Suppl. Table S2: annotation lines

ZFIN line designator	gene	transcript	NM number	coding strand	deleted nucleotides (coding strand)	inserted nucleotides (coding strand)	cDNA	protein	protein sequence (red: AS different from ref. protein sequence)	number of aminoacids
magi2a[cl604]	magi2a	ENSDART00000133644	NM_001327853	reverse	TCC	GCTA	c.69_71delinsGCTA	p.Pro24Leufs*76	MSKSLKKKSHWTNRVHEVVLSRGLEWGSRVRAAGRRGERTVPRYWRGETGQAQTAAGRAASGGKRYSSGRTDHQGCLGCGQALQRPCSVQVCQTRRCCG*	99
magi2a[cl605]	magi2a	ENSDART00000133644	NM_001327853	reverse	TGTGTTGTCCAGGGGTCC	A	c.54_71delinsA	p.Val19Glufs*75	MSKSLKKKSHWTNRVHEVEWGSRVRAAGRRGERTVPRYWRGETGQAQTAAGRAASGGKRYSSGRTDHQGCLGCGQALQRPCSVQVCQTRRCCG*	93
magi2a[cl606]	magi2a	ENSDART00000133644	NM_001327853	reverse	AGGGGTC	G	c.64_70delinsG	p.Arg22_Pro24delinsAla	MSKSLKKKSHWTNRVHEVVLSASGDLGFELQGGAENGQFPVIGEVKPDRRKLQQDELLLEVNDTPVAGLTIRDVWAVVRHCKDPVRFKCVKQGGVVDKDLRQYLNLRFQKGSLDHELQQIIRDNLYLRTVPCTTRQPREGEVPGVDYNFVTVERFVELERSGALLESGTYEDNYYGTPKPPAEPSPLLLNVAEQLLPGATPTSQGKRRRNKSVSNMEKAGIEPPEEEEEERPVINGNGVAITPESSEHEDKSTDASGEMATTCPSETSTDAPKEDTEPPKSPPKPDENDELGPLPDNWEMAYTEKGEVYFIDHNTKTTSWLDPRLAKKAKPPEECKENELPYGWEKIDDPIYGTYYVDHINRRTQFENPVLEAKRRLQHQQQMQSQGLSSLPLPAVYREKPLFTRDPTQLKGSFLSTPLQKSNMGFGFTIIGGDEPDEFLQVKSVIPDGPAAQDGKMATGDVIVYINDVCVLGTTHADVVKLFQSVPIGQSVTLVLCRGYPLPYDPEDAANTLLSPLGLIDRPLLVNGRNSYDSYMEYISRTARFVDPLQTTMVQPHPGDTHLDAGPLEDSVSMASSGAAGGELLTINMVKGADGFGFTIADSNGGQRVKQILEAQGCPGLCEGDLIVEINQQPALTLSHTQVVELLKECPIGTEATLVIQRGGTVCSFTLQVTFPLGRPLNRSLHICTGLQVQNLTWPNLTLMTCMRSPGLSMRIGVTEFQEVEVHLRRQKSGFGFRILGGEEPGQPILIGAIIEKSPADKDGRLRPGDELISVDGIVVAGKPHRYVIDLMHGAARTGQVKLTVRRRVQPTGEPFPENGRSPGSTQHSSPRSDFNSRMFCNNSAPSQNSAPSTTGSSPPDTAANQNAQPNDVSIQRKETEGFGFVIISSLNRPETAAAAAVPHKIGRIIEGSPADHCGKLKVGDRILAVNNQSIVNMPHADIVKLIKDAGLSVTLRIIPQEETNSTPSAGSSEKQSPMAQPSPVCQPNTVNQTGAAPLANSNAQQNSAPQPSPIKQPISEAQPSLVTQNSPANHPSSVTQQNPQTQPVQTYSHDSSYRSEVKARQDVKPDIRQPFTDYRQPPVDYRHPPVADYRQPPTLDYRHPPLLDYRPLPADPRTFPLPDYRMPQDFDFFTVELEKGMKGFGFSIRGGREYKMDLFVLRLAEDGPAIRNGRMRVGDQIIEINGESTRDMTHARAIELIKSGGRRVRLLLKRGTGQVPEYGMVSSSLSMCMKSDNHGSPYFFL	1272
