Variant	miRNA	Database	Conservation Score	Functional Effect	Context Score Change
	hsa-miR-1231	PolymiRTS Database 3.0	10	D	-0.246
c.*529A>G		MicroSNiPer	N/A	D	N/A
	hsa-miR-1299	PolymiRTS Database 3.0	11	D	-0.093
		MicroSNiPer	N/A	D	N/A
	hsa-miR-6128	PolymiRTS Database 3.0	11	D	-0.077
	hsa-miR-654-3p	PolymiRTS Database 3.0	12	D	-0.137`
		MicroSNiPer	N/A	D	N/A
	hsa-miR-875-3p	PolymiRTS Database 3.0	11	D	-0.071
		MicroSNiPer	N/A	С	N/A
	hsa-miR-3681-5p	MicroSNiPer	N/A	U	N/A
	hsa-miR-1254	PolymiRTS Database 3.0	10	С	-0.392
		MicroSNiPer	N/A	С	N/A
	hsa-miR-3116	PolymiRTS Database 3.0	10	С	-0.413
		MicroSNiPer	N/A	С	N/A
	hsa-miR-661	PolymiRTS Database 3.0	10	С	-0.15
		MicroSNiPer	N/A	С	N/A
	hsa-miR-4633-5p	MicroSNiPer	N/A	С	N/A
	hsa-miR-4254	MicroSNiPer	N/A	С	N/A

Supplemental Table 1. Predicted miRNA target effects for c.\*529A>G variant.

D: variant disrupts the predicted miRNA site; C: variant creates a predicted miRNA site; U: unaffected.

Untranslated Region	Variant	RNA-Binding Protein	Motif	Functional Effect	Z-score	P-value
	WT	CDCCO	cuckucy	D	1.670	4.75e-02
	c68T>C	58555			N/A	N/A
5 018	WT	DDMC	hauccar	С	N/A	N/A
	c68T>C	KDIVIO			2.775	2.76e-03
	WT		amayama	D	2.387	8.49e-03
	c.*529A>G	HINRINPL			N/A	N/A
	WT		rcahaca	U	2.519	5.88e-03
	c.*529A>G	TINKPLL			2.025	2.14e-02
	WT		vmahwca	D	1.986	2.35e-02
3'UTR	c.*529A>G	IGFZDFZ			N/A	N/A
	WT		Museuuk	D	2.420	7.76e-03
	c.*529A>G	KDIVI41	wuacwuk	D	N/A	N/A
	WT	CDCE2	wcwwc	D	2.402	8.15e-03
	c.*529A>G	34353			N/A	N/A
	WT	CDCEE	yywcwsg	С	N/A	N/A
	c.*529A>G	SUSLO			2.204	1.38e-02

Supplemental Table 2. Predicted RNA binding protein (RBP) effects with non-coding variation.

D: variant disrupts the predicted RBP motif site; C: variant creates a predicted RBP motif; U: unaffected. Z-score and P-value reflect the reliability of the predicted binding site

# Supp. Figure 1. In silico protein modeling.













Supp. Figure 1. *In silico* protein modeling. Protein structures for the solved MAB21L1 wild-type (5EOG) (de Oliveira Mann et al., 2016) (**A**,**C**) and the I-TASSER predicted mutants (Arg51Leu **B**,**D**; Arg62Cys **E**; Gly220Arg **F**). Amino acids (aa) of interest are highlighted as follows: aa51 orange, aa62pink, aa220 yellow. Alpha helices are purple, beta sheets green, linker regions blue. Red arrows (**B**,**D**,**E**,**F**) indicate observed structural changes upon mutation.

