

Table S2. Related to STAR METHODS. Amino acid sequence of internally linked PyIRS dimers.

<p>PM-MCP-OT_{v2,AA} <i>LCK₁₋₁₀</i> <i>HA</i> <i>MCP</i> <i>SPOT</i> <i>NES</i> <i>PyIRS^{AA}</i> <i>FUS₁₋₄₇₈</i></p>	<p>MGCVCSSNPEGTELAIAYPYDVPDYAGAPGSAGSAAGSGASNFTQFVLVDNNGTGDVTVAPSNFANGIAEWISSNSRSQAYKVTCSVRQSSAQNRKYTIKVEVPKGAWRSYLNMEITIPFATNSDCELVKAMQGLLKDGNPIPSAIAANSGLSGLSPDRVRAVSHWSSACPVPLQLPPLERLTLDDKKPLNTLISATGLWMSRTGTIHKIKHHEVSRSKIYIEMACGDHLVVNNSRSSRTARALRHHKYRKTCKRRCRVSDLEDLNKFLTKANEDQTSVKVKVVSAPTRTKKAMPKSVARAPKPLENTEAAQAQPSGSKFSPAIPVSTQESVSVPASVSTSISSISTGATASALVKGNTPITSMSAPVQASAPALTKSQTDRLEVLLNPKDEISLNSGKPFRELESELLSRRKKDLQIQIYAEERENYLGLKLEREITRFFVDRGFLEIKSPIPILEIYIERMGIDNDELTSKQIFRVDKNFCLRPMLAPNLNYLRLKLDRALPDPKIFEIGPCYRKESDGKEHLEEFMTLAFAMGSGCTRENLESIITDFLNHLGIDFKIVGDSCMVYGDTLDMHGDLELSSAVVGPIPLDREWIDKWPWAGAGFLERLLKVKHDFKNIKRAARSESYNGISTNLASNDYTQQATQSYGAYPTQPGQGYSSQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQNTGYGTQSTPQGYGSGTGGYGGSSQSSQSSYGGQSSYPGYGQQPAPSSTSGSYGSSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGGNYGQDQSSMSSGGSGGGYGNQDQSGGGGGGGYGGQDRGGRGRGGSGGGGGGGGGGNYRSSGGYEPGRGGGRGRGGMGGSDRGGFNKFGGPRDQGSRHDEQDSDNNTIFVQGLGENVTIESVADYFKQIGIIKTNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAIDWFDGKEFSGNPIKVSFATRRADFNRGGNGRGGRGRGGPMGRGGYGGGGSGGGGRGGFPSSGGGGGGQQRAGDWKCPNPTCENMNFWRNECNQCKAPKPDGPGGGPGGSHMGGNYGDDRRGGRGGDKKPLNTLISATGLWMSRTGTIHKIKHHEVSRSKIYIEMACGDHLVVNNSRSSRTARALRHHKYRKTCKRRCRVSDLEDLNKFLTKANEDQTSVKVKVVSAPTRTKKAMPKSVARAPKPLENTEAAQAQPSGSKFSPAIPVSTQESVSVPASVSTSISSISTGATASALVKGNTPITSMSAPVQASAPALTKSQTDRLEVLLNPKDEISLNSGKPFRELESELLSRRKKDLQIQIYAEERENYLGLKLEREITRFFVDRGFLEIKSPIPILEIYIERMGIDNDELTSKQIFRVDKNFCLRPMLAPNLNYLRLKLDRALPDPKIFEIGPCYRKESDGKEHLEEFMTLAFAMGSGCTRENLESIITDFLNHLGIDFKIVGDSCMVYGDTLDMHGDLELSSAVVGPIPLDREWIDKWPWAGAGFLERLLKVKHDFKNIKRAARSESYNGISTNL</p>
<p>ERM-MCP-OT_{v2,AF} <i>CYPIIC₁₋₂₇</i> <i>EWSR1₁₋₆₂₈</i> <i>HA</i> <i>MCP</i> <i>VSV-G</i> <i>NES</i> <i>PyIRS^{AF}</i> <i>FUS₁₋₄₇₈</i></p>	<p>MDPVVVLGLCLSCLLLLSLWKQSYGGMMASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTQAYGQQSYGTYGQPTDVSYTQAQTTATYGTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTATVTTTQASYAAQSAQYGTQPAYPAYGQQPAATAPTRPQDGNKPTETSQPSQSSGGYNQPSLGYGQSNYSYPQVPGSYPMQPVTAAPPSPPTSYSSTQPTSQDSSYSQQNTYGGPSSYGGQSSYGGQSSYGGQPPTSYPPQTGSYSQAPSQSSYGGQSSFRQDHPSSMGVYQESGGFSGPGENRSMSPDNRRGRGGFDRGGMSRGGRRGGMGMSAGERGGFNKPGGPMDEGPDLDLGPVDPDEDSDNSAIYVQGLNDSVTLDDLADFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGSKLKVSARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPMGRMGRRGGDRGGFPPRGRPRGSRGNPSSGGNVQHRAGDWQCPNPGCGNQNAWRTECNQCKAPKPEGFLPPPFPFGGDRGRGGP GGMRGGRRGLMDRGGPGMFRGGRRGGDRGGFRGGRRGMDRGGFGGRRGGPGGPPGLMEQAIAYPYDVPDYAGAPGSAGSAAGSGASNFTQFVLVDNNGTGDVTVAPSNFANGIAEWISSNSRSQAYKVTCSVRQSSAQNRKYTIKVEVPKGAWRSYLNMEITIPFATNSDCELVKAMQGLLKDGNPIPSAIAANSGLSGLSYTDIEMNRLGKACPVPLQLPPLERLTLDDKKPLNTLISATGLWMSRTGTIHKIKHHEVSRSKIYIEMACGDHLVVNNSRSSRTARALRHHKYRKTCKRRCRVSDLEDLNKFLTKANEDQTSVKVKVVSAPTRTKKAMPKSVARAPKPLENTEAAQAQPSGSKFSPAIPVSTQESVSVPASVSTSISSISTGATASALVKGNTPITSMSAPVQASAPALTKSQTDRLEVLLNPKDEISLNSGKPFRELESELLSRRKKDLQIQIYAEERENYLGLKLEREITRFFVDRGFLEIKSPIPILEIYIERMGIDNDELTSKQIFRVDKNFCLRPMLAPNLANYLRLKLDRALPDPKIFEIGPCYRKESDGKEHLEEFMTLNFQMGSGCTRENLESIITDFLNHLGIDFKIVGDSCMVYGDTLDMHGDLELSAVVGPIPLDREWIDKWPWAGAGFLERLLKVKHDFKNIKRAARSESYNGISTNLASNDYTQQATQSYGAYPTQPGQGYSSQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQNTGYGTQSTPQGYGSGTYGSSQSSQSSYGGQSSYPGYGQQPAPSSTSGSYGSSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGGNYGQDQSSMSSGGGGGGYGNQDQSGGGGGGGYGGQDRGGRGRGGSGGGGGGGGGGNYRSSGGYEPGRGGGRGGMGGSDRGGFNKFGGPR</p>

