

## Legends to the Supplementary Figures.

**Supplementary Figure 1. Phenotypic characterization of human CD4 Th cells.** Flow cytometric analyses of the indicated primary Th cells (ND8) or Th lines (NIH001, Jurkat) stained with a panel of indicated antibodies or their isotype IgG control antibodies are shown as histogram plots. The data tabulated below indicates the Th subtype, i.e., effector, effector memory, naïve etc. based on the combination of cell receptor expression.

**Supplementary Figure 2. Experimental depletion of WAS expression in normal (WT) Th cells.** (A) For CRISPR/Cas9-mediated WAS KO: location of gRNA guides on the *WAS* gene showing primer pairs with the expected amplicon length. (B) representative gel images showing clones with PCR amplicon patterns that is consistent with no KO, partial KO, and complete KO of *WAS*. (C) Western blot sequentially reprobed with anti-WASp and  $\alpha$ -tubulin loading control antibodies, to demonstrate complete *WAS* KO clones lacking WASp expression. (D) DNA sequencing of complete *WAS* KO clone show the expected gene region deletion. (E) RNA-interference-mediated depletion of WASp expression by shRNA vector. Shown is the western blot image of WASp expression in the indicated primary Th cells.

**Supplementary Figure 3. RNaseH1 expression into WT and WKO Th1 cells.** Flow cytometry (dot plot) of NIH001-WT and -WKO Th1 lines transfected with RNaseH1-eGFP construct or its empty vector control is shown as pre-sort (transfection efficiency) and post sort (purity) in 3 independent experiments. "X" denotes post-sort sample not tested for purity. The location of the gated population is shown, which was sorted for down-stream assays.

**Supplementary Figure 4. R loop modulation in DRB-treated Th1 cells.** *Left*, confocal images of WT Th1 cells dual-labelled with S9.6 antibody and DAPI. The image shown is representative of n=100 cells in DRB 100uM for 2 h treatment condition. *Right*, statistics of

S9.6+ foci changes under the indicated DRB dose/duration conditions. The displayed data is from n=100-150 cells analyzed for each condition. p-value: ns= nonsignificant by Mann-Whitney nonparametric test.

**Supplementary Figure 5. R-loop and DNA damage load in WASp-deficient Th2-cells. (A)**

Box-and-whisker plots comparing the magnitude of R-loop (S9.6+ foci) and DSB load (comet assay) in Th1 and Th2 cells, WASp-sufficient (WT) and WASp-deficient (WKOWKD). The data is representative of analyzing 20-30 z-stack images of at least 100 cells each from 2-3 independent experiments. (B) shown are the indicated immunofluorescence images overlaid on the corresponding Nomarski (DIC) images for Th1 and Th2 cells. Right, plot showing the range of individual (single) S9.6+ foci size in Th1 and Th2 cells. \*\*\*\*p<0.0001, Mann-Whitney.

**Supplementary Figure 6. Reconstituting nuclear but not cytosolic compartment of WASp-deficient Th1-cells is necessary to normalize R-loop frequency.**

Change in R-loop frequency in WAS Th1 line stably-transfected with NLS-deleted ( $\Delta$ NLS) or NES-deleted ( $\Delta$ NES) WASp mutants. Note, reconstituting only the nuclear compartment with WASp is sufficient to normalize the R-loop frequency (left panel), but reconstituting only the cytosolic compartment does not change the R-loop frequency (right panel). Also shown is the ChIP enrichment profile of  $\gamma$ H2A.X. Note, the DNA damage as reported by  $\gamma$ H2A.X enrichment is reduced by reconstituting only the nuclear compartment of WASp-deficient Th1 cells. Data is from n=3, mean+SEM.

**Supplementary Figure 7. The magnitude of R-loop accumulation and DNA-damage at non-Th1 genes in WASp-deficient Th1 cells. (A)**

R loop frequency at the 3'-ends of the indicated Th1 and non-Th1 genes in WAS Th1 line (NIH002) untransfected (control) or transfected with wt-WASp or the indicated pathogenic mutant. (B) DNA damage frequency at the same cis-region in the same set of genes. Data is from n=3, mean+SEM.

## Supplementary file 1

### Antibodies and Reagents

Antibody	Product number	Company name	Used for
AF488 anti-mouse IgG	A21202	Invitrogen	IF, FACS
AF488 anti-rabbit IgG	A21206	Invitrogen	FACS
AF488 anti-mouse IgG	A16119	ThermoFisher	IF
AF568 anti-rabbit IgG	A-11004	ThermoFisher	IF
AF594 anti-rabbit IgG	A11012	Invitrogen	FACS
AF594 anti-mouse IgG	A21203	Invitrogen	FACS
AF647 anti-mouse IgG	A32728	ThermoFisher	IF
Anti-CD28	302902	BioLegend	Cell culture
Anti-CD3	300402	BioLegend	Cell culture
Anti-IL-4	500815	BioLegend	Cell culture
anti-mouse IgG-HRP	sc-2055	Santa Cruz	WB
anti-rabbit IgG-HRP	sc-2054	Santa Cruz	WB
DNAPKcs	Ab18192	Abcam	ChIP
DNAPKcs	sc-5282	Santa Cruz	WB
DNA-RNA Hybrid (S9.6)	ENH001	Kerafast	DRIP, FACS, IF
Flag M2	F1804	Sigma	IP, WB, ChIP
H2A	ab13923	Abcam	FACS
phospho-Histone H2A.X (Ser139)	05-636	Millipore	FACS, ChIP
p-Histone H2A.X (Ser 139)	sc-101696	Santa Cruz	WB, IF
H2A.Z	ab4174	Abcam	FACS
Histone H3	ab1791	Abcam	WB, ChIP, FACS
IgG	sc-66931	Santa Cruz	Gel super-shift
LAMP1	H4A3	DSHB	WB
Normal Mouse IgG	12-371	Upstate	ChIP, FACS
Rabbit Control IgG	Ab46540	Abcam	IP, ChIP, FACS
RNA pol II	05-623	Millipore	ChIP
RNA pol II (Ser2)	Ab5095	Abcam	ChIP
RNA pol II (Ser5)	Ab5131	Abcam	ChIP
Reagent	Product number	Company	Used for
$\alpha$ -Amanitin	A2263	Sigma	Transcription inhibitor
Alexa Fluor™ 568 Phalloidin	A12380	ThermoFisher	IF
Amaya Cell line nucleofactor kitV	NC9041615	Fisher Scientific	Cell transfection
Agarose, low gelling temperature	A0701	Sigma-Aldrich	Single-Cell Gel Electrophoresis Assay
ChIP-IT Protein G Magnetic Beads	101945	Active Motif	ChIP, IP
CometSlide	4250-200-03	Trevigen	Single-Cell Gel Electrophoresis Assay
Control CRISPR/Cas9 Plasmid	Sc-418922	Santa Cruz	Control for KOs
Cytochalasin D	C8273	Sigma	Actin depolymerization
CytoFix/CytoPerm solutions	554714	BD Pharmingen	For intracellular FACS
DAPI	D3571	Invitrogen	IF
DRB	D1916	Sigma	Transcription inhibitor
Enzymatic shearing cocktail	101197	Active Motif	ChIP
Lysis Solution	4250-050-01	Trevigen	Single-Cell Gel Electrophoresis Assay
High Capacity cDNA Reverse Transcription kit	4368813	Applied Biosystems	cDNA synthesis
Latrunculin B	L5288	Sigma	Actin depolymerization
Myc-DDK-tagged ORF clone of Homo sapiens WAS	RC203457	Origene	Used as mammalian protein expression vector
NE-PER Nuclear & Cytoplasmic Extraction Reagents	78835	Pierce	To extract nuclear and cytoplasmic proteins

Perfecta qPCR SuperMix, LowROX™	95052-500	Quanta Biosciences	RT-PCR
Plasmid Transfection Medium	sc-108062	Santa Cruz	For transfection
Proteinsae K stop solution	Part#101942	Active Motif	ChIP
QuickChange II Site-Directed Mutagenesis (SDM) kit	200519	Stratagene	Site-Directed Mutation

WB: Western Blot

IF: Immunofluorescence

ChIP: Chromatin Immunoprecipitation

IP: Immunoprecipitation

FACS: Fluorescence-activated cell sorting

RT-PCR: Real Time Polymerase Chain Reaction

DRIP: DNA-RNA Immunoprecipitation

*Supplementary file 2*

*RT-qPCR Primers and Probes for mature mRNA and nascent pre-mRNA estimation*

Gene (AssayID)	Exon Boundary	Chromosome location
IFNG (Hs99999041_m1)	Ex1-2	Chr.12: 68154770 - 68159741
IFNG (Hs00989290_g1)	Ex2-3	Chr.12: 68154770 - 68159741
IFNG (Hs00174143_m1)	Ex3-4	Chr.12: 68154770 - 68159741
TBX21 (Hs00203436_m1)	Ex1-2	Chr.17: 47733240 - 47746122
TBX21 (Hs00894391_g1)	Ex2-3	Chr.17: 47733240 - 47746122
TBX21 (Hs00894392_m1)	Ex3-4	Chr.17: 47733240 - 47746122
TBX21 (Hs00894393_gH)	Ex4-5	Chr.17: 47733240 - 47746122
TBX21 (Hs00894394_g1)	Ex5-6	Chr.17: 47733240 - 47746122
TUBA1A (Hs04187782_g1)	Ex1-2	Chr.12: 49127782 - 49131521

TUBA1A	Ex2-3	5'-GGCTGTGTTTGTAGACTTGGA-3'
		5'-CTCATCAGGCAAGGAAGAT-3'
		5'-6FAM-TGATGAAGTTCGCACTGGCACCTA-3'
TUBA1A	Ex3-4	5'-CAAGGAAGATGCTGCCAATAAC-3'
		5'-GTCTTCAGGGCTTCTTGGTT-3'
		5'-6FAM-GTCTTCAGGGCTTCTTGGTT-3'
IFNG	5'-UTR	5'-GTTTCCGAGAGAATTAAGCCAAAG-3'
		5'-CATCTGAAGATCAGCTATTAGAAGAGA-3'
		5'-6FAM-TCAAGCTGATCAGGTCCAAAGGACT-3'
IFNG	Ex1-Int1	5'-TTTCAGCTCTGCATCGTTT-3'
		5'-AGCAAGTCGATATTCAGTCATT-3'
		5'-6FAM-ACATATGGGTCTTGGCAGTAACAGC-3'
IFNG	Ex2-Int2	5'-GGTCATTCAGATGTAGCGGATAA-3'
		5'-CCATCAGAAAGCAAGCAACAG-3'
		5'-6FAM-AGAGGTAAGCTGAATATTCCTTTGGCT-3'
IFNG	Int2-Ex3	5'-TCCTCTGTTTGTGCTCTTTCC-3'
		5'-CTTGATGGTCTCCACACTCTTT-3'
		5'-6FAM-ATGCAGAGCCAAATTGTCTCCTTT-3'

IFNG	Ex3-Int3	5'-AAAGAGTGTGGAGACCATCAAG-3'
		5'-CAAGACCCTCGGCAATGAA-3'
		5'-6FAM-AGCTGACTAATTATTCGGTGAGGCT-3'
IFNG	Int3-Ex4	5'-ACTGACCATCATGACATTAGCA-3'
		5'-CAGTTCAGCCATCACTTGGA-3'
		5'-6FAM-ACTGACTTGAATGTCCAACGCAAAGC-3'
IFNG	Ex4-3'-UTR	5'-TCCAAGTGATGGCTGAACTG-3'
		5'-CAAATATTGCAGGCAGGACAAC-3'
		5'-6FAM-TCGAGGTCTGAAGAGCATCCCAGTA-3'
IFNG	3'-UTR-polyA	5'-GTCAGGTGACCCTGATGAAA-3'
		5'-TTGGGTACAGTCACAGTTGTC-3'
		5'-6FAM-TCAGGAGATTTTCATGCCTGGTGCT-3'
TBX21	Ex1-Int1	5'-TCCAAGTTTAATCAGCACCAGA-3'
		5'-GACAATGCTTCTGACTCCGT-3'
		5'-6FAM-ATCATCACCAAGCAGGGACGGT-3'
TBX21	Int1-Ex2	5'-TGTC AAGCTGGAGCTGATG-3'
		5'-ACTACAGGATGTTTGTGGACG-3'
		5'-6FAM-TCTCTCTTCTCTCCAGGCGGATGT-3'
TBX21	Ex2-Int2	5'-ATGTTTGTGGACGTGGTCTT-3'
		5'-CTCTGTTTCGCTGGGACTG-3'
		5'-6FAM-GCAAGTGGGTGCAGTGTGGAAAG-3'
TBX21	Int2-Ex3	5'-GCATGTCAAAGAGGTGAACTG-3'
		5'-CATTTGGGAAACTAAAGCTCACA-3'
		5'-6FAM-ACAGGAAACCGCCTGTACGTCC-3'
TBX21	Ex3-Int3	5'-GCGCCAGGAAGTTTCATTTG-3'
		5'-AAAAGGTAGCCTCGCCCT-3'
		5'-6FAM-GCGTCCAACAATGTGACCCAGGTA-3'
TBX21	Int3-Ex4	5'-AACCGTCTTGCTCTGTCTAC-3'

		5'-CATATCGTTGAGGTGAACGACG-3'
		5'-6FAM-ATGATTGTGCTCCAGTCCCTCCAT-3'
TBX21	Ex4-Int4	5'-GCTTCCAACACGCATATCTTTAC-3'
		5'-CTTGGGAGGGATTTGAAA-3'
		5'-6FAM-ATTGCCGTGACTGCCTACCAGAAT-3'
TBX21	Int4-Ex5	5'-GTCTTCCTTGGGAGGGATTTG-3'
		5'-CAAAGGATTCCGGGAGAACTT-3'
		5'-6FAM-CCCAGACTCAGGACTCAGGTGACT-3'
TBX21	Ex5-Int5	5'-AAGGATTCCGGGAGAACTTTG-3'
		5'-CTGAGACACATCCTCTCCCT-3'
		5'-6FAM-GGGTTCAACTCAGCTTTGGTCCCT-3'
TBX21	Int5-Ex6	5'-TCTGCTTGTGACCCGTTT-3'
		5'-CTACCCAACCAGTATCCTGTTC-3'
		5'-6FAM-GCCTGGACCCAAGTCAATTCCT-3'
TUBA1A	Ex1-Int1	5'-CCTCCTAATCCCTAGCCACTA -3'
		5'-CGTTTGGAGGGCGGAA -3'
		5'-6FAM-TCCCGGCTGCTTTCAGGGAA -3'
TUBA1A	Int1-Ex2	5'-GGCGACAGACCTTATCTCTAAA -3'
		5'-ATCTCCATCCACGTTGGC -3'
		5'-6FAM-TTTCCTTCCCGCAGCGTGAGT -3'
TUBA1A	Ex2-Int2	5'-GGCTGTGTTTGTAGACTTGGAA -3'
		5'-TCACTCACTCACTCCCTCC -3'
		5'-6FAM-CCCACAGTCATTGGTGAGTTGACCT -3'
TUBA1A	Int2-Ex3	5'-CTTCTTGTCACTCACTC -3'
		5'-CAAGGAAGATGCTGCCAATAA -3'
		5'-6FAM-CGTCCTTCTCTCCCTCCTCCAGAT -3'
TUBA1A	Ex3-Int3	5'-CTACACCATTGGCAAGGAGAT -3'
		5'-TAGTTCAGTGCAAGTTGGG -3'
		5'-6FAM-TCGCAAGCTGGTAAGCACCATATA -3'

