

Supplemental Table 1: circRNA specific protein sequences

>LINC PINT

MLWLPPDRGSCSARSPSGMLRGAPGGWRYGRRRCRRRQSCCCCCCASHVGAPLSFHREASLVSHD
GHDIMKQHCGEESIRGAHGYKNK

>circSHPRH

MKIQLRDPGAKALVFSTWQDVLDIISKALTDNNMEFAQISRVTQFQENLSAFKRDPQINILLP
LHTGSNGLTIIIEATHVLLVEPILNPAHELQAIGRVHRIGQTKPTIVHRFLIKATIEERMQAMLK
TAERRAAILQKWLWSEL

>circFBXW7

MNQELLSVGSKRRRTGGSLRGNPSSSQVDEEQMNRVVEEEQQQQLRQQEEEHTARNGEVVGVEP
RPGGQNDSSQQGLEENNNRFISVDEDSSGNQEEQEEDEEHAGEQDEEDEEEEEE^{MDQESDDFDQS}
DDSSREDEHHTNSVTNSSSIVDLPVHQLSSPFYTKTKTKDYFLRIDCQKWSYWVRGM

>circCDH1

MEVTATDADDDVNTYNAAIAYTILSQDPELPDKNMFTINRNTGVISVTTGLDRESFPTYTLVV
QAADLQGEGLSTTATAVITVTDNDNPPIFNPTTYKGQVPENEANVVITTLKVTADAPNTPAW
EAVYTILNDDGGQFVVTNPNVNDGILKTAKGLDFEAKQQYILHVAVTNVVPFEVSLTTSTATV
TVDVLDVNEAPIFVPPEKRVEVSEDFGVGQEITSYTAQEPDTFMEQKITNLCDGGHSHRRGR

>circINSIG1

MVSITVVGLLYPCIDSHLGEPHKFKREWASVMRCIAVFVGINHASAVSLIFCATSRKLDFANNV
QLSLTLAALSLGLWWTFDRSRSGLGITIAFLATLITQFLVYNGVYHCCWPTVPLYRQSPRRT
PQI

>circNFIB

MNSGVNLQORSLSSPPSSKRPKTISIDENMEPSPTGDFYFSPSSPAAGSRTWHERDQDSGQSGSP
SHNDPAKNPPGYLEDSEFVKSGVFNVSELVVRVSRTPITQGTGVNFPIGEIPSQPYHDMNSGVNL
QORSLSSPPSSKRPKTISIDENMEPSPTGDFYFSPSSPAAGSRTWHERDQDSGQSGSPSHNDPAK
NPPGYLEDSEFVKSGVFNVSELVVRVSRTPITQGTGVNFPIGEIPSQPYHD

>ZNF609

MSLSSGASGGKGVDPANPVETYDSGDEWDIGVGNLIIDLADLEKDQQKLEMSGSKKEVGI PAPNA
VATLPDNIKFVTPVPGPQGKEGKSKRSKSGKDTSKPTPGTSLFTPSEGAASKKEVQGRSGDG
ANAGGLVAIAIPKGSEKAAKASRSVAGSKKEKENSSSKSKKERSEGVGTCSEKDPGVLQPVPLG
GRGGQYDGSAGVDTGAVEPLGSIAIEPGAALNPLGTKPEPEEGENE^{CRLLKKVKSEKQ}

>circYAP1

MAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMNSASGPLPDGWEQAMTQ
DGEIYYINHKNTTSWLDPRLDPRFAMNQRIQSAPVKQPPPLAPQSPQGGVMGGNSNSNQQQQM
RLQQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGM
SQELR TMTTNSSDPFLNRPVLMQALQEP

>FAM53B

MSSCRTSWRPLGSKVWTPVEKRRRCYSGGSVQRYSNGFSTMQRSSSFSLPSRANVLSSPCDQAGL
HHRFGGQPCQGVPGSAPCGQAGDTWSPDLHPVGGGRDLQORSLSCSHEQFSFVEYCPPSANSTP

ASTPELARSSSGLSRSRSQPCVLNDKKVGVKRRRPEEVQEQRPSLDLAKMAQKMTDGETWTGNA
LFRLTNRAPASGNACLKRTAHYGTGRQ

>TRCP

MMEKLKCGILWLLWTPVLLQGHSVYGPLWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIE
SNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHGTGSVL
CLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTC SKDRSIAVWDM
SPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNHGKRGIACLQYR
DRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP
RAPAGTLCRLTLVGTVFIQKQTS

