Supplementary File for Figure 1

Supplementary Material to *in silico* screen: The *in silico screen* that lead to NFAT5a and alternative potentially lipid-modified transcription factors

The *in-silico* screen

Protein sequence hits from Hidden Markov Model (HMM) searches [1] with protein domain models taken from PFAM [2] and SMART [3] annotated as nucleic acid binding domains against the non-redundant protein sequence database were scored for the presence of an N-terminal myristoylation signal [4,5], a prenylation site [6,7] or the GPI lipid anchor attachment motif [8]. The resulting list of a few thousand hits was to be further reduced with the goal to come up with singular targets for an experimental follow up. By excluding entries with doubtful sequence termini, we wished to exclude cases of technically correct prediction but possibly non-existing proteins. Considerations of accessibility of cDNA and cell lines restricted the search to protein entries from well-studied model organisms. The requirement for conservation of the predicted lipid anchor sites in other species enhances the reliability of prediction and the possibility to find biological results of more general value.

Finally, the restriction to experimentally verified transcription factor (TF) domains ensures that the candidate under investigation has truly the potential to act as TF. NFAT5a was finally selected as candidate protein for studying the feasibility of nuclear import of lipid-modified TFs because there is experimental evidence for the existence of this isoform [9-12]. Equally important, knowing NFAT5 as the osmotic stress response TF provided us initial hope that testing isoform a for nuclear import upon salt stress is an accessible functional assay [13,14].

About other TFs with predicted lipid anchors

The most interesting question for general biology is whether lipid-modified TFs that are imported into the nucleus in a regulated manner are a more general phenomenon and whether reversible palmitoylation as a mobilization mechanism might be found in contexts other than NFAT5a.

It appears impossible to get an exact overview with regard to lipid modified TFs from a renewed *in silico* screen. Despite more than a decade of availability of “complete genomes”, new releases of genome assemblies remain accompanied with addition/losses of thousands of proteins, not to speak about isoforms. Nevertheless, several more years of sequencing have improved the data situation since 2004 when we first aggressively unselected hits to come up with the single, hopefully easy-to-test example NFAT5a. Frequently, termini of proteins are described more reliably. The likelihood to find homologues in genomes of alternative species has increased and this improves chances to test the conservation of posttranslational modification sites. Therefore, cases that we *a priori* omitted previously might become worthwhile to be investigated now. For example, the human protein Q8WYA1 (named MOP9, CLIF or BMAL2), a transcriptional regulator with functions in circadian and hypoxia pathways [15], was considered as a potential candidate alongside with NFAT5a. Only two of its isoforms were known in 2004 but eight isoforms are described in the database today. Isoforms 6, 7 and 8 are predicted targets of myristoylation; yet, they do not have an obvious acylation site.

The following five examples all have at least one isoform reported to have an N-terminal glycine after the leading methionine as well as sequentially close cysteines. The proteins are predicted targets for myristoylation at the N-terminal glycines (with NMT/MyrPS [4]) and the cysteines in their vicinity are likely palmitoylation sites [16]. The sequence features are conserved in neighbouring species. (1) The human protein BTBD7 (Q9P203) and (2) the protein BAC20790 from *Oryza sativa* are predicted to possess a BTB/POZ domain (PFAM PF00651) which is known to occur in TFs [17]. Similarly, (3) the CAD60697

(*Podospora anserine*) is a predicted classical zinc finger protein. (4) The human proteins LZTS1/FEZ1 (Q9Y250, isoform 1) and (5) LZTS2/LAPSER1 (isoform AAK31577) are annotated as leucine zipper putative tumor suppressor 1 and 2, respectively. They harbour a Fez1 domain (PFAM PF06818) which contains a leucine-zipper region with similarity to the DNA-binding domain of the cAMP-responsive activating-transcription factor 5 [18]. There is evidence that Fez1 regulates mitosis and inhibits cancer cell growth [19]. As the accuracy of the protein sequences in the proteomes, especially of the isoforms, improves in the future, more protein examples might pass the selection criteria.

Supplementary Table 1: Taxonomic distribution of NFAT5 isoforms and their sequence conservation in the N-terminal region of human NFAT5a

This part contains Supplementary Table 1 (a list of sequence database entries with orthologues of NFAT5 isoforms) and Supplementary Figure 1.1 (an alignment figure of NFAT5 protein isoform sequence segments).

The Supplementary Table 1 lists the entries in non-redundant protein database or UniProt that carry sequences homologous to NFAT5. Generally, protein isoforms are not well studied and it is not surprising that explicit NFAT5a entries are available only for a few species at the time of writing (July 2011); yet, their number has grown since 2004 when the authors have first done this survey.