TUBA1A	Int3-Ex4	5'-CCTGTGCTTACATCAGTGAGA -3'
		5'-GTCTTCAGGGCTTCTTGGTT -3'
		5'-6FAM-TACAGGCTGACCAGTGCACC -3'

**e. RT-qPCR Primers and Probes for intron retention**

IFNG	Ex2-Int2	5'-AGATGTAGCGGATAATGGA ACTC -3'
		5'-GTTTGTGCTCTTTCCTTCCAAG -3'
		5'-6FAM-TCCTGTTGCTTGCTTTCTGATGGA -3'
TBX21	Ex4-Int3-Ex5	5'-CGTGACTGCCTACCAGAATG -3'
		5'-CTATTCCTTCTCTCTAGATTACTCAG -3'
		5'-6FAM-CGTGACTGCCTACCAGAATG -3'
IL13 (Hs01124271_g1)	Ex2-Int2-Ex3-2	Chr.5: 132658173 - 132661109

**f. RT-PCR Primers for intron retention and sequencing**

IFNG	Ex2-Int2-Ex3 [Forward]	5'-TGCAGGTCATTCAGATGTAGC -3'
	Ex2-Int2-Ex3 [Reverse]	5'-TGACCAGAGCATCCAAAAGA -3'
TBX21	Ex4-Int4-Ex5 [Forward]	5'-GCTGCATATCGTTGAGGTGA -3'
	Ex4-Int4-Ex5 [Reverse]	5'-CAAAGGATTCCGGGAGAACT -3'
TUBA1A	Ex2-Int2-Ex3 [Forward]	5'-CCGGGCTGTGTTTGTAGACT -3'
	Ex2-Int2-Ex3 [Reverse]	5'-ACACCATGGCAAGGAGATC -3'
IL13	Ex2-Int2-Ex3 [Forward]	5'-CAGCATGGTATGGAGCATCA -3'
	Ex2-Int2-Ex3 [Reverse]	5'-GAAGACCCAGAGGATGCTGA -3'

**g. Site-directed mutagenesis primer sets for generating WASp- mutants**

Primer	Sequence
T45M Forward	5'- TGCTTGGACGAAAATGCTTGATGCTGGCCACTG-3'
T45M Reverse	5'- CAGTGGCCAGCATCAAGCATTTTCGTCCAAGCA-3'
V75M Forward	5'-GGGGCTGTGTGCTTCATGAAGGATAACCCCC-3'



V75M Reverse	5'-GGGGGTTATCCTTCATGAAGCACACAGCCCC-3'
A236G Forward	5'-AGAAGAAGATCAGCAAAGGTGATATTGGTGCACCC-3'
A236G Reverse	5'-GGGTGCACCAATATCACCTTTGCTGATCTTCTTCT-3'
R477K Forward	5'-CACGTGATGCAGAAGAAAAGCAGAGCCATCCAC-3'
R477K Reverse	5'-GTGGATGGCTCTGCTTTTCTTCTGCATCACGTG-3'

**h. RT-qPCR Primers and Probes for mRNA estimation**

Gene (AssayID)	Exon Boundary	Chromosome location
IFNG (Hs00989290_g1)	Ex2-3	Chr.12: 68548550 - 68553521
TBX21 (Hs00894392_m1)	Ex3-4	Chr.17: 45810610 - 45823485
IL12RB2 (Hs02558264_s1)	Ex16-16	Chr.1: 67773047 - 67862583
GAPDH (Hs00266705_g1)	Ex2-3	Chr.12: 6643657 - 6647536

**i. ChIP-qPCR Primers and Probes based on NCBI36/hg18(Mar. 2006)**

Genes Names	Primer/Probes Sequence
<i>-1kbTSS IFNG</i> (1)	5'-GTTCAAGCCATTCTCCTGCCT-3'
	5'-AAATTAGCCAGGCATGGTGGT-3'
	5'-/56-FAM/CCTCCCTAG/ZEN/TAGCTGAGATTACAGGCA/3IABkFQ/-3'
<i>5'UTR-EXONI IFNG</i> (2)	5'-CGTAATCCTCAGGAGACTTCAA-3'
	5'-GATCTTTCTTCTTAATAGCTGATCTTC-3'
	5'-/56-FAM/AAATACCAG/ZEN/CAGCCAGAGGAGGTG/3IABkFQ/-3'
<i>EXONI-INTRON1 IFNG</i> (3)	5'-TTCAGCTCTGCATCGTTT-3'
	5'-GCAAGTCGATATTCAGTCATTT-3'
	5'-/56-FAM/ACATATGGG/ZEN/TCCTGGCAGTAACAGC/3IABkFQ/-3'
<i>Intron1a-intron1a IFNG</i> (4)	5'-ACCTTCTGCTCAGTTTGTATAGAG-3'
	5'-CTGAATGAGTCCACCACA-3'
	5'-/56-FAM/AGATGGGCA/ZEN/TAATATGGGTATGAAGCA/3IABkFQ/-3'
<i>Intron1b-intron1b IFNG</i> (5)	5'-GATTTCAACATTCTGCTTCTCTATC-3'
	5'-AAACATTCCTTAGCCAGAATCA-3'
	5'-/56-FAM/CGGAAGTTC/ZEN/GTTGCTCACTGGGAT/3IABkFQ/-3'
<i>Intron1c-intron1c IFNG</i> (6)	5'-CACACACACACACACAC-3'
	5'-CATCTACTGTGCCTTCCTGTAG-3'
	5'-/56-FAM/ACACTCGCA/ZEN/CATGTTTGGAATCT/3IABkFQ/-3'

<i>Intron1c-exon2a IFNG</i> (7)	5'-GGTCATTTCAGATGTAGCGGATAA-3'
	5'-CAGAAAGCAAGCAACAGGAAA-3'
	5'-/56-FAM/AGAGGTAAG/ZEN/CTGAATATTCCTTTGGCT/3IABkFQ/-3'
<i>Intron2a-exon3 IFNG</i> (8)	5'-TCCTCTGTTTGTGCTCTTTCC-3'
	5'-TTTGGATGCTCTGGTCATCTTT-3'
	5'-/56-FAM/ATGCAGAGC/ZEN/CAAATTGTCTCCTTT/3IABkFQ/-3'
<i>Exon4-3'UTR IFNG</i> (9)	5'-GTGTAAGTTCACAACACTTATGCTG-3'
	5'-TTTCCACAGCTAAGAAGACTCC-3'
	5'-/56-FAM/AGTGAGACC/ZEN/TGGAGTGAAAGAACTACCT/3IABkFQ/-3'
<i>+1.5KB3'UTR IFNG</i> (10)	5'-TCCCTCTCTGAGGTTGAT-3'
	5'-GGATCTTCTCCCTGTCTCATTC-3'
	5'-/56-FAM/TGGCCAGAC/ZEN/TGTGAGACATGAAAGA/3IABkFQ/-3'
<i>+6kb3'UTR IFNG</i> (11)	5'-AGGACAACACTAGAAGGGACTCA-3'
	5'-AGAAACAAAGGTCTGCTCTCC-3'
	5'-/56-FAM/AGCCCTCTC/ZEN/ACAGGAGTCCTGGTAA/3IABkFQ/-3'
<i>+3kb3'UTR IFNG</i> (12)	5'-CTTATCATCATGGAGGGCAGAA-3'
	5'-CCTAAAGTCTCCAGAAGGAACAA-3'
	5'-/56-FAM/AAATCAAGG/ZEN/CATCGGCAGGGC/3IABkFQ/-3'
<i>3'TBX21</i>	5'-CTCCAGTCCCTCCATAAGTACCA-3'
	5'-CTCTCCGTCGTTACCTCAAC-3'
	5'-6FAM-CCCCGGCTGCATAT-3'
<i>3'IL12RB2</i>	5'-GTGGTAGCTCATGCCTGTAATC-3'
	5'-CCATGTTAGCCAGAATGGTCTC-3'
	5'-/56-FAM/AGGCGGATC/Zen/ATGAGGTCAGGAGAT/3IABkFQ/-3'
<i>3'RUNX3</i>	5'-GATGTGTGGAAGGAGTCCAG-3'
	5'-CTGGGCAACAGCAGGAG-3'
	5'-/56-FAM/CCGGTTTCT/Zen/AGGGCTATGCATGGA/3IABkFQ/-3'
<i>3'TLR1</i>	5'-GGATCCACTTGTTTCTTTGCTATAA-3'
	5'-ACTAGAACACACATCACTGAAGAA-3'

	5'-/56-FAM/TCATGAAGT/Zen/CAAGGGAAGCACCTGT/3IABkFQ/-3'
<i>3'IL10</i>	5'-CAACAGAAGCTTCCATTCCAAG-3'
	5'-CCAAGCCCAGAGACAAGATAA-3'
	5'-/56-FAM/ACCACGCTT/ZEN/TCTAGCTGTTGAGCT/3IABkFQ/-3'
<i>3'FOXP3</i>	5'-GTCACAATCCTGTCCCTCAC-3'
	5'-GCTGTGCTTGTGTGTGATTG-3'
	5'-/56-FAM/AGCCTGCCT/ZEN/CAGTACACTCAAACA/3IABkFQ/-3'
<i>3'IL17A</i>	5'-GTGCTGTCTTGCCCTACTT-3'
	5'-TGGAGTGAAGAGGAAGGTCT-3'
	5'-/56-FAM/ATATTCTCA/ZEN/GGCCACTCTGCAGGC/3IABkFQ/-3'
<i>3'IL5</i>	5'TTTACTGCAGTGAGAATGAGG-3'
	5'-CTTTCTGGCAAAGTGTCAGTAT-3'
	5'-/56-FAM/ATTAAGGCC/ZEN/TGACTCTTTCTTGGC/3IABkFQ/-3'
<i>3'SNRPN</i>	5'-GAGCAATTAAGTGTGAGGTACTG -3'
	5'-AATCAACTGCTTAATAGGCATCAC-3'
	5'-/56-FAM/TGATGAGAT/Zen/CTTAAGTTACTGTGGATGAGG/3IABkFQ/- 3'
<i>3' ZNF544</i>	5'-GGAGGAGTTGCCATTACACTAC-3'
	5'-CTTGGCAAGATCCCATCCAT-3'
	5'-/56-FAM/AAGATTGGT/Zen/GGACGGGAATGCTGT/3IABkFQ/-3'