>circMET

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GATNYIIYVLNEEDLQKVAEYKTGPVLEHPDCFPQCDCSSKANLSGGVWKDNINMALVVDTYDD
QLISCGSVNRGTCQRHVFPHNHTADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRF
INFFVGNTINSSYFPDHPHSISVRRLKETKDGFMFMTDQSYIDVLPEFRDSYPIKYVHAFESN
NFIYFLTQVRETLDATFHTRIIRFCSINSGLHSYMEMPLECILTEKRKKRSTKKEVFNILQAA
YVSKPGAQLARQIGASLNDDILFGVFAQSKPDSEPMDRSAMCAFPKIYVNDFFNKIVNKNNVR
CLQHFYGPNEHCFNRINLS

>CAPG

MTALCWTGTSVARSISGRNIFAWCGGKSNILERNKARDLALAIRDSERQGKAQVEIVTDGEEPA
EMIQVLGPKPALKEGNPEEDLTADKANAAALYKVSDATGQMNLTKVADSSPFALELLISDDC
FVLNGLCGKIYIWKEHLRLVWVKVQHPGTQQGEGPGPHPGQ

>RSRC1

MIEDAGIDQAVALLMAPEGNEVEVVQGVGNPIEFRGLGQKAEQEEMGRSSDTEEEESRSKRKK
KHRRRSSSSSSSDSRTYSRKKGGRKSRKSRWSRDLQPRSHSYDRRRRHRSSSSSSSYGSRRKR
SRSRSRGRGKSYRVQRSRSKSRTRNGTSVIRY

>TMEFF1

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QEQIDIRHLGHCTD TDDTSLLGKKDDGLQYRPDVKDASDQREDVYIGNHMPCPENLNGYCIHGK
CEFIYSTQKASCRCVCNIDCSGYSFNPVCASDGSSYNNPCFVREASCIKQEQIDIRHLGHCTD
TDDTSLLGKKDDGLQYRPDVKDASDQREDVYIGNH

>PPP1R12A

MKPVLAFKHGNFDSLPLQMEISSIKKIGWVQWLIPVVSQHFGRRLRHVNCLSPGVQDQPGQHGET
PSLPKVQN

>GSPT1

MIGGASQADLAVLVISARKGEFETGFEEKGGQTREHAMLAKTAGVKHLIVLINKMDDPTVNWSNE
RYEECKEKLVPFLKKVGFNPKKDIHFMPCSGLTGANLKEQSDFCPWYIGLPFIPYLDNLPNFNR
SVDGPIRLPIDKYKDMGTVVLGKLESGSICKGQQLVMMPNKHNVVLGILSDDVETDTPAPGE
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>circMAPK14

MGADLNNIVKCQKLTDDHVQFLIYQILRGLKYIHSADI IHRDLKPSNLAVNEDCELKILDFGLA
RHTDDEMTGYVATRWRAP EIMLNWMHYNQTVDIWSVGCIMAE LLTGRTLFP GTDHDIDQLKLIL
RLVGTPGAELLKKISSSESARNYIQSLTQMPKMN FANVFIGANPLGIW

>PLCE1

MTSEEMTASVLIPVTQRKVVSAQSAADESSEKVS DINISKAHTVRRSGETSHTISQLNKLKEEP
SGSNLPKILSIAREKIVSDENSNEKCWEKIMPD SAKNLNINCNNILRNHQHGLPQRQFYEMYNS
VAEEDLCLETGIPSPLERKVFPGIQLELDRPSMGISPLGNQSVI IETGRAHPDSRRAVFHFHYE
VDRRMSDTFCTLSEN LILDDCGNCVPLPGGEEKQKKNYVAYTCKLMELAKNCDNKNEQLQCDHC
DTLNDKYFCFE GSC EKVDMVYSGDSFCRKDFTDSQA AKTFLSHFEDFPDNCDDVEEDAFKSKKE
RSTLLVRRFCKNDREVKKSVYTGTRAIVRTLPSGHIGLTAWSYIDQKRNGPLLPCGRVMEPPST
VEIRQDGSQRLSEAQWYPETGIIQTGF

>CTNNB1

MATQADLMELDMAMEPDRKAAVSHWQQQSYLD SGIHSGATTTAPSLSGKGNPEEEDVDTSQVLY
EWEQGFSQSFTQE QVADIDGQYAMTRAQRVRAAMFPETLDEGMQIPSTQFDAAHPTNVQRLAEP
SQMLKHAVVNLIN YQDDAELATRAIPELTKLLNDEDQVVVNKAAVMVHQLSKKEASRHAIMRSP
QMVSAIVRTMQNTNDVETARCTAGTLHNL SHHREGLLAI FKSGGIPALVKMLGSPVDSVLFYAI
TTLHNLLLHQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLIILASGG
PQALVNIMRTYTYEKL LWTTSRVLKVL SVCSSNKPAIVEAGYLKYTIQLF

> ARHGAP35

MMMARKQDVRIPTYNISVVGLSGTEKEKGQCGIGK SCLCNRFVRPSADEFHL DHTSVLSTSDFG
GRVVNNDHFLYWG EVSRSLED CVECKMHIVEQTEFID DQTFQPHRSTALQPYIKRAAATKLASA
EKL MYFCTDQLGLEQDFEQKQMPD GKL LVDGFL LGIDVSRGMNRNFDDQLKFVSNLYNQLAKTK
KPIVVVLTKCDEGVERYIRDAHTFALS KKNLQVVETSARSNVNVDLAFSTLVQLIDKSRGKTKI
IPYFEALKQQSQQIATAKDKYEWLVSRIVKNHNENWLSVSRKMQASPEYQDYVYLEGTQKAKKL
FLQHIHRLKHEHIERRRKL YLAALPLAFEALIPNLDEIDHLS CIKAKKLLET KPEFLKWFVVLE
ETPWDATSHIDNMENERIPFDLMDTVPAEQLYEAHLEKL RNERKRVEMRRAFKENLETSPFITP
GKPWEEARSFIMNEDFYQWLEESVYMDIYGKHQKQIIDKAKEEFQELLLEYSELFYELELDAKP
SKEKMGVIQDVLGEEQRFKALQKLQAERDALILKHIHFVYHPTKETCPSCPACVD AKIEHLISS
RFIRPSDRNQKNSLSDPNIDRINLVILGKDGLARELANEIRALCTNDDKYVIDGKMYELSLRPI
EGNVRLPVNSFQTPTFQPHGCLCLYNSKESLSYVVESIEKSRESTLGRRDNHLVHLPLTLILVN
KRGDTSGETLHSLIQGQQIASKLQCVFLDPASAGIGYGRNINEKQISQVLKGLLDSKRNLNLV
SSTASIKDLADV DLRIVMCLMCGDPFSADDILFPVLQSQTCKSSHCGSNNSVLELPIGLHKKR
IELSVLSYHSSFSIRKSRLVHG YIVFYSAKRKASLAMLRAFLCEVQDI IPIQLVALTDGAVDVL
DNDLSREQLTEGEEIAQEIDGRFTSIPCSQPQH KLEIFHPFFKDVVEKKNIEATHMYDNAAEA
CSTTEE VFNSPRAGSPLCNSNLQDSEEDIEPSYSLFREDTSLPSLSKDH SKLSMELEGN DGLSF
IMSNFESKLNNKVP PPVKPKPPVHFEITKGDLSYLDQGHRDGQRKSVSSSPWLPQDGFDP SDYA
EPMDAVVKPRNEEENIYSVPHDSTQGKIITIRNINKAQ SNGSGNGSDSEMDTSSLERGRKVSIV
SKPVLYRTRCTRLGRFASYRTSFSVGSDELGP IRRKEEDQASQGYKGDNAVIPYETDE DPRRR
NILRSLRRNTKKPKPKPRPSITKATWESNYFGVPLTTVVTP EKPIPIFIERCIEYIEATGRNVG
YLAMRGGEQ

>EGFR

MNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVWKYADAGHVCHLCHPNCTYGEPR
EFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVWKYA
DAGHVCHLCHPNCTYGEPRFVENSECIQCHPECLPQA

>APP

MISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPV DAR
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GGVVIATVIVITLVMLKKKQYTSIHG VVEMSCFRKSKTIQMTSWPT

>FNDC3B

MAMGRAIVVEVAEAAA VVVPELRKQSDEQEAAQSRMIQTCKVIEDSTGVRRVVVTPQSPECYPP
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GMSTYITREDQYSKPPHKKLKDRQIDRQNRLNSPPSSIYKSSCTTVYNGYGKGHSGGSGGGGSG
SGPGIKKTERRARSSPKSNSDSLQGD