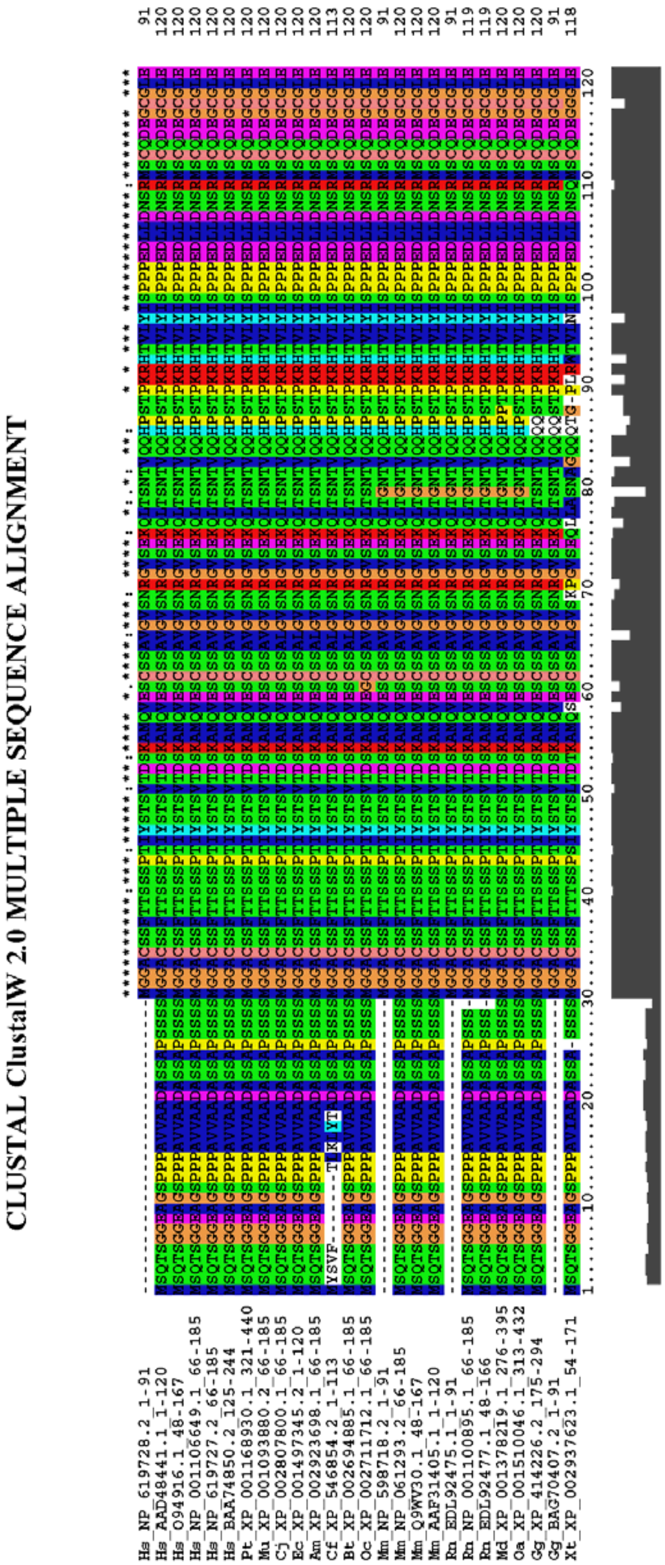
Supplementary Table 1

Species	NFAT5: isoform a	NFAT5: other isoforms
Homo sapiens (human)	NP_619728.2	AAD48441.1 (isoform b) O94916 (isoform c) NP_001106649.1 (isoform d) NP_619727.2 BAA74850.2[#]
Pan troglodytes (chimpanzee)		XP_001168930.1
Macaca mulatta (rhesus monkey)		XP_001093880.2
Callithrix jacchus (white-tufted-ear marmoset)		XP_002807800.1
Equus caballus (horse)		XP_001497345.2
Ailuropoda melanoleuca (giant panda)		XP_002923698.1
Canis familiaris (dog)		XP_546854.2
Bos taurus (cattle)		XP_002694885.1
Oryctolagus cuniculus (rabbit)		XP_002711712.1
Mus musculus (house mouse)	NP_598718.2	NP_061293.2 AAF31405.1 Q9WV30.1
Rattus norvegicus (Norway rat)	EDL92475.1	NP_001100895.1 EDL92477.1
Monodelphis domestica (gray short-tailed opossum)		XP_001378219.1
Ornithorhynchus anatinus (platypus)		XP_001510046.1
Gallus gallus (red jungle fowl)	BAG70407.2	XP_414226.2
Xenopus (Silurana) tropicalis (western clawed frog)		XP_002937623.1

[#] This sequence is annotated as KIAA0827 protein having a length of 1608 AAs. It is an N-terminally prolonged isoform c-type sequence that does not start with methionine. The 77 additional AAs are rich in P (27.9%), R (19.7%), and S (19.7%). Possibly, this is just a hypothetical translation with no real protein equivalent.

Supplementary Figure 1.1

The alignment figure below (created with CLUSTALX; [20-22]) shows that the protein sequence region in the environment of the human NFAT5a N-terminus is strongly conserved over a wide range of species. The species is encoded with a two-letter abbreviation in accordance with Supplementary Table 1. The N-terminal positions Gly2 and Cys5 are remarkably preserved throughout species.


CLUSTAL ClustalW 2.0 MULTIPLE SEQUENCE ALIGNMENT
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Hs_AAD48441.1_1-120 120
Hs_O94916.1_48-167 120
Hs_NP_001106649.1_66-185 120
Hs_NP_619727.2_66-185 120
Hs_BAA74850.2_125-244 120
Pt_XP_001168930.1_321-440 120
Mu_XP_001093880.2_66-185 120
Cj_XP_002807800.1_66-185 120
Ec_XP_001497345.2_1-120 120
Am_XP_002923698.1_66-185 120
Cf_XP_546854.2_1-113 113
Bt_XP_002694885.1_66-185 120
Oc_XP_002711712.1_66-185 120
Mm_NP_598718.2_1-91 91
Mm_NP_061293.2_66-185 120
Mm_Q9WV30.1_48-167 120
Mm_AAF31405.1_1-120 120
Rn_EDL92475.1_1-91 91
Rn_NP_001100895.1_66-185 119
Rn_EDL92477.1_48-166 119
Md_XP_001378219.1_276-395 120
Oa_XP_001510046.1_313-432 120
Gg_XP_414226.2_175-294 120
Gg_BAG70407.2_1-91 91
Xt_XP_002937623.1_54-171 118
1 10 20 30 40 50 60 70 80 90 100 110 120

Supplementary Figure 1.2: Sequences of all five human NFAT5a mRNA transcripts in the regions used for qPCR

The alignment figure below (created with CLUSTALX; [20-22]) shows the mRNA sequences of all five human transcripts in the region of the segments 2|B, -|X and 4|D used for quantitative RT-PCR.

