**Plasmid sequences**

Nucleotide sequences for constructs discussed in this paper. There are two classes of plasmids: those used to make recombinant protein in bacteria in the pCDF MBP-TEV or pGEX-TEV vector backbone, and those used to express full-length Dvl proteins in cells for signaling assays, which are in the pCS2+ vector backbone under the control of the SP6 promoter. The full sequence of each vector backbone is provided, including appropriate sequencing primers for each vector backbone. For analogous constructs between mammalian and bacterial expression, please refer to the bacterial expression constructs for the exact nucleotide sequence. Yellow highlights indicate either the mutated residue or extra sequences inserted inside the native open reading frame.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| *Construct ID* | *Description* | *Vector backbone* | *ORF Sequence and/or associated PCR primer oligonucleotides* |  |
| pCDFDuet His6-MBP-TEV Sequence with Mal-E (forward), T7-Term (reverse), or DuetDOWN1 (reverse)GGGGAATTGTGAGCGGATAACAATTCCCCTGTAGAAATAATTTTGTTTAACTTTAATAAGGAGATATACCATGGGCAGCAGCCATCACCATCATCACCACGGTTCTTCTATGAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAACGCCCAGAAAGGTGAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCCGCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCGAACAACAACAACAATAACAATAACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGTCGACAAGCTTGCGGCCGCATAATGCTTAAGTCGAACAGAAAGTAATCGTATTGTACACGGCCGCATAATCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCATCTTAGTATATTAGTTAAGTATAAGAAGGAGATATACATATGGCAGATCTCAATTGGATATCGGCCGGCCACGCGATCGCTGACGTCGGTACCCTCGAGTCTGGTAAAGAAACCGCTGCTGCGAAATTTGAACGCCAGCACATGGACTCGTCTACTAGCGCAGCTTAATTAACCTAGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAACCTCAGGCATTTGAGAAGCACACGGTCACACTGCTTCCGGTAGTCAATAAACCGGTAAACCAGCAATAGACATAAGCGGCTATTTAACGACCCTGCCCTGAACCGACGACCGGGTCATCGTGGCCGGATCTTGCGGCCCCTCGGCTTGAACGAATTGTTAGACATTATTTGCCGACTACCTTGGTGATCTCGCCTTTCACGTAGTGGACAAATTCTTCCAACTGATCTGCGCGCGAGGCCAAGCGATCTTCTTCTTGTCCAAGATAAGCCTGTCTAGCTTCAAGTATGACGGGCTGATACTGGGCCGGCAGGCGCTCCATTGCCCAGTCGGCAGCGACATCCTTCGGCGCGATTTTGCCGGTTACTGCGCTGTACCAAATGCGGGACAACGTAAGCACTACATTTCGCTCATCGCCAGCCCAGTCGGGCGGCGAGTTCCATAGCGTTAAGGTTTCATTTAGCGCCTCAAATAGATCCTGTTCAGGAACCGGATCAAAGAGTTCCTCCGCCGCTGGACCTACCAAGGCAACGCTATGTTCTCTTGCTTTTGTCAGCAAGATAGCCAGATCAATGTCGATCGTGGCTGGCTCGAAGATACCTGCAAGAATGTCATTGCGCTGCCATTCTCCAAATTGCAGTTCGCGCTTAGCTGGATAACGCCACGGAATGATGTCGTCGTGCACAACAATGGTGACTTCTACAGCGCGGAGAATCTCGCTCTCTCCAGGGGAAGCCGAAGTTTCCAAAAGGTCGTTGATCAAAGCTCGCCGCGTTGTTTCATCAAGCCTTACGGTCACCGTAACCAGCAAATCAATATCACTGTGTGGCTTCAGGCCGCCATCCACTGCGGAGCCGTACAAATGTACGGCCAGCAACGTCGGTTCGAGATGGCGCTCGATGACGCCAACTACCTCTGATAGTTGAGTCGATACTTCGGCGATCACCGCTTCCCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGCTAGCTCACTCGGTCGCTACGCTCCGGGCGTGAGACTGCGGCGGGCGCTGCGGACACATACAAAGTTACCCACAGATTCCGTGGATAAGCAGGGGACTAACATGTGAGGCAAAACAGCAGGGCCGCGCCGGTGGCGTTTTTCCATAGGCTCCGCCCTCCTGCCAGAGTTCACATAAACAGACGCTTTTCCGGTGCATCTGTGGGAGCCGTGAGGCTCAACCATGAATCTGACAGTACGGGCGAAACCCGACAGGACTTAAAGATCCCCACCGTTTCCGGCGGGTCGCTCCCTCTTGCGCTCTCCTGTTCCGACCCTGCCGTTTACCGGATACCTGTTCCGCCTTTCTCCCTTACGGGAAGTGTGGCGCTTTCTCATAGCTCACACACTGGTATCTCGGCTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTAAGCAAGAACTCCCCGTTCAGCCCGACTGCTGCGCCTTATCCGGTAACTGTTCACTTGAGTCCAACCCGGAAAAGCACGGTAAAACGCCACTGGCAGCAGCCATTGGTAACTGGGAGTTCGCAGAGGATTTGTTTAGCTAAACACGCGGTTGCTCTTGAAGTGTGCGCCAAAGTCCGGCTACACTGGAAGGACAGATTTGGTTGCTGTGCTCTGCGAAAGCCAGTTACCACGGTTAAGCAGTTCCCCAACTGACTTAACCTTCGATCAAACCACCTCCCCAGGTGGTTTTTTCGTTTACAGGGCAAAAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACTGAACCGCTCTAGATTTCAGTGCAATTTATCTCTTCAAATGTAGCACCTGAAGTCAGCCCCATACGATATAAGTTGTAATTCTCATGTTAGTCATGCCCCGCGCCCACCGGAAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATCGGTCGAGATCCCGGTGCCTAATGAGTGAGCTAACTTACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCCAGGGTGGTTTTTCTTTTCACCAGTGAGACGGGCAACAGCTGATTGCCCTTCACCGCCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCACGCTGGTTTGCCCCAGCAGGCGAAAATCCTGTTTGATGGTGGTTAACGGCGGGATATAACATGAGCTGTCTTCGGTATCGTCGTATCCCACTACCGAGATGTCCGCACCAACGCGCAGCCCGGACTCGGTAATGGCGCGCATTGCGCCCAGCGCCATCTGATCGTTGGCAACCAGCATCGCAGTGGGAACGATGCCCTCATTCAGCATTTGCATGGTTTGTTGAAAACCGGACATGGCACTCCAGTCGCCTTCCCGTTCCGCTATCGGCTGAATTTGATTGCGAGTGAGATATTTATGCCAGCCAGCCAGACGCAGACGCGCCGAGACAGAACTTAATGGGCCCGCTAACAGCGCGATTTGCTGGTGACCCAATGCGACCAGATGCTCCACGCCCAGTCGCGTACCGTCTTCATGGGAGAAAATAATACTGTTGATGGGTGTCTGGTCAGAGACATCAAGAAATAACGCCGGAACATTAGTGCAGGCAGCTTCCACAGCAATGGCATCCTGGTCATCCAGCGGATAGTTAATGATCAGCCCACTGACGCGTTGCGCGAGAAGATTGTGCACCGCCGCTTTACAGGCTTCGACGCCGCTTCGTTCTACCATCGACACCACCACGCTGGCACCCAGTTGATCGGCGCGAGATTTAATCGCCGCGACAATTTGCGACGGCGCGTGCAGGGCCAGACTGGAGGTGGCAACGCCAATCAGCAACGACTGTTTGCCCGCCAGTTGTTGTGCCACGCGGTTGGGAATGTAATTCAGCTCCGCCATCGCCGCTTCCACTTTTTCCCGCGTTTTCGCAGAAACGTGGCTGGCCTGGTTCACCACGCGGGAAACGGTCTGATAAGAGACACCGGCATACTCTGCGACATCGTATAACGTTACTGGTTTCACATTCACCACCCTGAATTGACTCTCTTCCGGGCGCTATCATGCCATACCGCGAAAGGTTTTGCGCCATTCGATGGTGTCCGGGATCTCGACGCTCTCCCTTATGCGACTCCTGCATTAGGAAATTAATACGACTCACTATA |  |
| Dvl2 DIX WT Dvl2 12-92 |  | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIX Y27D | Head intra-strand mutant | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTGACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIX K68A | Tail intra-strand mutant | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGGGGTGGTGGCGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIX M60A |  | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCGCGGATCAGGATTTTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIX G65D |  | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGATGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIX N82D |  | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCGATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIXDC | F64(+DC)G65 | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGACTGTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIXY27D/DC | Y27D, F64(+DC)G65 | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTGACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGACTGTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIXDE | M60(+DE)Q61 | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGACGAGGATCAGGATTTTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIX QQ | E22Q, E24Q | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATCAGGAACAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Dvl2 DIX KK | E22K, E24K | pCDFDuet His6-MBP-TEV | AACAACAACCTCGGGCCGGGTGCGGAAAACCTGTACTTTCAGGGATCCGGCGAGACGAAGGTGATTTACCATCTGGATAAAGAAAAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCATAATAAGTCGAC |
| Axin1 DAX WT Axin1 743-826 |  | pCDFDuet His6-MBP-TEV | GAAAACCTGTACTTTCAGGGATCCCCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCTACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCCCGTCTTTGAGGAGAAGATCATCGGCAAAGTGGAGAAGGTGGACTAATAAGTCGAC |
| Axin1 DAX Y760D | Head mutant | pCDFDuet His6-MBP-TEV | GAAAACCTGTACTTTCAGGGATCCCCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCGACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCCCGTCTTTGAGGAGAAGATCATCGGCAAAGTGGAGAAGGTGGACTAATAAGTCGAC |
| Axin1 DAX V800A, F801A | Tail mutant | pCDFDuet His6-MBP-TEV | GGATCCCCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCTACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGCGGCTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCC |
| Axin1 DAX Y760D, V800A, F801A | Head+Tail mutant | pCDFDuet His6-MBP-TEV | GGATCCCCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCGACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGCGGCTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCCCGTCTTTGAGGAGAAGATCATCGGCAAAGTGGAGAAGGTGGACTAATAAGTCGAC |