	<p>DQGSRRHDSEQDNSDNNTIFVQGLGENVTIESVADYFKQIGIHKTNKKTGQPMINLYTDRETGKLGKGEATVS FDDPPSAKAAIDWFDGKEFSGNPIKVSFATRRADFNRGGGNGRGGRRGGPMGRGGYGGGGSSGGG GRGGFPPSGGGGGGGQQRAGDWKCPNPTCENMNFWRNECNQCKAPKPDGPGGGPGGSHMGGNY GDDRRGGRRGGDKKPLNLTISATGLWMSRTGTIHKIKHHEVSRSKIYIEMACGDHLVVNNSRSSRTARAL RHHKYRKTCKRRCRVSEDLNKFLTKANEDQTSVKVKVVSAPTRTKKAMPKSVARAPKLENTEAAQAQ PSGSKFSPAIPVSTQESVSPASVSTSISSISTGATASALVKGNTNPITSMSAPVQASAPALTKSQTDRLE VLLNPKDEISLNSGKPFRELESELLSRRKKDLQQIYAEERENYLGKLEREITRFFVDRGFLEIKSPILIPLEYI ERMGIDNDELTSKQIFRVDKNFCLRPMLAPNLANYLRKLDRALPDIKIFEIGPCYRKESDQKEHLEEFM LNFCQMGSCTRENLESIITDFLNHLGIDFKIVGDSCMVFGDTLDMVHGDLELSSAVVGPIPLDREWGIDK PWIGAGFGLERLLKVKHDFKNIKRAARSESYNGISTNL</p>
<p>OMM-λ_{N22}⁻ OT_{v2,AF} <i>TOM20₁₋₇₀</i> <i>EWSR1₁₋₆₂₈</i> <i>Myc</i> λ_{N22} <i>VSV-G</i> <i>NES</i> <i>PyIRS^{AF}</i> <i>FUS₁₋₄₇₈</i></p>	<p>MVGRNSAIAAGVCGALFIGYCIYFDRKRRSDPNFKNRLRERRKKQKLAKERAGLSKLPDLKDAEAVQKFF MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTQAYGQQSYGTYGQPTDVSYTQAQTTATYGGTAYA TSYGGPPTGYTTPTAPQAYSQPVQGYGTGAYDTTATVTTTQASYAAQSAYGTQPAYPAYGQQPAATA PTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYPMQPVTAPPSYPTSYSSTQPTS YDQSSYSQQNTYQGPSSYGQSSYGQSSYGQQPPTSYPPTQGSYSQAPSQYSQQSSSYGQSSFR QDHPSSMGVYGQESGGFSGPGENRSMSPDNRGRGRGGFDRGGMSRGGRRGGGRRGGMGSAGERG GFNKPGGPMDEGPDLDLGPVDPDESDNSAIYVQGLNDSVTLDDLADFFKQCGVVKMNKRTGQPMIH IYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGSKLKVS LARKKPPMNSMRGGLPPREGRGM PPPLRGGPGGGPGGPMGRMGRRGGDRGGFPFRGPRGRSNGPSGGNVQHRAGDWQCPNPGC GNQNFARTECNQCKAPKPEGFLPPFPFPGDRGRGGPGGMRGGRRGGLMDRGGPGGMFRGGRG GDRGGFRGGRMDRGGFGGGRRGGPGPPGLMEQAIAGAPGSAGSAAGSGEQKLISEEDLLATMD AQTRRRERRAEKQAQWKAANPPLDGAGAGAGAGAGAGGLATMDAQTRRRERRAEKQAQWKAANPP LDGAGAGAGAGAGAGGLATMDAQTRRRERRAEKQAQWKAANPPLDGAGAGAGAGAGAGGLATMDA QTRRRERRAEKQAQWKAANPPLGLSYTDIEMNRLGKACPVPLQLPPLERLTLDDKKPLNLTISATGLWM SRTGTIHKIKHHEVSRSKIYIEMACGDHLVVNNSRSSRTARALRHHKYRKTCKRRCRVSEDLNKFLTKAN