CLUSTAL ClustalW 2.0 MULTIPLE SEQUENCE ALIGNMENT

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NM_138713.2|NFAT5d2_t2     ATGCCCTCGGACTTCATCTCATTGCTCAGCGCGGACCTAGACCTGGAATCGCCCAAGTCCCTCTACTCGCGAGATTCTCTGAAGTTACACCCATCACAGAATTTTCATAGAGCTGGACTATTGGAAGAATCTGTCTATGATCTTCTCCCA    150
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NM_173214.1|NFAT5a_t4      ATGCCCTCGGACTTCATCTCATTGCTCAGCGCGGACCTAGACCTGGAATCGCCCAAGTCCCTCTACTCGCGAG------------------------------------------------------AATCTGTCTATGATCTTCTCCCA     96
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isoform_d                  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD    150
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NM_138714.2|NFAT5a_t1      AAGGAGTTACAGTTACCTCCATCTAGAGAAACATCTGTAGCATCAATGAGTCAGACAAGCGGTGGTGAGGCAGGCTCGCCTCCTCCAGCTGTTGTTGCTGCTGGATTTGCCTCTGAAGCAGGGAGTGTCTGCATTAAAAATGACCTGTAG    300
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exon                       CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC-----------------------------------------------    254
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isoform_b                  ---------------------------------------------BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB-----------------------------------------------     59
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isoform_a                  XXXXXXXXXXXXXXX-----------------------------AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA    168
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NM_001113178.1|NFAT5d1_t6  TGGGGGTAAGTAACAGAGGGGTAAGTGAAAAGCAGTTAACCAGTAACACAGTTCAGCAGCATCCATCAACACCGAAGAGGCACACAGTCTTGTACATCTCACCACCACCTGAGGACTTGCTGGATAACAGTCGGATGTCCTGCCAGGATG    538
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CLUSTAL ClustalW 2.0 MULTIPLE SEQUENCE ALIGNMENT