| Axin1 DAXNQ/NG | D793N, E794Q, E815N, E816G | pCDFDuet His6-MBP-TEV | GGATCCCCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCTACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCAACCAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCCCGTCTTTAATGGGAAGATCATCGGCAAAGTGGAGAAGGTGGACTAATAAGTCGAC |
| Axin1 DAXNG | E815N, E816G | pCDFDuet His6-MBP-TEV | GGATCCCCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCTACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCCCGTCTTTAATGGGAAGATCATCGGCAAAGTGGAGAAGGTGGACTAATAAGTCGAC |
| Axin1 DI-DAX WT 599-826 |  | pCDFDuet His6-MBP-TEV | GGATCCGGCGTGGCGTGCAAAAGAAATGCCAAGAAGGCTGAGTCGGGGAAGAGCGCCAGCACCGAGGTGCCAGGTGCCTCGGAGGATGCGGAGAAGAACCAGAAAATCATGCAGTGGATCATTGAGGGGGAAAAGGAGATCAGCAGGCACCGCAGGACCGGCCACGGGTCTTCGTGGACGAGGAAGCCACAGCCCCATGAGAACTCCAGACCCTTGTCCCTTGAGCACCCCTGGGCCGGCCCTCAGCTCCGGACCTCCGTGCAGCCCTCCCACCTCTTCATCCAAGACCCCACCATGCCACCCCACCCAGCTCCCAACCCCCTAACCCAGCTGGAGGAGGCGGGCCGACGTCTGGAGGAGGAAGAAAAGAGAGCCAGCCGAGCACCCTCCAAGCAGAGGACAAGATCGCAGAGGAAGGTGGGCGGCGGGAGTGCCCAGCCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCTACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCCCGTCTTTGAGGAGAAGATCATCGGCAAAGTGGAGAAGGTGGACTAATAAGTCGAC |
| pGEX-TEVSequence with pGEX5 (forward) or pGEX3 (reverse)ACGTTATCGACTGCACGGTGCACCAATGCTTCTGGCGTCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCGTGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTTCTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGTATTCATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCACTCGACTTCTTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATACGGTGTTTCGAGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCGAAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGTGGATCCATATGTGGTGGCGGAGGGGAAAACCTGTATTTCCAAGGAGGAATTCTAGACTCCATGGGTCGACTCGAGCTCAAGCTTATTCATCGTGACTGACTGACGATCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATAATTCTTGAAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTGTTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGCAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATAAATTCCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAACGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGGATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCTTTGCCTGGTTTCCGGCACCAGAAGCGGTGCCGGAAAGCTGGCTGGAGTGCGATCTTCCTGAGGCCGATACTGTCGTCGTCCCCTCAAACTGGCAGATGCACGGTTACGATGCGCCCATCTACACCAACGTAACCTATCCCATTACGGTCAATCCGCCGTTTGTTCCCACGGAGAATCCGACGGGTTGTTACTCGCTCACATTTAATGTTGATGAAAGCTGGCTACAGGAAGGCCAGACGCGAATTATTTTTGATGGCGTTGGAATT |
| Axin1 DI-DAX Y760D | Head mutant | pGEX-TEV | TCGGATCTGGTTCCGCGTGGATCCATATGTGGTGGCGGAGGGGAAAACCTGTATTTCCAAGGAGGAATTCTAGACTCCATGGGTCGACTAGGCGTGGCGTGCAAAAGAAATGCCAAGAAGGCTGAGTCGGGGAAGAGCGCCAGCACCGAGGTGCCAGGTGCCTCGGAGGATGCGGAGAAGAACCAGAAAATCATGCAGTGGATCATTGAGGGGGAAAAGGAGATCAGCAGGCACCGCAGGACCGGCCACGGGTCTTCGGGGACGAGGAAGCCACAGCCCCATGAGAACTCCAGACCCTTGTCCCTTGAGCACCCCTGGGCCGGCCCTCAGCTCCGGACCTCCGTGCAGCCCTCCCACCTCTTCATCCAAGACCCCACCATGCCACCCCACCCAGCTCCCAACCCCCTAACCCAGCTGGAGGAGGCGCGCCGACGTCTGGAGGAGGAAGAAAAGAGAGCCAGCCGAGCACCCTCCAAGCAGAGGACAAGATCGCAGAGGAAGGTGGGCGGCGGGAGTGCCCAGCCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCGACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCCCGTCTTTGAGGAGAAGATCATCGGCAAAGTGGAGAAGGTGGACTGATAGAAGCTTAATTCATCGTGACTGACTGACGATCTGCCTCGCGCGTTTCGGTGATGACG |
