

Additional_result_file_4 to support figure 3c

APOBEC1 RNA-editing targets (predicted or experimentally validated by Rosenberg B.R. *et al*, 2011) x Tag-seq_4289_RT_CgtH_FDR

=> 53 transcripts in common between both lists (NCBI Gene IDs)

351, 567, 648, 987, 1386, 1810, 1997, 2313, 3615, 4942,
5218, 5358, 5567, 5796, 5925, 6102, 6319, 6428, 6601, 8539,
8924, 9191, 9373, 9403, 9510, 9730, 9741, 9849, 9989, 10001
10009, 22861, 22903, 23132, 23142, 23272, 23635, 26136, 27018, 29761
51742, 54776, 54918, 55754, 57120, 57132, 57515, 57799, 80218, 84162

116254, 133746, 552889 (underlined Gene ID represent experimentally validated APOBEC1 editing targets)

NB: Alteration of the NlaIII tag by APOBEC1 was checked only for experimentally validated APOBEC1 editing targets

Index	APOBEC1 RNA-editing target(Mouse)	Gene Symbol	Description	Human orthologue (blastn first hit)	Blast Score	E value	Entrez Gene ID (human)
1	NM_007471	APP	amyloid beta (A4) precursor protein	NM_201414	3646	0.0	<u>351</u>
2	NM_009735	B2M	beta-2-microglobulin	NM_004048	205	9e -50	<u>567</u>
3	NM_001025093	ATF2	activating transcription factor 2	NM_001880	2678	0.0	<u>1386</u>
4	NM_009029	RB1	retinoblastoma-associated protein	NM_000321	3439	0.0	<u>5925</u>
5	NM_053102	SEP15	15 kDa selenoprotein precursor	NM_004261	797	0.0	<u>9403</u>
6	NM_013918	USP25	ubiquitin carboxyl-terminal hydrolase 25	NM_013396	4353	0.0	<u>29761</u>
7	NM_133718	TMEM30A	transmembrane protein 30A	NM_018247	1797	0.0	<u>55754</u>
8	NM_019760	SERINC1	serine incorporator 1 precursor	NM_020755	1849	0.0	<u>57515</u>

RNA-editing table:

Index	APOBEC1 RNA-editing target(Mouse)	RNA editing status	Mouse mooring sequence in transcript	Human orthologue	Human mooring sequence (By similarity)	17 base <i>NlaIII</i> tag (RT) In human transcript	17 base <i>NlaIII</i> tag edition by APOBEC1
1	NM_007471	exp. validated	<u>ugaucac<u>uau</u></u> <u>g<u>aa</u>ucauugc</u>	NM_201414	tgatcactat conserved gaatcattgc conserved	ATCGCTTTCTACACTGT	No, because <i>NlaIII</i> tag is 3' to the mooring sequence
2	NM_009735	exp. validated	<u>ucauuacuu</u>	NM_004048	Not conserved	TGTACTTCCTAAGGTGA	Unlikely, because the mooring sequence is not conserved between mouse and human
3	NM_001025093	exp. validated	<u>aaauuacau</u>	NM_001880	Not conserved	AGTAAACCATCAGAGAA	Unlikely, because the mooring sequence is not conserved between mouse and human
4	NM_009029	exp. validated	<u>aaauugcuau</u>	NM_000321	aaattgctat conserved	AATATCATACAAATCAG	No, because <i>NlaIII</i> tag is 3' to the mooring sequence
5	NM_053102	exp. validated	<u>gcaugcuuac</u>	NM_004261	gcttgcttcc conserved	TGCTGTGTGCTCTTTGA	No, because <i>NlaIII</i> tag is 3' to the mooring sequence
6	NM_013918	exp. validated	<u>ugauuauuu</u>	NM_013396	tgattattt	ACTACAGCCATTTAAGT	No, because <i>NlaIII</i> tag is too distant from the mooring sequence
7	NM_133718	exp. validated	<u>agauuauau</u>	NM_018247	tgattaatat	CACCATTCAGTAAACAT	No, because <i>NlaIII</i> tag is 3' to the mooring sequence
8	NM_019760	exp. validated	<u>acuagaaaauaguau</u>	NM_020755	Not conserved	TAATTGAAATATATAGA	Unlikely, because the mooring sequence is not conserved between mouse and human

Legend:

Red nucleotides = mouse mooring sequence

Violet nucleotides = human mooring sequence (by similarity)

Green nucleotides = 17 base *NlaIII* tag in human transcript

Blue nucleotides = *NlaIII* "CATG" recognition site

Underlined nucleotides = Stretch of bases in which C to U edition could occur (3' to the mooring sequence)

1) APP, amyloid beta (A4) precursor protein

NM_007471	2690	--cctacgtattcttttcc tgatcactat gcatt-----ttgaacattt	2731	(Mm)
		. .		
NM_201414	2721	tgccctaagattcctttc tgatcactat gcattttaagttaaca--t	2768	(Hs)
NM_007471	3020	ttctccaaaattaattttctgcaggatgattgtaca gaatcattg cтта	3069	(Mm)
NM_201414	3054	ttctccaaa--caattttctgcaggatgattgtaca gaatcattg cтта	3101	(Hs)

>gi|228008405|ref|NM_201414.2| Homo sapiens amyloid beta (A4) precursor protein (APP), transcript variant 3, mRNA

GGATCAGCTGACTCGCCTGGCTCTGAGCCCCGCCGCCGCGCTCGGGCTCCGTCAGTTTCCTCGGCAGCGG
TAGGCGAGAGCACGCGGAGGAGCGTGC GCGGGGGCCCCGGGAGACGGCGGGCGGTGGCGGGCGGGCAGAG
CAAGGACGCGGCGGATCCCACCTCGCACAGCAGCGCACTCGGTGCCCGCGCAGGGTTCGCGATGCTGCCCCG
GTTTGGCACTGCTCCTGCTGGCCGCCTGGACGGCTCGGGCGCTGGAGGTACCCACTGATGGTAATGCTGG
CCTGCTGGCTGAACCCCAGATTGCCATGTTCTGTGGCAGACTGAACATGCACATGAATGTCCAGAATGGG
AAGTGGGATTCAGATCCATCAGGGACCAAACCTGCATTGATACCAAGGAAGGCATCCTGCAGTATTGCC
AAGAAGTCTACCCTGAACTGCAGATCACCAATGTGGTAGAAGCCAACCAACCAGTGACCATCCAGAACTG
GTGCAAGCGGGGCCGCAAGCAGTGCAAGACCCATCCCCACTTTGTGATTCCCTACCGCTGCTTAGTTGGT
GAGTTTGTAAAGTGATGCCCTTCTCGTTCCCTGACAAGTGCAAATCTTACACCAGGAGAGGATGGATGTTT
GCGAAACTCATCTTCACTGGCACACCGTCGCCAAAGAGACATGCAGTGAGAAGAGTACCAACTTGCATGA
CTACGGCATGTTGCTGCCCTGCGGAATTGACAAGTTCCGAGGGGTAGAGTTTGTGTGTTGCCCACTGGCT
GAAGAAAGTGACAATGTGGATTCTGCTGATGCGGAGGAGGATGACTCGGATGTCTGGTGGGGCGGAGCAG
ACACAGACTATGCAGATGGGAGTGAAGACAAAGTAGTAGAAGTAGCAGAGGAGGAAGAAGTGGCTGAGGT
GGAAGAAGAAGAAGCCGATGATGACGAGGACGATGAGGATGGTGTGATGAGGTAGAGGAAGAGGCTGAGGAA
CCCTACGAAGAAGCCACAGAGAGAACCACCAGCATTGCCACCACCACCACCACCACCACAGAGTCTGTGG
AAGAGGTGGTTTCGAGTTCCTACAACAGCAGCCAGTACCCCTGATGCCGTTGACAAGTATCTCGAGACACC
TGGGGATGAGAATGAACATGCCCATTTCCAGAAAGCCAAAGAGAGGGCTTGAGGCCAAGCACCCGAGAGAGA
ATGTCCCAGGTCATGAGAGAATGGGAAGAGGCAGAACGTCAAGCAAAGA ACTTGCTAAAGCTGATAAGA
AGGCAGTTATCCAGCATTTCAGGAGAAAAGTGGAACTTTGGAACAGGAAGCAGCCAACGAGAGACAGCA
GCTGGTGGAGACACACATGGCCAGAGTGGAAAGCCATGCTCAATGACCGCCGCCGCTGGCCCTGGAGAAC
TACATCACCGCTCTGCAGGCTGTTCCCTCCTCGGCCTCGTCACGTGTTCAATATGCTAAAGAAGTATGTCC
GCGCAGAACAGAAGGACAGACAGCACACCCTAAAGCATTTCGAGCATGTGCGCATGGTGGATCCCAAGAA
AGCCGCTCAGATCCGGTCCCAGGTTATGACACACCTCCGTGTGATTTATGAGCGCATGAATCAGTCTCTC
TCCCTGCTCTACAACGTGCCTGCAGTGGCCGAGGAGATTGAGGATGAAGTTGATGAGCTGCTTCAGAAAG
AGCAAAACTATTTCAGATGACGTCTTGCCCAACATGATTAGTGAACCAAGGATCAGTTACGGAAACGATGC