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isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC   934
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NM_006599.2|NFAT5c_t3      GCTTTCCTACAGTAAAGCTGGAAGGCCATAATGAACCTGTAGTGTTGCAAGTGTTTGTGGGCAACGACTCTGGACGAGTGAAACCACATGGATTTTATCAGGCCTGCAGAGTAACTGGACGAAATACAACTCCTTGCAAAGAAGTGGACA  1084
NM_173214.1|NFAT5a_t4      GCTTTCCTACAGTAAAGCTGGAAGGCCATAATGAACCTGTAGTGTTGCAAGTGTTTGTGGGCAACGACTCTGGACGAGTGAAACCACATGGATTTTATCAGGCCTGCAGAGTAACTGGACGAAATACAACTCCTTGCAAAGAAGTGGACA  1146
exon                       EEEEEEEEEEEEEEEEEFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF  1138
isoform_a                  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   918
isoform_b                  BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB   943
isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  1084
isoform_d                  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD  1138
                           ......1060......1070......1080......1090......1100......1110......1120......1130......1140......1150......1160......1170......1180......1190......1200
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NM_138713.2|NFAT5d2_t2     TTGAAGGCACTACTGTTATAGAAGTCGGCCTTGATCCTAGCAACAACATGACACTGGCGGTGGACTGCGTAGGGATATTGAAATTGAGGAATGCTGATGTCGAAGCCAGAATAGGAATTGCTGGTTCCAAGAAGAAAAGCACTCGTGCCA  1288
NM_001113178.1|NFAT5d1_t6  TTGAAGGCACTACTGTTATAGAAGTCGGCCTTGATCCTAGCAACAACATGACACTGGCGGTGGACTGCGTAGGGATATTGAAATTGAGGAATGCTGATGTCGAAGCCAGAATAGGAATTGCTGGTTCCAAGAAGAAAAGCACTCGTGCCA  1288
NM_138714.2|NFAT5a_t1      TTGAAGGCACTACTGTTATAGAAGTCGGCCTTGATCCTAGCAACAACATGACACTGGCGGTGGACTGCGTAGGGATATTGAAATTGAGGAATGCTGATGTCGAAGCCAGAATAGGAATTGCTGGTTCCAAGAAGAAAAGCACTCGTGCCA  1350
NM_006599.2|NFAT5c_t3      TTGAAGGCACTACTGTTATAGAAGTCGGCCTTGATCCTAGCAACAACATGACACTGGCGGTGGACTGCGTAGGGATATTGAAATTGAGGAATGCTGATGTCGAAGCCAGAATAGGAATTGCTGGTTCCAAGAAGAAAAGCACTCGTGCCA  1234
NM_173214.1|NFAT5a_t4      TTGAAGGCACTACTGTTATAGAAGTCGGCCTTGATCCTAGCAACAACATGACACTGGCGGTGGACTGCGTAGGGATATTGAAATTGAGGAATGCTGATGTCGAAGCCAGAATAGGAATTGCTGGTTCCAAGAAGAAAAGCACTCGTGCCA  1296
exon                       FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  1288
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isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  1234
isoform_d                  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD  1288
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NM_001113178.1|NFAT5d1_t6  GATTGGTTTTTCGAGTTAATATCATGAGGAAAGATGGCTCCACTTTGACACTGCAAACACCCTCTTCTCCAATTTTGTGTACTCAGCCAGCAGGAGTGCCAGAAATCTTAAAGAAAAGCTTGCATAGCTGTTCAGTGAAAGGAGAAGAAG  1438
NM_138714.2|NFAT5a_t1      GATTGGTTTTTCGAGTTAATATCATGAGGAAAGATGGCTCCACTTTGACACTGCAAACACCCTCTTCTCCAATTTTGTGTACTCAGCCAGCAGGAGTGCCAGAAATCTTAAAGAAAAGCTTGCATAGCTGTTCAGTGAAAGGAGAAGAAG  1500
NM_006599.2|NFAT5c_t3      GATTGGTTTTTCGAGTTAATATCATGAGGAAAGATGGCTCCACTTTGACACTGCAAACACCCTCTTCTCCAATTTTGTGTACTCAGCCAGCAGGAGTGCCAGAAATCTTAAAGAAAAGCTTGCATAGCTGTTCAGTGAAAGGAGAAGAAG  1384
NM_173214.1|NFAT5a_t4      GATTGGTTTTTCGAGTTAATATCATGAGGAAAGATGGCTCCACTTTGACACTGCAAACACCCTCTTCTCCAATTTTGTGTACTCAGCCAGCAGGAGTGCCAGAAATCTTAAAGAAAAGCTTGCATAGCTGTTCAGTGAAAGGAGAAGAAG  1446
exon                       GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH  1438
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isoform_b                  BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB  1243
isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  1384
isoform_d                  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD  1438
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NM_001113178.1|NFAT5d1_t6  AAGTGTTTTTAATCGGCAAGAACTTTCTGAAAGGAACTAAAGTTATTTTCCAAGAAAATGTTTCTGATGAAAACTCTTGGAAGTCAGAAGCTGAAATTGATATGGAACTATTTCATCAGAATCATCTTATTGTGAAGGTTCCTCCCTATC  1588
NM_138714.2|NFAT5a_t1      AAGTGTTTTTAATCGGCAAGAACTTTCTGAAAGGAACTAAAGTTATTTTCCAAGAAAATGTTTCTGATGAAAACTCTTGGAAGTCAGAAGCTGAAATTGATATGGAACTATTTCATCAGAATCATCTTATTGTGAAGGTTCCTCCCTATC  1650
NM_006599.2|NFAT5c_t3      AAGTGTTTTTAATCGGCAAGAACTTTCTGAAAGGAACTAAAGTTATTTTCCAAGAAAATGTTTCTGATGAAAACTCTTGGAAGTCAGAAGCTGAAATTGATATGGAACTATTTCATCAGAATCATCTTATTGTGAAGGTTCCTCCCTATC  1534
NM_173214.1|NFAT5a_t4      AAGTGTTTTTAATCGGCAAGAACTTTCTGAAAGGAACTAAAGTTATTTTCCAAGAAAATGTTTCTGATGAAAACTCTTGGAAGTCAGAAGCTGAAATTGATATGGAACTATTTCATCAGAATCATCTTATTGTGAAGGTTCCTCCCTATC  1596
exon                       HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK  1588
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isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  1534
isoform_d                  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD  1588
                           ......1510......1520......1530......1540......1550......1560......1570......1580......1590......1600......1610......1620......1630......1640......1650
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NM_001113178.1|NFAT5d1_t6  ATGACCAACATATAACTTTGCCTGTGTCAGTGGGAATATATGTAGTGACAAATGCTGGAAGATCTCATGATGTTCAACCATTCACTTACACTCCAGACCCAG---CAGCTGGTGCTTTGAATGTAAATGTGAAGAAGGAAATATCTAGTC  1735
NM_138714.2|NFAT5a_t1      ATGACCAACATATAACTTTGCCTGTGTCAGTGGGAATATATGTAGTGACAAATGCTGGAAGATCTCATGATGTTCAACCATTCACTTACACTCCAGACCCAGCAGCAGCTGGTGCTTTGAATGTAAATGTGAAGAAGGAAATATCTAGTC  1800
NM_006599.2|NFAT5c_t3      ATGACCAACATATAACTTTGCCTGTGTCAGTGGGAATATATGTAGTGACAAATGCTGGAAGATCTCATGATGTTCAACCATTCACTTACACTCCAGACCCAGCAGCAGCTGGTGCTTTGAATGTAAATGTGAAGAAGGAAATATCTAGTC  1684
NM_173214.1|NFAT5a_t4      ATGACCAACATATAACTTTGCCTGTGTCAGTGGGAATATATGTAGTGACAAATGCTGGAAGATCTCATGATGTTCAACCATTCACTTACACTCCAGACCCAGCAGCAGCTGGTGCTTTGAATGTAAATGTGAAGAAGGAAATATCTAGTC  1746
exon                       KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL  1738
