	+
HNRPF	+	+
PDAP1	+	+
SELE	+	+
n.a.	+	+
RCN1	+	+
GLDC	+	+
PMS1	+	+
PFKP	+	+
PDCD2	+	+
MGST2	+	+
NDUFB7	+	+
G22P1	+	+
n.a.	+	+
PBEF1	+	+
TBL2	+	+

HGNC Symbol	signEx_0 5Tc	signEx_0Tc
GCN5L2	+	+
CDK2AP1	+	+
NOL1	+	+
SLC29A1	+	+
BNIP1	+	+
DBN1	+	+
EIF4G1	+	+
B4GALT2	+	+
TMEM5	+	+
FVT1	+	+
ETF1	+	+
ATF4	+	+
ILF3	+	+
RAMP1	+	+
n.a.	+	+
ADCY3	+	+
AFG3L2	+	+
PRPS1	+	+
OPRS1	+	+
TOMM70A	+	+
APRT	+	+
FGFR4	+	+
DEFA6	+	+
ZNF9	+	+
RAC3	+	+
WNT10B	+	+
NFRKB	+	+
CDK5R2	+	+
CYCS	+	+
YES1	+	+
DLEU1	+	+
BNIP3	+	+
RAD23A	+	+
	+	+
UBE2G2	+	+
KCNQ3	-	+
MTA1	+	+
LIG3	+	+
ITGA2B	+	+
TOMM34	+	+
ITIH4	+	+
POLD1	+	+
IKBKAP	+	+
ASNS	+	+
MX1	-	+
XRCC5	+	+
XPO1	+	+
RAD54L	+	+
PTHLH	-	+
MSH2	+	+
CDKL1	+	+
ADA	+	+
n.a.	+	+
TGFB1	-	+
NPTX2	-	+
BAG1	+	+
BAG1	+	+

HGNC Symbol	signEx_0 5Tc	signEx_0Tc
SHB	+	+
EIF3S10	+	+
HTATIP2	-	+
CALCA	+	+
C6orf108	+	+
ACY1	+	+
PASK	+	+
CEBPZ	+	+
RAP1A	+	+
NID	-	+
IDE	+	+
HOXB7	-	+
GUCY1B2	+	+
SERPINA7	+	+
FPRL2	+	+
MTRR	+	+
THRA	+	+
POR	+	+
YWHAH	+	+
TRIM28	+	+
DHX30	+	+
CDK8	+	+
CCNH	+	+
RFK	+	+
RABGGTB	+	+
PLK4	+	+
CYP4B1	-	+
TP53BP2	+	+
NVL	+	+
ARF1	+	+
PLK2	+	+
GZMA	-	+
NOLA2	+	+
HMBS	+	+
ITIH2	-	+
SACS	+	+
GABPA	+	+
ETS2	+	+
IL8RA	+	+
API5	+	+
n.a.	+	+
ICT1	+	+
DFFB	+	+
USP7	+	+
PAP	+	+
BSG	+	+
YIF1	+	+
POLE	+	+
	+	+