TCTCATGCCATCTTTGACCGAAACGAAAACCACCGTGGAGCTCCTTCCCCTGAATGGAGAGTTCAGCCTG
GACGATCTCCAGCCGTGGCATTCTTTTTGGGGCTGACTCTGTGCCAGCCAACACAGAAAACGAAGTTGAGC
CTGTTGATGCCCCGCCCTGCTGCCGACCGAGGACTGACCACTCGACCAGGTTCTGGGTTGACAAATATCAA
GACGGAGGAGATCTCTGAAGTGAAGATGGATGCAGAATCCGACATGACTCAGGATATGAAGTTCATCAT
CAAAAATTGGTGTCTTTGCAGAAGATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCG
GTGTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGTGCTGAAGAAGAAACAGTACACATCCATTCA
TCATGGTGTGGTGGAGGTTGACGCCGCTGTCACCCCAGAGGAGCGCCACCTGTCCAAGATGCAGCAGAAC
GGCTACGAAAATCCAACCTACAAGTTCTTTGAGCAGATGCAGAACTAGACCCCCGCCACAGCAGCCTCTG
AAGTTGGACAGCAAACCATTGCTTCACTACCCATCGGTGTCCATTTATAGAATAATGTGGGAAGAAACA
AACCCGTTTTATGATTTACTCATTATCGCCTTTTGACAGCTGTGCTGTAACACAAGTAGATGCCTGAACT
TGAATTAATCCACACATCAGTAATGTATTCTATCTCTTTACATTTTGGTCTCTATACTACATTATTAA
TGGGTTTTGTGTACTGTAAAGAATTTAGCTGTATCAAAC TAGTGCATGAATAGATTCTCTCCTGATTATT
TATCACATAGCCCCTTAGCCAGTTGTATATTATTCTTGTGGTTTTGTGACCCAATTAAGTCCTACTTTACA
TATGCTTTAAGAATCGATGGGGGATGCTTCATGTGAACGTGGGAGTTCAGCTGCTTCTCTTGCCTAAGTA
TTCTTTCC**TGATCACTAT**GCATTTTAAAGTTAAACATTTTAAAGTATTTTCAGATGCTTTAGAGAGATTT
TTTTTCCATGACTGCATTTTACTGTACAGATTGCTGCTTCTGCTATATTTGTGATATAGGAATTAAGAGG
ATACACACGTTTGTTCCTCGTGCCTGTTTTATGTGCACACATTAGGCATTGAGACTTCAAGCTTTTCTT
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GCGGGTGGGGAGGGGTGCTCTGCTGGTCTTCAATTACCAAGAATTTCTCCAAAACAATTTTCTGCAGGATG
ATTGTACAGAATCATTGCTTATGA**CATGATCGCTTTCTACTGT**ATTACATAAATAAATTAATAAAAT
AACCCCGGGCAAGACTTTTCTTTGAAGGATGACTACAGACATTAATAAATCGAAGTAATTTTGGGTGGG
AGAAGAGGCAGATTCAATTTTCTTTAACAGTCTGAAGTTTCATTTATGATACAAAAGAAGATGAAAATG
GAAGTGGCAATATAAGGGGATGAGGAAGGCATGCCTGGACAAACCCTTCTTTAAGATGTGTCTTCAATT
TGTATAAAATGGTGTTTT**CATGTAAATAAATACATTCTT**GGAGGAGCAAAAAAAAAAAAAAAAAA

2) B2M, beta-2-microglobulin

NM_009735	657	tcata-----tgccaa-----accctctg-----	675	(Mm)
		. . .		
NM_004048	759	gcataagttaacttccaatttacatactctgcttagaatttgggggaaaa	808	(Hs)
NM_009735	676	-----tacttctc---attacttggatgca----gttactcat--	706	(Mm)
			
NM_004048	809	tttagaaatataattgacaggatta-ttgg---aatttgta-taatga	853	(Hs)

The mooring sequence is not conserved

3) ATF2, activating transcription factor 2

Mooring sequence is not conserved between human and mouse B2M transcripts (transcripts do not align)

1) RB1, retinoblastoma associated protein

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NM_009029      4533 tgtaccggttgaaactataca-ttcaaattgctatgttcctatthttcta- 4580
              ||||..||||.|||||.|||| ||.|||||||.|.|||||||
NM_000321      4674 tgtattggttaaaactgtacatttaaaattgctatgttactatthttctac 4723
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>gi|108773786|ref|NM_000321.2| Homo sapiens retinoblastoma 1 (RB1), mRNA
GCTCAGTTGCCGGGCGGGGAGGGCGCGTCCGGTTTTTCTCAGGGGACGTTGAAATTATTTTTGTAACGG
GAGTCGGGAGAGGACGGGGCGTGCCCCGACGTGCGCGCGCGTCTCCTCCCCGGCGCTCCTCCACAGCTC
GCTGGCTCCCGCCGCGGAAAGGCGTCATGCCGCCAAAACCCCCGAAAAACGGCCGCCACCGCCGCCGC
TGCCGCCGCGGAACCCCCGGCACCGCCGCCGCCGCCCTCTGAGGAGGACCCAGAGCAGGACAGCGGC
CCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTC
AGAAATTAAAGATAACCAGATCATGTCCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGA
TGGAGTATTGGGAGGTTATATTTCAAAGAAAAAGGAAGTGTGGGGAATCTGTATCTTTATTGCAGCAGTT
GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCT
TTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTA
TGATGTATTGTTTGCCTCTTTCAGCAAATTGGAAAGGACATGTGAAGTATATATTTGACACAACCCAGC
AGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTA
AAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCAATTCAGTTAATGCTATGTGTCCTTGACTA
TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATAACCCATTAATGGT
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GGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT
TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCCTATTTTAACTGACAGTGAATCCAA
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ACAGGGTTGTGTCGAAATTTGGATCACAGCGATACAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAA
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TCTTGATTCTGGAACAGATTTGCTTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT
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GAAAATCACCTTGTCTAACTCAGAATTATTTTTAAAAAGAAATCTGGTCTTGTTAGAAAACAAAATTTTA
TTTTGTGCTCATTTAAGTTTCAAACCTTACTATTTTGACAGTTATTTTGATAACAATGACACTAGAAAAC

TGACTCCATTTTCATCATTGTTTCTG**CATGAATATCATACAAATCAG**TTAGTTTTTTAGGTCAAGGGCTTAC
TATTTCTGGGTCTTTTGGCTACTAAGTTCACATTAGAATTAGTGCCAGAATTTTAGGAACTTCAGAGATCG
TGTATTGAGATTTCTTAAATAATGCTTCAGATATTATTGCTTTATTGCTTTTTTTGTATTGGTTAAAAC**CTG**
TACATTTAAAATTGCTATGTTACTATTTTCTACAATTAATAGTTTGTCTATTTTAAAATAAATTAGTTGT
TAAGAGTCTTAA

2) SEP15, 15kDa selenoprotein precursor

NM_053102 842 taacttagttttg**catgcttac**attggtcatcctttttatgtacat---- 887
 |||.|||||||||.|||||.|||||.|||.|.|||. |||.|
NM_004261 879 taatntagttttg**cttgcttc**cattgatcagtcctt-----tacttgagg

>gi|42741647|ref|NM_004261.3| Homo sapiens 15 kDa selenoprotein (SEP15), transcript variant 1, mRNA

GGAGAAGAAGGCGGGGCTAAAACTGGCGAAGGCGTGGCTTCTTGGCTGCTTGACGAAGTGTTCGTGAATAA
AAGAAAGGAGACCGCAGAAGTAAAGAAGTGGGGAGTTTAGGCAAGTGCCTGATTTGGGTAATCGAAAGCA
CCCAGTGATTGTATTTGATGACTTTTAAAGCTTTCATATGCCGTTATTTAATACCTGTCACTTCCAAATGA
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GGGTCCTTCTAGGCAGCCAGAAACCTGCGGAAAATGGTAGCGATGGCGGCTGGGCCGAGTGGGTGTCTGG
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GTTACCTTATCAAATGAAATATTACAGCACCTAGAAAATAATTTAGTTTT**GCTTGCTTCC**ATTGATCAGT
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TGGCAAGCTTAACAAAACCCATTTTTTATAAATGTCCATCCTCCTGCATTTGTTGATAACCACTAACAAA
TGCTTTGTAACAGACTTGCGGTTAATTATGCAAATGATAGTTTGTGATAATTGGTCCAGTTTTACGAACA
ACAGATTTCTAAATTAGAGAGGTTAACAAGACAGATGATTACTATGCCT**CATGTGCTGTGTGCTCTTTGA**
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TGCATAAAAACCTTTGTAGCTTCAATTATTGTAAAACATATTCAGATCCTACAGTAAGAGTGAAACATTCA
CAAAGATTTGCGTTAATGAAGACTACACAGAAAACCTTCTAGGGATTTGTGTGGATCAGATACATACTT

GGCAAATTTTTGAGTTTTACATTCTTACAGAAAAGTCCATTTAAAAGTGATCATTTGTAAGACCAAATA
TAAATAAAAAGTTTTCAAAAATCTATCTGAATTTGGAATTTCTTCTGGTTTGTTCATGTTTAAAAATG
ATGTTTTTCAATGCATTTTTTTCATGTAAGCCCTTTTTTTAGCCAAAATGTAAAAATGGCTGTAATATTT
AAAACCTTATAACATCTTATTGTTGGTAATAGTGCTTTATATTTGTCTGATTTTATTTTTCAAAGTTTTTT
CATTTATGAACACATTTTCATTGGTATATTATTTAAGGAATATCTCTTGATATAGAATTTTTTATATTA
AATGATTTTTCTTTGCTTAAAAA

3) USP25, carboxyl-terminal hydrolase 25

NM_013918 3902 -cttttctgtatgtataaataata-----caagg**tgattattt**caagaga 3945
 ||||| |..|||||..|.|||| ||||| ||||| ||||| |||||
NM_013396 4129 actttt-taaatgtatttacaatatacagcaagg**tgattattt**caagaga 4177