EDQTSVKVKVVSAPTRTKKAMPKSVARAPKLENTEAAQAQPSGSKFSPAIPVSTQESVSPASVSTSI SISTGATASALVKGNTNPITSMSAPVQASAPALTKSQTDRLEVLLNPKDEISLNSGKPFRELESELLSRRK KDLQQIYAEERENYLGKLEREITRFFVDRGFLEIKSPILIPLEYIERMGIDNDELTSKQIFRVDKNFCLRPML APNLANYLRKLDRALPDIKIFEIGPCYRKESDQKEHLEEFMNLNFCQMGSCTRENLESIITDFLNHLGID FKIVGDSCMVFGDTLDMVHGDLELSSAVVGPIPLDREWGIDKPWIGAGFGLERLLKVKHDFKNIKRAARS ESYNGISTNLASNDYTQATQSYGAYPTQPGQGYSSQSSQPYGQQSYSGYSQSTDTSGYGQSSYSS YGQSQNTGYGTQSTPQGYGSTGGYSSQSSQSSYGQSSYPGYGQQPAPSSTSGSYGSSSSQSSSY GQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQNSSSSGGGGGGGGGGNYGQDQSSMS SGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRRGGSGGGGGGGGGYNRSSGGYEPRGRGGG RGGRRGGMGGSDRGGFNKFGGPRDQGSRRHDSEQDNSDNNTIFVQGLGENVTIESVADYFKQIGIHKTNK KTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFDGKEFSGNPIKVSFATRRADFNRGGGNGR GGRGRGGPMGRGGYGGGGSGGGGRGGFPPSGGGGGGGQQRAGDWKCPNPTCENMNFWRNECN QCKAPKPDGPGGGPGGSHMGGNYGDDRRGGRRGGDKKPLNLTISATGLWMSRTGTIHKIKHHEVSRSKI YIEMACGDHLVVNNSRSSRTARALRHHKYRKTCKRRCRVSEDLNKFLTKANEDQTSVKVKVVSAPTRTK KAMPKSVARAPKLENTEAAQAQPSGSKFSPAIPVSTQESVSPASVSTSISSISTGATASALVKGNTNP ITSMSAPVQASAPALTKSQTDRLEVLLNPKDEISLNSGKPFRELESELLSRRKKDLQQIYAEERENYLGK EREITRFFVDRGFLEIKSPILIPLEYIERMGIDNDELTSKQIFRVDKNFCLRPMLAPNLANYLRKLDRALPDI KIFEIGPCYRKESDQKEHLEEFMNLNFCQMGSCTRENLESIITDFLNHLGIDFKIVGDSCMVFGDTLDM HGDLELSSAVVGPIPLDREWGIDKPWIGAGFGLERLLKVKHDFKNIKRAARSESYNGISTNL</p>
<p>OMM-λ_{N22}⁻ OT_{v2,AA} <i>TOM20₁₋₇₀</i> <i>EWSR1₁₋₆₂₈</i> <i>Myc</i></p>	<p>MVGRNSAIAAGVCGALFIGYCIYFDRKRRSDPNFKNRLRERRKKQKLAKERAGLSKLPDLKDAEAVQKFF MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTQAYGQQSYGTYGQPTDVSYTQAQTTATYGGTAYA TSYGGPPTGYTTPTAPQAYSQPVQGYGTGAYDTTATVTTTQASYAAQSAYGTQPAYPAYGQQPAATA PTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYPMQPVTAPPSYPTSYSSTQPTS YDQSSYSQQNTYQGPSSYGQSSYGQSSYGQQPPTSYPPTQGSYSQAPSQYSQQSSSYGQSSFR QDHPSSMGVYGQESGGFSGPGENRSMSPDNRGRGRGGFDRGGMSRGGRRGGGRRGGMGSAGERG</p>