>RTN4

MDLKEQPGNTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYLG NLSAVASTEGTIEETLN
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CSAALHNPQESPATLT KVVKEDGVMSPEKTMDIFNEMKMSVVAPVREEYADFKPFEQAW EVKDT
YEGSRDVLAARANMESKVDKKCFEDSLEQKGHGKDSESRNENASFPRTPELVKDGS RAYITCDS
FSSATESTAANIFPVLEDHTSENKTDEKKIEERKAQIITEKTS PKTSNPFLVAIHDSEADYVTT
DNLSKVTEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQL
CPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPY
EEAMSVALKTSDSKEEIKEPESFNAAQAEAEAPYIS IACDLIKETKLSTEPSPEFSNYSEIAKF
EKSVDPDHCELVD DSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESL TEVSETVTQHKKKERLS
ASPQEVGKPYLESFQPNLHITKDAASNEIPTLT KKETISLQMEEFN TAIYSNDDLSSKEDKMK
ESETFSDSSPIEIIDEFPTFVSAKDDSPKEYTDLEVS NKSEIANVQSGANSLPCSELPCDLSFK
NTYPKDEAHVSDEF SKSRSSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAE EKLPDTEKE
DRSLTAVLSAELNKTSDETLFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETA
ASLPSLSPLSTVSFKEHGYLG NLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLE
YSEMGS SFNGSPKGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLT KVVKEDGVMS
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LEQKGHGKDSESRNENASFPRTPELVKDGS RAYITCDSFSSATESTAANIFPVLEDHTSENKTD
EKKIEERKAQIITEKTS PKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA
CESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNS
LLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAA
AQAEAEAPYIS IACDLIKETKLSTEPSPEFSNYSEIAKF EKSVDPDHCELVD DSSPESEPVDLFS
DSIPEVPQTQEEAVMLMKESL TEVSETVTQHKKKERLSASPQEVGKPYLESFQPNLHITKDAAS
NEIPTLT KKETISLQMEEFN TAIYSNDDLSSKEDKMK ESETFSDSSPIEIIDEFPTFVSAKDD
SPKEYTDLEVS NKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVSDEF SKSRSSSVSKVPL
LLPNVSALESQIEMGNIVKPKVLTKEAE EKLPDTEKEDRSLTAVLSAELNKTSDETLFALPAA
SEPVI PSSAEKI

>NLGN1

MALPRCTWP NYVWRAVMACLVHRGLGAPLTLCMLGCLLQAGHVLSQKLDDVDPLVATNFGKIRG
IKKELNNEILGPVIQFLGVPYAAPPTGERRFQPPEPPSPWSDIRNATQFAPVCPQNIIDGRLPE
VM LPVWF TNNLDVVS SYVQDQSEDCLYLN IYVPTEDGYRPAANWI

>AXIN1

MNIQEQQGFPLDLGASFTEADAPRPPVPGEEGELVSTDPRPASYSFCSGKGVGIKGETSTATPRRS
DLDLGYEPEGSASPTPPYLKWAESLHSLDDQDGLSLFRTFLKQEGCADLLDFWFACTGFRKLE
PCDSNEEKRLKLARAIYRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQAT
MEENTYPSFLKSDIYLEYTRTGSESPKVCSDQSSSGSGTGKGISGYLPTLNEDEEWKCDQDMDED
DGRDAAPPGRLPQKLLLETAAPRVSSRRYSEGREFRTD

>EIF6

MKPSLAPLPPACGIPSLTASPESPSKLFHGLLALDCGQPSPHSAQSVPDAGREVAESSLGLRGW
APNPFPPVLIAWIYHYCKNLLCCAGWQALWLLAEGSAVLCHPIKVQFPPVCSRASSPIPSPWCT
RLSPAAASSGACVWGTGTVSWYPTIPPTRSCNTFATASQTQCRLGGWRSGSQPWAMSPAMTTW
PWSTQWTWGRQKKFWQMCSRWKSSDRQWPTRC

>HER2

MCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP

>MAPT 12 to 7

MPDLKNVSKSIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPV
DLSKVTSCGSLGNIHHKPGGGQVEVKSEKLDLKDRVQSKIGSLDNITHVPGGGNKKGADGKTK
IATPRGAAPPQKGQANATRIPAKTTPAPKTPSSGEPKSGDRSGYSSPGSPGTPGSRSRTPS
LPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPLKNVSKSIGSTENLKHQPGGGKVQII
NKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVLDLSKVTSCGSLGNIHHKPGGGQVEVKSE
KLDLKDRVQSKIGSLDNITHVPGGGNKKGADGKTKIATPRGAAPPQKGQANATRIPAKTTPAP
KTPSSGEPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRL
QTAPVP