| pCS2+ M2-FlagSequence with Sp6CGCCATTCTGCCTGGGGACGTCGGAGCAAGCTTGATTTAGGTGACACTATAGAATACAAGCTACTTGTTCTTTTTGCAGGATCCCATCGATTCGAATTCGCCACCATGGACTACAAAGACGATGACGACGACAAGGGACCCATCTTGAGGCCACATTGGGTCTGTGCCCTTGGCCTGGCAAGTTTCAGCCTGGTGCCCTTCATAGTGCCTGGGCTCAGCCTGGCGGCTGGTGCCTACCAAAACGTTTTTGCCACTGTGACTCTCACCAGCAGTGCCTGGTCCTTCCCCCTCTTCCTCCGGGGTAGATGGGGACCTTTGGTTATTTTTAGCTTTATTTTTTATAAGCTTTTTGGGGGGTTAAAATAGACTTTCTTATATTTGGGGGAGTATTTTTTTGTAGATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAATTCGCGGCCGCGGCGCCAATGCATTGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGTCGACCATAGCCAATTCAATATGGCGTATATGGACTCATGCCAATTCAATATGGTGGATCTGGACCTGTGCCAATTCAATATGGCGTATATGGACTCGTGCCAATTCAATATGGTGGATCTGGACCCCAGCCAATTCAATATGGCGGACTTGGCACCATGCCAATTCAATATGGCGGACTTGGCACTGTGCCAACTGGGGAGGGGTCTACTTGGCACGGTGCCAAGTTTGAGGAGGGGTCTTGGCCCTGTGCCAAGTCCGCCATATTGAATTGGCATGGTGCCAATAATGGCGGCCATATTGGCTATATGCCAGGATCAATATATAGGCAATATCCAATATGGCCCTATGCCAATATGGCTATTGGCCAGGTTCAATACTATGTATTGGCCCTATGCCATATAGTATTCCATATATGGGTTTTCCTATTGACGTAGATAGCCCCTCCCAATGGGCGGTCCCATATACCATATATGGGGCTTCCTAATACCGCCCATAGCCACTCCCCCATTGACGTCAATGGTCTCTATATATGGTCTTTCCTATTGACGTCATATGGGCGGTCCTATTGACGTATATGGCGCCTCCCCCATTGACGTCAATTACGGTAAATGGCCCGCCTGGCTCAATGCCCATTGACGTCAATAGGACCACCCACCATTGACGTCAATGGGATGGCTCATTGCCCATTCATATCCGTTCTCACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCACTTGGCAGTACATCAATATCTATTAATAGTAACTTGGCAAGTACATTACTATTGGAAGGACGCCAGGGTACATTGGCAGTACTCCCATTGACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGACGTCAATGGGGAGGGGCAATGACGCAAATGGGCGTTCCATTGACGTAAATGGGCGGTAGGCGTGCCTAATGGGAGGTCTATATAAGCAATGCTCGTTTAGGGAAC |
| Dvl2 WT | 2-736 | pCS2+ M2-Flag | GTTACCGCGGGCAGCAGCGCGGGGGGCGGTGGTGTAGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTTACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCAGATACCCCACAGCCTGAGGTGGCTCCCCCAGCCCATGAGTCTCGGACAGAACTGGTTCCTCCGCCTCCACCCTTACCCCCTTTGCCACCAGAAAGGACCAGTGGAATTGGGGACTCAAGGCCTCCATCCTTCCACCCTAATGTATCCAGCAGCCATGAAAATCTAGAGCCTGAGACAGAGACCGAATCTGTCGTATCACTGAGGCGAGACCGACCTAGGAGGAGAGACAGCAGTGAACATGGCGCTGGTGGCCACAGGCCTGGTGGCCCCTCGAGGCTGGAGCGCCACCTGGCTGGCTACGAGAGCTCTTCCACCCTCATGACCAGTGAGCTGGAGAGTACCAGCCTAGGAGACTCGGATGAGGATGACACCATGAGTAGGTTCAGCAGCTCCACTGAGCAGAGCAGTGCCTCCCGCCTCCTCAAGCGCCACCGAAGGCGAAGGAAGCAGCGGCCGCCACGCATGGAGAGGACCTCATCCTTCAGCAGTGTCACCGATTCCACAATGTCTCTCAACATCATCACGGTCACGCTCAACATGGAGAAGTACAACTTCCTGGGCATCTCCATTGTGGGCCAAAGTAACGAGCGTGGTGATGGGGGCATCTACATCGGCTCCATCATGAAAGGGGGCGCGGTGGCTGCGGACGGGCGGATCGAGCCTGGAGACATGCTTTTGCAGGTAAATGATATGAACTTTGAGAACATGAGCAACGACGATGCTGTACGAGTGCTGAGAGACATCGTGCACAAGCCAGGCCCCATCGTGCTCACCGTGGCCAAGTGTTGGGACCCGTCTCCCCAGGCCTACTTCACCCTCCCTCGAAATGAGCCCATCCAGCCCATCGACCCAGCCGCCTGGGTGTCGCACTCGGCTGCGCTGACTGGAGCCTTCCCTGCTTACCCTGGCTCCTCATCTATGAGCACTATCACATCTGGCTCCTCTCTGCCTGATGGCTGCGAAGGCCGGGGTCTCTCTGTCCACATGGACATGGCCTCTGTCACCAAGGCCATGGCAGCCCCAGAGTCTGGGCTCGAAGTCCGGGACCGCATGTGGCTCAAGATCACCATCCCAAACGCCTTTCTAGGCTCCGATGTGGTGGACTGGCTGTACCATCACGTGGAAGGTTTTCCTGAGCGCCGGGAGGCCCGCAAGTATGCCAGTGGGCTGTTGAAGGCGGGACTCATCCGGCACACCGTCAACAAGATTACTTTCTCTGAGCAGTGCTATTATGTCTTCGGGGACCTCAGTGGTGGCTGTGAGAGTTACCTAGTTAACCTCTCTCTGAATGACAATGACGGTTCCAGTGGGGCTTCAGACCAGGATACCCTGGCACCTCTGCCTGGAGCTACTCCCTGGCCCCTGCTGCCCACCTTCTCCTACCAGTATCCAGCGCCACACCCCTACAGCCCCCAGCCTCCACCCTACCACGAGCTTTCTTCGTACACCTATGGTGGAGGCAGTGCCAGCAGCCAGCACAGTGAGGGGAGCCGGAGCAGCGGGTCGACAAGAAGCGATGGGGGGGCTGGGCGCACAGGCAGGCCTGAGGAACGGGCCCCTGAGTCCAAGTCCGGCAGTGGCAGTGAGTCAGAACTCTCCAGCCGGGGAGGCAGCCTTCGGCGGGGTGGGGAGCCTGGTGGGACTGGTGATGGCGGCCCTCCTCCATCCAGGGGCTCGACAGGCGCTCCTCCTAATCTCCGAGCTCTTCCCGGGCTCCATCCCTATGGAGCCCCATCTGGCATGGCTCTCCCCTATAACCCCATGATGGTAGTTATGATGCCTCCACCCCCACCCCCTGTCTCCACAGCAGTGCAGCCCCCTGGTGCCCCTCCAGTCAGAGACCTGGGCTCCGTGCCCCCAGAACTGACAGCTAGCCGTCAGAGCTTCCACATGGCCATGGGCAACCCCAGTGAGTTTTTTGTGGATGTTATGTAG |
| Dvl2 Y27D | Head mutant | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIX |
| Dvl2 K68A | Tail mutant | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIX |
| Dvl2 M60A |  | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIX |
| Dvl2 G65D |  | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIX |
| Dvl2 N82A |  | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIX |
| Dvl2DC | F64(+DC)G65 | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIX |
| Dvl2DE | M60(+DE)Q61 | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIX |
| Dvl2 QQ | E22Q, E24Q | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIX |
| Dvl2 KK | E22K, E24K | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIX |
| Dvl2 ΔDIX | Deletion of Dvl2 residues 2-92  | pCS2+ M2-Flag | GATACCCCACAGCCTGAGGTGGCTCCCCCAGCCCATGAGTCTCGGACAGAACTGGTTCCTCCGCCTCCACCCTTACCCCCTTTGCCACCAGAAAGGACCAGTGGAATTGGGGACTCAAGGCCTCCATCCTTCCACCCTAATGTATCCAGCAGCCATGAAAATCTAGAGCCTGAGACAGAGACCGAATCTGTCGTATCACTGAGGCGAGACCGACCTAGGAGGAGAGACAGCAGTGAACATGGCGCTGGTGGCCACAGGCCTGGTGGCCCCTCGAGGCTGGAGCGCCACCTGGCTGGCTACGAGAGCTCTTCCACCCTCATGACCAGTGAGCTGGAGAGTACCAGCCTAGGAGACTCGGATGAGGATGACACCATGAGTAGGTTCAGCAGCTCCACTGAGCAGAGCAGTGCCTCCCGCCTCCTCAAGCGCCACCGAAGGCGAAGGAAGCAGCGGCCGCCACGCATGGAGAGGACCTCATCCTTCAGCAGTGTCACCGATTCCACAATGTCTCTCAACATCATCACGGTCACGCTCAACATGGAGAAGTACAACTTCCTGGGCATCTCCATTGTGGGCCAAAGTAACGAGCGTGGTGATGGGGGCATCTACATCGGCTCCATCATGAAAGGGGGCGCGGTGGCTGCGGACGGGCGGATCGAGCCTGGAGACATGCTTTTGCAGGTAAATGATATGAACTTTGAGAACATGAGCAACGACGATGCTGTACGAGTGCTGAGAGACATCGTGCACAAGCCAGGCCCCATCGTGCTCACCGTGGCCAAGTGTTGGGACCCGTCTCCCCAGGCCTACTTCACCCTCCCTCGAAATGAGCCCATCCAGCCCATCGACCCAGCCGCCTGGGTGTCGCACTCGGCTGCGCTGACTGGAGCCTTCCCTGCTTACCCTGGCTCCTCATCTATGAGCACTATCACATCTGGCTCCTCTCTGCCTGATGGCTGCGAAGGCCGGGGTCTCTCTGTCCACATGGACATGGCCTCTGTCACCAAGGCCATGGCAGCCCCAGAGTCTGGGCTCGAAGTCCGGGACCGCATGTGGCTCAAGATCACCATCCCAAACGCCTTTCTAGGCTCCGATGTGGTGGACTGGCTGTACCATCACGTGGAAGGTTTTCCTGAGCGCCGGGAGGCCCGCAAGTATGCCAGTGGGCTGTTGAAGGCGGGACTCATCCGGCACACCGTCAACAAGATTACTTTCTCTGAGCAGTGCTATTATGTCTTCGGGGACCTCAGTGGTGGCTGTGAGAGTTACCTAGTTAACCTCTCTCTGAATGACAATGACGGTTCCAGTGGGGCTTCAGACCAGGATACCCTGGCACCTCTGCCTGGAGCTACTCCCTGGCCCCTGCTGCCCACCTTCTCCTACCAGTATCCAGCGCCACACCCCTACAGCCCCCAGCCTCCACCCTACCACGAGCTTTCTTCGTACACCTATGGTGGAGGCAGTGCCAGCAGCCAGCACAGTGAGGGGAGCCGGAGCAGCGGGTCGACAAGAAGCGATGGGGGGGCTGGGCGCACAGGCAGGCCTGAGGAACGGGCCCCTGAGTCCAAGTCCGGCAGTGGCAGTGAGTCAGAACTCTCCAGCCGGGGAGGCAGCCTTCGGCGGGGTGGGGAGCCTGGTGGGACTGGTGATGGCGGCCCTCCTCCATCCAGGGGCTCGACAGGCGCTCCTCCTAATCTCCGAGCTCTTCCCGGGCTCCATCCCTATGGAGCCCCATCTGGCATGGCTCTCCCCTATAACCCCATGATGGTAGTTATGATGCCTCCACCCCCACCCCCTGTCTCCACAGCAGTGCAGCCCCCTGGTGCCCCTCCAGTCAGAGACCTGGGCTCCGTGCCCCCAGAACTGACAGCTAGCCGTCAGAGCTTCCACATGGCCATGGGCAACCCCAGTGAGTTTTTTGTGGATGTTATGTAG |
| DAX-ΔDIX-Dvl2 | Residues 2-92 of Dvl2 substituted wtih Axin1 743-826 | pCS2+ M2-Flag | CCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCTACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCCCGTCTTTGAGGAGAAGATCATCGGCAAAGTGGAGAAGGTGGACGATACCCCACAGCCTGAGGTGGCTCCCCCAGCCCATGAGTCTCGGACAGAACTGGTTCCTCCGCCTCCACCCTTACCCCCTTTGCCACCAGAAAGGACCAGTGGAATTGGGGACTCAAGGCCTCCATCCTTCCACCCTAATGTATCCAGCAGCCATGAAAATCTAGAGCCTGAGACAGAGACCGAATCTGTCGTATCACTGAGGCGAGACCGACCTAGGAGGAGAGACAGCAGTGAACATGGCGCTGGTGGCCACAGGCCTGGTGGCCCCTCGAGGCTGGAGCGCCACCTGGCTGGCTACGAGAGCTCTTCCACCCTCATGACCAGTGAGCTGGAGAGTACCAGCCTAGGAGACTCGGATGAGGATGACACCATGAGTAGGTTCAGCAGCTCCACTGAGCAGAGCAGTGCCTCCCGCCTCCTCAAGCGCCACCGAAGGCGAAGGAAGCAGCGGCCGCCACGCATGGAGAGGACCTCATCCTTCAGCAGTGTCACCGATTCCACAATGTCTCTCAACATCATCACGGTCACGCTCAACATGGAGAAGTACAACTTCCTGGGCATCTCCATTGTGGGCCAAAGTAACGAGCGTGGTGATGGGGGCATCTACATCGGCTCCATCATGAAAGGGGGCGCGGTGGCTGCGGACGGGCGGATCGAGCCTGGAGACATGCTTTTGCAGGTAAATGATATGAACTTTGAGAACATGAGCAACGACGATGCTGTACGAGTGCTGAGAGACATCGTGCACAAGCCAGGCCCCATCGTGCTCACCGTGGCCAAGTGTTGGGACCCGTCTCCCCAGGCCTACTTCACCCTCCCTCGAAATGAGCCCATCCAGCCCATCGACCCAGCCGCCTGGGTGTCGCACTCGGCTGCGCTGACTGGAGCCTTCCCTGCTTACCCTGGCTCCTCATCTATGAGCACTATCACATCTGGCTCCTCTCTGCCTGATGGCTGCGAAGGCCGGGGTCTCTCTGTCCACATGGACATGGCCTCTGTCACCAAGGCCATGGCAGCCCCAGAGTCTGGGCTCGAAGTCCGGGACCGCATGTGGCTCAAGATCACCATCCCAAACGCCTTTCTAGGCTCCGATGTGGTGGACTGGCTGTACCATCACGTGGAAGGTTTTCCTGAGCGCCGGGAGGCCCGCAAGTATGCCAGTGGGCTGTTGAAGGCGGGACTCATCCGGCACACCGTCAACAAGATTACTTTCTCTGAGCAGTGCTATTATGTCTTCGGGGACCTCAGTGGTGGCTGTGAGAGTTACCTAGTTAACCTCTCTCTGAATGACAATGACGGTTCCAGTGGGGCTTCAGACCAGGATACCCTGGCACCTCTGCCTGGAGCTACTCCCTGGCCCCTGCTGCCCACCTTCTCCTACCAGTATCCAGCGCCACACCCCTACAGCCCCCAGCCTCCACCCTACCACGAGCTTTCTTCGTACACCTATGGTGGTGGAGGCAGTGCCAGCAGCCAGCACAGTGAGGGGAGCCGGAGCAGCGGGTCGACAAGAAGCGATGGGGGGGCTGGGCGCACAGGCAGGCCTGAGGAACGGGCCCCTGAGTCCAAGTCCGGCAGTGGCAGTGAGTCAGAACTCTCCAGCCGGGGAGGCAGCCTTCGGCGGGGTGGGGAGCCTGGTGGGACTGGTGATGGCGGCCCTCCTCCATCCAGGGGCTCGACAGGCGCTCCTCCTAATCTCCGAGCTCTTCCCGGGCTCCATCCCTATGGAGCCCCATCTGGCATGGCTCTCCCCTATAACCCCATGATGGTAGTTATGATGCCTCCACCCCCACCCCCTGTCTCCACAGCAGTGCAGCCCCCTGGTGCCCCTCCAGTCAGAGACCTGGGCTCCGTGCCCCCAGAACTGACAGCTAGCCGTCAGAGCTTCCACATGGCCATGGGCAACCCCAGTGAGTTTTTTGTGGATGTTATGTAG |
| DAX Y760D-ΔDIX-Dvl2 | DAX head mutant for DAX-substituted Dvl2 | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Axin1 DAX Y760D |
| DAXNQ/NG-ΔDIX-Dvl2 | DAX mutations at D793N, E794Q, E815N, E816G for DAX-substituted Dvl2 | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Axin1 DAXNQ/NG |
| T2SAM-ΔDIX-Dvl2 | Residues of 2-92 of Dvl2 substituted for human tankyrase2 867-940 | pCS2+ M2-Flag | GAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGGACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTGAGATGGGGCACAAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTCGAGAGACTTATCTCCGGACAACAAGGTCTTGATACCCCACAGCCTGAGGTGGCTCCCCCAGCCCATGAGTCTCGGACAGAACTGGTTCCTCCGCCTCCACCCTTACCCCCTTTGCCACCAGAAAGGACCAGTGGAATTGGGGACTCAAGGCCTCCATCCTTCCACCCTAATGTATCCAGCAGCCATGAAAATCTAGAGCCTGAGACAGAGACCGAATCTGTCGTATCACTGAGGCGAGACCGACCTAGGAGGAGAGACAGCAGTGAACATGGCGCTGGTGGCCACAGGCCTGGTGGCCCCTCGAGGCTGGAGCGCCACCTGGCTGGCTACGAGAGCTCTTCCACCCTCATGACCAGTGAGCTGGAGAGTACCAGCCTAGGAGACTCGGATGAGGATGACACCATGAGTAGGTTCAGCAGCTCCACTGAGCAGAGCAGTGCCTCCCGCCTCCTCAAGCGCCACCGAAGGCGAAGGAAGCAGCGGCCGCCACGCATGGAGAGGACCTCATCCTTCAGCAGTGTCACCGATTCCACAATGTCTCTCAACATCATCACGGTCACGCTCAACATGGAGAAGTACAACTTCCTGGGCATCTCCATTGTGGGCCAAAGTAACGAGCGTGGTGATGGGGGCATCTACATCGGCTCCATCATGAAAGGGGGCGCGGTGGCTGCGGACGGGCGGATCGAGCCTGGAGACATGCTTTTGCAGGTAAATGATATGAACTTTGAGAACATGAGCAACGACGATGCTGTACGAGTGCTGAGAGACATCGTGCACAAGCCAGGCCCCATCGTGCTCACCGTGGCCAAGTGTTGGGACCCGTCTCCCCAGGCCTACTTCACCCTCCCTCGAAATGAGCCCATCCAGCCCATCGACCCAGCCGCCTGGGTGTCGCACTCGGCTGCGCTGACTGGAGCCTTCCCTGCTTACCCTGGCTCCTCATCTATGAGCACTATCACATCTGGCTCCTCTCTGCCTGATGGCTGCGAAGGCCGGGGTCTCTCTGTCCACATGGACATGGCCTCTGTCACCAAGGCCATGGCAGCCCCAGAGTCTGGGCTCGAAGTCCGGGACCGCATGTGGCTCAAGATCACCATCCCAAACGCCTTTCTAGGCTCCGATGTGGTGGACTGGCTGTACCATCACGTGGAAGGTTTTCCTGAGCGCCGGGAGGCCCGCAAGTATGCCAGTGGGCTGTTGAAGGCGGGACTCATCCGGCACACCGTCAACAAGATTACTTTCTCTGAGCAGTGCTATTATGTCTTCGGGGACCTCAGTGGTGGCTGTGAGAGTTACCTAGTTAACCTCTCTCTGAATGACAATGACGGTTCCAGTGGGGCTTCAGACCAGGATACCCTGGCACCTCTGCCTGGAGCTACTCCCTGGCCCCTGCTGCCCACCTTCTCCTACCAGTATCCAGCGCCACACCCCTACAGCCCCCAGCCTCCACCCTACCACGAGCTTTCTTCGTACACCTATGGTGGTGGAGGCAGTGCCAGCAGCCAGCACAGTGAGGGGAGCCGGAGCAGCGGGTCGACAAGAAGCGATGGGGGGGCTGGGCGCACAGGCAGGCCTGAGGAACGGGCCCCTGAGTCCAAGTCCGGCAGTGGCAGTGAGTCAGAACTCTCCAGCCGGGGAGGCAGCCTTCGGCGGGGTGGGGAGCCTGGTGGGACTGGTGATGGCGGCCCTCCTCCATCCAGGGGCTCGACAGGCGCTCCTCCTAATCTCCGAGCTCTTCCCGGGCTCCATCCCTATGGAGCCCCATCTGGCATGGCTCTCCCCTATAACCCCATGATGGTAGTTATGATGCCTCCACCCCCACCCCCTGTCTCCACAGCAGTGCAGCCCCCTGGTGCCCCTCCAGTCAGAGACCTGGGCTCCGTGCCCCCAGAACTGACAGCTAGCCGTCAGAGCTTCCACATGGCCATGGGCAACCCCAGTGAGTTTTTTGTGGATGTTATGTAG |