>gi|50312665|ref|NM_013396.3| Homo sapiens ubiquitin specific peptidase 25 (USP25), mRNA

GCGGCCGCGCTGGCCCTCACAGTCGGCGTTTCGCCGCTGCCGCGGTGCCGCGCACGCCGGCCGCCAT
CGCCTTCGCGCCTGGCTGGCGGGGGCGCTGTCTCCAGGCCGTCCGCGCCGCTCCCTGGAGCTCGGCGG
AGCGCGGCAGCCAGGGCCGGGAGGCGGAGGAGCCGGGCGCCACCGCCGCGCCGCGCCGCGCCGCGC
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AATCAACTGAGAGAAATTACGGGGATTAATGACACCCAGATACTACAGCAAGCCTTGAAGGATAGTAATG
GAACTTGGAATTAGCAGTGGCTTTCCTTACTGCGAAGAATGCTAAGACCCCTCAGCAGGAGGAGACAAC
TTACTACCAACAGCACTTCCTGGCAATGATAGATACATCAGTGTGGGAAGCCAAGCAGATACAAATGTG
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CAAATGACTCACAGCAGCAAGATGTGAGTGAGTTTACACACAAATTTAGATTGGTTAGAAGATGCCTT
CCAAATGAAAGCTGAAGAGGAGACGGATGAAGAGAAGCCAAAGAACCCCATGGTAGAGTTGTTCTATGGC
AGATTCTGGCTGTGGGAGTACTTGAAGGTAAAAAATTTGAAAACACTGAAATGTTTGGTCAGTACCCAC
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GATCAAGAGACTGAAAGATTACCTCACGGTATTACAACAAAGGCTAGAAAGATATTTAAGCTATGGTTCC
GGTCCCAAACGATTCCCTTGGTAGATGTTCTTCAGTATGCATTGGAATTTGCCCTCAAGTAAACCTGTTT

GCACTTCTCCTGTTGACGATATTGACGCTAGTTCCCCACCTAGTGGTTCATACCATCACAGACATTACC
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ATTTTCATCGAGATCAGTAATACACAAACCATTTACTCAGTCCCGGATACCTCCAGATTTGCCCATGCATC
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AATAGAAAATGACACCAGAGATTTGCAGGAAAGCATATCCAGAATCCATCGAACAATTGAATTAATGTAC
TCTGACAAATCTATGATACAAGTTCCTTATCGATTACATGCCGTTTTAGTTTACGAAGGCCAAGCTAATG
CTGGGCACTACTGGGCATATATTTTTGATCATCGTGAAAGCAGATGGATGAAGTACAATGATATTGCTGT
GACAAAATCATCATGGGAAGAGCTAGTGAGGGACTCTTTTGGTGGTTATAGAAATGCCAGTGCATACTGT
TTAATGTACATAAATGATAAGGCACAGTTCCTAATACAAGAGGAGTTTAATAAAGAACTGGGCAGCCCC
TTGTTGGTATAGAAACATTACCACCGGATTTGAGAGATTTTGTGAGGAAGACAACCAACGATTTGAAAA
AGAAGTAGAAGAATGGGATGCACAACCTGCCAGAAAGCTTTGCAGGAAAAGCTTTTAGCGTCTCAGAAA
TTGAGAGAGTCAGAGACTTCTGTGACAACAGCACAAGCAGCAGGAGACCCAGAATATCTAGAGCAGCCAT
CAAGAAGTGATTTCTCAAAGCACTTGAAAGAAGAACTATTCAAATAATTACCAAGGCATCACATGAGCA
TGAAGATAAAAGTCCTGAAACAGTTTTTGCAGTCGGCAATTAAGTTGGAATATGCAAGGTTGGTTAAGTTG
GCCAAGAAGACACCCACCAGAAACCGATTATCGTTTACATCATGTAGTGGTCTACTTTATCCAGAACC
AGGCACCAAAGAAAATTTATTGAGAAAACATTACTAGAACAATTTGGAGATAGAAATTTGAGTTTTGATGA
AAGGTGTCACAACATAATGAAAGTTGCTCAAGCCAACTGGAAATGATAAACCTGAAGAAGTAACTTG
GAGGAATATGAGGAGTGGCATCAGGATTATAGGAAATTCAGGGAAACAACCTATGTATCTCATAATTGGGC
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AGAAGTCTTGTCTAAAGGCTTATACAGAGGACATGATGAAGAATTGATATCACATTATAGAAGAGAATGT
TTGCTAAAATTTAATGAGCAAGCCGCAGAACTCTTCGAATCTGGAGAGGATCGAGAAGTAAACAATGGTT
TGATTATCATGAATGAGTTTATTGTCCCATTTTTGCCATTATTACTGGTGGATGAAATGGAAGAAAAGGA
TATACTAGCTGTAGAAGATATGAGAAATCGATGGTGTTCCTACCTGGTCAAGAAATGGAACCCACACCTC
CAAGAAAAGCTGACAGATTTTTTGCCTAACTGCTTGATTGTTCTATGGAGATTAAGTTTCCATGAGC
CACCGAAGTTACCTTCATATTCCACGCATGAACTCTGTGAGCGATTTGCCCGAATCATGTTGTCCCTCAG
TCGAAGTCTGCTGATGGAAGATAAACTGCACACTTTCCCTGAACACACTGTATAAACTCTTTTTAGTTC
TTAACCCTTGCCCTTCTGTACAGGGTTTTGCTTGTGCTGCTATAGTTTTTAACTTTTTTTTTATTTAAT
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CGCTCAGACATTTTAAACCGGAACTGATGTATAATCACAAATCTAATTGATTTTATTATGGCAAACTATG
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GTAAATGAAATAAAGAATAAAGTTTTATTTATGGCTACCTATGTGTTTGTAAAGCAGGTATATTGTATATT
AGTGTATTAGTAATACTAGATAAATGAATTTTGTCTGGGGATTAAGATTGGATAGTTAATAGATTAATAC
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TATTTTTAACAAAGTTCTTGAAGTTAGTATGGCACCAGGAACTGTTTTGAATTCAGTCAGTTTTTACTC
AAGTAAGTGGTTGATTTTTTTTTAAGTCAAACACTGAACTTTTTATCCTTTTCTTAGATTAATCTTAC
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CTATTGTAATAATTTAAAGAAATATTTATATATACACATATATACACATACACACATGTATATATATATT

CTTCATAATGGAGGACAATGTTTTGCAATATATAAATCATTCTATTTTTGTAAATTGTATATCACTTTAA
 TTGAAAATGTTCTCTACTAATTAATACTGTGAAACAAAATTGATGTTGTTAACTAGAA GTTATGAGTAT
 CTTAACTGCCTTTATTCTTTTTCAAAAAGGAAAAAGCTGTAGAACATTTTGTAGATGAAACTACTGTTTA
 AGATTAATGAATTAATATTGTGAATGAAAATCAAATCCATACTTTAAAGGTAATCATGTTACTAACAAC
 CTATTTTTGAATTCATAAAAATTTCTTTATAAATGATGTTTTGTGAACATAGTAAAATAGACCATTATAC
 TATGTGTATGTTTGATACAGCGTCGCCAAAAC TAGTGTTCTTTATTAGTGCCTCTCACAAAAGATCCTGG
 ATGGAGGAGTAAGATGAAATATTATGCTATTATATGATGCTGTTTGTAAAGGTATTAATGTACTAGTAAG
 GTGTTAATGACAAGGAATTAGTACTATTCCTGTTGTAAAGTTAGATTTTGCATATTGTATCTATCAAAAT
 ATGTTTTGGTTTTAGATTTTAAAGTTGTCTACTGAGCAGATTTCTGCATTGGTTTTCCAGTCCTGTTAAAAG
 TTTAGAAACTTCATATGTGTCATCACAGCTTTTGTAAAGAAAGTATCCTTAATATTTTATGACATTCT

4) TMEM30A, transmembrane protein 30A

NM_133718 2767 tgggtaacatatcagttt**agattaatat**gtgctt-----aaaagaaga 2809
 ||| | | | | . | | | | . | | | | | | | | | | | | | . | | | | |
 NM_018247 2824 tgggtaatgtat-actttt**gattaatat**atacttttttttaaaaaacaa-a 2871

>gi|221219060|ref|NM_018247.3| Homo sapiens transmembrane protein 30A (TMEM30A), transcript variant 1, mRNA