isoform_a                  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  1518
isoform_b                  BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB  1543
isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  1684
isoform_d                  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD  1738
                           ......1660......1670......1680......1690......1700......1710......1720......1730......1740......1750......1760......1770......1780......1790......1800
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NM_001113178.1|NFAT5d1_t6  CAGCAAGACCTTGCTCTTTTGAAGAGGCCATGAAAGCAATGAAAACTACTGGATGTAATTTAGATAAGGTAAATATTATCCCTAATGCCCTGATGACTCCACTCATACCAAGCAGTATGATTAAGAGTGAAGATGTTACTCCAATGGAAG 1885
NM_138714.2|NFAT5a_t1      CAGCAAGACCTTGCTCTTTTGAAGAGGCCATGAAAGCAATGAAAACTACTGGATGTAATTTAGATAAGGTAAATATTATCCCTAATGCCCTGATGACTCCACTCATACCAAGCAGTATGATTAAGAGTGAAGATGTTACTCCAATGGAAG 1950
NM_006599.2|NFAT5c_t3      CAGCAAGACCTTGCTCTTTTGAAGAGGCCATGAAAGCAATGAAAACTACTGGATGTAATTTAGATAAGGTAAATATTATCCCTAATGCCCTGATGACTCCACTCATACCAAGCAGTATGATTAAGAGTGAAGATGTTACTCCAATGGAAG 1834
NM_173214.1|NFAT5a_t4      CAGCAAGACCTTGCTCTTTTGAAGAGGCCATGAAAGCAATGAAAACTACTGGATGTAATTTAGATAAGGTAAATATTATCCCTAATGCCCTGATGACTCCACTCATACCAAGCAGTATGATTAAGAGTGAAGATGTTACTCCAATGGAAG 1896
exon                       LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM 1888
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isoform_b                  BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB 1693
isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1834
isoform_d                  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD 1888
                           ......1810......1820......1830......1840......1850......1860......1870......1880......1890......1900......1910......1920......1930......1940......1950
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NM_138713.2|NFAT5d2_t2     TAACAGCAGAAAAAAGATCTTCCACTATTTTTAAGACTACAAAGTCTGTTGGATCAACTCAGCAAACATTAGAAAACATCTCAAACATAGCAGGAAATGGCTCTTTTTCATCACCATCATCTTCCCACCTACCTTCTGAAAATGAAAAAC 2038
NM_001113178.1|NFAT5d1_t6  TAACAGCAGAAAAAAGATCTTCCACTATTTTTAAGACTACAAAGTCTGTTGGATCAACTCAGCAAACATTAGAAAACATCTCAAACATAGCAGGAAATGGCTCTTTTTCATCACCATCATCTTCCCACCTACCTTCTGAAAATGAAAAAC 2035
NM_138714.2|NFAT5a_t1      TAACAGCAGAAAAAAGATCTTCCACTATTTTTAAGACTACAAAGTCTGTTGGATCAACTCAGCAAACATTAGAAAACATCTCAAACATAGCAGGAAATGGCTCTTTTTCATCACCATCATCTTCCCACCTACCTTCTGAAAATGAAAAAC 2100
NM_006599.2|NFAT5c_t3      TAACAGCAGAAAAAAGATCTTCCACTATTTTTAAGACTACAAAGTCTGTTGGATCAACTCAGCAAACATTAGAAAACATCTCAAACATAGCAGGAAATGGCTCTTTTTCATCACCATCATCTTCCCACCTACCTTCTGAAAATGAAAAAC 1984
NM_173214.1|NFAT5a_t4      TAACAGCAGAAAAAAGATCTTCCACTATTTTTAAGACTACAAAGTCTGTTGGATCAACTCAGCAAACATTAGAAAACATCTCAAACATAGCAGGAAATGGCTCTTTTTCATCACCATCATCTTCCCACCTACCTTCTGAAAATGAAAAAC 2046
exon                       MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2038
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isoform_b                  BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB 1843
isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1984
isoform_d                  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD 2038
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NM_001113178.1|NFAT5d1_t6  AGCAGCAGATTCAGCCCAAGGCATACAACCCAGAGACCCTGACAACTATTCAAACCCAGGACATCTCACAGCCTGGTACTTTTCCAGCAGTTTCTGCTTCTAGTCAGCTGCCCAACAGCGATGCACTATTGCAGCAGGCTACACAGTTTC 2185
NM_138714.2|NFAT5a_t1      AGCAGCAGATTCAGCCCAAGGCATACAACCCAGAGACCCTGACAACTATTCAAACCCAGGACATCTCACAGCCTGGTACTTTTCCAGCAGTTTCTGCTTCTAGTCAGCTGCCCAACAGCGATGCACTATTGCAGCAGGCTACACAGTTTC 2250
NM_006599.2|NFAT5c_t3      AGCAGCAGATTCAGCCCAAGGCATACAACCCAGAGACCCTGACAACTATTCAAACCCAGGACATCTCACAGCCTGGTACTTTTCCAGCAGTTTCTGCTTCTAGTCAGCTGCCCAACAGCGATGCACTATTGCAGCAGGCTACACAGTTTC 2134
NM_173214.1|NFAT5a_t4      AGCAGCAGATTCAGCCCAAGGCATACAACCCAGAGACCCTGACAACTATTCAAACCCAGGACATCTCACAGCCTGGTACTTTTCCAGCAGTTTCTGCTTCTAGTCAGCTGCCCAACAGCGATGCACTATTGCAGCAGGCTACACAGTTTC 2196
exon                       NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2188
isoform_a                  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1968
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NM_001113178.1|NFAT5d1_t6  AGACAAGAGAAACTCAGTCTAGAGAGATATTACAGTCAGATGGTACAGTGGTTAATTTGTCACAACTGACTGAGGCATCACAACAACAGCAGCAGTCACCACTACAAGAACAAGCACAGACTTTACAGCAGCAGATTTCATCAAATATTT 2335
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NM_006599.2|NFAT5c_t3      AGACAAGAGAAACTCAGTCTAGAGAGATATTACAGTCAGATGGTACAGTGGTTAATTTGTCACAACTGACTGAGGCATCACAACAACAGCAGCAGTCACCACTACAAGAACAAGCACAGACTTTACAGCAGCAGATTTCATCAAATATTT 2284
NM_173214.1|NFAT5a_t4      AGACAAGAGAAACTCAGTCTAGAGAGATATTACAGTCAGATGGTACAGTGGTTAATTTGTCACAACTGACTGAGGCATCACAACAACAGCAGCAGTCACCACTACAAGAACAAGCACAGACTTTACAGCAGCAGATTTCATCAAATATTT 2346
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isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 2284
isoform_d                  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD 2338
                           ......2260......2270......2280......2290......2300......2310......2320......2330......2340......2350......2360......2370......2380......2390......2400
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NM_138713.2|NFAT5d2_t2      TTCCATCACCAAATAGTGTGAGTCAGCTTCAGAATACTATTCAGCAGCTGCAAGCAGGGAGTTTCACAGGCAGTACTGCTAGTGGCAGCAGTGGAAGTGTTGACTTGGTCCAACAAGTTTTAGAGGCACAGCAGCAGTTATCTTCAGTTT  2488
NM_001113178.1|NFAT5d1_t6   TTCCATCACCAAATAGTGTGAGTCAGCTTCAGAATACTATTCAGCAGCTGCAAGCAGGGAGTTTCACAGGCAGTACTGCTAGTGGCAGCAGTGGAAGTGTTGACTTGGTCCAACAAGTTTTAGAGGCACAGCAGCAGTTATCTTCAGTTT  2485