#### Supp. Figure 2. Multi-species sequence comparisons of MAB21L1 non-coding regions.

#### **A** 5' UTR sequence; 13:36050329 – 36050370 (forward sequence)

Human Individual 2 Chimp Gorilla Orangutan Gibbon Baboon Green monkey Marmoset Squirrel monkey Chinese tree shrew Squirrel Lesser Egyptian jerboa Prairie vole Chinese hamster Golden hamster Mouse Rat Naked mole-rat Guinea pig Chinchilla Brush-tailed rat Rabbit Pika Pig Alpaca Bactrian camel Killer whale Tibetan antelope COW Sheep Domestic goat Horse White rhinoceros Cat Ferret Panda Pacific walrus Weddell seal Megabat David's myotis (bat) Microbat Big brown bat Hedgehog Shrew Star-nosed mole Cape elephant shrew Manatee Cape golden mole Tenrec Aardvark Armadillo Opossum Tasmanian devil Wallaby Platypus Saker falcon Peregrine falcon Collared flycatcher White-throated sparrow Medium ground finch Zebra finch Tibetan ground jay Budgerigar Parrot Scarlet macaw Rock pigeon Mallard duck Chicken American alligator Green seaturtle Painted turtle Chinese softshell turtle Lizard Coelacanth Tetraodon Fugu Yellowbelly pufferfish Nile tilapia Zebra mbuna Medaka Southern platyfish Stickleback Atlantic cod Zebrafish Mexican tetra (cavefish) Lamprey

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ggttctctccgaagttggctcccgcgccagcagccgcattg	J
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tttctcctctgaagttggctccagccttagcagccgcattg	3
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ttctttcgctgcgctgcccgcccacccgttcgcgttgd	J