ATCCTCCTCCCCTTTCCCCTCCCCATGTCCTCCTTCTTCTCCCTCCTCCTCCTCCTCCTCCTCCTGCGG
 TCTCCAGCCGACTTTCGCTTCCCGTCAGCAGCCTTTGGCGGAAGAGTGTCCC GCCTCTTCCGCTCTACAG
 CGGAGGTGGCTGTGGCGGTGGCGCTGGTGGCTGCGGCGGCGGCAGCGGCGCTCGAGCGGTTCTT
 GTCAGGGTCAGCCGGCGGGCCCCCTGGGTGGTCCACCTGCAAATCGCGGAGCGGCGCCCCAGGGATCGAT
 GGCGATGAACTATAACGCGAAGGATGAAGTGGACGGTGGGCCCCCGTGTGCTCCGGGGGGCACCGCGAAG
 ACTCGGAGACCGGATAACACGGCCTTCAAACAGCAACGGCTGCCAGCTTGGCAGCCCATCCTTACGGCTG
 GCACGGTGCTACCTATTTTCTTCATCATCGGTCTCATCTTCATTCCCATCGGCATTGGCATTTTTGTAC
 CTCCAACAACATCCGCGAGATCGAGATTGATTATACCGGAACAGAGCCTTCCAGTCCCTGTAATAAATGT
 TTATCTCCGGATGTGACACCTTGCTTTTTGTACCATTAACCTCACACTGGAAAAGTCATTTGAGGGCAACG
 TGTTTATGTATTATGGACTGTCTAATTTCTATCAAAACCATCGTCGTTACGTGAAATCTCGAGATGATAG
 TCAACTAAATGGAGATTCTAGTGCTTTGCTTAATCCCAGTAAGGAATGTGAACCTTATCGAAGAAATGAA
 GACAAACCAATTGCTCCTTGTGGAGCTATTGCCAACAGCATGTTTAATGATACATTAGAATTGTTTCTCA
 TTGGCAATGATTCTTATCCTATAACCTATCGCTTTGAAAAGAAAGGTATTGCTTGGTGGACAGATAAAAA
 TGTGAAATTCAGAAATCCCCCTGGAGGAGACAACCTGGAAGAACGATTTAAAGGTACAACAAAGCCTGTG
 AACTGGCTTAAACCAGTTTACATGCTGGATTCTGACCCAGATAATAATGGATTTCATAAATGAGGATTTTA
 TTGTTTGGATGCGTACTGCAGCATTACCTACTTTTCGCAAGTTGTATCGTCTTATAGAAAGGAAAAGTGA
 TTTACATCCAACATTACCAGCTGGCCGATACTCTTTGAATGTCACATACAATTACCCTGTACATTATTTT
 GATGGACGAAAACGGATGATCTTGAGCACTATTTTCATGGATGGGAGGAAAAAATCCATTTTTTGGGGATTG

CTTACATCGCTGTTGGATCCATCTCCTTCCTTCTGGGAGTTGTACTGCTAGTAATTAATCATAAATATAG
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CAAGGCCAGTCCATTTCAACCTAGCTTTTCGAATGCTGATATCTGGTTAGTATGTCATTTTGAAGTTGGCA
CATAACTTTTCTAAAAAAGCAGTCTTTGTTGTTTGCTTCTTCCCTACGGATGACTTCTAAAAATATAT
GACGGGTATAAAAAAATTAGCTATATTGATCATATCAACACTGTAAGTCTGAAATGGCATTCTAATGTT
TGCTTTTTTATTTCGGACAGGCCACATGATGCATAGAGCCTCTTTCATGTGACTTGTGTCTACTGCTTAAAT
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TTTCCCTTGAAGCTTATACTTTATAAGGGAAGAAAGAATTCAGGTGATATGGGAAAACCTGCTTGGCAGAC
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GGAGAGGGGTTTTCTGCCACTCTTCCAGATTGAGTCTGTGCTGTTTAAAGGAGGACTACCATCCTGCAACT
CTTTTTCTAACTGGGGCACAGAGGATGTCGCTAAAGAAAAGTTGAAGAGCCCTTTCAGCACTTCTCATC
TGTGGAGAAGATGGAATCTTAAAATACATTTGGAGTTTTATCTGTTTTACAAGTCCATTGATGGCCTAAG
TTCTCCTGTTTTCTGCTGTTTGATCTCTAAGGAACCTCTGTTGCTAAATATGAAGAGTATGGAACATTC
GTATAGTCTCTGTGAAGCATGGGGGGAGGGAAGACATTTCTTTTTCTTATAGGCTTTATGCTCAAATGTC
ATAGTCTCCTTTCAAAGAATTGTGTTGCATTTTAAATGCACCCAGCTTAAGTAGAAGACATTGAAGGATG
CATTAAATTTTCAGGAACATTTTTGAATTATGAAAAGATTCCCAATTGAAAAAATTATTCAACAAGTAAAA
GCTAAGAAATTTCAATTGAAATCATAAGGCAGTTTAAAGCATAAATTGATAAAAAATAGCTGTGTACTACTAA
TTAATAGAAAATCATTCAACCAAGAGAAGAGTCAAGTGAATATCGTTTGTTTATTTGCTAGTGAGTTTCT
TTGTAACGTTGATTTTATTAAATGATAATATTTGGTTAGTATGTCCTATGTTAATAAAAAATGAACAAAAT
TAATTTTGCTATGTTTCAGGTGTCTTGATAAAATAACAATGCTCCAGTGTGTTGCTTACATTTAGCACTA

AATTTTAAACACAGCGTCAGTGAGTCCAGGTTTTAACTTCTTCATGCCTGGATGGGATAAAAATGTAATTCA
 TTGTTAAATTAATTCATATTTGTATTTATTAATCACTGTGACAACATTAACCATTTGTTCTTACCAGGAA
 GTGGTCAGATTATCATCTGAGTTACAGTTAGACTGGCTAAGTTTGGTATTAGATCAAGGGGAATGTCCAG
 TAAACAGAGAGGTAAGCATGATGGAAATAATGAAGTGGGGTACACAGGAAAAACCTGACTAGTGAGGAGG
 AGCAGCTGAGAGATAGGGTCAGTGAATGCGGTTTCAGCCTGCTACCTCTCCTGTCTTCATAGAACCATTGC
 CTTAGAATTATTGTATGACACATTTTTTTGTTGGTTAAGCTGTAAGGTTTTGTTCTTTGTGAACATGGGTA
 TTTTGAGGGGAGGGTGGAGGGAGTAGGGAAGTGGTCCTTTTACAAGAATTTTGATGCATAAGTGTCTATT
 GTAGGGTTTGGATGATCTAGTAAAGTGTTTTAGAACCCCTTTTTATCCCATGCACCATTGAGTAAACATA
 AAAATCACAATTCTGCTAATGTCATTTGGAACCTCAAATAAATATCTTGTCTAAAAACAAATC

5) SERINC1, serine incorporator 1 precursor

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NM_019760      2644  catgcaattga-----tatagtaa---atcgactagaaaaat---  2676
                ||||.|||||          |||.|||  .||.||..|||||
NM_020755      2870  catgtaattgaaatatatagattattgtaacctttcaacctgaaaatcaa  2919

NM_019760      2677  -tagtatgccacttaattaagataaaaaatgcttagttatt--tatgt---  2720
                .|||||          |||  |.|||||||  |||||
NM_020755      2920  gcagtatg-----aga-----gtttagttatttgtatgtgtc  2951
  
```

Mooring sequence is not conserved between human and mouse

Supplementary information for Figure 3d

APOBEC1 RNA-editing targets (predicted or experimentally validated by Rosenberg B.R. et al, 2011) x Tag-seq_1123_RT_CgtH_FDR
 => 12 transcripts in common, namely 3251, 7009, 8904, 10056, 10237, 26999, 55610, 64770, 79868, 84726, 170506 and 219771 (NCBI Gene IDs)

Orthology table:

Index	APOBEC1 RNA-editing target(Mouse)	Gene Symbol	Description	Human orthologue (blastn first hit)	Blast Score	E value	Gene ID (human)
1	NM_013556	HPRT1	hypoxanthine phosphoribosyltransferase 1	NM_000194	1279	0.0	3251
2	NM_026669	TMBIM6	transmembrane BAX inhibitor motif containing 6	NM_003217	985	0.0	7009

3	NM_170588	CPNE1	copine I	NM_152928	1679	0.0	8904
4	NM_011811	FARSB	phenylalanyl-tRNA synthetase, beta subunit	NM_005687	1731	0.0	10056
5	NM_016752	SLC35B1	solute carrier family 35, member B1	NM_005827	1178	0.0	10237
6	NM_133769	CYFIP2	cytoplasmic FMR1 interacting protein 2	NM_001037333	4785	0.0	26999
7	NM_024260	CCDC132	coiled-coil domain containing 132	NM_017667	3376	0.0	55610
8	NM_172824	CCDC14	coiled-coil domain containing 14	NM_022757	222	5e-56	64770
9	NM_177130	ALG13	asparagine-linked glycosylation 13 homolog	NM_018466	440	e-122	79868
10	NM_001159634	PRRC2B	proline-rich coiled-coil 2B	NM_013318	7685	0.0	84726
11	NM_028136	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	NM_020865	3190	0.0	170506
12	NM_026484	CCNY	cyclin Y	NM_145012	1350	0.0	219771

RNA-editing table:

Index	APOBEC1 RNA-editing target(Mouse)	RNA editing status	Mouse mooring sequence in transcript	Human orthologue	Human mooring sequence (By similarity)	17 base NlaIII tag (RT) In human transcript	17 base NlaIII tag edition by APOBEC1
1	NM_013556	exp. validated	ugauuugcac	NM_000194	ttatttgcac conserved	TATCTTCTAAGAATTTT	No, because NlaIII tag is too distant from the mooring sequence
2	NM_026669	exp. validated	cuauuuugaa	NM_003217	ctattttga conserved	CCACCCCGAATGGCTCA	No, because NlaIII tag is too distant from the mooring sequence
3	NM_170588	predicted	ucaauaaaauuauau	NM_152928 (U83246)	Not conserved	GAGCAGCTGGACGCTGA	No, the mooring sequence is not conserved
4	NM_011811	predicted	ucucuggaaaaucauu	NM_005687	tcctagaatca atgt (rather conserved)	CCCTGCTCCTCCCTAGA	Possible. NlaIII tag and APOBEC1 putative editing sites are overlapping.
5	NM_016752	predicted	acacuuauuuuuu	NM_005827	atatttaagt tat (rather	CAGTGGGTGGGCACTGT	No, because NlaIII tag is too distant from the mooring sequence

					conserved)		
6	NM_133769	predicted	ucuguguuguuuacuau	NM_001037333	tctgtgtggattacta (conserved)	CTGGTTTCTCCATAGCA	No, because NlaIII tag is too distant from the mooring sequence
7	NM_024260	Predicted	acucucauaauuuuuu	NM_017667	Not conserved	TAAGTAAAATAGTTGAA	No, the mooring sequence is not conserved
8	NM_172824	predicted	acuacaagaucauuau	NM_022757	attgcaagatcatat	TAAGCAGCACGTTTTAA	No, because NlaIII tag is too distant from the mooring sequence
9	NM_177130	predicted	acaauuaaaucuuu	NM_018466	ataatataattataa	AAGTGCCTGTTTGTAC	No, because NlaIII tag is too distant from the mooring sequence
10	NM_001159634	predicted	ucaccaaaaucuuu	NM_013318	Not conserved	GCCAGACCCCTCCCACC	No, the mooring sequence is not conserved
11	NM_028136	predicted	acucuaaaauuuuu	NM_020865	Not conserved	CCCACTCTTTGGGAGTA	No, the mooring sequence is not conserved
12	NM_026484	predicted	ucuaucuaaguuuuu	NM_145012	tctagatcacatg	GCGCAGACTTCCAAATA	No, because NlaIII tag is too distant from the mooring sequence

1) HPRT1, hypoxanthine phosphoribosyltransferase 1