HSLEGLTLEGGSAK		Medium	CS(Carbamidonet NP100-150.raw	3	591.96265	1773.8739	2.58	48.97	Unambiguous	Isoform Beta-1 of	3	3.47	0	1	Q02880-2	1		0	1.37336E-06	722	MS2	60
HYDYVDQVWGK	High		NP100-250.raw	2	679.26017	1357.71396	1.45	46.53	Unambiguous	Isoform Beta-1 of	3	4.94	0	1	Q02880-2	1				312	MS2	22
HYDYVDQVWGK		High	NP100-150.raw	2	453.24943	1357.71396	1.22	42.87	Unambiguous	Isoform Beta-1 of	3	3.88	0	1	Q02880-2	1				385	MS2	44
HYDYVDQVWGK		High	NP200-250.raw	2	679.36328	1357.71396	6.04	43.21	Unambiguous	Isoform Beta-1 of	3	4.78	0	1	Q02880-2	1				345	MS2	22
HYDYVDQVWGK			NP200-250.raw	3	453.24374	1357.71396	4.12	43.22	Unambiguous	Isoform Beta-1 of	3	3.79	0	1	Q02880-2	1				363	MS2	44
IFDEELVNAADNK	High		NP100-150.raw	2	731.38513	1461.76235	3.10	55.16	Unambiguous	Isoform Beta-1 of	8	3.99	0	2	Q02880-2:P11388	1	0.000153	0.00043761		361	MS2	24
IFDEELVNAADNK		High	NP150-250.raw	3	487.92593	1461.76235	3.27	55.25	Unambiguous	Isoform Beta-1 of	8	3.79	0	2	Q02880-2:P11388	1	0	4.4581E-07		437	MS2	48
IFDEELVNAADNK		High	NP100-150.raw	2	731.38489	1461.76235	2.76	57.65	Unambiguous	Isoform Beta-1 of	8	4.25	0	2	Q02880-2:P11388	1				375	MS2	24
IFDEELVNAADNK		High	NP100-150.raw	3	487.92542	1461.76235	2.21	57.77	Unambiguous	Isoform Beta-1 of	8	4.15	0	2	Q02880-2:P11388	1				467	MS2	48
IFDEELVNAADNK		High	NP200-250.raw	2	731.38617	1461.76235	4.52	57.87	Unambiguous	Isoform Beta-1 of	8	4.15	0	2	Q02880-2:P11388	1				344	MS2	24
IFDEELVNAADNK		Medium	NP200-250.raw	3	487.92667	1461.76235	4.78	57.92	Unambiguous	Isoform Beta-1 of	8	3.41	0	2	Q02880-2:P11388	1				418	MS2	48
IMN	High		NP100-150.raw	2	487.92037	1461.76235	1.64	57.94	Selected	Isoform Beta-1 of	12	1.32	0	2	Q02880-2:P11388	1				103	MS2	48
IMmImTQQDQDQSHK	High		M2(Oxidation): M-NP100-150.raw	3	588.69425	1763.79819	2.40	29.97	Unambiguous	Isoform Beta-1 of	7	4.73	0	2	Q02880-2:P11388	1	0.029567	0.3010378		1127	MS2	56
IMmImTQQDQDQSHK		High	M2(Oxidation): M-NP100-150.raw	3	588.69413	1763.79827	2.20	32.20	Unambiguous	Isoform Beta-1 of	7	4.34	0	2	Q02880-2:P11388	1				1135	MS2	56
KEWLNTHNEDR	High		M8(Oxidation): NP100-250.raw	3	495.56495	1464.69880	4.64	46.09	Unambiguous	Isoform Beta-1 of	7	3.87	1	2	Q02880-2:P11388	1	0	9.6166E-05		662	MS2	40
KEWLNTHNEDR		High	NP150-250.raw	3	490.23584	1468.69297	2.70	55.79	Unambiguous	Isoform Beta-1 of	7	4.11	1	2	Q02880-2:P11388	1	0	9.82995E-05		649	MS2	40
KSPSRLWK	High		NP100-250.raw	3	320.84402	960.51752	2.68	34.48	Unambiguous	Isoform Beta-1 of	7	2.75	1	2	Q02880-2:P11388	1	0.009094	0.1049212		329	MS2	28
KIETVQDLK	High		NP150-250.raw	2	638.84711	1236.68994	2.80	45.03	Unambiguous	Isoform Beta-1 of	4	2.37	1	2	Q02880-2	1	0.041685	0.4132991		220	MS2	18
KIETVQDLK		Medium	NP200-250.raw	3	412.90094	1236.68827	3.88	47.81	Unambiguous	Isoform Beta-1 of	4	3.25	1	2	Q02880-2	1				223	MS2	36
LAQAAGALK	High		NP100-250.raw	3	370.29929	1108.61332	2.10	23.79	Unambiguous	Isoform Beta-1 of	3	3.16	0	1	Q02880-2	1	0.000188	0.001322709		236	MS2	40
LAQAAGALK		High	NP150-250.raw	2	554.80981	1108.61235	1.23	23.84	Unambiguous	Isoform Beta-1 of	3	3.07	0	1	Q02880-2	1	0.000153	0.000446094		244	MS2	20
LAQAAGALK		High	NP100-150.raw	2	554.81061	1108.61394	2.66	25.98	Unambiguous	Isoform Beta-1 of	3	4.01	0	1	Q02880-2	1				229	MS2	20
LNnPTK	High		NP150-250.raw	2	491.75644	982.50560	2.99	44.41	Unambiguous	Isoform Beta-1 of	7	2.73	0	2	Q02880-2:P11388	1	0.00027	0.003062967		389	MS2	14
LKDQVALMTR		Medium	NP100-150.raw	3	425.57724	1274.71717	2.67	54.45	Unambiguous	Isoform Beta-1 of	3	3.63	1	1	Q02880-2	1				178	MS2	40
LKDQVALMTR		High	NP200-250.raw	3	425.57723	1274.72863	3.82	54.65	Unambiguous	Isoform Beta-1 of	3	3.65	1	1	Q02880-2	1				180	MS2	40
LHGPEQLRYGTATK	High		NP150-250.raw	3	558.96777	1674.88877	2.22	52.52	Unambiguous	Isoform Beta-1 of	3	2.98	0	1	Q02880-2	1	0.000188	0.000885451		396	MS2	56
LIEVVK	Medium		NP150-250.raw	2	350.73497	700.46166	1.81	34.28	Unambiguous	Cytochrome c oxii	7	1.20	0	2	H18R45:Q02880-	1	0.034639	0.3454588		97	MS2	10
LIEVVK		Medium	NP100-250.raw	2	350.73477	700.46227	2.68	41.30	Selected	Cytochrome c oxii	7	1.49	0	2	H18R45:Q02880-	1	0.015618	0.1641186		105	MS2	10
LLPFAVDNLLK	High		NP150-250.raw	2	679.39264	1357.77800	3.94	65.93	Unambiguous	Isoform Beta-1 of	3	2.88	0	1	Q02880-2	1	0.000188	0.00146149		142	MS2	22
LLPFAVDNLLK		Medium	NP100-150.raw	2	679.39209	1357.77890	3.13	68.26	Unambiguous	Isoform Beta-1 of	3	3.01	0	1	Q02880-2	1				123	MS2	22
LLPFAVDNLLK		Medium	NP200-250.raw	2	679.39331	1357.77934	4.93	68.44	Unambiguous	Isoform Beta-1 of	3	2.75	0	1	Q02880-2	1				137	MS2	22
LLPFAVDNLLK		High	NP100-150.raw	4	572.78790	2288.12978	2.76	63.59	Unambiguous	Isoform Beta-1 of	3	4.30	2	1	Q02880-2	1				1186	MS2	102
LLPFAVDNLLK		High	NP100-150.raw	2	635.85522	1270.70317	2.34	50.03	Unambiguous	Isoform Beta-1 of	3	3.82	0	1	Q02880-2	1				181	MS2	20
LLPFAVDNLLK		High	NP200-250.raw	2	635.85522	1270.70337	4.07	50.09	Unambiguous	Isoform Beta-1 of	3	3.63	0	1	Q02880-2	1				155	MS2	20
LLPFAVDNLLK		High	NP150-250.raw	3	682.66888	2045.95210	3.20	65.18	Unambiguous	Isoform Beta-1 of	3	2.70	1	1	Q02880-2	1	0.00027	0.002485287		1076	MS2	60
LLPFAVDNLLK		High	NP150-250.raw	2	773.40283	1545.79839	2.71	46.83	Unambiguous	Isoform Beta-1 of	7	4.41	0	2	Q02880-2:P11388	1	0	7.0743E-05		340	MS2	24
LLPFAVDNLLK		High	NP100-150.raw	2	773.40240	1545.79753	2.16	49.33	Unambiguous	Isoform Beta-1 of	7	4.26	0	2	Q02880-2:P11388	1				315	MS2	24
LLPFAVDNLLK		High	NP150-250.raw	2	765.40552	1529.80376	2.93	51.92	Unambiguous	Isoform Beta-1 of	7	4.40	0	2	Q02880-2:P11388	1	0	2.8749E-06		337	MS2	24
LLPFAVDNLLK		High	NP100-150.raw	2	765.40515	1529.80303	2.45	54.46	Unambiguous	Isoform Beta-1 of	7	4.05	0	2	Q02880-2:P11388	1				319	MS2	24
LLPFAVDNLLK		High	NP200-250.raw	2	765.40222	1529.79717	-1.38	54.60	Unambiguous	Isoform Beta-1 of	7	3.50	0	2	Q02880-2:P11388	1				376	MS2	24
LLPFAVDNLLK		High	NP100-150.raw	3	651.00110	1830.98094	1.41	52.14	Unambiguous	Isoform Beta-1 of	3	4.69	1	1	Q02880-2	1				290	MS2	60
LLPFAVDNLLK		High	NP100-150.raw	2	564.84167	1128.67607	2.19	54.36	Unambiguous	Isoform Beta-1 of	3	4.86	0	1	Q02880-2	1				123	MS2	22
LLPFAVDNLLK		High	NP200-250.raw	2	564.84253	1128.67778	3.70	54.67	Unambiguous	Isoform Beta-1 of	3	4.75	0	1	Q02880-2	1				133	MS2	22
LLPFAVDNLLK		High	NP150-250.raw	2	416.71481	832.42235	2.85	38.48	Unambiguous	Isoform Beta-1 of	7	2.40	0	2	Q02880-2:P11388	1	0.001998	0.02812004		231	MS2	12
LLPFAVDNLLK		Medium	NP150-250.raw	2	926.43304	1851.85881	2.13	65.75	Unambiguous	Isoform Beta-1 of	3	5.62	0	1	Q02880-2	1	0	3.24447E-07		1005	MS2	30
LLPFAVDNLLK		Medium	NP100-150.raw	3	617.95850	1851.86094	3.28	68.21	Unambiguous	Isoform Beta-1 of	3	3.64	0	1	Q02880-2	1				1168	MS2	60
LLPFAVDNLLK		High	NP100-150.raw	2	521.26617	2082.04287	1.84	43.75	Unambiguous	Isoform Beta-1 of	3	4.21	1	1	Q02880-2	1				906	MS2	102
LLPFAVDNLLK		High	NP150-250.raw	3	360.86502	1080.58051	0.77	24.11	Unambiguous	Isoform Beta-1 of	3	2.95	0	1	Q02880-2	1	0.000188	0.0005673		289	MS2	32
LLPFAVDNLLK		High	NP200-250.raw	2	926.43628	1851.86238	5.63	68.42	Unambiguous	Isoform Beta-1 of	3	3.50	0	1	Q02880-2	1	0.026846	0.2786565		167	MS2	12
LLPFAVDNLLK		High	NP150-250.raw	2	834.91272	1668.81816	3.92	56.07	Unambiguous	Isoform Beta-1 of	3	4.39	0	1	Q02880-2	1	0	3.46867E-05		663	MS2	30
LLPFAVDNLLK		High	NP100-150.raw	2	834.91168	1668.81609	2.68	58.51	Unambiguous	Isoform Beta-1 of	3	5.21	0	1	Q02880-2	1				648	MS2	30
LLPFAVDNLLK		High	NP200-250.raw	2	834.91358	1668.81988	4.95	58.76	Unambiguous	Isoform Beta-1 of	3	5.22	0	1	Q02880-2	1				656	MS2	30
LLPFAVDNLLK		High	NP150-250.raw	2	456.24405	851.48082	3.98	49.88	Unambiguous	Isoform Beta-1 of	7	2.31	0	2	Q02880-2:P11388	1	0.001589	0.02026924		187	MS2	12
LLPFAVDNLLK		High	NP100-150.raw	2	666.35730	1331.70732	3.37	61.71	Unambiguous	Isoform Beta-1 of	3	3.43	0	1	Q02880-2	1				321	MS2	20
LLPFAVDNLLK		High																				

Human Jurkat Th1 cells: nuclear fraction ( 2 step IP with anti-Flag and -Myc Abs)

P1187	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=1 - [TOP2A_HUMAN]	31.90	B3	13	25	D3	25	E3	95	F3	765	G3	90.7	H3	Modifications	Spectrum File	Charge	m/z [Da]	MH+ [Da]	ΔPM [ppm]	RT [min]	PSM Ambiguity	Protein Description	# Proteins	XCorr	Missed Cleavage #	Protein Group/Stein Group	Accession	Engine Rank	q-Value	PEP	Peptides Matched	MS Order	Total Ions	
	Sequence	A3																																	
	AEEVATFFAK															Koustat1.1.raw	2	556.78809	1112.56890	5.92	45.48	Unambiguous	DNA topoisomerase 1	1	3.73	0	1	P1187	1	0.00071099	347	MS2	18		
	AEEVATFFAK															Koustat1.1.raw	2	556.78850	1112.56720	6.03	45.21	Unambiguous	DNA topoisomerase 1	1	3.75	0	1	P1187	1	0.00105806	339	MS2	18		
	AEEVATFFAK															Koustat1.1.raw	2	556.78818	1112.56920	6.07	45.12	Unambiguous	DNA topoisomerase 1	1	3.72	0	1	P1187	1	0.0154077	375	MS2	18		
	AEEVATFFAK															Koustat1.1.raw	2	556.78760	1112.56920	5.94	44.74	Unambiguous	DNA topoisomerase 1	1	3.14	0	1	P1187	1	0.00083405	307	MS2	18		
	AEEVATFFAK															Koustat1.10.raw	2	556.78772	1112.56816	5.26	45.03	Unambiguous	DNA topoisomerase 1	1	3.28	0	1	P1187	1	0.00021748	391	MS2	18		
	AGNEKEEGTADTVGGSLSR															C10(Carbamidomethyl) Koustat1.2.raw	3	728.11796	2182.9393	2.42	25.75	Unambiguous	DNA topoisomerase 1	1	6.61	1	1	P1187	1	0.11239E-07	1904	MS2	76		
	AGNEKEEGTADTVGGSLSR															C10(Carbamidomethyl) Koustat1.2.raw	3	728.11895	2182.94292	3.17	25.17	Unambiguous	DNA topoisomerase 1	1	5.81	1	1	P1187	1	0.44137E-08	915	MS2	76		
	AGNEKEEGTADTVGGSLSR															C10(Carbamidomethyl) Koustat1.2.raw	3	728.11781	2182.93888	2.21	25.47	Unambiguous	DNA topoisomerase 1	1	6.79	1	1	P1187	1	0.81009E-09	1187	MS2	76		
	ANALYFDIK															Koustat1.4.raw	2	520.29620	1039.5853	2.72	51.25	Unambiguous	DNA topoisomerase 1	1	4.40	0	1	P1187	1	0.000911	0.02371258	119	MS2	16	
	ANALYFDIK															Koustat1.3.raw	2	520.29218	1039.58708	4.60	50.82	Unambiguous	DNA topoisomerase 1	1	2.36	0	1	P1187	1	0.008325	0.0667895	102	MS2	16	
	ANALYFDIK															Koustat1.6.raw	2	520.29706	1039.58684	4.37	50.15	Unambiguous	DNA topoisomerase 1	1	2.57	0	1	P1187	1	0.003308	0.06540293	118	MS2	16	
	ANALYFDIK															Koustat1.2.raw	2	520.29700	1039.58672	4.25	50.55	Unambiguous	DNA topoisomerase 1	1	2.36	0	1	P1187	1	0.017113	0.184966	116	MS2	16	
	ANALYFDIK															Koustat1.9.raw	2	520.29694	1039.58660	4.13	50.25	Unambiguous	DNA topoisomerase 1	1	2.41	0	1	P1187	1	0.003941	0.0386868	90	MS2	16	
	ANALYFDIK															Koustat1.0.raw	2	520.29651	1039.58574	3.31	50.49	Unambiguous	DNA topoisomerase 1	1	2.61	0	1	P1187	1	0.007102	0.08381958	112	MS2	16	
	cdFTIQSQYFK															C1(Carbamidomethyl) Koustat1.2.raw	2	735.80872	1470.61016	4.96	38.38	Unambiguous	DNA topoisomerase 1	1	4.11	0	1	P1187	1	0.00088073	467	MS2	20		
	cdFTIQSQYFK															C1(Carbamidomethyl) Koustat1.0.raw	2	735.80869	1470.61211	6.29	37.58	Unambiguous	DNA topoisomerase 1	1	4.22	0	1	P1187	1	4.0103E-06	508	MS2	20		
	cdFTIQSQYFK															C1(Carbamidomethyl) Koustat1.0.raw	2	735.80865	1470.61003	4.88	38.23	Unambiguous	DNA topoisomerase 1	1	4.41	0	1	P1187	1	0.000133	0.000495193	466	MS2	20	
	DEDDADYFK															Koustat1.4.raw	2	598.26239	1195.51790	5.11	14.15	Unambiguous	DNA topoisomerase 1	1	2.63	0	1	P1187	1	0.000999	0.002927681	357	MS2	18	
	ELTAPDENPAK															Koustat1.2.raw	2	649.33942	1297.67156	6.22	31.46	Unambiguous	DNA topoisomerase 1	1	3.20	0	1	P1187	1	0.003346	0.01649453	275	MS2	22	
	ELTAPDENPAK															Koustat1.4.raw	2	649.33807	1297.66887	4.15	30.42	Unambiguous	DNA topoisomerase 1	1	3.17	0	1	P1187	1	0.000185	2.7247E-05	317	MS2	22	
	ELTAPDENPAK															Koustat1.3.raw	2	649.33911	1297.66655	2.36	31.09	Unambiguous	DNA topoisomerase 1	1	2.97	0	1	P1187	1	0.000969	0.01582824	349	MS2	22	
	ELTAPDENPAK															Koustat1.2.raw	2	649.33917	1297.67107	5.84	30.47	Unambiguous	DNA topoisomerase 1	1	3.22	0	1	P1187	1	0.000789	0.01679976	316	MS2	22	
	ELTAPDENPAK															Koustat1.2.raw	2	649.33942	1297.67156	6.22	31.46	Unambiguous	DNA topoisomerase 1	1	3.20	0	1	P1187	1	0.003346	0.01649453	275	MS2	22	
	ELTAPDENPAK															Koustat1.9.raw	2	649.33942	1297.67156	6.22	31.46	Unambiguous	DNA topoisomerase 1	1	3.20	0	1	P1187	1	0.003346	0.01649453	275	MS2	22	
	ELTAPDENPAK															Koustat1.0.raw	2	649.33942	1297.67156	6.22	31.46	Unambiguous	DNA topoisomerase 1	1	3.20	0	1	P1187	1	0.003346	0.01649453	275	MS2	22	
	ELTAPDENPAK															Koustat1.0.raw	2	649.33942	1297.67156	6.22	31.46	Unambiguous	DNA topoisomerase 1	1	3.20	0	1	P1187	1	0.003346	0.01649453	275	MS2	22	
	FAWAdmWDEDFEY															Koustat1.0.raw	2	649.33942	1297.67156	6.22	31.46	Unambiguous	DNA topoisomerase 1	1	3.20	0	1	P1187	1	0.003346	0.01649453	275	MS2	22	
	GPVAFPPFLPFLPK															Koustat1.3.raw	2	877.46478	1753.92229	3.57	51.63	Unambiguous	DNA topoisomerase 1	1	3.28	0	1	P1187	1	0.000136	0.00257263	347	MS2	30	
	GPVAFPPFLPFLPK															Koustat1.0.raw	2	877.46622	1753.92522	5.24	51.23	Unambiguous	DNA topoisomerase 1	1	3.52	0	1	P1187	1	0.01331471	303	MS2	30		
	GPVAFPPFLPFLPK															Koustat1.9.raw	2	877.46621	1753.92515	5.20	51.23	Unambiguous	DNA topoisomerase 1	1	3.43	0	1	P1187	1	0.00012006	0.359	MS2	30		
	GPVAFPPFLPFLPK															Koustat1.0.raw	2	877.46515	1753.92302	3.99	51.19	Unambiguous	DNA topoisomerase 1	1	3.15	0	1	P1187	1	0.00012006	0.359	MS2	30		
	HQLQMEGLTAK															Koustat1.0.raw	2	678.35714	1355.70788	4.68	46.71	Unambiguous	DNA topoisomerase 1	1	4.45	0	1	P1187	1	0.00078038	0.00011497	247	MS2	22	
	HQLQMEGLTAK															Koustat1.2.raw	2	678.35724	1355.70517	4.68	46.71	Unambiguous	DNA topoisomerase 1	1	3.76	0	1	P1187	1	0.000119891	371	MS2	22		
	HQLQMEGLTAK															Koustat1.9.raw	2	678.35645	1355.70561	5.00	46.73	Unambiguous	DNA topoisomerase 1	1	3.71	0	1	P1187	1	0.000119508	302	MS2	22		
	IMPEDIIISLK															M2(Oxidation): C1Koustat1.0.raw	2	724.86213	1448.71977	5.66	44.22	Unambiguous	DNA topoisomerase 1	1	2.63	0	1	P1187	1	0.00011497	366	MS2	22		
	IMPEDIIISLK															M2(Oxidation): C1Koustat1.2.raw	2	724.86208	1448.72008	5.48	44.22	Unambiguous	DNA topoisomerase 1	1	3.41	0	1	P1187	1	0.000465129	441	MS2	22		
	IMPEDIIISLK															M2(Oxidation): C1Koustat1.9.raw	2	724.86366	1448.72035	5.25	43.46	Unambiguous	DNA topoisomerase 1	1	3.24	0	1	P1187	1	0.000118114	396	MS2	22		
	ITVAWIK															M2(Oxidation): C1Koustat1.0.raw	2	724.86366	1448.72035	5.25	43.46	Unambiguous	DNA topoisomerase 1	1	3.24	0	1	P1187	1	0.000118114	396	MS2	22		
	ITVAWIK															M2(Oxidation): C1Koustat1.2.raw	2	724.86366	1448.72035	5.25	43.46	Unambiguous	DNA topoisomerase 1	1	3.24	0	1	P1187	1	0.000118114	396	MS2	22		
	ITVAWIK															M2(Oxidation): C1Koustat1.9.raw	2	724.86366	1448.72035	5.25	43.46	Unambiguous	DNA topoisomerase 1	1	3.24	0	1	P1187	1	0.000118114	396	MS2	22		
	ITVAWIK															M2(Oxidation): C1Koustat1.0.raw	2	439.23547	877.46367	4.10	36.63														