## **B 3' UTR sequence;** 13:36048652 – 36048681 (forward sequence)

Individual 3	CU	-gga	la-cllcc-a	<b>q</b>	ccac-laac-	-d
Chimp	ct	-gga	ta-cttcc-aq	gacatttt	ccac-taac	-a
Gorilla	ct	-gga	ta-cttcc-ao	g <mark>a</mark> catttt	ccac-taac	-a
Orangutan Cibban	ct	-gga	ta-cttcc-ao	g <b>a</b> catttt	ccac-taac	-a
Baboon	ct	-cda	ta-cttcc-ac	acatttt		-a
Green monkey	ct	-cga	ta-cttcc-ac	gacctttt	ccac-taac	-a
Marmoset	ct	-gga	ta-cttcc-a	g <mark>a</mark> catttt	ccac-taac	-a
Squirrel monkey	ct	-gga	ta-cttcc-a <u>c</u>	g <b>a</b> catttt	ccac-taac	-a
Chinese tree shrew	tt	-gga	ta-cttcc-ao	g <b>a</b> catttt	tcac-taac	-a
Lesser Egyptian jerboa	ct	-gga	tt-cttcc-ac	acatttt	tcac-taac	-a
Prairie vole	t	-qqa	aa-tttcc-ad	g <b>a</b> cacttt	ccac-gaac	-a
Chinese hamster	t	-gga	aa-cttcc-aq	g <mark>a</mark> cacttt	ccac-gagc	-a
Golden hamster	t	-gga	aa-cttcc-aq	g <b>a</b> cacttt	ccac-gaac	-a
Mouse	tt	-gga	aa-ctttc-aq	g <b>a</b> catttc	ccacagaac	-a
Naked mole-rat	tt	-ggg	ta-cttcc-a	racatttt	ccacayaac	-a
Guinea pig	tt	-gga	ta-cttcc-ad	g <b>a</b> catttt	ccac-taac	-a
Chinchilla	tt	-gga	ta-ctccc-ac	g <mark>a</mark> catttt	ccac-taac	-a
Brush-tailed rat	tt	-gga	ga-cttcc-ag	g <b>a</b> catttt	ccac-taac	-a
Rabbit	tt	-gga	ta-cttcc-ac	g <b>a</b> catttt	ccac-taac-	-a
Pika Dia	ttt	-gga	ta-ctccc-ao	gacatttt	ccac-caac	-a
Alpaca	tt	-gga -gga	ta-cttcc-ac	gcatttt	ccac-taac	-a
Bactrian camel	tt	-gga	ta-cttcc-a	gacatttt	ccac-taac	-a
Dolphin	tt	-gga	ta-cttcc-a	g <mark>a</mark> catttt	ccac-taac	-a
Killer whale	tt	-gga	ta-cttcc-a <u>c</u>	g <b>a</b> catttt	ccac-taac	-a
Tibetan antelope	tt	-gga	ta-cttcc-ao	<b>ja</b> catttt	ccac-taac	-a
Sheep	tt	-gga -gga	ta-cttcc-ac	acatttt		-a
Domestic goat	tt	-qqa	ta-cttcc-ad	g <b>a</b> catttt	ccac-taac	-a
Horse	tt	-gga	ta-cttcc-ac	g <mark>a</mark> catttt	ccac-taac	-a
White rhinoceros	tc	-gga	caacttcc-ao	g <mark>a</mark> catttt	ccac-caac	-a
Cat	tt	-gga	ta-cttcc-ao	g <b>a</b> catttt	ccgc-taac-	-a
Panda	tt	-gga	ga-cttcc-a	racatttt	ccac-taac	-a
Pacific walrus	tt	-qqa	ga-cttcc-ad	g <b>a</b> cagttt	ccac-taac	-a
Weddell seal	tt	-gga	ga-cttcc-ag	g <mark>a</mark> catttt	ccac-taac	-a
Megabat	tt	-gga	ta-cttcc-ao	g <b>a</b> catttt	ccac-taac	-g