```
NM_013556      961 cgtccccagacttttgatttgcacatgagcctatagc---cagcctac 1007 (Mm)
               |.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|
NM_000194      985 cattcctaaactgttatttgcacatgagcctatagactatcag--ttc 1032 (Hs)
```

```
>gi|164518913|ref|NM_000194.2| Homo sapiens hypoxanthine phosphoribosyltransferase 1 (HPRT1), mRNA
GGCGGGGCCTGCTTCTCCTCAGCTTCAGGCGGCTGCGACGAGCCCTCAGGCGAACCTCTCGGCTTTCCCG
CGCGGCGCCGCTCTTGCTGCGCCTCCGCCTCCTCCTCTGCTCCGCCACCGGCTTCCTCCTCCTGAGCAG
TCAGCCCGCGCGCCGGCTCCGTTATGGCGACCCGCAGCCCTGGCGTCGTGATTAGTGATGATGAAC
CAGGTTATGACCTTGATTTATTTGCATACCTAATCATTATGCTGAGGATTTGGAAAGGGTGTTTATTCC
TCATGGACTAATTATGGACAGGACTGAACGTCTTGCTCGAGATGTGATGAAGGAGATGGGAGGCCATCAC
ATTGTAGCCCTCTGTGTGCTCAAGGGGGGCTATAAATTCCTTGTGCTGACCTGCTGGATTACATCAAAGCAC
TGAATAGAAATAGTGATAGATCCATTCTATGACTGTAGATTTTATCAGACTGAAGAGCTATTGTAATGA
CCAGTCAACAGGGGACATAAAAGTAATTGGTGGAGATGATCTCTCAACTTTAACTGGAAAGAATGTCTTG
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CAAAGATGGTCAAGGTCGCAAGCTTGCTGGTGAAAAGGACCCACGAAGTGTTGGATATAAGCCAGACTT
TGTTGGATTTGAAATTCAGACAAGTTTGTTGTAGGATATGCCCTTGACTATAATGAATACTTCAGGGAT
```

TTGAATCATGTTTGTGTCATTAGTGAAACTGGAAAAGCAAATACAAAGCCTAAGATGAGAGTTCAAGTT
 GAGTTTGGAAACATCTGGAGTCCTATTGACATCGCCAGTAAAATTATCAATGTTCTAGTTCTGTGGCCAT
 CTGCTTAGTAGAGCTTTTTG**CATGTATCTTCTAAGAATTTT**ATCTGTTTTGTACTTTAGAAATGTCAGTT
 GCTGCATTCCCTAAACTGT**TTATTTGCAC**TATGAGCCTATAGACTATCAGTTCCCTTTGGGCGGATTGTTG
 TTTAACTTGTAATGAAAAAATCTCTTAAACCACAGCACTATTGAGTGAAACATTGAACTCATATCTGT
 AAGAAATAAAGAGAAGATATATTAGTTTTTTAATTGGTATTTTAAATTTTATATATGCAGGAAAGAATAG
 AAGTGATTGAATATTGTTAATTATACCACCGTGTGTTAGAAAAGTAAGAAGCAGTCAATTTTTCACATCAA
 AGACAGCATCTAAGAAGTTTTGTTCTGTCTGGAATTATTTTAGTAGTGTTCAGTAATGTTGACTGTAT
 TTTCCAACCTTGTTCAAATTATTACCAGTGAATCTTTGTCAGCAGTTCCCTTTTAAATGCAAATCAATAAA
 TTCCCAAAAATTTAAAAA

2) TMBIM6, transmembrane BAX inhibitor motif containing 6

NM_026669	928	gataatg-aaagcatcaggaaagcttttgtacttagtggttttct ctatt	976	(Mm)
		. . .		
NM_003217	934	gataatgaaaagcatcagaaaagcttttgtactttgtggtttcct ctatt	983	(Hs)
NM_026669	977	ttgaa attttttgatc-aaaaactgattag-tgaatatagtttgagttt	1024	(Mm)
		.		
NM_003217	984	ttg-a attttttgatcaaaaaactgattagcagaatatagtttgagttt	1032	(Hs)

>gi|148746208|ref|NM_003217.2| Homo sapiens transmembrane BAX inhibitor motif containing 6 (TMBIM6), transcript variant 1, mRNA
 GAGAGGCGAACGCCGGGTAAAAGATCGGGAGCGGAAGTGGGCGAGTCAGAGCACATCCGGTGTTAGAAGC
 GCTGGTAGGCCTTGGAGAGGCGGGTTAGGAAGAGTGGAGACTGCTGCACGGACTCTGGAACCATGAACAT
 ATTTGATCGAAAGATCAACTTTGATGCGCTTTTAAAATTTTCTCATATAACCCCGTCAACGCAGCAGCAC
 CTGAAGAAGGTCTATGCAAGTTTTGCCCTTTGTATGTTTGTGGCGGCTGCAGGGCCCTATGTCCATATGG
 TCACTCATTTTCATTGAGGCTGGCCTGCTGTCTGCCTTGGGCTCCCTGATATTGATGATTTGGCTGATGGC
 AACACCTCATAGCCATGAACTGAACAGAAAAGACTGGGACTTCTTGCTGGATTTGCATTCCTTACAGGA
 GTTGGCCTGGGCCCTGCCCTGGAGTTTTGTATTGCTGTCAACCCAGCATCCTTCCCCTGCTTTCATGG
 GCACGGCAATGATCTTTACCTGCTTCACCCTCAGTGCACCTATGCCAGGCGCCGTAGCTACCTCTTTCT
 GGGAGGTATCTTGATGTCAGCCCTGAGCTTGTTGCTTTTGTCTTCCCTGGGGAATGTTTTCTTTGGATCC
 ATTTGGCTTTTCCAGGCAAACCTGTATGTGGGACTGGTGGTCAATGTGTGGCTTCGTCTTTTGGATACTC
 AACTCATTATTGAAAAGGCCGAACATGGAGATCAAGATTATATCTGGCACTGCATTGATCTCTTCTTAGA
 TTTCATTACTGTCTTCAGAAAACCTCATGATGATCCTGGCCATGAATGAAAAGGATAAGAAGAAAGAGAAG
 AAATGAAGTGACCATCCAGCCTTCCCAATTAGACTTCTCTCCTTCCACCCCTCATTTCTTTTGCAC

ACATTACAGGTGGTGTGTTCTGTGATAATGAAAAGCATCAGAAAAGCTTTTGTACTTTGTGGTTTCCTCT
ATTTTGAATTTTTTGGATCAAAAAACTGATTAGCAGAATATAGTTTGGAGTTTGGCTTCATCTTCCTGGGG
 TTCCCCTCACTCCCTTTTTTGTCAACCCCATCTGTAGCCTCTTCCTCTACTCAGGCAGTCGACCCGCCAC
 GATGAGAAGTGGGACCAGCAGAGGGCGCCAACTTCAGGAGTCCGCTTTCCCACCAGGCTTCATTCACCCA
 GTGGACCTGAAGTGTGGTAGAGCCACCCGGCCCTTCCCTTCCTCATTGTTGTTGGTATGCGCACAGTT
 CCTGTGGGACTGGGCCGTGAGTTTTCCATTGGAAAGAAGTTCAGTGGTCCCATTGTTAACTCAGCCTCAA
 ATCTCAACTGTCAGGCCCTACAAAGAAAATGGAGAGCCTCTTCTGGTGGATGCTTTGCTCCCTCTGAGCT
 GCCCATGCTGGTCTGGCAAACACACCTTTCTGCTTTGCCTTACAAAAGTAATGTGTTCCCTTTCCCACC
 CCTTGCCTGACCCTCAGGGAGTCAGCCTGCTTCCATCCATGGGTGGGAAGACTTCAGCACAAAGGAAAGA
 CTAATTCTTGTGAGGCATTTTTGAAAAGGCTGATTATGTGTATCAAGGTACAGCATCGTAGGGTTCCCTT
 AAACCTTGCCCTGTTTTTGTTTTTTAGTTTGTATCCCTTACTGAGCGGCCTCTACTAGGTGGCTGTGA
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 ATTTGTGGCCTTTTAGGCGGGAGTTAGGCGACCAAACCAGTGAGAGCCCAATCCCTGCAGTTTTGTGGC
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 GAGCCATTGAAAGCTCATTACCAGTAGGACATAATTTTTGGCTCTCCCTATTCACAACCAGTGCACAGTT
 TGACACAGTGGCCTCAGGTTACAGTGCACCATGTCACTGTGCTATCCTACGAAATCATTTGTTTCTAAG
 TTGTGTTTATTCTGGAGTGA**CATGCCACCCGAATGGCTCA**CTTTCACTGAGGATGCTGTCTCTGATT
 TAGCTGCTGCCTCCAGCCTCTGGCTTGAGAACTTACTAAAGGCACTTCCCTTCCTGTTAAACCCCTGTTAA
 CTCTCCATAAATTTGGTGATTCTCTGCTAGGCCTAAGATTTTTGAGTTAACATCTCTTGAAGCCAAACTCC
 ACCTTCTGTGCTTTTTGCTTGGGATAATGGAGTTTTTCTTTAGAAACAGTGCCAAGAATGACAAGATATT
 AAAAAAAAAAAGAAAGAAAAAAAAAAAAACACCTACTTTTAAAGAAAATACCTAACAGATTTTAAATAT
 AGTTATCTCTACCCTTTCTTTTCTAGTTTCTTGATTTTTCAGCTCAGGCTGCATTCTAACTCATACTGTG
 AAGACAAAGGTGTTTTTGTTCAGAAATATATGAAATCTGCATAGTCTTAATTTGTAAAAAATAAAGAAA
 ATTCCTTAACCTTTA

3) CPNEI, copine I

NM_170588	3476	aaaatatatctatgta tcaataaaattaatat atccacctcctcaaaaaa	3525	(Mm)
U83246	1985	-----	1985	(Hs)
NM_170588	3526	aaaaaaaaaaaaaaaa	3542	

The mouse NM_170588 transcript is longer than the human NM_152928 (U83246). The mooring sequence is close to the 3' boundary.