DPALNSGVSQSPQAPAK					High	Koustat10.raw	3	541.95135	1623.8951	3.54	22.18	Unambiguous	DNA topoisomerase	4	3.65	0	1	P11388	1	0	0.000163673	503	MS2	60			
DPALNSGVSQSPQAPAK					High	Koustat10.raw	2	812.2426	1623.8123	4.60	22.49	Unambiguous	DNA topoisomerase	4	4.38	0	1	P11388	1	0	0.00016648	291	MS2	30			
ELALTTRELEAFKAF					High	Koustat10.raw	3	602.97465	1623.9101	5.07	72.84	Unambiguous	DNA topoisomerase	7	4.86	0	1	P11388	1	0	1.8758E-05	606	MS2	60			
EDVNR					Medium	Koustat10.raw	2	429.24744	857.48760	4.22	23.86	Unambiguous	DNA topoisomerase	4	1.89	0	0	0.019623	0.238615	0.262	MS2	12	MS2	12			
EQKQZQVQLGK					High	Koustat10.raw	3	443.2323	1327.6014	4.40	22.26	Unambiguous	DNA topoisomerase	4	2.67	1	1	P11388	1	0.00776	0.00329137	323	MS2	44			
EQKQZQVQLGK					High	Koustat10.raw	2	664.34930	1327.6013	4.55	22.32	Unambiguous	DNA topoisomerase	4	4.4	1	1	P11388	1	0.00001	0.00078905	360	MS2	44			
EQKQZQVQLGK					High	Koustat10.raw	3	443.23480	1327.68985	3.44	22.88	Unambiguous	DNA topoisomerase	4	2.98	1	1	P11388	1	0	0.00029208	360	MS2	44			
ELLFNSNDR					High	Koustat11.raw	2	718.8582	1436.70774	5.64	48.4	Unambiguous	Isoform Beta-1 of	7	4.19	0	0	0.02880-2P11388	1	0	0.4944E-12	485	MS2	22			
ELLFNSNDR					High	Koustat10.raw	2	718.8582	1436.70774	6.06	48.4	Unambiguous	Isoform Beta-1 of	7	4.08	0	0	0.02880-2P11388	1	0	0.3138E-05	445	MS2	22			
ELLFNSNDR					High	Koustat10.raw	3	479.57410	1436.70774	4.23	48.3	Unambiguous	Isoform Beta-1 of	7	3.47	0	0	0.02880-2P11388	1	0	0.00036014	549	MS2	44			
EMTTLQPK					High	Koustat10.raw	2	480.74655	960.48833	4.04	23.3	Selected	Isoform Beta-1 of	7	1.74	0	0	0.02880-2P11388	1	0.003073	0.0452011	248	MS2	14			
EQLELTLK					High	Koustat10.raw	2	480.74655	960.48833	5.06	23.6	Selected	Isoform Beta-1 of	7	1.87	0	0	0.02880-2P11388	1	0.023427	0.2276727	294	MS2	14			
EQLELTLK					High	Koustat10.raw	2	488.25546	975.50365	4.70	26.11	Unambiguous	DNA topoisomerase	4	1.70	0	0	0.02880-2P11388	1	0	0.002554	0.0531746	294	MS2	14		
EQLELTLK					High	Koustat10.raw	2	566.30591	1131.60454	3.59	22.90	Unambiguous	DNA topoisomerase	4	2.19	1	1	P11388	1	0.001201	0.0192252	497	MS2	16			
EQVLFNTHGTR					High	Koustat10.raw	2	752.3731	1503.7999	1.94	33.72	Unambiguous	DNA topoisomerase	4	2.72	0	0	0.001123	0.00011673	543	MS2	24					
EQVLFNTHGTR					High	Koustat10.raw	2	744.7817	1487.7900	5.36	41.29	Unambiguous	DNA topoisomerase	4	3.50	1	1	P11388	1	0	0.13256E-05	208	MS2	24			
EQVLFNTHGTR					High	Koustat15.raw	2	576.8195	1152.6362	2.29	48.52	Unambiguous	Isoform Beta-1 of	8	1.93	0	0	0.02880-2P11388	1	0.025379	0.2842081	191	MS2	18			
EQVLFNTHGTR					High	Koustat12.raw	2	576.81800	1152.62993	-0.04	49.84	Unambiguous	Isoform Beta-1 of	8	1.86	0	0	0.02880-2P11388	1	0.013775	0.2519483	177	MS2	18			
EQVLFNTHGTR					High	Koustat10.raw	2	576.81824	1152.62950	-0.68	48.2	Unambiguous	Isoform Beta-1 of	8	2.12	0	0	0.02880-2P11388	1	0.037075	0.3508853	184	MS2	18			
EQVLFNTHGTR					High	Koustat10.raw	2	710.86499	1402.72270	6.01	57.18	Unambiguous	DNA topoisomerase	4	4.12	0	0	1	P11388	1	0	0.42848E-06	299	MS2	24		
EQVLFNTHGTR					High	Koustat10.raw	2	702.80761	1404.72795	6.19	66.48	Unambiguous	DNA topoisomerase	4	4.35	0	0	1	P11388	1	0	5.74703E-06	260	MS2	24		
EQVLFNTHGTR					High	Koustat10.raw	3	468.3170	1404.72564	5.19	66.56	Unambiguous	DNA topoisomerase	4	2.55	0	0	1	P11388	1	0.0130708	0.1594313	366	MS2	48		
EQVLFNTHGTR					High	Koustat10.raw	2	678.80200	1356.59673	5.74	48.24	Unambiguous	Isoform Beta-1 of	7	3.27	0	0	0.02880-2P11388	1	0	0.00014908	514	MS2	18			
EQVLFNTHGTR					High	Koustat10.raw	2	670.80497	1360.6246	6.29	59.36	Unambiguous	Isoform Beta-1 of	7	2.95	0	0	0.02880-2P11388	1	0.002041	0.009012374	487	MS2	18			
EQVLFNTHGTR					High	Koustat10.raw	2	462.19133	919.39098	4.72	22.36	Unambiguous	DNA topoisomerase	4	1.80	0	0	1	P11388	1	0.007102	0.08348662	157	MS2	12		
EQVLFNTHGTR					High	Koustat10.raw	2	452.20010	903.29293	1.34	32.81	Unambiguous	DNA topoisomerase	4	1.65	0	0	1	P11388	1	0.013046	0.15835	295	MS2	12		
EQVLFNTHGTR					High	Koustat11.raw	2	668.3856	1335.76384	5.92	62.72	Unambiguous	DNA topoisomerase	4	3.17	0	0	1	P11388	1	0.005067	0.0055292	155	MS2	20		
EQVLFNTHGTR					High	Koustat12.raw	2	668.38800	1335.76387	5.98	61.2	Unambiguous	DNA topoisomerase	4	3.81	0	0	1	P11388	1	0.005005	0.01725714	119	MS2	20		
EQVLFNTHGTR					High	Koustat9.raw	2	668.3823	1335.7618	6.93	61.63	Unambiguous	DNA topoisomerase	4	3.78	0	0	1	P11388	1	0.004283	0.04189776	150	MS2	20		
EQVLFNTHGTR					High	Koustat10.raw	2	668.3817	1335.76506	6.84	62.44	Unambiguous	DNA topoisomerase	4	3.38	0	0	1	P11388	1	0.001242	0.01897861	145	MS2	20		
EQVLFNTHGTR					High	Koustat10.raw	2	668.3817	1335.76421	6.84	62.44	Unambiguous	DNA topoisomerase	4	3.68	0	0	1	P11388	1	0.000546	0.006949006	136	MS2	20		
EQVLFNTHGTR					High	Koustat9.raw	2	535.7519	1070.49590	5.34	29.22	Unambiguous	Isoform Beta-1 of	7	1.93	0	0	0.02880-2P11388	1	0.044705	0.1748599	525	MS2	14			
EQVLFNTHGTR					High	Koustat10.raw	2	535.75067	1070.49496	3.63	29.17	Unambiguous	Isoform Beta-1 of	7	2.26	0	0	0.02880-2P11388	1	0.008062	0.01301193	506	MS2	14			
EQVLFNTHGTR					High	Koustat10.raw	2	542.89246	1048.81782	4.63	24.47	Unambiguous	DNA topoisomerase	4	2.64	1	1	P11388	1	0.000520	0.008024514	264	MS2	14			
EQVLFNTHGTR					High	Koustat11.raw	2	455.73700	910.46672	4.19	23.41	Unambiguous	DNA topoisomerase	4	2.05	0	0	1	P11388	1	0.00317	0.02240768	391	MS2	14		
EQVLFNTHGTR					High	Koustat9.raw	2	455.73715	910.46703	4.52	23.71	Unambiguous	DNA topoisomerase	4	2.51	0	0	1	P11388	1	0.002468	0.02780445	391	MS2	14		
EQVLFNTHGTR					High	Koustat10.raw	2	455.73630	910.46522	2.64	23.79	Unambiguous	DNA topoisomerase	4	2.57	0	0	1	P11388	1	0.001522	0.02358445	285	MS2	14		
EQVLFNTHGTR					High	Koustat10.raw	2	455.73630	910.46522	2.64	23.79	Unambiguous	DNA topoisomerase	4	2.57	0	0	1	P11388	1	0.001522	0.02358445	285	MS2	14		
EQVLFNTHGTR					High	Koustat10.raw	2	632.60358	1895.76118	5.07	46.48	Unambiguous	DNA topoisomerase	4	2.37	0	0	1	P11388	1	0	0.4701E-06	101	MS2	64		
EQVLFNTHGTR					High	Koustat13.raw	2	813.91195	1626.85661	4.89	52.90	Unambiguous	DNA topoisomerase	4	4.89	1	1	P11388	1	0	8.56509E-07	262	MS2	28			
EQVLFNTHGTR					High	Koustat10.raw	2	542.89246	1048.81782	4.60	52.07	Unambiguous	DNA topoisomerase	4	4.60	0	0	1	P11388	1	0	0.00000000	367	MS2	56		
EQVLFNTHGTR					High	Koustat11.raw	2	813.93372	1626.86106	7.06	53.11	Unambiguous	DNA topoisomerase	4	2.87	0	0	1	P11388	1	0.007461	0.08606581	309	MS2	28		
EQVLFNTHGTR					High	Koustat10.raw	2	813.93219	1626.86710	5.19	52.62	Unambiguous	DNA topoisomerase	4	5.01	0	0	1	P11388	1	0	1.74223E-05	274	MS2	28		
EQVLFNTHGTR					High	Koustat10.raw	2	542.89246	1048.81782	6.34	52.07	Unambiguous	DNA topoisomerase	4	4.27	0	0	1	P11388	1	0	7.7176E-07	366	MS2	56		
EQVLFNTHGTR					Medium	Koustat10.raw	2	439.76016	878.51305	4.07	22.04	Unambiguous	Isoform Beta-1 of	8	1.56	0	0	0.02880-2P11388	1	0.013197	0.1744991	156	MS2	14			
EQVLFNTHGTR					High	S7(Phospho)	Koustat10.raw	2	428.77671	2794.11559	0.96	48.81	Unambiguous	DNA topoisomerase	4	4.06	0	0	1	P11388	2	0	0.00024004	2408	MS2	148	
EQVLFNTHGTR					High	S8(Phospho)	Koustat10.raw	2	428.77671	2794.11559	0.96	48.81	Unambiguous	DNA topoisomerase	4	4.06	0	0	1	P11388	2	0	6.5729E-05	490	MS2	148	
EQVLFNTHGTR					High	S9(Phospho)	Koustat10.raw	2	428.77671	2794.11559	0.96	48.81	Unambiguous	DNA topoisomerase	4	4.06	0	0	1	P11388	2	0	0.00018825	27407E-05	1086	MS2	100
EQVLFNTHGTR					High	S10(Phospho)	Koustat10.raw	2	428.77671	2794.11559	0.96	48.81	Unambiguous	DNA topoisomerase	4	4.06	0	0	1	P11388	2	0	0.00012000	9400E-05	2408	MS2	148
EQVLFNTHGTR					High	S11(Phospho)	Koustat10.raw	2	428.77671	2794.11559	0.96	48.81	Unambiguous	DNA topoisomerase	4	4.06	0	0	1	P11388	2	0	0.00012000	9400E-05	2408	MS2	148
EQVLFNTHGTR					High	S12(Phospho)	Koustat10.raw	2	428.77671	2794.11559	0.96	48.81	Unambiguous	D													