NM_138714.2|NFAT5a_t1       TTCCATCACCAAATAGTGTGAGTCAGCTTCAGAATACTATTCAGCAGCTGCAAGCAGGGAGTTTCACAGGCAGTACTGCTAGTGGCAGCAGTGGAAGTGTTGACTTGGTCCAACAAGTTTTAGAGGCACAGCAGCAGTTATCTTCAGTTT  2550
NM_006599.2|NFAT5c_t3       TTCCATCACCAAATAGTGTGAGTCAGCTTCAGAATACTATTCAGCAGCTGCAAGCAGGGAGTTTCACAGGCAGTACTGCTAGTGGCAGCAGTGGAAGTGTTGACTTGGTCCAACAAGTTTTAGAGGCACAGCAGCAGTTATCTTCAGTTT  2434
NM_173214.1|NFAT5a_t4       TTCCATCACCAAATAGTGTGAGTCAGCTTCAGAATACTATTCAGCAGCTGCAAGCAGGGAGTTTCACAGGCAGTACTGCTAGTGGCAGCAGTGGAAGTGTTGACTTGGTCCAACAAGTTTTAGAGGCACAGCAGCAGTTATCTTCAGTTT  2496
exon                        NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  2488
isoform_a                   AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  2268
isoform_b                   BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB  2293
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NM_138713.2|NFAT5d2_t2      TATTTTCTGCTCCAGATGGTAATGAGAATGTTCAAGAGCAGCTTAGTGCAGATATTTTTCAACAAGTCAGTCAAATTCAGAGTGGTGTAAGCCCTGGAATGTTTTCCTCAACAGAGCCAACAGTCCATACCAGACCAGATAATTTATTAC  2638
NM_001113178.1|NFAT5d1_t6   TATTTTCTGCTCCAGATGGTAATGAGAATGTTCAAGAGCAGCTTAGTGCAGATATTTTTCAACAAGTCAGTCAAATTCAGAGTGGTGTAAGCCCTGGAATGTTTTCCTCAACAGAGCCAACAGTCCATACCAGACCAGATAATTTATTAC  2635
NM_138714.2|NFAT5a_t1       TATTTTCTGCTCCAGATGGTAATGAGAATGTTCAAGAGCAGCTTAGTGCAGATATTTTTCAACAAGTCAGTCAAATTCAGAGTGGTGTAAGCCCTGGAATGTTTTCCTCAACAGAGCCAACAGTCCATACCAGACCAGATAATTTATTAC  2700
NM_006599.2|NFAT5c_t3       TATTTTCTGCTCCAGATGGTAATGAGAATGTTCAAGAGCAGCTTAGTGCAGATATTTTTCAACAAGTCAGTCAAATTCAGAGTGGTGTAAGCCCTGGAATGTTTTCCTCAACAGAGCCAACAGTCCATACCAGACCAGATAATTTATTAC  2584
NM_173214.1|NFAT5a_t4       TATTTTCTGCTCCAGATGGTAATGAGAATGTTCAAGAGCAGCTTAGTGCAGATATTTTTCAACAAGTCAGTCAAATTCAGAGTGGTGTAAGCCCTGGAATGTTTTCCTCAACAGAGCCAACAGTCCATACCAGACCAGATAATTTATTAC  2646
exon                        NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  2638
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isoform_c                   CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  2584
isoform_d                   DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD  2638
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NM_138713.2|NFAT5d2_t2      CTGGAAGAGCTGAAAGTGTTCATCCACAGTCTGAAAACACGTTATCTAATCAACAGCAGCAGCAGCAGCAGCAACAGCAAGTGATGGAATCTTCAGCCGCAATGGTGATGGAGATGCAACAGAGTATCTGCCAGGCAGCTGCCCAGATTC  2788
NM_001113178.1|NFAT5d1_t6   CTGGAAGAGCTGAAAGTGTTCATCCACAGTCTGAAAACACGTTATCTAATCAACAGCAGCAGCAGCAGCAGCAACAGCAAGTGATGGAATCTTCAGCCGCAATGGTGATGGAGATGCAACAGAGTATCTGCCAGGCAGCTGCCCAGATTC  2785
NM_138714.2|NFAT5a_t1       CTGGAAGAGCTGAAAGTGTTCATCCACAGTCTGAAAACACGTTATCTAATCAACAGCAGCAGCAGCAGCAGCAACAGCAAGTGATGGAATCTTCAGCCGCAATGGTGATGGAGATGCAACAGAGTATCTGCCAGGCAGCTGCCCAGATTC  2850
NM_006599.2|NFAT5c_t3       CTGGAAGAGCTGAAAGTGTTCATCCACAGTCTGAAAACACGTTATCTAATCAACAGCAGCAGCAGCAGCAGCAACAGCAAGTGATGGAATCTTCAGCCGCAATGGTGATGGAGATGCAACAGAGTATCTGCCAGGCAGCTGCCCAGATTC  2734
NM_173214.1|NFAT5a_t4       CTGGAAGAGCTGAAAGTGTTCATCCACAGTCTGAAAACACGTTATCTAATCAACAGCAGCAGCAGCAGCAGCAACAGCAAGTGATGGAATCTTCAGCCGCAATGGTGATGGAGATGCAACAGAGTATCTGCCAGGCAGCTGCCCAGATTC  2796
exon                        NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  2788
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isoform_b                   BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB  2593
isoform_c                   CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  2734
isoform_d                   DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD  2788
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NM_001113178.1|NFAT5d1_t6   AGTCAGAGTTATTCCCTTCAACTGCTTCAGCAAATGGAAACCTTCAGCAATCGCCAGTTTACCAGCAGACTTCTCACATGATGAGTGCATTGTCTACCAATGAGGATATGCAAATGCAGTGTGAATTGTTTTCTTCTCCTCCTGCAGTTT  2935
NM_138714.2|NFAT5a_t1       AGTCAGAGTTATTCCCTTCAACTGCTTCAGCAAATGGAAACCTTCAGCAATCGCCAGTTTACCAGCAGACTTCTCACATGATGAGTGCATTGTCTACCAATGAGGATATGCAAATGCAGTGTGAATTGTTTTCTTCTCCTCCTGCAGTTT  3000
NM_006599.2|NFAT5c_t3       AGTCAGAGTTATTCCCTTCAACTGCTTCAGCAAATGGAAACCTTCAGCAATCGCCAGTTTACCAGCAGACTTCTCACATGATGAGTGCATTGTCTACCAATGAGGATATGCAAATGCAGTGTGAATTGTTTTCTTCTCCTCCTGCAGTTT  2884
NM_173214.1|NFAT5a_t4       AGTCAGAGTTATTCCCTTCAACTGCTTCAGCAAATGGAAACCTTCAGCAATCGCCAGTTTACCAGCAGACTTCTCACATGATGAGTGCATTGTCTACCAATGAGGATATGCAAATGCAGTGTGAATTGTTTTCTTCTCCTCCTGCAGTTT  2946
exon                        NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  2938
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isoform_b                   BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB  2743
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NM_001113178.1|NFAT5d1_t6 CTGGAAATGAAACTTCTACAACTACCACACAGCAGGTTGCAACCCCTGGCACTACCATGTTTCAGACATCAAGTTCAGGAGATGGAGAAGAAACTGGAACACAAGCAAAACAGATTCAGAACAGTGTCTTTCAGACCATGGTCCAAATGC  3085
NM_138714.2|NFAT5a_t1     CTGGAAATGAAACTTCTACAACTACCACACAGCAGGTTGCAACCCCTGGCACTACCATGTTTCAGACATCAAGTTCAGGAGATGGAGAAGAAACTGGAACACAAGCAAAACAGATTCAGAACAGTGTCTTTCAGACCATGGTCCAAATGC  3150
NM_006599.2|NFAT5c_t3     CTGGAAATGAAACTTCTACAACTACCACACAGCAGGTTGCAACCCCTGGCACTACCATGTTTCAGACATCAAGTTCAGGAGATGGAGAAGAAACTGGAACACAAGCAAAACAGATTCAGAACAGTGTCTTTCAGACCATGGTCCAAATGC  3034
NM_173214.1|NFAT5a_t4     CTGGAAATGAAACTTCTACAACTACCACACAGCAGGTTGCAACCCCTGGCACTACCATGTTTCAGACATCAAGTTCAGGAGATGGAGAAGAAACTGGAACACAAGCAAAACAGATTCAGAACAGTGTCTTTCAGACCATGGTCCAAATGC  3096
exon                      NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  3088
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NM_001113178.1|NFAT5d1_t6 AACATAGTGGGGACAATCAACCTCAAGTTAACCTTTTTTCATCCACAAAAAGTATGATGAGTGTTCAGAATAGTGGTACCCAACAACAAGGTAATGGTTTATTCCAGCAAGGGAATGAGATGATGTCACTTCAATCTGGAAATTTTTTGC  3235
NM_138714.2|NFAT5a_t1     AACATAGTGGGGACAATCAACCTCAAGTTAACCTTTTTTCATCCACAAAAAGTATGATGAGTGTTCAGAATAGTGGTACCCAACAACAAGGTAATGGTTTATTCCAGCAAGGGAATGAGATGATGTCACTTCAATCTGGAAATTTTTTGC  3300