λ_{N22}

SPOT

NES

PyIRS^{AA}

FUS₁₋₄₇₈

GFNKPGGPMDEGPDLDLGPPVDPDESDNSAIYVQGLNDSVTLDDLADFFKQCQGVVKMNKRTGQPMIH
IYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGSKLKVS LARKKPPMNSMRGGLPPREGRGM
PPPLRGGPGGGPGGPGGPMGRMGRRGGDRGGFPPRGRGSRGNPSGGGNVQHRAGDWQCPNPGC
GNQNFARTECNQCKAPKPEGFLPPFPFPPGGDRGRGGPGGMRGGRGGLMDRGGPGGMFRGGRG
GDRGGFRGGRGMDRGGFGGGRRGGPGGPPGLMEQAIAGAPGSAGSAAGSGEQKLISEEDLLATMD
AQTRRRERRAEKQAQWKAANPPLDGAGAGAGAGAGAGGLATMDAQTRRRERRAEKQAQWKAANPP
LDGAGAGAGAGAGAGGLATMDAQTRRRERRAEKQAQWKAANPPLDGAGAGAGAGAGAGGLATMDA
QTRRRERRAEKQAQWKAANPPLGLSPDRVRAVSHWSSACPVPLQLPPLERLTLDDKKPLNTLISATGL
WMSRTGTIHKIKHHEVSRSKIYIEMACGDHLVNNRSRSTARALRHHKYRKTCKRCRVSDLEDLNKFLTK
ANEDQTSVKVKVVSAPTRTKKAMPKSVARAPKPLENTEAAQAQPSGSKFSPAIPVSTQESVSPASVST
SISSISTGATASALVKGNTNPITSMSAPVQASAPALTKSQTDRLEVLLNPKDEISLNSGKPFRELESELLSR
RKKDLQQIYAEERENYLGKLEREITRFFVDRGFLEIKSPILIPLEYIERMGIDNDELTSKQIFRVDKNFCLRP
MLAPNLNYLRKLDRALPDPIKIFEIGPCYRKESDGKEHLEEFTMLAFAQMGSCTRENLESIITDFLNHL
GIDFKIVGDSCMVYGD TLDVMHGDLELSSAVVGPIPLDREWIDKWPWIGAGFGLERLLKVKHDFKNIKRA
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SYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGGNYGQDQSS
MSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGGSGGGGGGGGGYNRSSGGYEPGRGRG
GGRGGRGGMGGS DRGGFNKFGGPRDQGSRHDSEQDNSDNNTIFVQGLGENVTIESVADYFKQIGIIKT
NKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFDGKEFSGNPIKVSFATRRADFNRRGGNG
RGGRRGRGPMGRGGYGGGGSGGGGRRGGFPSSGGGGGGGQQRAGDWKCPNPTCENMNFWRNEC
NQCKAPKPDGPGGGPGGSHMGGNYGDDRRGGRRGGDKKPLNTLISATGLWMSRTGTIHKIKHHEVSR
KIYIEMACGDHLVNNRSRSTARALRHHKYRKTCKRCRVSDLEDLNKFLTKANEDQTSVKVKVVSAPTR
TKKAMPKSVARAPKPLENTEAAQAQPSGSKFSPAIPVSTQESVSPASVSTSISSISTGATASALVKGNT
NPITSMSAPVQASAPALTKSQTDRLEVLLNPKDEISLNSGKPFRELESELLSRKKDLQQIYAEERENYLG
KLEREITRFFVDRGFLEIKSPILIPLEYIERMGIDNDELTSKQIFRVDKNFCLRPMLAPNLNYLRKLDRALP
DPIKIFEIGPCYRKESDGKEHLEEFTMLAFAQMGSCTRENLESIITDFLNHLGIDFKIVGDSCMVYGD TLD
VMHGDLELSSAVVGPIPLDREWIDKWPWIGAGFGLERLLKVKHDFKNIKRAARSESYNGISTNL