EDVAGmGSK					Medium	M7(Oxidation)	Koustat10.rzw	2	511.74652	1022.48577	3.34	19.60	Unambiguous	Isomform Beta-1 of	3	3.31	0	2 Q0280-2-B4DLVG	1	0.016191	0.2051855	318	MS2	18	
EDVAGmGSK						High	M7(Oxidation)	Koustat10.rzw	2	511.74689	1022.48580	4.05	20.21	Unambiguous	Isomform Beta-1 of	3	3.51	0	2 Q0280-2-B4DLVG	1	0.000133	0.00052604	247	MS2	18
EDVAGmGSK						High	Koustat16.rzw	2	503.74979	1006.42323	3.82	18.80	Unambiguous	Isomform Beta-1 of	3	2.53	0	1 Q0280-2	1	0.000245	0.00083963	288	MS2	12	
EDVNWV					Medium		Koustat16.rzw	2	422.24094	843.47460	7.43	18.80	Unambiguous	Isomform Beta-1 of	3	3.01	0	1 Q0280-2	1	0.041517	0.4178283	284	MS2	12	
EDVNWV						High	Koustat12.rzw	2	422.24005	843.47283	5.33	18.60	Unambiguous	Isomform Beta-1 of	3	2.18	0	1 Q0280-2	1	0.022856	0.2261099	285	MS2	12	
EDVNWV						High	Koustat11.rzw	2	422.23935	843.47242	3.66	18.80	Unambiguous	Isomform Beta-1 of	3	1.93	0	1 Q0280-2	1	0.06664	0.07019494	286	MS2	12	
ELLUSNSDNER					High		Koustat11.rzw	2	718.85852	1436.70976	5.64	48.42	Unambiguous	Isomform Beta-1 of	7	4.19	0	2 Q0280-2-P11388	1	0	4.944612	485	MS2	22	
ELLUSNSDNER						High	Koustat10.rzw	2	718.85883	1436.71037	6.06	48.16	Unambiguous	Isomform Beta-1 of	7	4.08	0	2 Q0280-2-P11388	1	0	1.13108E-05	245	MS2	22	
ELLUSNSDNER						High	Koustat10.rzw	2	479.12943	1436.71774	4.23	48.30	Unambiguous	Isomform Beta-1 of	7	3.43	0	2 Q0280-2-P11388	1	0.00030414	0.3748599	525	MS2	14	
EMHTLQPK						High	Koustat10.rzw	2	480.74655	960.48831	4.04	23.32	Selected	Isomform Beta-1 of	7	1.74	0	1 Q0280-2	1	0.000763	0.0452011	448	MS2	14	
EMHTLQPK						High	Koustat10.rzw	2	480.74655	960.48831	4.04	23.32	Selected	Isomform Beta-1 of	7	1.74	0	1 Q0280-2	1	0.000763	0.0452011	448	MS2	14	
EMHTLQPK						High	Koustat15.rzw	2	576.81995	1152.62622	2.29	48.20	Unambiguous	Isomform Beta-1 of	8	1.93	0	2 Q0280-2-P11388	1	0.025379	0.2842081	184	MS2	18	
EMHTLQPK						High	Koustat10.rzw	2	576.81995	1152.62623	2.04	48.20	Unambiguous	Isomform Beta-1 of	8	1.96	0	2 Q0280-2-P11388	1	0.017175	0.3518463	177	MS2	18	
EMHTLQPK						High	Koustat10.rzw	2	576.81824	1152.62920	-0.68	49.04	Unambiguous	Isomform Beta-1 of	8	2.12	0	1 Q030775	1	0.030775	0.3508553	191	MS2	18	
EMHTLQPK						High	M7(Oxidation)	Koustat10.rzw	2	678.80200	1356.59673	5.74	48.20	Unambiguous	Isomform Beta-1 of	7	3.27	0	2 Q0280-2-P11388	1	0	0.00014908	514	MS2	18
EMHTLQPK						High	Koustat10.rzw	2	678.80487	1360.62046	6.20	48.20	Unambiguous	Isomform Beta-1 of	7	2.95	0	2 Q0280-2-P11388	1	0.00021	0.00012231	487	MS2	18	
EMHTLQPK						High	M6(Oxidation)	Koustat10.rzw	2	718.80322	1436.71916	7.02	49.80	Unambiguous	Isomform Beta-1 of	4	4.20	0	2 Q0280-2	1	0	2.9066E-05	386	MS2	24
EMHTLQPK						High	Koustat10.rzw	2	530.72638	1060.49458	4.73	35.94	Unambiguous	Isomform Beta-1 of	3	2.26	0	1 Q0280-2	1	0.001522	0.0241999	330	MS2	14	
EMHTLQPK						High	Koustat10.rzw	2	535.75139	1070.49599	5.24	39.21	Unambiguous	Isomform Beta-1 of	3	1.83	0	2 Q0280-2-P11388	1	0.040705	0.3748599	525	MS2	14	
EMHTLQPK						High	Koustat10.rzw	2	535.75967	1070.49606	3.63	29.17	Unambiguous	Isomform Beta-1 of	7	2.20	0	2 Q0280-2-P11388	1	0.000662	0.01301193	506	MS2	14	
EMHTLQPK						High	Koustat10.rzw	2	478.23315	955.45933	3.82	24.33	Unambiguous	Isomform Beta-1 of	3	2.33	0	1 Q0280-2	1	0.030775	0.3502531	464	MS2	14	
EMHTLQPK						High	C7(Carbamidomethyl)	Koustat10.rzw	2	445.25758	889.49428	1.90	21.30	Unambiguous	Isomform Beta-1 of	3	2.63	0	2 Q0280-2-B4DLVG	1	0.001739	0.0271622	271	MS2	16
EMHTLQPK						High	Koustat10.rzw	2	800.94073	1604.91919	6.02	53.44	Unambiguous	Isomform Beta-1 of	3	5.50	0	1 Q0280-2	1	0	1.8623E-07	363	MS2	28	
EMHTLQPK						High	Koustat13.rzw	2	547.62933	1048.87345	5.57	53.46	Unambiguous	Isomform Beta-1 of	3	4.55	0	1 Q0280-2	1	0	1.5311E-06	347	MS2	56	
EMHTLQPK						High	Koustat10.rzw	2	547.62915	1048.87290	5.23	53.25	Unambiguous	Isomform Beta-1 of	3	4.52	0	1 Q0280-2	1	0	1.1294E-07	331	MS2	56	
EMHTLQPK						High	Koustat10.rzw	2	820.94061	1604.91955	5.87	53.29	Unambiguous	Isomform Beta-1 of	3	5.66	0	1 Q0280-2	1	0	8.4312E-06	363	MS2	28	
EMHTLQPK						High	Koustat10.rzw	2	439.76016	878.51305	4.07	22.04	Unambiguous	Isomform Beta-1 of	8	1.56	0	2 Q0280-2-P11388	1	0.01397	0.1744991	156	MS2	14	
EMHTLQPK						High	Koustat11.rzw	2	808.41622	2423.23441	5.85	57.99	Unambiguous	Isomform Beta-1 of	8	1.53	0	1 Q0280-2	1	0	3.8724E-16	113	MS2	84	
EMHTLQPK						High	Koustat10.rzw	2	808.41381	2423.23688	2.74	56.93	Unambiguous	Isomform Beta-1 of	3	7.11	0	1 Q0280-2	1	0	5.4665E-08	837	MS2	84	
EMHTLQPK						High	Koustat10.rzw	2	447.71521	894.42114	3.10	17.93	Unambiguous	Isomform Beta-1 of	3	2.32	0	1 Q0280-2	1	0.022235	0.2635889	166	MS2	14	
EMHTLQPK						High	Koustat14.rzw	2	510.61948	1528.83888	4.94	64.04	Unambiguous	Isomform Beta-1 of	3	3.94	0	1 Q0280-2	1	0	2.7426E-07	237	MS2	48	
EMHTLQPK						High	Koustat10.rzw	2	510.61968	1528.84024	3.18	63.77	Unambiguous	Isomform Beta-1 of	3	3.18	0	1 Q0280-2	1	0	0.00068694	241	MS2	48	
EMHTLQPK						High	Koustat12.rzw	2	510.62015	1529.84889	6.26	64.16	Unambiguous	Isomform Beta-1 of	3	3.55	0	1 Q0280-2	1	0	0.001594545	232	MS2	48	
EMHTLQPK						High	Koustat10.rzw	2	510.61969	1528.84852	5.36	64.71	Unambiguous	Isomform Beta-1 of	3	4.47	0	1 Q0280-2	1	0	1.1474E-07	234	MS2	48	
EMHTLQPK						High	Koustat10.rzw	2	765.42607	1528.84977	4.53	64.66	Unambiguous	Isomform Beta-1 of	3	4.19	0	1 Q0280-2	1	0	1.6707E-06	233	MS2	24	
EMHTLQPK						High	Koustat10.rzw	2	510.61938	1529.84860	4.77	65.30	Unambiguous	Isomform Beta-1 of	3	3.50	0	1 Q0280-2	1	0.000292	0.00321812	234	MS2	48	
EMHTLQPK						High	C5(Carbamidomethyl)	Koustat10.rzw	2	591.96343	1173.87575	3.91	42.24	Unambiguous	Isomform Beta-1 of	3	3.79	0	1 Q0280-2	1	0.000133	0.00037152	652	MS2	60
EMHTLQPK						High	Koustat13.rzw	2	679.36218	1357.71709	4.42	36.03	Unambiguous	Isomform Beta-1 of	3	4.48	0	1 Q0280-2	1	0	2.3357E-06	279	MS2	22	
EMHTLQPK						High	Koustat10.rzw	2	679.36218	1357.71709	4.42	36.03	Unambiguous	Isomform Beta-1 of	3	4.48	0	1 Q0280-2	1	0	2.3357E-06	279	MS2	22	
EMHTLQPK						High	Koustat10.rzw	2	679.36292	1357.71855	5.50	36.04	Unambiguous	Isomform Beta-1 of	3	4.93	0	1 Q0280-2	1	0	2.3091E-05	289	MS2	22	
EMHTLQPK						High	Koustat15.rzw	2	487.52691	1461.76518	5.28	51.03	Unambiguous	Isomform Beta-1 of	8	3.72	0	2 Q0280-2-P11388	1	0	1.1048E-07	420	MS2	48	
EMHTLQPK						High	Koustat10.rzw	2	731.38715	1461.76520	4.85	51.03	Unambiguous	Isomform Beta-1 of	8	4.25	0	2 Q0280-2-P11388	1	0	6.9431E-09	349	MS2	48	
EMHTLQPK						High	Koustat10.rzw	2	731.38593	1461.76457	4.18	51.37	Unambiguous	Isomform Beta-1 of	8	3.29	0	2 Q0280-2-P11388	1	0	0.00020797	360	MS2	48	
EMHTLQPK						High	Koustat13.rzw	2	487.52599	1461.76343	3.40	51.40	Unambiguous	Isomform Beta-1 of	8	3.85	0	2 Q0280-2-P11388	1	0	1.0831E-07	427	MS2	48	
EMHTLQPK						High	Koustat10.rzw	2	731.38713	1461.76378	4.10	51.38	Unambiguous	Isomform Beta-1 of	8	4.10	0	2 Q0280-2-P11388	1	0	9.0661E-13	352	MS2	48	
EMHTLQPK						High	Koustat10.rzw	2	487.52639	1461.76462	4.21	51.03	Unambiguous	Isomform Beta-1 of	8	4.23	0	2 Q0280-2-P11388	1	0	2.3039E-08	424	MS2	48	
EMHTLQPK						High	Koustat10.rzw	2	731.38690	1461.76453	5.52	51.9	Unambiguous	Isomform Beta-1 of	8	3.85	0	2 Q0280-2-P11388	1	0.000292	0.002716907	341	MS2	24	
EMHTLQPK						High	Koustat10.rzw	2	487.52648	1461.76490	4.40	51.17	Unambiguous	Isomform Beta-1 of	8	3.88	0	2 Q0280-2-P11388	1	0	5.4522E-06	412	MS2	48	
EMHTLQPK						High	M8(Oxidation)	Koustat10.rzw	2	516.29590	1031.58452	3.79	34.32	Unambiguous	Isomform Beta-1 of	3	1.42	0	2 Q0280-2-B4DLVG	1	0.003198	0.04100775	176	MS2	16
EMHTLQPK						High	C11(Carbamidomethyl)	Koustat10.rzw	2	404.29199	2414.14644	5.29	46.65	Unambiguous	Isomform Beta-1 of	3	3.71	0	1 Q0280-2	1	0	0.00023428	1778	MS2	114
EMHTLQPK						High	Koustat10.rzw	2	405.28617	2414.14395	4.38	46.57	Unambiguous	Isomform Beta-1 of	3	3.26	0	1 Q0280-2	1	0	4.2013E-08	1859	MS2	76	
EMHTL																									