⇒ The mooring sequence is not conserved

4) FARSB, phenylalanyl-tRNA synthetase, beta subunit

NM_011811	1699	tcctgatgttatcaccaaatttgagctgacccatgcccctgttccctctctg	1748	(Mm)
		.		
NM_005687	1730	tcctgacgttatcaccaaatttgagctgacccatgcccctgtcctccctag	1779	(Hs)
NM_011811	1749	aatcaatatgagccctttttgtg-aggttggtctctg-----	1786	(Mm)
		. .		
NM_005687	1780	aatcaatgttgaccctttttgtgaagattggtctctgtggtgtgattc	1829	(Hs)

>gi|124028524|ref|NM_005687.3| Homo sapiens phenylalanyl-tRNA synthetase, beta subunit (FARSB), mRNA
AGCTCGCTGCGCAGGCGCAGTGTGAGTTCGACACACCATGCCGACTGTCAGCGTGAAGCGTGATCTGCTCTT
CCAAGCCCTGGGCCGCACCTACACTGACGAAGAATTTGATGAACTATGTTTTGAATTTGGTCTGGAGCTT
GATGAAATTACATCTGAGAAGGAAATAATAAGTAAAGAACAAGGTAATGTAAAGGCAGCAGGAGCCTCTG
ATGTTGTTCTTTACAAAATTGACGTCCCTGCCAATAGATATGATCTCCTGTGTCTGGAAGGATTGGTTTCG
AGGACTTCAGGTCTTCAAAGAAAGGATAAAGGCTCCAGTGTATAAACGGGTAATGCCTGATGGAAAAATC
CAGAAATTGATTATCACAGAAGAGACAGCTAAGATACGTCCTTTTGCGGTAGCAGCAGTTCTCCGTAATA
TAAAGTTTACTAAAGATCGATATGACAGCTTCATTGAACTTCAGGAGAAATTACATCAGAATATTTGCAG
GAAAAGAGCACTGGTTGCCATTGGTACCCATGATTTGGACACTTTGTCTGGGCCCATTTACTTATACTGCA
AAGCGTCTTCAGATATCAAATTCAGCCTCTAAATAAGACCAAGGAGTATACAGCCTGTGAACTGATGA
ACATATAACAAGACTGACAATCACCTGAAACATTATTTACATATCATTGAAAACAACCCCTGTATCCAGT
TATCTATGATAGCAATGGTGTCTCCTTTCAATGCCTCCCATCATCAATGGGGATCATTCCAGAATAACA
GTAAATACTAGAAATATTTTTATTGAATGCACGGGAACTGACTTTACTAAGGCAAAAATAGTTCTTGATA
TTATTGTCACCATGTTTCAGTGAATATTGTGAGAATCAATTTACGGTTCGAAGCTGCTGAAGTGGTTTTTCC
TAATGGAAAATCACATACCTTTCCAGAATTAGCTTACCGAAAGGAGATGGTGAGAGCTGACCTAATTAAC
AAAAAAGTTGGAATCAGAGAACTCCAGAAAATCTTGCCAAACTTCTGACCAGGATGTATTTAAAATCAG
AAGTCATAGGTGATGGGAATCAGATTGAGATTGAAATCCCTCCAACCAGAGCTGACATTATCCATGCATG
TGATATTGTAGAAGATGCAGCTATTGCTTATGGATATAACAACATTCAGATGACTCTCCCGAAAACCTTAC
ACCATAGCTAATCAATTTCTCTTAATAAGCTCACTGAACTTCTCCGACATGACATGGCAGCCGCTGGCT
TCACTGAAGCACTTACCTTTGCCCTGTGCTCCCAAGAAGATATTGCTGATAAACTAGGTGTGGATATCTC
TGCAACAAAGGCAGTCCACATAAGTAATCCTAAAACAGCTGAATTTTCAGGTGGCACGCACTACCCTTCTT
CCTGGCCTCCTGAAGACCATAGCAGCAAATCGTAAGATGCCCTTCCACTGAAACTGTTTGAAATCTCTG
ACATTGTAATAAAAAGATTCTAATACAGATGTAGGTGCAAAAACTACAGACATCTCTGTGCTGTTTATTA
CAACAAGAATCCTGGGTTTGAGATCATTCATGGGCTGCTGGACAGAATTATGCAGTTGCTCGATGTGCC
CCTGGTGAAGACAAGGGGGATATGTGATCAAAGCATCAGAAGGCCTGCTTTCTTCCCGGGCGATGTG

CAGAGATCTTTGCCAGGGGTCAAAGCGTCGGGAAGCTTGGGGTCCTTCATCCTGACGTTATCACCAAATT
 TGAGCTGACCCATGCCCTGCTCCTCCCTAGAAATCAATGTTGGACCCTTTTTGTGAAGATTGGTCTCTGTG
 GTGTGATTCTCTTCCCAGGTGTCCCTTTCTCCTCCCCTAGTGTCTTAAGTCTCCTCCACAGGGAACAT
 CTATTTGGGCTTTGATGTTTAATAAAGTAGAAAGCACTGTCTGGCTGTGTGGGTAGAGACCATCCTTTCC
 CTGCATATTAGGCCAGCTTGTGCCATATAACCAGTGTGGTGTCTGTGTGTGAAGCTGCATTGTTGGGTAAA
 AGCCCCGTGGAGTGTGGAGAAATGCACTAGCAGAGTGCAGGATCTGTTCTGAAAGGCAGACGTGCTCCT
 CAGACATCAGAACATCACATTGGAACGGATTACTCCTGCATAACAAGATCCCATTTCTTTCCTTATTGAT
 AAAACAAGATAATCGATGAGAATTCATGTTGCATGAGTTCGAGATAACTGAGGGGTTTAGCTT

5) SLC35B1, solute carrier family 35, member B1

NM_016752	1050	cccactaggaagaaagaggcttcctctac-tccagaaacacttaaattat	1098	(Mm)
NM_005827	1049	cccactaggaagagagagactacctccacatcaag-aatatttaagttat	1097	(Hs)
NM_016752	1099	tatctcgaacagtggca--tcttgggaaaatggactcgggtcat---gat	1143	(Mm)
NM_005827	1098	tatctcaaacagtgcacatctcttgggaaaatggact----taataggaat	1143	(Hs)

>gi|5032212|ref|NM_005827.1| Homo sapiens solute carrier family 35, member B1 (SLC35B1), mRNA

GATGTCCGGCTGGAGCTGTCGCCTCCGCCGCCGCTGCTGCCGGTGCCGGTTGTGAGCGGGTCTCCAGTCG
 GCTCCTCTGGGCGTCTCATGGCCTCTAGCAGCTCCCTGGTGCCCGACCGGCTGCGCCTGCCGCTCTGCTT
 CCTGGGTGTCTTTGTCTGCTATTTTTACTATGGGATCCTGCAGGAAAAGATAACAAGAGGAAAGTATGGG
 GAAGGAGCCAAGCAGGAGACGTTACCTTTGCCTTAACTTTGGTCTTCATTCAATGTGTGATCAATGCTG
 TGTTTGCCAAGATCTTGATCCAGTTTTTTTGACACTGCCAGGGTGGATCGTACCCGGAGCTGGCTCTATGC
 TGCCTGTTCTATCTCCTATCTGGGTGCCATGGTCTCCAGCAATTCAGCACTACAGTTTGTCAACTACCCA
 ACTCAGGTCCTTGGTAAATCCTGCAAGCCAATCCCAGTCATGCTCCTTGGGGTGACCCTCTTGAAGAAGA
 AGTACCCGTTGGCCAAGTACCTGTGTGTGCTGTTAATTGTGGCTGGAGTGGCCCTTTTCATGTACAAACC
 CAAGAAAGTTGTTGGGATAGAAGAACACACAGTCGGCTATGGAGAGCTACTCTTGCTATTATCGCTGACC
 CTGGATGGACTGACTGGTGTTCAGGACCATGCGGGCTCATTACCAAACAGGCTCCAACCACATGA
 TGCTGAACATCAACCTTTGGTGCACATTGCTGCTGGGAATGGGAATCCTGTTCACTGGGGAGCTCTGGGA
 GTTCTTGAGCTTTGCTGAAAGGTACCCTGCCATCATCTATAACATCCTGCTCTTTGGGCTGACCAGTGCC
 CTGGGTGAGAGCTTCATCTTTATGACGGTTGTGATTTTTGGTCCCCTGACCTGCTCCATCATCACTACAA
 CTCGAAAGTTCTTCACAATTTTGGCCTCTGTGATCCTCTTCGCCAATCCCATCAGCCCCATGCAGTGGGT
GGGCACTGTGCTTGTGTTCTGGGTCTTGGTCTTGATGCCAAGTTTGGGAAAGGAGCTAAGAAGACATCC
 CACTAGGAAGAGAGAGACTACCTCCACATCAAGAATATTTAAGTTATTATCTCAAACAGTGACATCTCTT
 GGGAAAATGGACTTAATAGGAATATGGGACTGAGTTCAGTCTTTTTTAATAAAAATAAAATCAAGC

6) CYFIP2, cytoplasmic FMR1 interacting protein 2

NM_133769 857 tgaggagctgctggcagacattgtcaaca**tctgtgttgattactat**gaga 906 (Mm)
|||||||.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.
NM_001037333 840 tgaggagctgctggctgacattgtcaaca**tctgtgttgattactac**gaga 889 (Hs)

>gi|82617633|ref|NM_001037333.1| Homo sapiens cytoplasmic FMR1 interacting protein 2 (CYFIP2), transcript variant 1, mRNA

CGGGGCCGGGGCGGGGCCGAGCGCGGCGCAGCGGAGCGGGGCAGAGCATCCTGCGCCCCGGCGCGGGGCC
CTGCGGTAGCCTCAGGCCCTCCCCTGGACCCGCCGAGAGCCAGTGCAGAATACAGAACTGCAGCCAT
GACCACGCACGTCACCCTGGAAGATGCCCTGTCCAACGTGGACCTGCTTGAAGAGCTTCCCCTCCCCGAC
CAGCAGCCATGCATCGAGCCTCCACCTTCCCTCCATCATGTACCAGGCTAACTTTGACACAAACTTTGAGG