>MAPT 12 to 10 v377M

MEVKSEKLDLKDRVQSKIGSLDNITHVPGGGNKKVQIINKKLDLSNVQSKCGSKDNIKHVPGGG
SVQIVYKPVLDLSKVTSCGSLGNIHHKPGGGQMEVKSEKLDLKDRVQSKIGSLDNITHVPGGGN
KKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVLDLSKVTSCGSLGNIHHKPGGGQ

>MAN2A1

MVEFGSKDLTLLMNLMTNLNPFKSLWCLIPITTQGQLSMLQEKIDHLERLLAENNEIISNIRD
SVINLSESVEDGPKSSQSNFSQGAGSHLLPSQLSLSVDTADCLFASQSGSHNSDVQMLDVYSLI
SFDNPDGGVWKQGFDTYESNEWDTEPLQVFVPHSHNDPGPALNVARKNRPFGAFAFAS

>SDHAF2

MTGIFTTGPQMLALSRLHSLLSPLLSVTSFRRFYRGDSPTDSQKDMIEIPLPPWQERTDESIETK
RARLLYESRKRGMLENCILLSLFAKEHLOHMTTEKQLNLYDRLINEPSNDWDIYYWATDACSVKA
QPIVSFAQCDDIIQTLLQR

>SLC8A1

MYNMRRLSLSPTFSMGFHLLVTVSLLFSHVDHVIAETEMELEGNETGECTGSYYCKKGVILPIW
EPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPNGETTKTTVR
IWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIALLCVYVVPD
GETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTFFFFPICVVFVAWADRRL
LFYKYVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSHVENFLDGALVLEVDERDQDDE

EARREMARILKELKQKHPDKEIEQLIELANYQVLSQQQKSRAFYRIQATRLMTGAGNILKRHAA
DQARKAVSMHEVNTEVTENDPVSKIFFEQGTYQCLENCGTVALTIIRRGGDLTNTVFVDFRTED
GTANAGSDYEFTEGTVVFKPGDTQKEIRVGIIDDDIFEEDENFLVHLSNVKVSSEASEDGILEA
NHVSTLACLGSPSTATVTIFDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKT
IEGTARGGGEDFEDTCGELEFQONDEIVRL

Supplemental Table 2: Characteristics of circRNA encoded proteins.

	circular RNA	% disordered residues ¹	% MoRF residues ²	phase separation propensity ³
1	LINC-PINT	32	64	0.16
2	circ-SHPRH	2	0	0.01
3	circFBXW7	96	29	1.0
4	circCDH1 CircCadherin	2	4	0.17
5	circINSIG1	5		0.01
6	circNFIB	95	20	0.91
7	circZNF609	100	22	1.0
8	circYAP	100	5	1.0
9	circFAM53B	71	2	0.97
10	circ Beta TRCP official name BTRC in our data	0	1	0.56
11	circMET	1	0	0.39
12	circCAPG	31	0	1.0
13	circRsrc1	100	28	1.0
14	CircTmeff1	20	15	0.07
15	circPPP1R12A	43	79	0.23
16	circGSPT1	0	4	0
17	circMAPK14	0	0	0
18	circPLCE1	19	0	1.0
19	circCTNNB1	29	4	0.03
20	circARHGAP35	3	0	1.0
21	circEGFR	1	0	0
22	Circ APP	50	0	0.01
23	circFNDC3B	72	24	1.0
24	circRTN4 (mouse)	4	3	1.0
25	Nlgn (mouse)	11	0	0.02
26	AXIN1	55	14	0.95
27	EIF6	6	0	1.0
28	HER2	0	9	1.0
29	MAPT 12 to7	100	32	1.0
30	MAPT12 to 10	100	33	0.88
31	MAN2A1-400	28	2	0.21
32	SDHAF2	18	14	0.012
33	SLC8A1	3	0	0.298

¹Percentage of disordered residues predicted with fIDPnn as implemented in DEPICTER2 (<http://biomine.cs.vcu.edu/servers/DEPICTER2/>).

²Molecular Recognition Feature (MoRF) predicted with fMoRFPred as implemented in DEPICTER2.

³Calculated with MolPhase (<https://molphase.sbs.ntu.edu.sg>). Propensity range is 0-1.0 with higher values corresponding to increased propensity.