TPALSDYK		High	Koustav10.raw	2	504.27603	1007.54479	3.94	34.95	Unambiguous	Isomform Beta-1 of	3	3.47	0	1	Q02880-2	1	0.000241	0.001125244	224	MS2	16
TPALSDYHEHFDITVK		High	Koustav10.raw	3	694.68793	2022.04923	4.90	37.65	Unambiguous	Isomform Beta-1 of	3	4.18	1	1	Q02880-2	1	0	6.01871E-07	817	MS2	68
TVTQVYK		High	Koustav10.raw	2	463.24455	925.48142	3.90	30.59	Unambiguous	Isomform Beta-1 of	3	2.02	0	1	Q02880-2	1	0.014272	0.1752489	435	MS2	12
VHELANER	High	Medium	Koustav16.raw	3	360.86707	1080.58664	6.44	19.67	Unambiguous	Isomform Beta-1 of	3	2.96	0	1	Q02880-2	1	0.000529	0.009874636	293	MS2	32
VHELANER		High	Koustav10.raw	3	360.86624	1080.58417	4.15	19.37	Unambiguous	Isomform Beta-1 of	3	3.00	0	1	Q02880-2	1	0	0.000120842	296	MS2	32
VHELANER		High	Koustav10.raw	2	940.79523	1080.58318	3.24	19.41	Unambiguous	Isomform Beta-1 of	3	2.81	0	1	Q02880-2	1	0.000292	0.001973292	277	MS2	16
VLFYGFK		Medium	CS(Carbamidomet)Koustav10.raw	2	457.74637	914.48546	5.45	45.53	Unambiguous	Isomform Beta-1 of	7	1.71	0	2	Q02880-2-P11388	1	0.025164	0.2968945	155	MS2	12
VSDPESHSSHWNGK		High	Koustav10.raw	2	943.49341	1885.97954	7.44	62.98	Unambiguous	Isomform Beta-1 of	3	5.45	0	1	Q02880-2	1	0	1.4007E-07	356	MS2	32
VSDPESHSSHWNGK		High	Koustav10.raw	3	629.33087	1885.97906	6.66	63.10	Unambiguous	Isomform Beta-1 of	3	4.39	0	1	Q02880-2	1	0.000292	0.001459657	464	MS2	64
VYVPAFLGQLLTSNSYDDEKX		High	Koustav10.raw	3	872.45093	2615.33823	5.43	72.77	Unambiguous	Isomform Beta-1 of	3	1.84	1	1	Q02880-2	1	0	4.78276E-06	567	MS2	88
YAGREDDAATLAFSK		High	Koustav11.raw	2	834.91382	1668.82036	5.24	52.37	Unambiguous	Isomform Beta-1 of	3	3.50	0	1	Q02880-2	1	0	5.3084E-08	615	MS2	30
YAGREDDAATLAFSK	High	High	Koustav10.raw	2	834.91257	1668.81987	4.94	51.93	Unambiguous	Isomform Beta-1 of	3	6.04	0	1	Q02880-2	1	0	1.1411E-07	611	MS2	30
YAGREDDAATLAFSK		High	Koustav10.raw	3	556.94507	1668.82065	5.41	52.05	Unambiguous	Isomform Beta-1 of	3	3.79	0	1	Q02880-2	1	0	5.88193E-05	810	MS2	60
YETVQDRK		High	Koustav10.raw	2	554.80048	1108.59368	4.67	45.54	Unambiguous	Isomform Beta-1 of	4	3.03	0	1	Q02880-2	1	0.000292	0.004304536	268	MS2	16
YGVFLR		High	Koustav10.raw	2	426.24435	851.48143	4.70	45.56	Unambiguous	Isomform Beta-1 of	7	2.30	0	2	Q02880-2-P11388	1	0.000506	0.01278071	185	MS2	12
YGVFLR		High	Koustav10.raw	2	426.24411	851.48094	4.12	46.06	Unambiguous	Isomform Beta-1 of	7	2.28	0	1	Q02880-2-P11388	1	0.001301	0.01525877	168	MS2	12
YIFMLSLAR		High	MS(Oxidation) Koustav10.raw	2	666.35846	1331.70964	5.11	55.37	Unambiguous	Isomform Beta-1 of	3	3.97	0	1	Q02880-2	1	0	0.000285482	327	MS2	20
YIFMLSLAR		High	MS(Oxidation) Koustav10.raw	2	666.35894	1331.71001	5.39	55.94	Unambiguous	Isomform Beta-1 of	3	3.77	0	1	Q02880-2	1	0	1.9688E-05	322	MS2	20
YIFMLSLAR		High	Koustav12.raw	2	658.36267	1315.71807	7.71	66.25	Unambiguous	Isomform Beta-1 of	3	3.10	0	1	Q02880-2	1	0.000905	0.01977624	292	MS2	20
YIFMLSLAR		High	Koustav10.raw	2	658.36169	1315.71611	6.23	66.83	Unambiguous	Isomform Beta-1 of	3	3.51	0	1	Q02880-2	1	0.000783	0.0164029	296	MS2	20

PCR Array Catalog #:	Qiagen	PAHS-025Y			
Position	Unigene	Refseq	Symbol	Description	Gname
A01	Hs.19383	NM_00029	AGT	Angiotensinogen (serpin peptidase inhibitor, clade A)	ANHU/SERPINA8
A02	Hs.525622	NM_005163	AKT1	V-akt murine thymoma viral oncogene homolog 1	AKT/CWS6/PKB/PKB-ALPHA/PRKBA/RAC/RAC-ALPHA
A03	Hs.648565	NM_005171	ATF1	Activating transcription factor 1	EWS-ATF1/FUS/ATF-1/TREB36
A04	Hs.227817	NM_004049	BCL2A1	BCL2-related protein A1	ACC-1/ACC-2/ACC1/ACC2/BCL2L5/BFL1/GRS/HBPA1
A05	Hs.516966	NM_138578	BCL2L1	BCL2-like 1	BCL-XL/SBCL2L/BCL-XL/BCLXL/BCLXS/Bcl-xL/PPP1R32/bcl-xL/bcl-xS
A06	Hs.31210	NM_005178	BCL3	B-cell CLL lymphoma 3	BCL4/D19S37
A07	Hs.696238	NM_001166	BIRC2	Baculoviral IAP repeat containing 2	API1/HIAP2/Hap-2/MIHB/RNF48/c-IAP1/cIAP1
A08	Hs.648101	NM_032415	CARD11	Caspase recruitment domain family, member 11	BENTA/BIMP3/CARMA1/IMD11/PPBL
A09	Hs.2490	NM_033292	CASP1	Caspase 1, apoptosis-related cysteine peptidase (h)	ICE1/L1BC/P45
A10	Hs.599762	NM_001228	CASP8	Caspase 8, apoptosis-related cysteine peptidase	ALPS2B/CAP4/Casp-8/FLICE/MACH/MCH5
A11	Hs.303649	NM_002982	CCL2	Chemokine (C-C motif) ligand 2	GDCF-2/H11/HSMCR30/MCAF/MCP-1/MCP1/SCYA2/SMC-CF
A12	Hs.514821	NM_002985	CCL5	Chemokine (C-C motif) ligand 5	D17S136E/RANTES/SCYA5/SIS-delta/SISd/TCP228/eoCP
B01	Hs.472860	NM_001250	CD40	CD40 molecule, TNF receptor superfamily member	Bp50/CDW40/TNFRSF5/p50
B02	Hs.390736	NM_003879	CFLAR	CASP8 and FADD-like apoptosis regulator	CASH/CASP8A1/CLARP/Casper/FLAME/FLAME-1/FLAME1/FLIP1/FLICE/MRIT/c-FLIP/c-FLIPL/c-FLIPR/c-
B03	Hs.198998	NM_001276	CHUK	Conserved helix-loop-helix ubiquitous kinase	IKKKA/IKK-alpha/IKK1/IKKAVNFKBIA/TCF16
B04	Hs.173894	NM_000757	CSF1	Colony stimulating factor 1 (macrophage)	CSF-1/MCSF
B05	Hs.1349	NM_000758	CSF2	Colony stimulating factor 2 (granulocyte-macrophage)	GM-CSF
B06	Hs.2233	NM_000759	CSF3	Colony stimulating factor 3 (granulocyte)	C17orf33/CSF3OS/GCSF
B07	Hs.488293	NM_005228	EGFR	Epidermal growth factor receptor	ERBB/ERBB1/HER1/NISBD2/PIG6/1mENA
B08	Hs.326035	NM_001964	EGR1	Early growth response 1	AT225/G0S30/KROX-24/NGFI-A/TIS8/ZIF-268/ZNF225
B09	Hs.181128	NM_005229	ELK1	ELK1, member of ETS oncogene family	-
B10	Hs.86131	NM_003824	FADD	Fas (TNFRSF6)-associated via death domain	GIG3/MORT1
B11	Hs.2007	NM_000639	FASLG	Fas ligand (TNF superfamily, member 6)	ALPS1B/APT1/LG1/APTL/CD178/CD95-L/CD95L/FASL/TNFSF6
B12	Hs.25647	NM_005252	FOS	FBJ murine osteosarcoma viral oncogene homolog	AP-1/C-FOS/p55
C01	Hs.727017	NM_002133	HMOX1	Heme oxygenase (decycling) 1	HMOX1/DHCO-1/HSP32/hk286B10
C02	Hs.37026	NM_024013	IFNA1	Interferon, alpha 1	IFN/IFN-ALPHA/IFN-alpha/IFNA3/IFNA@
C03	Hs.856	NM_000619	IFNG	Interferon, gamma	IFG/IFI
C04	Hs.597664	NM_001566	IKKB	Inhibitor of kappa light polypeptide gene enhancer 1	IKK-beta/IKK2/IKKB/IMD15/NFKBKB
C05	Hs.43505	NM_003639	IKBK	Inhibitor of kappa light polypeptide gene enhancer 1	AMCBX1/FIP-3/FIP3/Fip3p/IKK-gamma/IMD33/IP1P1/IP2/IPD2/NEMO/ZC2HC9
C06	Hs.193717	NM_000572	IL10	Interleukin 10	CSIF/GVHDS/IL-10/IL10A/TGIF
C07	Hs.1722	NM_000575	IL1A	Interleukin 1, alpha	IL-1A/IL1/IL1-ALPHA/IL1F1
C08	Hs.126256	NM_000576	IL1B	Interleukin 1, beta	IL-1B/IL1-BETA/IL1F2
C09	Hs.701982	NM_000877	IL1R1	Interleukin 1 receptor, type 1	CD121A/D2S1473/IL-1R-alpha/IL1R/IL1RA/P80
C10	Hs.522819	NM_001569	IRAK1	Interleukin-1 receptor-associated kinase 1	IRAK/pelle
C11	Hs.449207	NM_001570	IRAK2	Interleukin-1 receptor-associated kinase 2	IRAK2
C12	Hs.696684	NM_002228	JUN	Jun proto-oncogene	AP-1/AP1/c-Jun
D01	Hs.36	NM_000595	LTA	Lymphotoxin alpha (TNF superfamily, member 1)	L7/TNFb/TNFSF1
D02	Hs.1116	NM_002342	LTBR	Lymphotoxin beta receptor (TNFR superfamily, member 1)	CD18/D12S370/LT-BETA-R/TNF-R-III/TNFCR/TNFR-RP/TNFR2-RP/TNFR3/TNFRSF3
D03	Hs.601217	NM_173844	MALT1	Mucosa associated lymphoid tissue lymphoma transmembrane protein 1	IMD12/MLT/MLT1
D04	Hs.653654	NM_005921	MAP3K1	Mitogen-activated protein kinase kinase kinase 1	IMAPKK1/MEKK/MEKK1/MEKK1/SRXY6
D05	Hs.82116	NM_002468	MYD88	Myeloid differentiation primary response gene (88)	MYD88D
D06	Hs.73090	NM_002502	NFKB2	Nuclear factor of kappa light polypeptide gene enhancer 1	CD101/H2TF1/LYT-10/LYT10/NF-kB2/p100/p52
D07	Hs.738731	NM_006092	NOD1	Nucleotide-binding oligomerization domain containing	CARD4/CLR7_1/NLRC1
D08	Hs.658434	NM_021444	PSIP1	PC4 and SFRS1 interacting protein 1	DF570/LEDGF/PAIP/PSIP2/p52/p75
D09	Hs.159130	NM_002880	RAF1	V-raf-1 murine leukemia viral oncogene homolog 1	CMO1/NNCRAF/NSS/Raf-1/c-Raf
D10	Hs.633266	NM_002908	REL	V-rel reticuloendotheliosis viral oncogene homolog	C-Rel
D11	Hs.502875	NM_021975	RELA	V-rel reticuloendotheliosis viral oncogene homolog	NFKB3/p65
D12	Hs.654402	NM_006509	RELB	V-rel reticuloendotheliosis viral oncogene homolog	IL-REL/IREL/REL-B
E01	Hs.247077	NM_001664	RHOA	Ras homolog gene family, member A	ARH12/ARHARHO12/RHOH12
E02	Hs.519842	NM_003804	RIPK1	Receptor (TNFRSF)-interacting serine-threonine kinase	RIP/RIP1
E03	Hs.642990	NM_007315	STAT1	Signal transducer and activator of transcription 1, 9	CANDF7/IMD31A/IMD31B/IMD31C/ISGF-3/STAT91
E04	Hs.505874	NM_013254	TBK1	TANK-binding kinase 1	NAK/T2K
E05	Hs.29344	NM_182919	TICAM1	Toll-like receptor adaptor molecule 1	IAE6/MvD88-3/PRV1TRB/TICAM-1/TRIF
E06	Hs.522832	NM_003254	TIMP1	TIMP metalloproteinase inhibitor 1	CLG/IEP/AE/POHC/TIMP
E07	Hs.654532	NM_003263	TLR1	Toll-like receptor 1	CD281/TL1L1_LPRS5/rsc786
E08	Hs.519033	NM_003264	TLR2	Toll-like receptor 2	CD282/TL4
E09	Hs.657724	NM_003265	TLR3	Toll-like receptor 3	CD283/IAE2
E10	Hs.174312	NM_138554	TLR4	Toll-like receptor 4	ARMOD1/CD284/TLR-4/TOLL
E11	Hs.575090	NM_006068	TLR6	Toll-like receptor 6	CD286
E12	Hs.87968	NM_017442	TLR9	Toll-like receptor 9	CD289
F01	Hs.591834	NM_003844	TNFRSF10A	Tumor necrosis factor receptor superfamily, member 10	AP02/CD261/DR4/TRAILR-1/TRAILR1
F02	Hs.661668	NM_003842	TNFRSF10B	Tumor necrosis factor receptor superfamily, member 10	CD262/DR5/KILLER/DR5/TRAILR-2/TRAILR2/TRICK2/TRICK2A/TRICK2B/TRICK2B/ZNFR9
F03	Hs.713833	NM_001065	TNFRSF1A	Tumor necrosis factor receptor superfamily, member 1	CD120a/FFP/MSS/TBP1/TNF-R/TNF-R-ITNF-R55/TNFAR/TNFR1/TNFR1-d2/TNFR55/TNFR60/p55/p55-R55
F04	Hs.478275	NM_003810	TNFSF10	Tumor necrosis factor (ligand) superfamily, member 10	AP02L/Apo-2L/CD253/TL2/TRAIL
F05	Hs.460996	NM_003789	TRADD	TNFRSF1A-associated via death domain	Hs.89892
F06	Hs.522506	NM_021138	TRAF2	TNF receptor-associated factor 2	MGC45012/TRAP/TRAP3
F07	Hs.510528	NM_003300	TRAF3	TNF receptor-associated factor 3	CAP-1/CAP1/CD40bp/CRAF1/IAE5/LAP1
F08	Hs.591983	NM_004620	TRAF6	TNF receptor-associated factor 6	MGC3310/RNF85
F09	Hs.127799	NM_001165	BIRC3	Baculoviral IAP repeat containing 3	AIP1/API2/CIAP2/HAI1/HAI1/MAL2/MIHC/RNF49/c-IAP2
F10	Hs.75498	NM_004591	CCL20	Chemokine (C-C motif) ligand 20	Ckb4/Exodus/LARC/MIP-3-alpha/MIP-3a/MIP3A/SCYA20/ST38
F11	Hs.595133	NM_004233	CD83	CD83 molecule	BL11/HB15
F12	Hs.75765	NM_002089	CXCL2	Chemokine (C-X-C motif) ligand 2	CINC-2a/GRO2/GROb/MGSA-b/MIP-2a/MIP2/MIP2A/SCYB2
G01	Hs.89690	NM_002090	CXCL3	Chemokine (C-X-C motif) ligand 3	CINC-2b/GRO3/GROg/MIP-2b/MIP2B/SCYB3
G02	Hs.643447	NM_002091	ICAM1	Intercellular adhesion molecule 1	BB2/CD54/IF38
G03	Hs.624	NM_000584	CXCL8	Interleukin 8	GCP-1/GCP1/IL8/LECTALUCTL/YNAP/MDNCF/MONAP/NAF/NAP-1/NAP1
G04	Hs.436061	NM_002198	IRF1	Interferon regulatory factor 1	IRF-1/MAR
G05	Hs.618430	NM_003998	NFKB1	Nuclear factor of kappa light polypeptide gene enhancer 1	EBP-1/KBF1/NF-kB1/NF-kappa-B/NF-kappaB/NFKB-p105/NFKB-p50/NFKBp105/p50
G06	Hs.81328	NM_020529	NFKBIA	Nuclear factor of kappa light polypeptide gene enhancer 1	IKBAM/MAD-3/NFKBI
G07	Hs.458276	NM_004556	NFKBIE	Nuclear factor of kappa light polypeptide gene enhancer 1	IKBE
G08	Hs.118958	NM_003764	STX11	Syntaxin 11	FHL4/HLH4/HPLH4
G09	Hs.310640	NM_052864	TIFA	TRAF-interacting protein with forkhead-associated	T2BP/T6BP/TIFA
G10	Hs.241570	NM_000594	TNF	Tumor necrosis factor	DIF/TNF-alpha/TNFA/TNFSF2
G11	Hs.525607	NM_006291	TNFAIP2	Tumor necrosis factor, alpha-induced protein 2	B94/EXOC3L3
G12	Hs.211600	NM_006290	TNFAIP3	Tumor necrosis factor, alpha-induced protein 3	A20/OTUD7C/TNFAIP2
control genes					
H01	Hs.520640	NM_001101	ACTB	Actin, beta	BRWS1/PS1TP5BP1
H02	Hs.546285	NM_001002	RPLP0	Ribosomal protein, large, P0	L10E/LP0/P/PRLP0/RPPO