Microbat Big brown bat	tt	-gga	ta-cttcc-ao	g <b>a</b> catttt	cctc-taac	-a
Hedgebog	ttttttaaaaa	aaaa	ta-cttcc-ac	rctatttt		-a
Shrew	tt	-qqa	ta-cttcc-ad	g <b>a</b> catttt	ccac-taac	-a
Star-nosed mole	tt	-gga	ta-cttcc-ao	g <mark>a</mark> catttt	ccac-aaac	-a
Cape elephant shrew	cc	-gga	gg-ccccc-aq	g <b>a</b> cctttc	tcac-ttac	-a
Manatee Capa goldon molo	tg	-gga	ga-ctggc-gg	g <b>a</b> catttt	ccac-taac-	-a
Aardvark	tt	-aaa	ga-actcc-a	accttcc		- a
Armadillo	tt	-gaa	ta-cttcc-c	g <b>a</b> catttt	cctc-taac	-a
Opossum	ttt	-gga	ta-cttc <mark>a</mark> -gg	g <mark>a</mark> catt <mark>ct</mark>	ctgc-taat	-g
Tasmanian devil	ttt	-gga	ta-cttca-gg	g <b>a</b> cattct	ctgc-taat	-9
Wallaby	ttg	-gga	ta-cttca-go	g <b>a</b> catttt	ctgc-taat-	-9
Saker falcon	tt	-gga	ta-cttcaag	racauttt	ctgc-taaaga	-9
Peregrine falcon	tt	-ada	ta-cttcaag	r <b>a</b> cagttt	ctgc-taaaga	-0
Collared flycatcher	tt	-gga	ta-cttcaag	gacatttt	ctgc-taaaaa	-g
White-throated sparrow	tt	-gga	ta-cttcaagg	g <mark>a</mark> catttt	ctgc-taaaaa	-g
Medium ground finch	tt	-gga	ta-cttcaagc	g <b>a</b> cattttt	ctgc-taaaaa	-9
Zebra IInch Tibetan ground jay	tt	-gga	ta-cttcaag	Jacatttt	ctgc-taaaaa	-9
Budgerigar	tt	-gga -gga	ta-cttcaagc	acatttt	ctgc-taaaga	-a
Parrot	tt	-gga	ta-cttcaagc	gacattgt	ctgc-taaaga	-g
Rock pigeon	tt	-gga	ta-cttcaag	g <b>a</b> caattt	ctgc-taaaga	-ġ
Mallard duck	tt	-gga	ta-cttcaago	g <b>a</b> catttt	ctgc-taaaga	-g
Chicken	tt	-gga	ta-cttcaago	<b>ja</b> catttt	ctgc-taacga	-9
American alligator	tt	-dda	ta-cttca-gc	racatttt	ctqc-taaa	-0
Green seaturtle	tc	-qqa	ta-cttca-gc	g <b>a</b> catttt	ctgc-taaa	-q
Painted turtle	tc	-gga	ta-cttca-gg	g <mark>a</mark> catttt	ctgc-taaa	-g
Chinese softshell turtle	tc	-gga	ta-cttca-go	g <b>a</b> catttt	ctgc-taaa	-9
Lizard Coolacanth	tt	-gga	tg-cttct-gc	g <b>a</b> catttt	ccac-tgaa	-9
Tetraodon	tt	-gga -tgctca	tc-ttttt-g	a autttacat	-t-ctgc-caag	-9
Nile tilapia	tt	-ttttc-	tt-tatct-g		g-taga	-a
Medaka	tt	-aaaaatc-	ca-cgtcg-ga	aactttctcttta	at-ctga-taga	-a
Southern platyfish	tt	-aaa	tct-ga	acttttttcttta	at-ctgc-taga-	-a
Atlantic cod	tt	-acatt-	tc-atcct-c	acallugccaca	it-ataa-tata	-a
Zebrafish	tt	-taaca-	tt-cqcct-qc	attatttctgaa	agagaga-aaga	-a
Spotted gar	tt	-atgaa-	ta-acttc-ac	gattttt	ctgc-taga	aa