| Sm1-ΔDIX-Dvl2 | Residues of 2-92 of Dvl2 substituted for Sm1 1-77 | pCS2+ M2-Flag | ATGCCGCCTCGGCCACTTGACGTACTTAACAGATCCCTTAAATCTCCCGTGATTGTAAGGCTGAAGGGGGGCCGGGAATTTAGAGGAACGCTGGATGGATATGACATTCACATGAACCTGGTCTTGTTGGACGCCGAGGAGATTCAGAACGGCGAGGTAGTACGAAAGGTCGGCAGCGTAGTAATCAGGGGCGACACTGTAGTGTTTGTAAGTCCTGCCCCAGGTGGAGAAGATACCCCACAGCCTGAGGTGGCTCCCCCAGCCCATGAGTCTCGGACAGAACTGGTTCCTCCGCCTCCACCCTTACCCCCTTTGCCACCAGAAAGGACCAGTGGAATTGGGGACTCAAGGCCTCCATCCTTCCACCCTAATGTATCCAGCAGCCATGAAAATCTAGAGCCTGAGACAGAGACCGAATCTGTCGTATCACTGAGGCGAGACCGACCTAGGAGGAGAGACAGCAGTGAACATGGCGCTGGTGGCCACAGGCCTGGTGGCCCCTCGAGGCTGGAGCGCCACCTGGCTGGCTACGAGAGCTCTTCCACCCTCATGACCAGTGAGCTGGAGAGTACCAGCCTAGGAGACTCGGATGAGGATGACACCATGAGTAGGTTCAGCAGCTCCACTGAGCAGAGCAGTGCCTCCCGCCTCCTCAAGCGCCACCGAAGGCGAAGGAAGCAGCGGCCGCCACGCATGGAGAGGACCTCATCCTTCAGCAGTGTCACCGATTCCACAATGTCTCTCAACATCATCACGGTCACGCTCAACATGGAGAAGTACAACTTCCTGGGCATCTCCATTGTGGGCCAAAGTAACGAGCGTGGTGATGGGGGCATCTACATCGGCTCCATCATGAAAGGGGGCGCGGTGGCTGCGGACGGGCGGATCGAGCCTGGAGACATGCTTTTGCAGGTAAATGATATGAACTTTGAGAACATGAGCAACGACGATGCTGTACGAGTGCTGAGAGACATCGTGCACAAGCCAGGCCCCATCGTGCTCACCGTGGCCAAGTGTTGGGACCCGTCTCCCCAGGCCTACTTCACCCTCCCTCGAAATGAGCCCATCCAGCCCATCGACCCAGCCGCCTGGGTGTCGCACTCGGCTGCGCTGACTGGAGCCTTCCCTGCTTACCCTGGCTCCTCATCTATGAGCACTATCACATCTGGCTCCTCTCTGCCTGATGGCTGCGAAGGCCGGGGTCTCTCTGTCCACATGGACATGGCCTCTGTCACCAAGGCCATGGCAGCCCCAGAGTCTGGGCTCGAAGTCCGGGACCGCATGTGGCTCAAGATCACCATCCCAAACGCCTTTCTAGGCTCCGATGTGGTGGACTGGCTGTACCATCACGTGGAAGGTTTTCCTGAGCGCCGGGAGGCCCGCAAGTATGCCAGTGGGCTGTTGAAGGCGGGACTCATCCGGCACACCGTCAACAAGATTACTTTCTCTGAGCAGTGCTATTATGTCTTCGGGGACCTCAGTGGTGGCTGTGAGAGTTACCTAGTTAACCTCTCTCTGAATGACAATGACGGTTCCAGTGGGGCTTCAGACCAGGATACCCTGGCACCTCTGCCTGGAGCTACTCCCTGGCCCCTGCTGCCCACCTTCTCCTACCAGTATCCAGCGCCACACCCCTACAGCCCCCAGCCTCCACCCTACCACGAGCTTTCTTCGTACACCTATGGTGGTGGAGGCAGTGCCAGCAGCCAGCACAGTGAGGGGAGCCGGAGCAGCGGGTCGACAAGAAGCGATGGGGGGGCTGGGCGCACAGGCAGGCCTGAGGAACGGGCCCCTGAGTCCAAGTCCGGCAGTGGCAGTGAGTCAGAACTCTCCAGCCGGGGAGGCAGCCTTCGGCGGGGTGGGGAGCCTGGTGGGACTGGTGATGGCGGCCCTCCTCCATCCAGGGGCTCGACAGGCGCTCCTCCTAATCTCCGAGCTCTTCCCGGGCTCCATCCCTATGGAGCCCCATCTGGCATGGCTCTCCCCTATAACCCCATGATGGTAGTTATGATGCCTCCACCCCCACCCCCTGTCTCCACAGCAGTGCAGCCCCCTGGTGCCCCTCCAGTCAGAGACCTGGGCTCCGTGCCCCCAGAACTGACAGCTAGCCGTCAGAGCTTCCACATGGCCATGGGCAACCCCAGTGAGTTTTTTGTGGATGTTATGTAG |
| Sm1-DIX-Dvl2 | Sm1 residues 1-77 fused to WT Dvl2 | pCS2+ M2-Flag | ATGCCGCCTCGGCCACTTGACGTACTTAACAGATCCCTTAAATCTCCCGTGATTGTAAGGCTGAAGGGGGGCCGGGAATTTAGAGGAACGCTGGATGGATATGACATTCACATGAACCTGGTCTTGTTGGACGCCGAGGAGATTCAGAACGGCGAGGTAGTACGAAAGGTCGGCAGCGTAGTAATCAGGGGCGACACTGTAGTGTTTGTAAGTCCTGCCCCAGGTGGAGAAGTTACCGCGGGCAGCAGCGCGGGGGGCGGTGGTGTAGGCGAGACGAAGGTGATTTACCATCTGGATGAAGAAGAGACTCCTGACCTGGTGAAGATCCCTGTCCCGGCGGAGCGCATCACGCTCGGCGATTTCAAGAGCGTTTTGCAGCGGCCCGCGGGCGCCAAGTACTTTTTCAAGTCCATGGATCAGGATTTTGGGGTGGTGAAGGAAGAGATCTCCGATGACAATGCCCGCCTACCTTGCTTCAATGGAAGGGTTGTCTCCTGGCTTGTGTCGTCAGATACCCCACAGCCTGAGGTGGCTCCCCCAGCCCATGAGTCTCGGACAGAACTGGTTCCTCCGCCTCCACCCTTACCCCCTTTGCCACCAGAAAGGACCAGTGGAATTGGGGACTCAAGGCCTCCATCCTTCCACCCTAATGTATCCAGCAGCCATGAAAATCTAGAGCCTGAGACAGAGACCGAATCTGTCGTATCACTGAGGCGAGACCGACCTAGGAGGAGAGACAGCAGTGAACATGGCGCTGGTGGCCACAGGCCTGGTGGCCCCTCGAGGCTGGAGCGCCACCTGGCTGGCTACGAGAGCTCTTCCACCCTCATGACCAGTGAGCTGGAGAGTACCAGCCTAGGAGACTCGGATGAGGATGACACCATGAGTAGGTTCAGCAGCTCCACTGAGCAGAGCAGTGCCTCCCGCCTCCTCAAGCGCCACCGAAGGCGAAGGAAGCAGCGGCCGCCACGCATGGAGAGGACCTCATCCTTCAGCAGTGTCACCGATTCCACAATGTCTCTCAACATCATCACGGTCACGCTCAACATGGAGAAGTACAACTTCCTGGGCATCTCCATTGTGGGCCAAAGTAACGAGCGTGGTGATGGGGGCATCTACATCGGCTCCATCATGAAAGGGGGCGCGGTGGCTGCGGACGGGCGGATCGAGCCTGGAGACATGCTTTTGCAGGTAAATGATATGAACTTTGAGAACATGAGCAACGACGATGCTGTACGAGTGCTGAGAGACATCGTGCACAAGCCAGGCCCCATCGTGCTCACCGTGGCCAAGTGTTGGGACCCGTCTCCCCAGGCCTACTTCACCCTCCCTCGAAATGAGCCCATCCAGCCCATCGACCCAGCCGCCTGGGTGTCGCACTCGGCTGCGCTGACTGGAGCCTTCCCTGCTTACCCTGGCTCCTCATCTATGAGCACTATCACATCTGGCTCCTCTCTGCCTGATGGCTGCGAAGGCCGGGGTCTCTCTGTCCACATGGACATGGCCTCTGTCACCAAGGCCATGGCAGCCCCAGAGTCTGGGCTCGAAGTCCGGGACCGCATGTGGCTCAAGATCACCATCCCAAACGCCTTTCTAGGCTCCGATGTGGTGGACTGGCTGTACCATCACGTGGAAGGTTTTCCTGAGCGCCGGGAGGCCCGCAAGTATGCCAGTGGGCTGTTGAAGGCGGGACTCATCCGGCACACCGTCAACAAGATTACTTTCTCTGAGCAGTGCTATTATGTCTTCGGGGACCTCAGTGGTGGCTGTGAGAGTTACCTAGTTAACCTCTCTCTGAATGACAATGACGGTTCCAGTGGGGCTTCAGACCAGGATACCCTGGCACCTCTGCCTGGAGCTACTCCCTGGCCCCTGCTGCCCACCTTCTCCTACCAGTATCCAGCGCCACACCCCTACAGCCCCCAGCCTCCACCCTACCACGAGCTTTCTTCGTACACCTATGGTGGTGGAGGCAGTGCCAGCAGCCAGCACAGTGAGGGGAGCCGGAGCAGCGGGTCGACAAGAAGCGATGGGGGGGCTGGGCGCACAGGCAGGCCTGAGGAACGGGCCCCTGAGTCCAAGTCCGGCAGTGGCAGTGAGTCAGAACTCTCCAGCCGGGGAGGCAGCCTTCGGCGGGGTGGGGAGCCTGGTGGGACTGGTGATGGCGGCCCTCCTCCATCCAGGGGCTCGACAGGCGCTCCTCCTAATCTCCGAGCTCTTCCCGGGCTCCATCCCTATGGAGCCCCATCTGGCATGGCTCTCCCCTATAACCCCATGATGGTAGTTATGATGCCTCCACCCCCACCCCCTGTCTCCACAGCAGTGCAGCCCCCTGGTGCCCCTCCAGTCAGAGACCTGGGCTCCGTGCCCCCAGAACTGACAGCTAGCCGTCAGAGCTTCCACATGGCCATGGGCAACCCCAGTGAGTTTTTTGTGGATGTTATGTAG |
| Sm1-DIXY27D-Dvl2 | Sm1 residues 1-77 fused to Dvl2 Y27D | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Dvl2 DIXY27D |
| Sm1-DAX-ΔDIX-Dvl2 | Sm1 residues 1-77 fused to DAX-ΔDIX-Dvl2 | pCS2+ M2-Flag | ATGCCGCCTCGGCCACTTGACGTACTTAACAGATCCCTTAAATCTCCCGTGATTGTAAGGCTGAAGGGGGGCCGGGAATTTAGAGGAACGCTGGATGGATATGACATTCACATGAACCTGGTCTTGTTGGACGCCGAGGAGATTCAGAACGGCGAGGTAGTACGAAAGGTCGGCAGCGTAGTAATCAGGGGCGACACTGTAGTGTTTGTAAGTCCTGCCCCAGGTGGAGAACCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCTACCGCACCCTGGTGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCAAGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGGCCGTCCTGCCCGTCTTTGAGGAGAAGATCATCGGCAAAGTGGAGAAGGTGGACGATACCCCACAGCCTGAGGTGGCTCCCCCAGCCCATGAGTCTCGGACAGAACTGGTTCCTCCGCCTCCACCCTTACCCCCTTTGCCACCAGAAAGGACCAGTGGAATTGGGGACTCAAGGCCTCCATCCTTCCACCCTAATGTATCCAGCAGCCATGAAAATCTAGAGCCTGAGACAGAGACCGAATCTGTCGTATCACTGAGGCGAGACCGACCTAGGAGGAGAGACAGCAGTGAACATGGCGCTGGTGGCCACAGGCCTGGTGGCCCCTCGAGGCTGGAGCGCCACCTGGCTGGCTACGAGAGCTCTTCCACCCTCATGACCAGTGAGCTGGAGAGTACCAGCCTAGGAGACTCGGATGAGGATGACACCATGAGTAGGTTCAGCAGCTCCACTGAGCAGAGCAGTGCCTCCCGCCTCCTCAAGCGCCACCGAAGGCGAAGGAAGCAGCGGCCGCCACGCATGGAGAGGACCTCATCCTTCAGCAGTGTCACCGATTCCACAATGTCTCTCAACATCATCACGGTCACGCTCAACATGGAGAAGTACAACTTCCTGGGCATCTCCATTGTGGGCCAAAGTAACGAGCGTGGTGATGGGGGCATCTACATCGGCTCCATCATGAAAGGGGGCGCGGTGGCTGCGGACGGGCGGATCGAGCCTGGAGACATGCTTTTGCAGGTAAATGATATGAACTTTGAGAACATGAGCAACGACGATGCTGTACGAGTGCTGAGAGACATCGTGCACAAGCCAGGCCCCATCGTGCTCACCGTGGCCAAGTGTTGGGACCCGTCTCCCCAGGCCTACTTCACCCTCCCTCGAAATGAGCCCATCCAGCCCATCGACCCAGCCGCCTGGGTGTCGCACTCGGCTGCGCTGACTGGAGCCTTCCCTGCTTACCCTGGCTCCTCATCTATGAGCACTATCACATCTGGCTCCTCTCTGCCTGATGGCTGCGAAGGCCGGGGTCTCTCTGTCCACATGGACATGGCCTCTGTCACCAAGGCCATGGCAGCCCCAGAGTCTGGGCTCGAAGTCCGGGACCGCATGTGGCTCAAGATCACCATCCCAAACGCCTTTCTAGGCTCCGATGTGGTGGACTGGCTGTACCATCACGTGGAAGGTTTTCCTGAGCGCCGGGAGGCCCGCAAGTATGCCAGTGGGCTGTTGAAGGCGGGACTCATCCGGCACACCGTCAACAAGATTACTTTCTCTGAGCAGTGCTATTATGTCTTCGGGGACCTCAGTGGTGGCTGTGAGAGTTACCTAGTTAACCTCTCTCTGAATGACAATGACGGTTCCAGTGGGGCTTCAGACCAGGATACCCTGGCACCTCTGCCTGGAGCTACTCCCTGGCCCCTGCTGCCCACCTTCTCCTACCAGTATCCAGCGCCACACCCCTACAGCCCCCAGCCTCCACCCTACCACGAGCTTTCTTCGTACACCTATGGTGGTGGAGGCAGTGCCAGCAGCCAGCACAGTGAGGGGAGCCGGAGCAGCGGGTCGACAAGAAGCGATGGGGGGGCTGGGCGCACAGGCAGGCCTGAGGAACGGGCCCCTGAGTCCAAGTCCGGCAGTGGCAGTGAGTCAGAACTCTCCAGCCGGGGAGGCAGCCTTCGGCGGGGTGGGGAGCCTGGTGGGACTGGTGATGGCGGCCCTCCTCCATCCAGGGGCTCGACAGGCGCTCCTCCTAATCTCCGAGCTCTTCCCGGGCTCCATCCCTATGGAGCCCCATCTGGCATGGCTCTCCCCTATAACCCCATGATGGTAGTTATGATGCCTCCACCCCCACCCCCTGTCTCCACAGCAGTGCAGCCCCCTGGTGCCCCTCCAGTCAGAGACCTGGGCTCCGTGCCCCCAGAACTGACAGCTAGCCGTCAGAGCTTCCACATGGCCATGGGCAACCCCAGTGAGTTTTTTGTGGATGTTATGTAG |
| Sm1-DAX Y760D-ΔDIX-Dvl2 | Sm1 residues 1-77 fused to DAX Y760D-ΔDIX-Dvl2 | pCS2+ M2-Flag | For more information, see equivalent constructs in MBP-Axin1 DAXY760D |
| Sm1 |  |  | Sm1 amino acid sequence: MPPRPLDVLNRSLKSPVIVRLKGGREFRGTLDGYDIHMNLVLLDAEEIQNGEVVRKVGSVVIRGDTVVFVSPAPGGEMinigene from IDT (codon optimized for human cells):ATGCCGCCTCGGCCACTTGACGTACTTAACAGATCCCTTAAATCTCCCGTGATTGTAAGGCTGAAGGGGGGCCGGGAATTTAGAGGAACGCTGGATGGATATGACATTCACATGAACCTGGTCTTGTTGGACGCCGAGGAGATTCAGAACGGCGAGGTAGTACGAAAGGTCGGCAGCGTAGTAATCAGGGGCGACACTGTAGTGTTTGTAAGTCCTGCCCCAGGTGGAGAA |