		Up-Down Regulation (comparing to control group: WAS Th1 cells; untransfected)								
		Group 1 ( WAS Th1; wt-WASp transfected)		Group 2 (WAS Th1; RNaseH1 transfected)						
		Fold Regulation	Comments	Fold Regulation	Comments					
A01	AGT	96.687	A	70.2779	A					
A02	AKT1	23.9798		22.8227						
A03	ATF1	34.2148		21.8885						
A04	BCL2A1	47.5393		38.245						
A05	BCL2L1	-1.1013		-1.7589						
A06	BCL3	14.0194		10.8521						
A07	BIRC2	26.2264		14.998						
A08	CARD11	9.8468		8.6231						
A09	CASP1	92.8835		57.6081						
A10	CASP8	13.0697		9.8485						
A11	CCL2	-1.4907		-17.5366						
A12	CCL5	3.2151		2.5394						
B01	CD40	3.2523		2.3953						
B02	CFLAR	4.9814		5.0312						
B03	CHUK	26.241		17.8704						
B04	CSF1	4.3962		2.9506						
B05	CSF2	-51.9824		-77.1396						
B06	CSF3	1993.8622	A	30.19	A					
B07	EGFR	63.2218	A	64.2712	A					
B08	EGR1	2.2583		-1.0898						
B09	ELK1	10.1877		4.9157						
B10	FADD	34.5724		22.4229						
B11	FASLG	1157.6232	A	812.1486	A					
B12	FOS	29.0779	A	20.9576	A					
C01	HMOX1	55.5668	A	43.0965	A					
C02	IFNA1	319.318	A	200.0477	A					
C03	IFNG	66.6831		50.0258						
C04	IKBKB	4.1654		3.6933						
C05	IKBKG	4.1409		2.7123						
C06	IL10	176.5643	A	158.9798	A					
C07	IL1A	1.6785		1.4464						
C08	IL1B	9.2404		4.9509						
C09	IL1R1	66.8729	A	56.9293	A					
C10	IRAK1	9.3544		7.3773						
C11	IRAK2	8.6984		7.4071						
C12	JUN	5.257		2.7566						
D01	LTA	3.0023		1.9592						
D02	LTBR	13.6285		11.0678						
D03	MALT1	91.8845		66.6947						
D04	MAP3K1	61.0809	A	29.3645	A					
D05	MYD88	23.8538		13.6876						
D06	NFKB2	3.2566		2.8499						
D07	NOD1	21.4789		16.2864						
D08	PSIP1	28.6358		21.9067						
D09	RAF1	6.6587		5.0037						
D10	REL	5.6889		5.0169						
D11	RELA	7.8112		5.8417						
D12	RELB	25.7099		15.1737						
E01	RHOA	24.3078		14.2126						
E02	RIPK1	9.0678		4.2416						



the other sample suggesting that the actual fold-change value is at least as large as the calculated and reported fold-change result.						
This fold-change result may also have greater variations if p value > 0.05; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene.						
B: This gene's average threshold cycle is relatively high (> 30), meaning that its relative expression level is low, in both control and test samples, and the p-value for the fold-change is either unavailable or relatively high (p > 0.05).						
This fold-change result may also have greater variations; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene.						
C: This gene's average threshold cycle is either not determined or greater than the defined cut-off value (default 35), in both samples meaning that its expression was undetected, making this fold-change result erroneous and un-interpretable.						
<b>Fold Change &amp; Fold Regulation:</b>						
Fold-Change ( $2^{-(\Delta\Delta Ct)}$ ) is the normalized gene expression ( $2^{-(\Delta Ct)}$ ) in the Test Sample divided the normalized gene expression ( $2^{-(\Delta Ct)}$ ) in the Control Sample.						
Fold-Regulation represents fold-change results in a biologically meaningful way. Fold-change values greater than one indicate a positive- or an up-regulation, and the fold-regulation is equal to the fold-change.						
Fold-change values less than one indicate a negative or down-regulation, and the fold-regulation is the negative inverse of the fold-change.						
Fold-change and fold-regulation values greater than 2 are indicated in red; fold-change values less than 0.5 and fold-regulation values less than -2 are indicated in blue.						



**Up-Down Regulation (comparing to control group: Normal Th1 cells)**

		Group 1 (WAS Th1, untransfected)		Group 2 (WAS Th1, wt-WASp transfected)		Group 3 (WAS Th1, RNaseH1 transfected)	
		Fold Regulation	Comments	Fold Regulation	Comments	Fold Regulation	Comments
A01	AGT	-211.6079	A	-2.1886		-3.011	
A02	AKT1	-60.286		-2.514		-2.6415	
A03	ATF1	-69.8675		-2.042		-3.192	
A04	BCL2A1	-59.7576		-1.257		-1.5625	
A05	BCL2L1	-1.9463		-2.1435		-3.4234	
A06	BCL3	-31.1109		-2.2191		-2.8668	
A07	BIRC2	-56.6086		-2.1585		-3.7744	
A08	CARD11	-21.2538		-2.1585		-2.4648	
A09	CASP1	-161.7195		-1.7411		-2.8072	
A10	CASP8	-26.3211		-2.0139		-2.6726	
A11	CCL2	-1.2605		-1.879		-22.1058	
A12	CCL5	-7.5415		-2.3457		-2.9698	
B01	CD40	-4.4427		-1.366		-1.8548	
B02	CFLAR	-7.709		-1.5476		-1.5322	
B03	CHUK	-49.9963		-1.9053		-2.7977	
B04	CSF1	-2.094		2.0994		1.4091	
B05	CSF2	23.9168		-2.1735		-3.2253	
B06	CSF3	-4244.415	A	-2.1287		-140.59	
B07	EGFR	-112.3885	A	-1.7777		-1.7487	
B08	EGR1	-3.7199		-1.6472		-4.054	
B09	ELK1	-16.665		-1.6358		-3.3902	
B10	FADD	-66.7895		-1.9319		-2.9786	
B11	FASLG	-1987.7905	A	-1.7171		-2.4476	
B12	FOS	-44.6891	A	-1.5369		-2.1324	
C01	HMOX1	-84.2234	A	-1.5157		-1.9543	
C02	IFNA1	-738.7027	A	-2.3134		-3.6926	
C03	IFNG	-103.1965		-1.5476		-2.0629	
C04	IKBKB	-6.3575		-1.5263		-1.7214	
C05	IKBKG	-6.9161		-1.6702		-2.5499	
C06	IL10	-286.8296	A	-1.6245		-1.8042	
C07	IL1A	-3.3338		-1.9862		-2.3048	
C08	IL1B	-19.0003		-2.0562		-3.8377	
C09	IL1R1	-103.4902	A	-1.5476		-1.8179	
C10	IRAK1	-12.7785		-1.366		-1.7321	
C11	IRAK2	-19.9837		-2.2974		-2.6979	
C12	JUN	-8.9647		-1.7053		-3.2521	
D01	LTA	-6.2595		-2.0849		-3.1949	
D02	LTBR	-20.5142		-1.5052		-1.8535	
D03	MALT1	-195.5983		-2.1287		-2.9327	
D04	MAP3K1	-92.5814	A	-1.5157		-3.1528	
D05	MYD88	-54.4232		-2.2815		-3.9761	
D06	NFKB2	-5.0748		-1.5583		-1.7807	
D07	NOD1	-30.7998		-1.434		-1.8911	
D08	PSIP1	-48.1595		-1.6818		-2.1984	
D09	RAF1	-10.0928		-1.5157		-2.0171	
D10	REL	-9.7011		-1.7053		-1.9337	
D11	RELA	-11.7578		-1.5052		-2.0127	
D12	RELB	-35.8587		-1.3947		-2.3632	
E01	RHOA	-48.9538		-2.0139		-3.4444	
E02	RIPK1	-13.0932		-1.4439		-3.0869	
E03	STAT1	-48.673		-1.9453		-2.6223	
E04	TBK1	-18.6765		-1.8277		-2.9376	
E05	TICAM1	-6.4123		-1.6472		-1.7936	
E06	TIMP1	-15.2121		-1.6472		-5.8574	
E07	TLR1	-418.6353	A	-1.5263		-11.3086	
E08	TLR2	-126.5751	A	-1.4044		-2.433	
E09	TLR3	-18.2086		-1.5692		-3.1161	
E10	TLR4	-10.4857		-1.5369		-2.8158	

E11	TLR6	-123.7127	A	-1.5369	-2.399
E12	TLR9	-12.2469		-1.4044	-1.9319
F01	TNFRSF10A	-3.83		-1.3472	-1.4169
F02	TNFRSF10B	-1.8174		-1.6472	-2.7178
F03	TNFRSF1A	-22.1042		-1.7777	-2.4874
F04	TNFSF10	-2.9576		-1.3287	-1.4079
F05	TRADD	-29.2964		-1.5052	-3.4384
F06	TRAF2	-3.5693		-1.5052	-1.6123
F07	TRAF3	-7.4464		-1.4641	-2.063
F08	TRAF6	-8.9176		-1.5157	-1.837
F09	BIRC3	-4.8001		-1.8921	-2.6267
F10	CCL20	-2.8028		-1.6021	-1.6423
F11	CD83	1.0385		-1.7532	-2.5063
F12	CXCL2	-3.1146		-1.5476	-2.6234
G01	CXCL3	-76.8914	A	-1.7777	-3.4587
G02	ICAM1	1.9175		-1.8277	-1.8588
G03	CXCL8	-3.5842		-1.8532	-2.1755
G04	IRF1	-4.2692		-1.6472	-1.8678
G05	NFKB1	-5.0028		-1.6702	-2.3912
G06	NFKBIA	-1.7936		-1.6702	-2.1141
G07	NFKBIE	-12.8978		-1.6586	-1.9713
G08	STX11	-14.5067		-1.4241	-2.1369
G09	TIFA	-98.6228		-1.2924	-2.8358
G10	TNF	-2.4761		-1.6472	-2.2025
G11	TNFAIP2	9.9704		-1.8025	-2.1834
G12	TNFAIP3	-3.2055		-1.6586	-2.1512

control genes

H01	ACTB	-1.0203		1.6586	1.732
H02	RPLP0	1.0203		-1.6586	-1.732

**Comments:**

A: This gene's average threshold cycle is relatively high (> 30) in either the control or the test sample, and is reasonably low in the other sample (< 30).

These data mean that the gene's expression is relatively low in one sample and reasonably detected in the other sample suggesting that the actual fold-change value is at least as large as the calculated and reported fold-change result.

This fold-change result may also have greater variations if p value > 0.05; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene.

B: This gene's average threshold cycle is relatively high (> 30), meaning that its relative expression level is low, in both control and test samples, and the p-value for the fold-change is either unavailable or relatively high (p > 0.05).

This fold-change result may also have greater variations; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene.

C: This gene's average threshold cycle is either not determined or greater than the defined cut-off value (default 35), in both samples meaning that its expression was undetected, making this fold-change result erroneous and un-interpretable.

