

Additional_result_file_3 to support figure 3a

APOBEC1 RNA-editing targets (predicted or experimentally validated by Rosenberg B.R. *et al*, 2011) x L-SAGE_372_RT_CgtH_FDR
=> 5 transcripts were in common between both lists, namely 4942, 9741, 10049, 10492 and 27018 (NCBI Gene IDs)

NB: Rosenberg B.R. *et al*. study was carried out in mouse

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_016978	OAT	Ornithine aminotransferase	NM_000274	1027	0.0	4942
2	NM_008640	LAPTM4A	lysosomal protein transmembrane 4 alpha	NM_014713	1039	0.0	9741
3	NM_001037940	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	NM_058246	860	0.0	10049
4	NM_019796	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	NM_001159677	5765	0.0	10492
5	NM_001110234	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	NM_206917	329	7e ⁻⁸⁹	27018

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_016978	predicted	acaguuaaaucuuau	NM_000274	aaagtgaatcattgtat (conserved)	TGTACTTCCTAAGGTGA	No, because NlaIII tag is too distant from the mooring sequence
2	NM_008640	predicted	ucauugguaauuacuau	NM_014713	tcatcgtaattactat (conserved)	TTTCTAGTTTGTATATG	No, because NlaIII tag is 3' to the mooring sequence
3	NM_001037940	predicted	acuucaaaucuuau	NM_058246	acttcaaatcgatat (conserved)	TATTTTAAATGCCACCT	No, because NlaIII tag is 3' to the mooring sequence
4	NM_019796	predicted	ucaggaaaauuuuau ucauagaaaauaguau	NM_001159677	aaagtgaatcattgtat (conserved)	GCAAAACAATCATTTTGC	No, because NlaIII tag is 3' to the mooring sequence
5	NM_001110234	predicted	acugaaauaauuuau	NM_206917	not conserved	GAAAAATTTAAAGCTAA	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 *Nla*III tag in human transcript

Blue nucleotides = *Nla*III "CATG" recognition site

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

1) OAT, Ornithine amino transférase

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NM_016978      1795  ---acagttaaatcattataatcaatgaatggt---aagttgattgaagg      1838      (Mm)
                |.||||.|||||||.|.||  |||||.||  |||  |||||.|.||
NM_000274      1847  tataaagtgaaatcattggtat---tgaattttaggaag--gattaatgg      1891      (Hs)
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>gi|284507296|ref|NM_000274.3| Homo sapiens ornithine aminotransferase (OAT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA

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CCGCGTGTACCCGTTGTCCTCAGGCGCTGTCAGATCTGTGGTTTTTCTACTTGAAGGACACAATGTTTT
CCAAACTAGCACATTTGCAGAGGTTTGCTGTAAGTTCAGTCGCGGAGTTCATTCTTCAAGTGGCTTCTGCTAC
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 TGGGTATTGCATAAAAGGCTTCATCTTAT**AAAGTGAAATCATTGTTAT**TGAATTTTAGGAAGGATTAATG
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 GTAAAAAATGTTTATTTTCAATACTTCTTTAAATTTAAAATAAAGCTTATATTTCAAATGTCAAAAAAAA
 AA

2) LAPTM4A, lysosomal protein transmembrane 4 alpha

NM_008640	1065	agtatgaag tcattgtaattactat tcatctgagagaatggctgataat	1114	(Mm)
NM_014713	696	agtatgaag tcatcggtaattactat tcgtctgagagaatggctgataat	745	(Hs)

>gi|196049387|ref|NM_014713.4| Homo sapiens lysosomal protein transmembrane 4 alpha (LAPTM4A), mRNA
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 GTCTCCCTTTTTCCATTAAATGCCTCTTTTCTTGCGGGTCTCATCTCGGGAATAGTGC ACTACGGGGACA
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 TGGAAGATGATGGTTG**CATGTTTCTAGTTTGTATATG**TTTCCATCTTTGTGATAAGATGATTTAATAAAT
 CTCTTTAAATACTTAAAAAAAAAAAAAAAAAAAA

3) DNAJB6, DnaJ (Hsp40) homolog, subfamily B, member 6

NM_001037940	780	acgtcatttggcggcagtggaatgggca acttcaaatcaatat caacttc	829	(Mm)
NM_058246	686	acgtcatttgggtggtagtgggcatgggca acttcaaatcgatat caacttc	735	(Hs)

>gi|34328906|ref|NM_058246.3| Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA

GAGAAAGGAGAGAAAGGAAAGCGCGAGGAGCCGCCACCACCAGCGCAGCAGTCCTGGAGCTGTGAGG
 AGATTCGGGCGTCACCCCTGCCTCCCCTGCGTCCCGCCACCGGCCCTTCTGTCCTCGGACCCATTCCAA
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AATAAAACATAAGCATATTGAATACAAAAA

4) SYNCRIP, synaptotagmin binding, cytoplasmic RNA interacting protein

ucaggaaaauuuuau mooring sequence could not be located in NM_019796 mouse transcript

NM_019796	3058	ttgaagttttttcataaa	tcatagaaattagatat	atggctgtagtttagc	3107	(Mm)
NM_001159677	3240	ttgaagttttttcataaa	tcatagaaattagatat	atggctgtagtttagc	3289	(Hs)

>gi|228008399|ref|NM_001159677.1| Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), transcript variant 6, mRNA

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 GGACGAGCAGTTTTGGCCACTTCCATCAGGACAAGACTTTTTAGGTCACTTAGTGCAGGTTTTAGTTTCT
 ATTTTGGATTAACAACATTTATATTGATTATCGAAAAGAAGCTTTCATCATTTTCAGAACAGTCCTGGAAG
 TTTGACTTTGAGTGTGGGAGAAGTCCTAATAAACCATTTTGGAAATTAAAAA