ACAGGAATGCATTTGTCACGGGCATTGCAAGGTACATTGAGCAGGCTACAGTCCACTCCAGCATGAATGA
GATGCTGGAGGAAGGACATGAGTATGCGGTCATGCTGTACACCTGGCGCAGCTGTTCCCGGGCCATTCCC
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GCGGCTGTGCCATGCCGAGCGCAGGAAGGACTTTGTCTCTGAGGCCTACCTCCTGACCCTTGGCAAGTTC
ATCAACATGTTTGCTGTCTGGATGAGCTAAAGAACATGAAGTGCAGCGTCAAGAATGACCACTCTGCCT
ACAAGAGGGCAGCACAGTTCCTGCGGAAGATGGCAGATCCCCAGTCTATCCAGGAGTCGCAGAACCTTTC
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GAGGAGCTGCTGGCTGACATTGTCACA**TCTGTGTGGATTACTAC**GAGAACAAGATGTACCTGACTCCCA
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GTGCCCTTTTTCGGCGACATGCAGATAGAGCTGGCCAGATACATTAAGACCAGTGCTCACTATGAAGAGA
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GCGTGAGCCCCTGCGGCAGGCGGTACGGAAGAAGAAGAATGTCTCATCAGCGTCTACAGGCAATTCGA
AAGACCATCTGTGACTGGGAGGGAGGGCGAGAGCCCCCTAATGACCCATGCTTGAGAGGGGAGAAGGACC
CCAAAGGTGGATTTGATATCAAGGTGCCCCGGCGTGTGTGGGGCCATCCAGCACACAGCTGTACATGGT
GCGGACCATGCTTGAATCACTCATTGCAGACAAAAGCGGCTCCAAGAAGACCCTGAGGAGCAGCCTGGAT
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TGTCTACAAGCTGGCAGACCAGATCTTTGCTTACTACAAAGCCATGGCTGGCAGTGTCCCTGTTGGATAAA
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TGCTGAAGCAGAGACACGTCCAGCTGTTGGGTAGATCAATTGACTTGAACAGACTCATTACCCAGCGCAT
CTCTGCCGCCATGTATAAATCCTTGGACCAAGCTATCAGCCGCTTTGAGAGTGAGGACCTGACCTCCATT
GTGGAGCTGGAGTGGCTGCTGGAGATTAACCGGCTCACGCATCGGCTGCTCTGTAAGCATATGACGCTGG
ACAGCTTCGATGCCATGTTCCGAGAGGCCAATCACAATGTGTCCGCCCCCTATGGCCGTATCACCTGCA
TGTCTTCTGGGAAC TGAAC TTTGACTTTCTCCCCAACTACTGCTACAATGGGTCCACTAACCGTTTTGTG
CGGACTGCCATTCCTTTACCCAAGAACCACAACGAGACAAACCTGCCAACGTCCAGCCTTATTACCTCT
ATGGATCCAAGCCTCTCAACATTGCCTACAGCCACATCTACAGCTCCTACAGGAATTTTCGTGGGGCCACC
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ATTGTGAAGAGCTTGCTCCAAGGAACCATTCTCCAGTATGTGAAAACACTGATAGAGGTGATGCCCAAGA
TATGCCGCTTGCCCCGACATGAGTATGGCTCCCCAGGGATCCTGGAGTTCTTCCACCACCAGCTGAAGGA
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TTCTGCCTCCTCATAGAGCAAGCTCTGTCTCAGGAGGAGGTCTGCGATTTGCTCCATGCCGCACCCTTCC
AAAACATCTTGCTTAGAGTCTACATCAAAGAGGGGGAGCGCCTGGAGGTCCGGATGAAACGTCTGGAAGC
CAAGTATGCCCCGCTCCACCTGGTCCCTCTGATCGAGCGGCTGGGGACCCCTCAGCAAATCGCCATTGCT
CGCGAGGGTGACCTCCTGACCAAGGAGCGGCTGTGCTGTGGCCTGTCCATGTTTCGAGGTCATCCTGACCC
GCATTCGGAGCTACCTGCAGGACCCCATCTGGCGGGGCCACCGCCCACCAATGGCGTCATGCACGTCGA
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ATGCTCTCCCATGACATCTC **CATGCTGGTTTTCTCCATAGCA**TAAATGAAAAAAAAAAAAAAAAAAGTAAAC
AGGGCAGTGTGTGCTTTTTCTTTTCTCCCCCTCAACTATATTAAGAACTCCTAGTTTCACCCTTTCTCC
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GCCCTTGTGTGACCCAGGACTCAAGTCTCAGACTGTGAACAGATGTGGCCATGCCCAGAGACGCCAGCC
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CTCTCAGGGAAGCCCTAGAGAGAGGTCCAAAAGCATTACAGCTGTATCACACTCTATGCAGGTGGGGT
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CCAAATTAGGGACAACGTCTTGGCACAGAATTGCTTATCAAGGAACATTTCCACAAGAAAGAAAATATTA
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AATGAGCTTTTAATACCAAGATACACCCCCTGCCCCCAAAGAAGAGTCCTCTTTTAGGGAATCAGAACCT
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 AATTTTTGTACAATGAATTTACATTTATTTATGGTGACATATTTACGCTTGTGATCAAATAATGATGTTA
 AATTCTTAAATCATATTTGCTATGCAGCTGAAGATGATATTTTGATTTGTATTTTGGGGGTACCTGTGTT
 GAGTTGATAAACATTTCCATCTTCATTAAAACCTGCTTCCAAACTAGTAAAACCAGCAA

7) CCDC132, coiled-coil domain containing 132

NM_024260	3234	ccttttctgaaattatctt ac ----- tctcat --- aattat tatgtgac	3275	(Mm)
			
NM_017667	3236	-----tctgaaatgatggtt ccgcctt gtc ataacaat ggttatgtgac	3279	(Hs)
NM_024260	3276	tacaattacacatggttgcaaaagagtgtactataaatacatagttggaag	3325	(Mm)
			
NM_017667	3280	tacagttatacattttacagaagaatgtaccataagtatataattagaa-	3328	(Hs)

The mooring sequence is not conserved

8) CCDC14, coiled-coil domain containing 14

NM_172824 583 -----gacac-----agcacagcgttggtcactacaagatcat 615 (Mm)
 ||||| |||.|.| |||||.|.|||||
NM_022757 515 gaaagagacacatcagacctagagcaaac--tggtcattgcaagatcat 562 (Hs)
NM_172824 616 tatagaatgtactcaccgataatataccaagccctctgtgagcatgtgca 665 (Mm)
 |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
NM_022757 563 tatagaatgtattcacccataatataccaagccctctgtgagcagctgca 612 (Hs)

>gi|169646280|ref|NM_022757.4| Homo sapiens coiled-coil domain containing 14 (CCDC14), mRNA

GACAAGCCGGGAAGCTTGGAGGGGTCTATTGCGTACGCCAAGGCGCTGGGCCTGGAGCAGGAGAAAGGG
AGTGGAGGCGCGTCGGAGACTATGAAGCGCGGCATTTCGGCGGGATCCTTTCCGGAAGCGGAAGCTCGGCG
GGCGGGCCAAGAAGGTCCGGGAGCCACGGCGGTTAATTCTTTTTACCGTGAGGCTTCACTTCCCTCGGT
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AACAGTTTCTGCAACCTGTACTGATGTTCTACGGAATTCATTTAATACCAGTCCTGGAGTTCCATGTAGC
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AACAAAGGAATTCATAAGGAAACAGACCTACTAAAATGTATTCAAACATATTTGTCTCTTTTTTCGATCTCA
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GCAGCTACAACACAGCTAGTCAGCAACAGCGGACTTGCTGTCTCTGGAAAAGAAAATAAACTGTGTACAC
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TCCATTAGCATCTTTAATTTTATTTAGTATTCATGAATTAATTTATTGGCATCTTATTTGGAGGTAATAG
GCCACAACCTTTTAAACAAATAAGTTTCAGAAATAAAAAATAATAAAAAAGGAAAAAA

9) ALG13, asparagine-linked glycosylation 13 homolog

>gi|270309164|ref|NM_018466.4| Homo sapiens asparagine-linked glycosylation 13 homolog (S. cerevisiae) (ALG13), transcript variant 2, mRNA