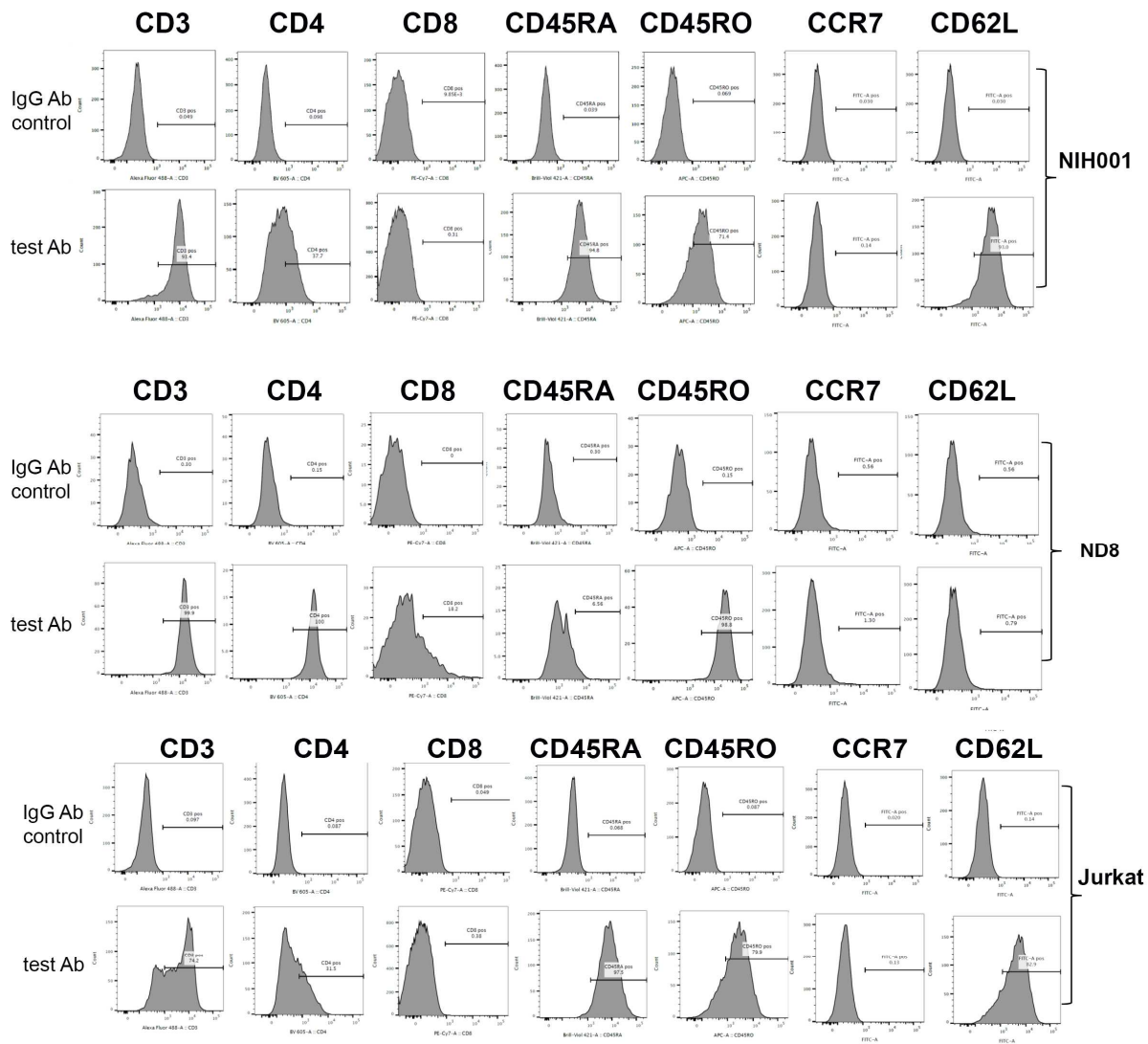
**Fold Change & Fold Regulation:**

Fold-Change ( $2^{\Delta\Delta Ct}$ ) is the normalized gene expression ( $2^{\Delta Ct}$ ) in the Test Sample divided the normalized gene expression ( $2^{\Delta Ct}$ ) in the Control Sample.

Fold-Regulation represents fold-change results in a biologically meaningful way. Fold-change values greater than one indicate a positive- or an up-regulation, and the fold-regulation is equal to the fold-change.

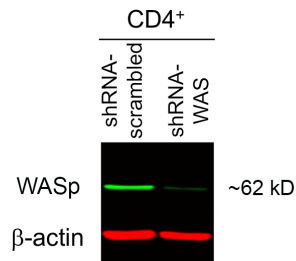
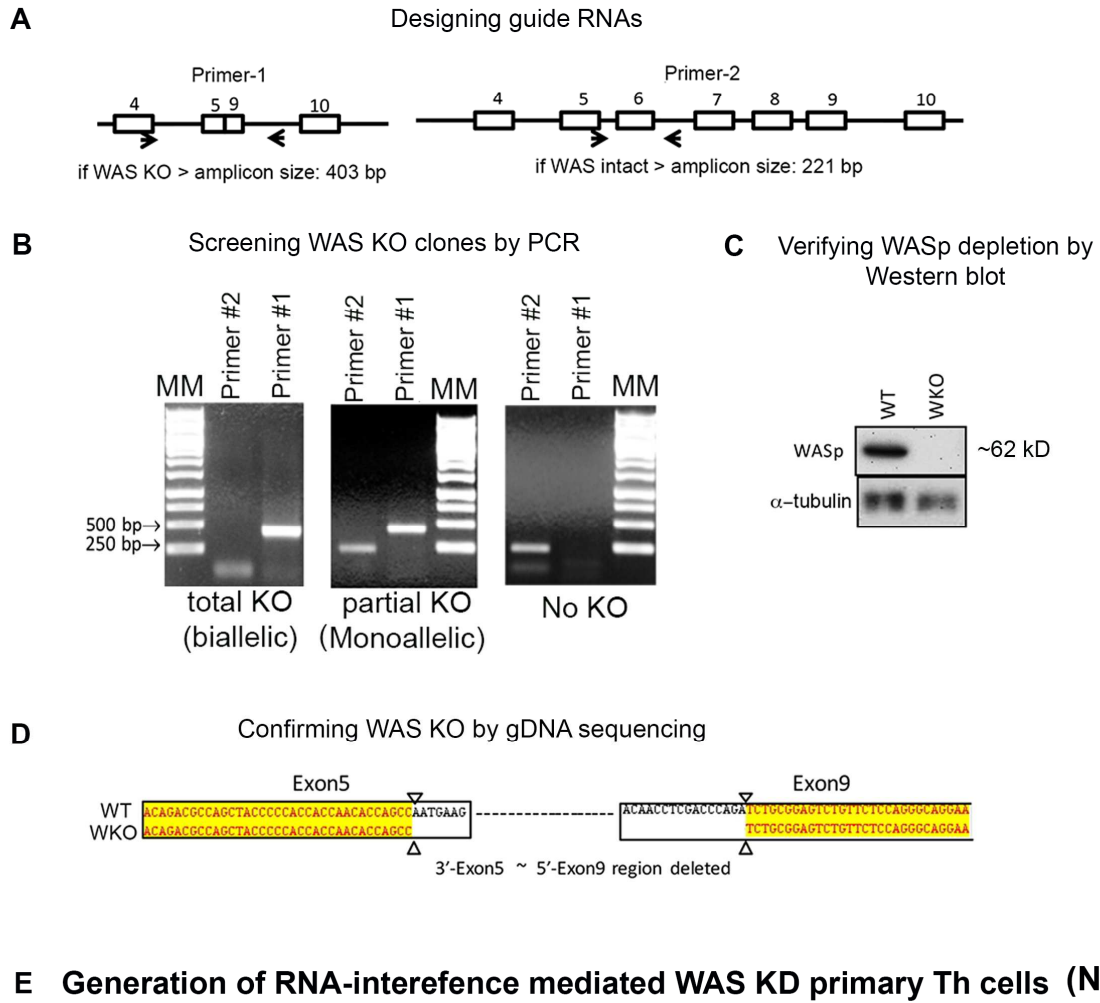
Fold-change values less than one indicate a negative or down-regulation, and the fold-regulation is the negative inverse of the fold-change.

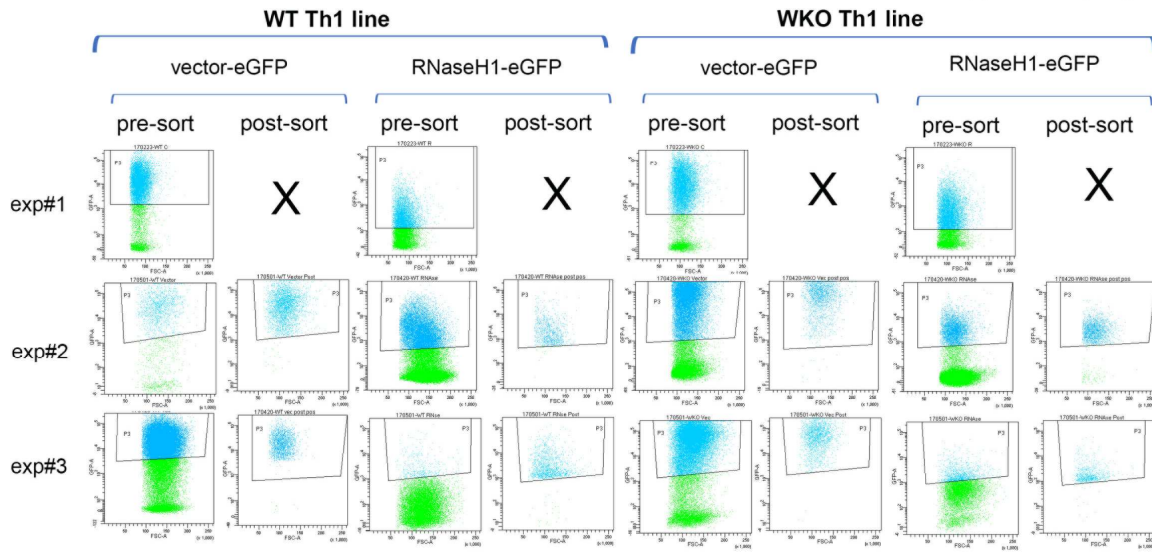
Fold-change and fold-regulation values greater than 2 are indicated in red; fold-change values less than 0.5 and fold-regulation values less than -2 are indicated in blue.



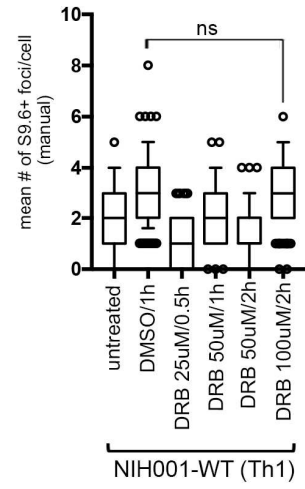
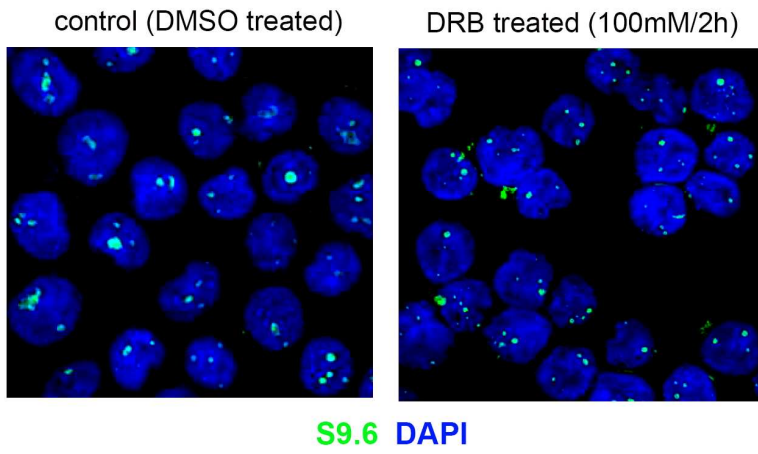
	CD3	CD4	CD8	CD45RA	CD45RO	CCR7	CD62L	<i>Th subtype</i>
<b>NIH001</b>	+	+	-	+	+	-	+	<b>Effector cell</b> (not naïve or central memory cell)
<b>Milan008</b>	+	+	-	-	+	-	-	<b>Effector memory cell</b> (not naïve or central memory cell)
<b>Jurkat</b>	+	+	-	+	+	-	+	<b>Effector cell</b> (not naïve or central memory cell)

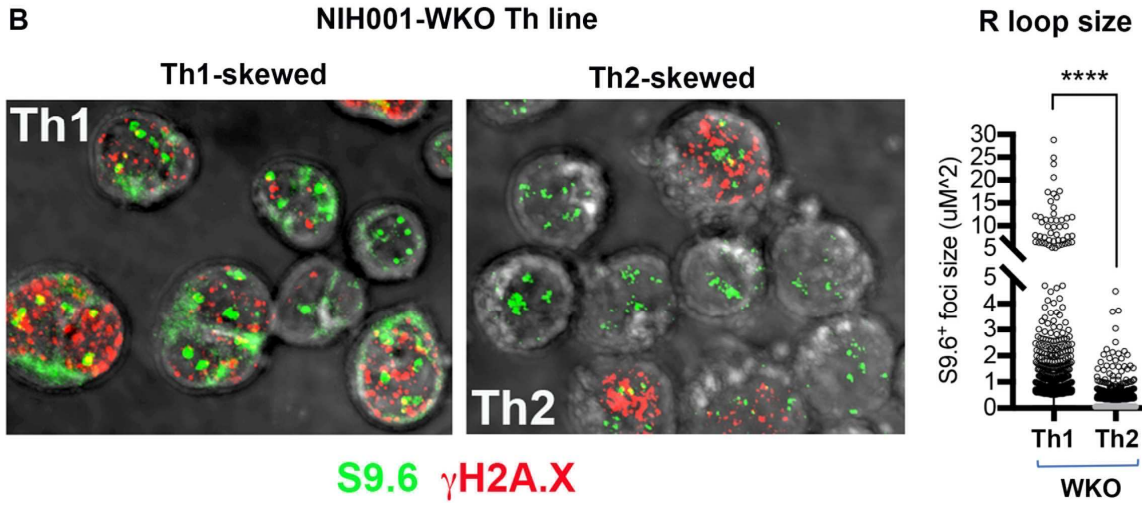
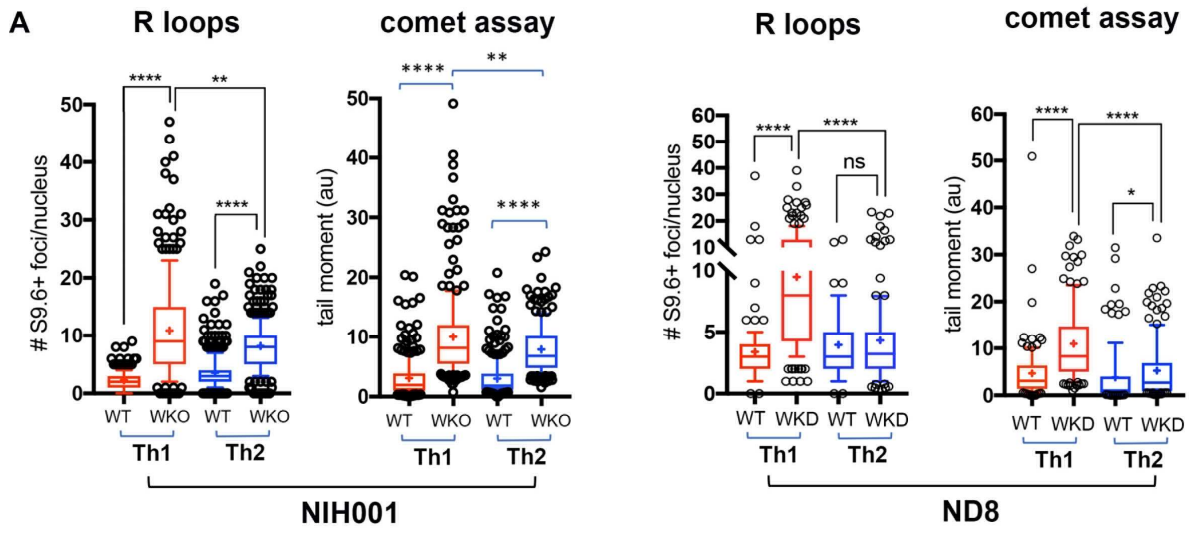
## Generation of CRISPR/Cas9-mediated WAS KO Th cell line (NIH001)





**Confocal imaging**







Supplementary Figure-6

DRIP/ChIP-qPCR: 3' end of genes