### Supp. Figure 2. Multi-species sequence comparisons of *MAB21L1* non-coding regions.

Nucleotide alignments for 5'UTR (**A**) and 3'UTR (**B**) are shown using data generated by UCSC Multiz Alignments of 100 Vertebrates. Identical nucleotides are shaded in grey; positions of variant nucleotides are indicated in bold; non-coding variants in Individuals 2 (**A**) and 3 (**B**) are shown in red.

## Supp. Figure 3. Alignment of full-length MAB21L1 and related proteins.

MAB21L1 MAB21L2 mMab2111 cMab2111 mab2111 mab2111 Mab-21	MIAAQAKLVYHLNKYYNEKCQARKAAIAKTIREVCKVVSDVLKEVEVQEPRFISSLNE-M MIAAQAKLVYQLNKYYTERCQARKAAIAKTIREVCKVVSDVLKEVEVQEPRFISSLSE-I MIAAQAKLVYHLNKYYNEKCQARKAAIAKTIREVCKVVSDVLKEVEVQEPRFISSLNE-M MIAAQAKLVYHLNKYYNEKCQARKAAIAKTIREVCKVVSDVLKEVEVQEPRFISSLNE-M MIAAQAKLVYHLNKYYNEKCQSRKAAISKTIREVCKVVSDVLKEVEVQEPRFISSLNE-M MIAAQAKLVYHLNKYYNEKCQSRKAAISKTIREVCKVVSDVLKEVEVQEPRFISSLNE-M MLGHNQNVVYQVNNYFNEKVQHRKVRVTKTVQRIAKVVQEILKEVEAQEPRFINTLSETT L	59
MAB21L1 MAB21L2 mMab21I1 cMab21I1 mab21I1 mab21I1 mab-21 Individual 2	DNRYEGLEVI-SPTEFEVVLYLNOMGVFNFVDDGSLPGCAVLKLSDGRKRSMSLWVEFIT DARYEGLEVI-SPTEFEVVLYLNOMGVFNFVDDGSLPGCAVLKLSDGRKRSMSLWVEFIT DNRYEGLEVI-SPTEFEVVLYLNOMGVFNFVDDGSLPGCAVLKLSDGRKRSMSLWVEFIT DNRFEGLEVI-SPTEFEVVLYLNOMGVFNFVDDGSLPGCAVLKLSDGRKRSMSLWVEFIT TGRFDGI-VVHSPSEYEAVLYLNOMGVFNFVDDGTIQGCAVLKLSDGRKRSMSLWVEFIT C	118
MAB21L1 MAB21L2 mMab21l1 cMab21l1 mab21l1 mab21l1	ASGYLSARKIRSRFOTLVAQAVDKCSYRDVVKMVADTSEVKLRIRDRYVVQITP ASGYLSARKIRSRFOTLVAQAVDKCSYRDVVKMIADTSEVKLRIRERYVVQITP ASGYLSARKIRSRFOTLVAQAVDKCSYRDVVKMVADTSEVKLRIRDRYVVQITP ASGYLSARKIRSRFOTLVAQAVDKCSYRDVVKMVADTSEVKLRIRDRYVVQITP ASGYLSARKIRSRFOTLVAQAVDKCSYRDVVKMVADTSEVKLRIRDRYVVQITP ASGYLSARKIRSRFOTLVAQAVDKCSYRDVVKMVADTSEVKLRIRDRYVVQITP ASGYLSARKIRHRFQNIVAQVLQTPQFSDYCKLLQDNTDVRVRVDDKYTVQITC	172
MAB21L1 MAB21L2 mMab21I1 cMab21I1 mab21I1 mab21I1 mab-21 Individual 3	AFKCTGIWPRSAAHWPLPHIPWPGPNR-VA-EVKAEGFNLLSKECHSLAGKOSSA AFKCTGIWPRSAAQWPMPHIPWPGPNR-VA-EVKAEGFNLLSKECYSLTGKOSSA AFKCTGIWPRSAAHWPLPHIPWPGPNR-VA-EVKAEGFNLLSKECHSLAGKOSSA AFKCTGIWPRSAAHWPLPHIPWPGPNR-VA-EVKAEGFNLLSKECYSLNGKOSSA AFKCTGIWPRSAAHWPLPHIPWPGPNR-VA-EVKAEGFNLLSKECYSLNGKOSSA AFKCTGIWPRSASHWPLAGLPWPNAALANQTKAEGFDLTSRET-AITQQNNPNKQASS <b>R</b>	225
MAB21L1 MAB21L2 mMab21I1 cMab21I1 mab21I1 mab21I1	-ESDAWVLQFAEAENRLQMGGCRKKCLSILKTLRDRHLELPGQPLNNYHMKTLVSYECEK -ESDAWVLQFGEAENRLIMGGCRNKCLSVLKTLRDRHLELPGQPLNNYHMKTLLLYECEK -ESDAWVLQFAEAENRLQMGGCRKKCLSILKTLRDRHLELPGQPLNNYHMKTLVSYECEK -ESDAWVLQFAEAENRLQMGGCRKKCLSILKTLRDRHLELPGQPLNNYHMKTLVSYECEK -ESDAWVLQFAEAENRLILGGCRKKCLSLLKTLRDRHLELPGQPLNNYHMKTLVSYECEK MEADAWAMKMHGAENMLLTGG-RRKTLSILKCLRDAHMDFPGTPVTNYILKTLVLYECEK	284
MAB21L1 MAB21L2 mMab21I1 cMab21I1 mab21I1 mab21I1	HPRESDWDESCLGDRLNGILLQLISCLQCRRCPHYFLPNLDLFQGKP-HSALENAAKQTW HPRETDWDESCLGDRLNGILLQLISCLQCRRCPHYFLPNLDLFQGKP-HSALESAAKQTW HPRESDWDESCLGDRLNGILLQLISCLQCRRCPHYFLPNLDLFQGKP-HSALENAAKQTW HPRESDWDESCLGDRLNGILLQLISCLQCRRCPHYFLPNLDLFQGKP-HSALENAAKQTW HPRESDWDENCLGDRLNGILLQLISCLQCRRCPHYFLPNLDLFQGKP-HSALENAAKQTW HCSEYEWEDPNIGDRLVGILLQLVSCLQCRRCAHYFLPSLDLLRSKPVHS-IEHSAQLAW	343
MAB21L1 MAB21L2 mMab21l1 cMab21l1 mab21l1 mab21l1	RLAREILTNPKSLEKL 359 RLAREILTNPKSLDKL RLAREILTNPKSLEKL RLAREILTNPKSLEKL RLAREILTNPKSLEKL HLVRKLMIDPNALQSL	

Supp. Figure 3. Alignment of full-length MAB21L1 and related proteins. Identical amino acids are shaded in grey; positions of variant amino acids are indicated in bold and variants identified in Individuals 1a, 1b, 2 and 3 are shown in red. Note high conservation between different vertebrate MAB21L1/Mab21l1/mab21l1 proteins as well as with its close human homolog MAB21L2 and *C. elegans* mab-21. Human MAB21L1 (NP\_005575.1), human MAB21L2 (NP\_006430.1), mouse Mab21l1 (NP\_034880.1), chicken Mab21l1 (NP\_989864.1), zebrafish mab21l1 (NP\_694506.2) and *C. elegans* mab-21 (NP\_497940.2).