magi2a[cl607]	magi2a	ENSDART00000133644	NM_001327853	reverse	TCCAGGGGTCCGA	GGG	c.61_73delinsGGG	p.Ser2_Met218del	MEKAGIEPPEEEEEERPVINGNGVAITPESSEHEDKSTDASGEMATTCPSETSTDAPKEDTEPPKSPPKPDENDELGPLPDNWEMAYTEKGEVYFIDHNTKTTSWLDPRLAKKAKPPEECKENELPYGWEKIDDPIYGTYYVDHINRRTQFENPVLEAKRRLQHQQQMQSQGLSSLPLPAVYREKPLFTRDPTQLKGSFLSTPLQKSNMGFGFTIIGGDEPDEFLQVKSVIPDGPAAQDGKMATGDVIVYINDVCVLGTTHADVVKLFQSVPIGQSVTLVLCRGYPLPYDPEDAANTLLSPLGLIDRPLLVNGRNSYDSYMEYISRTARFVDPLQTTMVQPHPGDTHLDAGPLEDSVSMASSGAAGGELLTINMVKGADGFGFTIADSNGGQRVKQILEAQGCPGLCEGDLIVEINQQPALTLSHTQVVELLKECPIGTEATLVIQRGGTVCSFTLQVTFPLGRPLNRSLHICTGLQVQNLTWPNLTLMTCMRSPGLSMRIGVTEFQEVEVHLRRQKSGFGFRILGGEEPGQPILIGAIIEKSPADKDGRLRPGDELISVDGIVVAGKPHRYVIDLMHGAARTGQVKLTVRRRVQPTGEPFPENGRSPGSTQHSSPRSDFNSRMFCNNSAPSQNSAPSTTGSSPPDTAANQNAQPNDVSIQRKETEGFGFVIISSLNRPETAAAAAVPHKIGRIIEGSPADHCGKLKVGDRILAVNNQSIVNMPHADIVKLIKDAGLSVTLRIIPQEETNSTPSAGSSEKQSPMAQPSPVCQPNTVNQTGAAPLANSNAQQNSAPQPSPIKQPISEAQPSLVTQNSPANHPSSVTQQNPQTQPVQTYSHDSSYRSEVKARQDVKPDIRQPFTDYRQPPVDYRHPPVADYRQPPTLDYRHPPLLDYRPLPADPRTFPLPDYRMPQDFDFFTVELEKGMKGFGFSIRGGREYKMDLFVLRLAEDGPAIRNGRMRVGDQIIEINGESTRDMTHARAIELIKSGGRRVRLLLKRGTGQVPEYGMVSSSLSMCMKSDNHGSPYFFLM	
	magi2a	ENSDART00000133644	NM_001327853	reverse	TCCAGGGGTCCGA	GGG	c.61_73delinsGGG	p.Ser21Profs*4	MSKSLKKKSHWTNRVHEVVLGVGI*	24
magi2b[cl608]	magi2b	ENSDART00000110879.3	n/a	reverse	GACCTAGTGCA	n/a	c.620_630del	p.Pro208Glyfs*6	MSKSLKKKNHWTNKVHEALLGRNKEGELGFDLKGGAENGNFPYFGEVKQGKVAIQSGKLSQDELLLEVNDTPVAGLTIRDVLAVIKHCKDPFRLKCVKQGGVVDKDLRHYLNLRFQKGSVDHELQQIIRDNLYLRTVPCTTRQPKEGEVPGVDYNFVSVERFMELEKSGALLESGTYEDNFYGTPKPPAEPTPMLFNVTDQLLPGARGEKEEK	213
magi2b[cl609]	magi2b	ENSDART00000110879.3	n/a	reverse	GCAGA	n/a	c.628_632del	p.Ala210Glyfs*6	MSKSLKKKNHWTNKVHEALLGRNKEGELGFDLKGGAENGNFPYFGEVKQGKVAIQSGKLSQDELLLEVNDTPVAGLTIRDVLAVIKHCKDPFRLKCVKQGGVVDKDLRHYLNLRFQKGSVDHELQQIIRDNLYLRTVPCTTRQPKEGEVPGVDYNFVSVERFMELEKSGALLESGTYEDNFYGTPKPPAEPTPMLFNVTDQLLPGARPSGEKEEK	215