NM_006599.2|NFAT5c_t3     AACATAGTGGGGACAATCAACCTCAAGTTAACCTTTTTTCATCCACAAAAAGTATGATGAGTGTTCAGAATAGTGGTACCCAACAACAAGGTAATGGTTTATTCCAGCAAGGGAATGAGATGATGTCACTTCAATCTGGAAATTTTTTGC  3184
NM_173214.1|NFAT5a_t4     AACATAGTGGGGACAATCAACCTCAAGTTAACCTTTTTTCATCCACAAAAAGTATGATGAGTGTTCAGAATAGTGGTACCCAACAACAAGGTAATGGTTTATTCCAGCAAGGGAATGAGATGATGTCACTTCAATCTGGAAATTTTTTGC  3246
exon                      NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  3238
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isoform_d                 DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD  3238
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NM_001113178.1|NFAT5d1_t6 AGCAGTCTTCTCATTCACAGGCCCAACTTTTTCATCCTCAAAATCCTATTGCCGATGCTCAGAACCTTTCCCAGGAAACTCAAGGTTCTCTCTTTCATAGTCCAAATCCTATTGTCCACAGTCAGACTTCTACAACCTCCTCTGAACAAA  3385
NM_138714.2|NFAT5a_t1     AGCAGTCTTCTCATTCACAGGCCCAACTTTTTCATCCTCAAAATCCTATTGCCGATGCTCAGAACCTTTCCCAGGAAACTCAAGGTTCTCTCTTTCATAGTCCAAATCCTATTGTCCACAGTCAGACTTCTACAACCTCCTCTGAACAAA  3450
NM_006599.2|NFAT5c_t3     AGCAGTCTTCTCATTCACAGGCCCAACTTTTTCATCCTCAAAATCCTATTGCCGATGCTCAGAACCTTTCCCAGGAAACTCAAGGTTCTCTCTTTCATAGTCCAAATCCTATTGTCCACAGTCAGACTTCTACAACCTCCTCTGAACAAA  3334
NM_173214.1|NFAT5a_t4     AGCAGTCTTCTCATTCACAGGCCCAACTTTTTCATCCTCAAAATCCTATTGCCGATGCTCAGAACCTTTCCCAGGAAACTCAAGGTTCTCTCTTTCATAGTCCAAATCCTATTGTCCACAGTCAGACTTCTACAACCTCCTCTGAACAAA  3396
exon                      NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  3388
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                          ......3310......3320......3330......3340......3350......3360......3370......3380......3390......3400......3410......3420......3430......3440......3450
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NM_138713.2|NFAT5d2_t2    TGCAGCCTCCAATGTTTCACTCTCAAAGTACCATTGCTGTGTTACAGGGCTCTTCAGTTCCTCAAGACCAGCAGTCAACCAACATATTTCTTTCCCAGAGTCCCATGAATAATCTTCAGACTAACACAGTAGCCCAAGAAGCATTTTTTG  3538
NM_001113178.1|NFAT5d1_t6 TGCAGCCTCCAATGTTTCACTCTCAAAGTACCATTGCTGTGTTACAGGGCTCTTCAGTTCCTCAAGACCAGCAGTCAACCAACATATTTCTTTCCCAGAGTCCCATGAATAATCTTCAGACTAACACAGTAGCCCAAGAAGCATTTTTTG  3535
NM_138714.2|NFAT5a_t1     TGCAGCCTCCAATGTTTCACTCTCAAAGTACCATTGCTGTGTTACAGGGCTCTTCAGTTCCTCAAGACCAGCAGTCAACCAACATATTTCTTTCCCAGAGTCCCATGAATAATCTTCAGACTAACACAGTAGCCCAAGAAGCATTTTTTG  3600
NM_006599.2|NFAT5c_t3     TGCAGCCTCCAATGTTTCACTCTCAAAGTACCATTGCTGTGTTACAGGGCTCTTCAGTTCCTCAAGACCAGCAGTCAACCAACATATTTCTTTCCCAGAGTCCCATGAATAATCTTCAGACTAACACAGTAGCCCAAGAAGCATTTTTTG  3484
NM_173214.1|NFAT5a_t4     TGCAGCCTCCAATGTTTCACTCTCAAAGTACCATTGCTGTGTTACAGGGCTCTTCAGTTCCTCAAGACCAGCAGTCAACCAACATATTTCTTTCCCAGAGTCCCATGAATAATCTTCAGACTAACACAGTAGCCCAAGAAGCATTTTTTG  3546
exon                      NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  3538
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NM_138713.2|NFAT5d2_t2     CAGCACCGAACTCAATTTCTCCACTTCAGTCAACATCAAACAGTGAACAACAAGCTGCTTTCCAACAGCAAGCTCCAATATCACACATCCAGACTCCTATGCTTTCCCAAGAACAGGCACAACCCCCGCAGCAGGGTTTATTTCAGCCTC 3688
NM_001113178.1|NFAT5d1_t6  CAGCACCGAACTCAATTTCTCCACTTCAGTCAACATCAAACAGTGAACAACAAGCTGCTTTCCAACAGCAAGCTCCAATATCACACATCCAGACTCCTATGCTTTCCCAAGAACAGGCACAACCCCCGCAGCAGGGTTTATTTCAGCCTC 3685
NM_138714.2|NFAT5a_t1      CAGCACCGAACTCAATTTCTCCACTTCAGTCAACATCAAACAGTGAACAACAAGCTGCTTTCCAACAGCAAGCTCCAATATCACACATCCAGACTCCTATGCTTTCCCAAGAACAGGCACAACCCCCGCAGCAGGGTTTATTTCAGCCTC 3750
NM_006599.2|NFAT5c_t3      CAGCACCGAACTCAATTTCTCCACTTCAGTCAACATCAAACAGTGAACAACAAGCTGCTTTCCAACAGCAAGCTCCAATATCACACATCCAGACTCCTATGCTTTCCCAAGAACAGGCACAACCCCCGCAGCAGGGTTTATTTCAGCCTC 3634
NM_173214.1|NFAT5a_t4      CAGCACCGAACTCAATTTCTCCACTTCAGTCAACATCAAACAGTGAACAACAAGCTGCTTTCCAACAGCAAGCTCCAATATCACACATCCAGACTCCTATGCTTTCCCAAGAACAGGCACAACCCCCGCAGCAGGGTTTATTTCAGCCTC 3696
exon                       NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3688
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                           ......3610......3620......3630......3640......3650......3660......3670......3680......3690......3700......3710......3720......3730......3740......3750
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NM_001113178.1|NFAT5d1_t6  AGGTGGCCCTGGGCTCCCTTCCACCTAATCCAATGCCTCAAAGCCAACAAGGAACCATGTTCCAGTCACAGCACTCAATAGTTGCCATGCAGAGTAACTCTCCATCCCAGGAACAGCAGCAGCAGCAGCAACAGCAGCAGCAACAGCAGC 3835
NM_138714.2|NFAT5a_t1      AGGTGGCCCTGGGCTCCCTTCCACCTAATCCAATGCCTCAAAGCCAACAAGGAACCATGTTCCAGTCACAGCACTCAATAGTTGCCATGCAGAGTAACTCTCCATCCCAGGAACAGCAGCAGCAGCAGCAACAGCAGCAGCAACAGCAGC 3900
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exon                       NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3838
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NM_001113178.1|NFAT5d1_t6  AGCAACAACAACAGAGCATTTTATTCAGTAATCAGAATACCATGGCTACAATGGCGTCTCCAAAGCAACCACCACCAAACATGATATTCAACCCAAATCAAAATCCAATGGCTAATCAGGAGCAACAGAACCAGTCAATTTTTCACCAAC 3985
NM_138714.2|NFAT5a_t1      AGCAACAACAACAGAGCATTTTATTCAGTAATCAGAATACCATGGCTACAATGGCGTCTCCAAAGCAACCACCACCAAACATGATATTCAACCCAAATCAAAATCCAATGGCTAATCAGGAGCAACAGAACCAGTCAATTTTTCACCAAC 4050
NM_006599.2|NFAT5c_t3      AGCAACAACAACAGAGCATTTTATTCAGTAATCAGAATACCATGGCTACAATGGCGTCTCCAAAGCAACCACCACCAAACATGATATTCAACCCAAATCAAAATCCAATGGCTAATCAGGAGCAACAGAACCAGTCAATTTTTCACCAAC 3934
NM_173214.1|NFAT5a_t4      AGCAACAACAACAGAGCATTTTATTCAGTAATCAGAATACCATGGCTACAATGGCGTCTCCAAAGCAACCACCACCAAACATGATATTCAACCCAAATCAAAATCCAATGGCTAATCAGGAGCAACAGAACCAGTCAATTTTTCACCAAC 3996
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isoform_c                  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 4084
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CLUSTAL ClustalW 2.0 MULTIPLE SEQUENCE ALIGNMENT