5) NGFRAP1, nerve growth factor receptor (TNFRSF16) associated protein 1

NM_001110234	786	ccattagcatggaaagcaatgtcaagtcaataaagca actgaataatcat	835	(Mm)
			
NM_206917	870	ccatttgcagtgaaa--aatttaaagctaataaagcaatttaa-----	910	(Hs)
NM_001110234	836	tatt gtgtccttaaagcataaataaacagttaagattaaaaaaaaa	880	(Mm)
		. .		
NM_206917	911	-----aaagcaaaaaaaaa-----aaaaaaaa	932	(Hs)

Mooring sequence is not conserved

>gi|46094061|ref|NM_206917.1| Homo sapiens nerve growth factor receptor (TNFRSF16) associated protein 1 (NGFRAP1), transcript variant 1, mRNA
 GGCTGTGCGCTCTGGGGCACCTCATGCAGACGGGAGTAGGGAGGCTGTTTTTTGCGCGTGCATATGGCGG
 TGCGGGTGGGGGAAGGGGAGATCCTGCTGCACTGGCCGCCCAAGTTGGGGGCGAGCTCGGTGGTGA

CGCGCGGCCCTCACGTGACCCAGAGCTGCAGAGCGACGCAGCCTTCGGTGCAGTCGTCACTCGCGTCTGG
 CTACCAGCTCCCCGCTGCCCTGAGCTCGGCGGGCTGGCATTTCGGCCCCGGGAAAAGCGGAGCAGGTCTGC
 GAGGCTAAGTGTCTCCGCGGCGCACCTCGCGGCGAGAATCCGGAGGAGAAGGAGACTGCAAGGATAGGCC
 CAGGAAAACGAAGAGATGGAGCAGCCTATGCAGAATGGAGAGGAAGACCGCCCTTTGGGAGGAGGTGAAG
 GCCACCAGCCTGCAGGAAATCGACGGGGACAGGCTCGCCGACTTGCCCTAATTTTCGATGGGCCATACC
 CAATAGGCAGATCAATGATGGGATGGGTGGAGATGGAGATGATATGGAAATATTCATGGAGGAGATGAGA
 GAAATCAGAAGAAAACCTTAGGGAGCTGCAGTTGAGGAATTGTCTGCGTATCCTTATGGGGGAGCTCTCTA
 ATCACCATGACCATCATGATGAATTTTGCCTTATGCCTTGACTCCTGCCATTTATCATGAGATTAATACT
 GTGATTTCCGCTGTTTTCTTTTTCTTTCCTTGCATTTTTCCTAATATGCCTTTACTGATCCGTTTGCTGTGAACC
 CTATGTTATTTCCATGTGTCAAGTGGGTCTTGTGTTGCCAGCTTCTATTTGAAGATTGCCTTTGCACTCA
 GTGTAAGTTTCTGTCAGCAGTAGTTTCACCCATTTG**CATGGAAAATTTAAAGCTAA**TAAAGCAATTTAA
 AAAGCAAAAAAAAAAAAAAAAAAAAA

Supplementary information for figure 3b

APOBEC1 RNA-editing targets (predicted or experimentally validated by Rosenberg B.R. *et al*, 2011) x L-SAGE_17_RT_HgtC_FDR
 => 1 transcript in common between both lists, namely 567 (NCBI Gene ID)

Orthology table:

Index	APOBEC1 RNA-editing target(Mouse)	Gene Symbol	Description	Human orthologue (blastn first hit)	Blast Score	E value	Entrez Gene ID (human)
1	NM_009735	B2M	beta-2-microglobulin	NM_004048	205	9e -50	567

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_009735	exp. validated	uc<u>auu</u>acuu	NM_004048	Not conserved	TGTA<u>CTTCCTA</u>AGGTGA	Unlikely, because the mooring sequence is not conserved between mouse and human

1) B2M, Homo sapiens beta-2-microglobulin (B2M)

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-ttggg---aatttgтта-taatga	853	(Hs)

The mooring sequence is not conserved

>gi|37704380|ref|NM_004048.2| Homo sapiens beta-2-microglobulin (B2M), mRNA
AATATAAGTGGAGGCGTCGCGCTGGCGGGCATTCCCTGAAGCTGACAGCATTCCGGGCCGAGATGTCTCGCT
CCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAGGCTATCCAGCGTACTCCAAAGAT
TCAGGTTTACTCACGTCATCCAGCAGAGAATGGAAAGTCAAATTTCCCTGAATTGCTATGTGTCTGGGTTT
CATCCATCCGACATTGAAGTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCCAGACT
TGTCTTTCAGCAAGGACTGGTCTTCTATCTCTTGTACTACACTGAATTCACCCCACTGAAAAAGATGA
GTATGCCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGATCGAGACATGTAA
GCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTTCTGCTTGCTTGCTTTT
TAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTAGGGTTATAATAATGTTAACATGGAC
ATGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTCCATGTTTGATGTATCTGAGCAGGTTGCTCCACA
GGTAGCTCTAGGAGGGCTGGCAACTTAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTT
GGTCAGATTTGAACTCTTCAATCTCTTGCACACTCAAAGCTTGTTAAGATAGTTAAGCGTGCATAAGTTAAC
TTCCAATTTACATACTCTGCTTAGAATTTGGGGGAAAATTTAGAAATATAATTGACAGGATTATTGGAAA
TTTGTTATAATGAATGAAACATTTTGTATATAAGATTCATATTTACTTCTTATACATTTGATAAAGTAA
GG**CATGGTTGTGGTTAATCTGGT**TTATTTTTGTTCCACAAGTTAAATAAATCATAAACTTGATGTGTTA
TCTCTTA