ACGGATTTCGCGCTCCCTCACAGAAGGCAGTCACTGCAACGTGCGTGGCCTCAGTTGCGTCATATCCGGC
CCTTGCGATCAGGGCTTGAGGAACCCGCGCCATGAAGTGCGTGTGGTTACCGTAGGGACCACCAGCTTT
GACGACCTCATTGCGTGTGTGTCGGCGCCCGACAGTCTGCAAAAAATCGAGAGCCTTGTTTACAACCGAC
TTATCCTGCAAAATGGTAGAGGAACGGTGGTACCTGAACCCTTCAGTACTGAGTCGTTTACTCTGGATGT
TTACAGGTACAAGGATTCCTTGAAAGAAGACATTCAGAAAGCAGATCTTGTTATTAGTCACGCAGGTGCA
GGAAGCTGTTTGGAGACTCTGGAAAAAGGAAAGCCACTCGTAGTGTTATAAACGAAAAGTTGATGAACA
ATCATCAGCTGGAAGTGGCAAAGCAGCTACACAAAGAGGGTTCATCTCTTCTATTGTACCTGCAGCACGCT
TCCTGGGCTGTTACAGTCAATGGACTTATCAACACTGAAATGTTATCCTCCTGGCCAGCCAGAAAAATTT
TCTGCATTTTTGGATAAAGTTGTTGGATTACAAAAATAAACACTAACTCTCAACACTTTAAAAGCAACC
CCCAAATCAACCTATGTAATGTGATTAAATCAAATTAATACATAATATATATTTACAAAATAATATA
TTAATAAACTTCCCTACATCTATAGAATGTATAGGAAATTTTATGTTGTGCACATTTGCATTGGGTCCAAA
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TTTTCTCCTAGAATCTCAAGTGGAATTGGAATCATAAAAAATGAATGAGATTTGAAAACCTTCACAAAGATT
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CTGTGAAATGAAAAGTTCAATCATTGCCTAAAAAAGATGATCAAGTTAGTTGATCTCTTGTACTTGGAAA
AGCTACTTTTTTCTAAAGAACAGAGTGGAGTGGATATATTTACTTTTTTTTTCTAAAACATACAAAGTG
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TACAATTTATGTGCTTATAAAATTAGTTTTATGAATGAACAATAAACTGATGCATATAATGGCTTAAATA
TATGGTTTTTAAAATTGACTTAACTTGAGCAAGATACATTATGAAGTTCTTTCTGATTAGAGTGTGTGGTC
TCAAGACCTTTACAGTAGATTATCCTTAAGTGTCCATAGCTCTCTGGTACAATGTTTATAGATATAGTTTAT
CTATCAAAATAGAACATTCACTATAAAGACCTCTCTTCCATTCCAATCATATTATCCCAACATGCTAAAT
GTTCCAAACATTTTATTTGGAATGCATTTTATCATGTTTTTATAGGTTTATTTTTCTGATTGTGTTTTAT
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AGGAAGCCAACCTGGATTAAAATTTGCTGAGAATAATCTAAAAGTGAGTAATCTGGTTGAGAATTCAC
AGCACCATAATCATAATTGTATATCAATGTTATGTTTTTAGGAAAGGTCCATTCAAATCCAGGGAGAGAA
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ACTTAGTTTTTATAGTTTATGATGAAGAATTAAGAGAAACAAATGAAAGGCAAGGTCTACTCAAATATC
AGACAACATAAAGGCTATACAGCCCCTAAATCCTTTGCTATCTACTTCCCAGAAATAATGCATAACCTAA
ATTCCATTATTTCAATTTAGCAGAGGTTAAGCCGTTGTTGTCAATTGTGTGCAGTAACGCCTCTGACTTC
CCTTTTGTGGAATTTTGTATCGATTTTGGATTTTAAAGTCAAAGGAGACTTTAAAATCATTTTGTATTTGG
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TTTGGCAGAACTGCCCTAGGAGCAGCTCCTTGATTCCCAGTCCCCTGCTCTTTCTACCCTGCATAATAT
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 GCGTATGACAACCTTACCTAGGACTTAGAAATCTGTGATTTCTGAGTTTTTGAATTTAGGAAAATGCT
 CTGGGTAGGATTGATAGTAGATTGAATAAATTAAGACTTTAAGACAGAATTGTAGACTTTTGGAGTTGGG
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 GGTTTCATTACATGACAGAGCTGCAGGTCTTGATATTAATGAGTAAGTGAATGCAGTTTATTTAGCAG
 TGTTCTATTAGAGGTACTGAAATTTTCAGGGATAAGGAAATGAAAGAGAGTTTAGCATTGGGAAATTTGC
 ACCATGGATAGATTAAGAGGTAGACAGTTAATAGAACATTTACGGGTTGGAGT

10) PRRC2B, proline-rich coiled-coil 2B

NM_001159634	7814	cttatc acccaaaatca ----- atata aaggacacaggtgaacacctat-	7855	(Mm)
			
NM_013318	7893	ctcat cg tg aac cc act tg gt gat gg ag gga -----gtggacc cg tg g	7937	(Hs)

The mooring sequence is not conserved

11) DHX36, DEAH (Asp-Glu-Ala-His) box polypeptide 36

NM_028136	4881	ttgtaaaacaaagtct actctaaaattattat tttggtatctgcaccagg	4930	(Mm)
NM_020865	3625	-----	3625	(Hs)

The mooring sequence is not conserved

NM_028136 and NM_020865 do not align

12) CCNY, cyclin Y

NM_026484	2258	ctatccctctcctgcctagtt-----ccaagaacattctat tctagatt	2300	(Mm)
			
NM_145012	1907	gtatccctttccctccttattcctcacc ca agaacat---- tctaga-t	1951	(Hs)
NM_026484	2301	aatatg gggtgcttgtgccttccagttttcttgcaattgggttcttgggt	2350	(Mm)

NM_145012 1952 .|.|||||.....|.....|.||| cacatgggtgcttgtgccttccgattttcttgcatttg----- 1989 (Hs)

>gi|190341111|ref|NM_145012.4| Homo sapiens cyclin Y (CCNY), transcript variant 1, mRNA
AGGCCCGCCGCCGCCGCTGCTGACCCGGCGGCCGCCGCTTCCGCCCCCTCCCGTGGCGGCGAG
CGGGCGGGCCTCCCCACACGCCCCCGCCGCCCGCGCCCGCGTCCACCCGCGCCCCGCTCCCGGGGACTG
GGAGAACAGGATAGCAGCAGGAGTCGGGGGGCCGCCGAAGATGGGGAACACTACCTCGTGCTGCGTGTCG
TCCAGTCCCAAGCTCCGGAGGAATGCCCACTCCCGGCTGGAGTCTACCCGGCCAGACACGGACCTGAGCC
GCGAGGACACGGGCTGCAACCTGCAGCACATCAGCGACCCGGGAGAACATAGACGATTTGAACATGGAATT
CAATCCTTCAGATCATCCTCGGGCCAGCACAAATATTCTCAGTAAATCTCAGACGGACGTGAGAGAAAAA
CGCAAGAGTCTCTTCATTAACCATCATCCTCCAGGACAAATAGCAAGGAAATACAGTTCCTGCTCCACCA
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AAGACTTTTAAACATACGCAGAGATAGATATCTGTCCGGCCAACCTGGAAGCGGATTGTTTTAGGGGCGATC
CTGCTGGCCTCCAAGGTGTGGGATGACCAGGCTGTATGGAATGTGGATTACTGCCAGATCCTGAAAGACA
TCACGGTGGAGGACATGAACGAGCTAGAGCGACAGTTTCTTGAATTGCTGCAGTTCAACATCAATGTTCC
TTCCAGTGTCTATGCCAAGTATTATTTTGTCTTCTGTTCTCTGGCAGAAGCGAACAACCTGAGCTTTCCC
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AGGACCTAAGAAGATCCGCGAGGAAGCGCTCAGCCAGTGCAGACAACCTGACTCTGCCCCGGTGGTCCCC
AGCCATCATCTCTTAACTACGGAGGCCCGCCGGAGGCCACACCATCCCTTAGTTCCTTTAGTTTGGAG
AAAAGACAGACTTGGGGTGGGTTTGTTTTTGTTTTTCTTTCTTTTCTTTTTTACGCATAGCTCCGTC
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GCTGTGCTTGTTCATTTCTGTACACCCTTATTTTATACCGTTTTTCTTCAACAATGGCGAAATGACTG
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TGCCTGGAACCTACCGAGTAGGAGCCATTTCTTTGTACCCCTGCCTAATCCATTCCTCTCCTTCCAAGTCC
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AGTAAAATGAAAGTTGATGATAGAATATCAAATAGTGAATTTGATATGAAATCTAAGAGTGTGAGTCACT
TGCATATGTAATGCTTTGGGTTTTTGCATATTTTCTTAGGTCACAGTGACAGGTTTCTGAGTTGTTTCCC
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