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NM_001113178.1|NFAT5d1_t6 CATCTTCGCCTCAACCACAGGCTACTTTATTTCACAACACAGCAGGAGGCACAATGAACCAACTGCAGAATTCTCCTGGCTCATCTCAGCAGACATCAGGAATGTTCTTATTTGGCATTCAAAATAACTGTAGTCAGCTTTTAACCTCTG  4435
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NM_006599.2|NFAT5c_t3     CATCTTCGCCTCAACCACAGGCTACTTTATTTCACAACACAGCAGGAGGCACAATGAACCAACTGCAGAATTCTCCTGGCTCATCTCAGCAGACATCAGGAATGTTCTTATTTGGCATTCAAAATAACTGTAGTCAGCTTTTAACCTCTG  4384
NM_173214.1|NFAT5a_t4     CATCTTCGCCTCAACCACAGGCTACTTTATTTCACAACACAGCAGGAGGCACAATGAACCAACTGCAGAATTCTCCTGGCTCATCTCAGCAGACATCAGGAATGTTCTTATTTGGCATTCAAAATAACTGTAGTCAGCTTTTAACCTCTG  4446
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NM_138714.2|NFAT5a_t1     GACCAGCTACATTGCCTGATCAGTTGATGGCCATAAGTCAGCCAGGCCAACCACAAAACGAGGGCCAGCCACCTGTGACAACACTTCTTTCTCAGCAAATGCCAGAGAATTCTCCACTGGCATCCTCTATAAACACCAACCAGAACATCG  4650
NM_006599.2|NFAT5c_t3     GACCAGCTACATTGCCTGATCAGTTGATGGCCATAAGTCAGCCAGGCCAACCACAAAACGAGGGCCAGCCACCTGTGACAACACTTCTTTCTCAGCAAATGCCAGAGAATTCTCCACTGGCATCCTCTATAAACACCAACCAGAACATCG  4534
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NM_138714.2|NFAT5a_t1     AAAAGATTGATTTGCTTGTTTCATTGCAAAACCAAGGGAACAACTTGACTGGCTCCTTTTAA  4712
NM_006599.2|NFAT5c_t3     AAAAGATTGATTTGCTTGTTTCATTGCAAAACCAAGGGAACAACTTGACTGGCTCCTTTTAA  4596
NM_173214.1|NFAT5a_t4     AAAAGATTGATTTGCTTGTTTCATTGCAAAACCAAGGGAACAACTTGACTGGCTCCTTTTAA  4658
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isoform_c                 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  4596
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