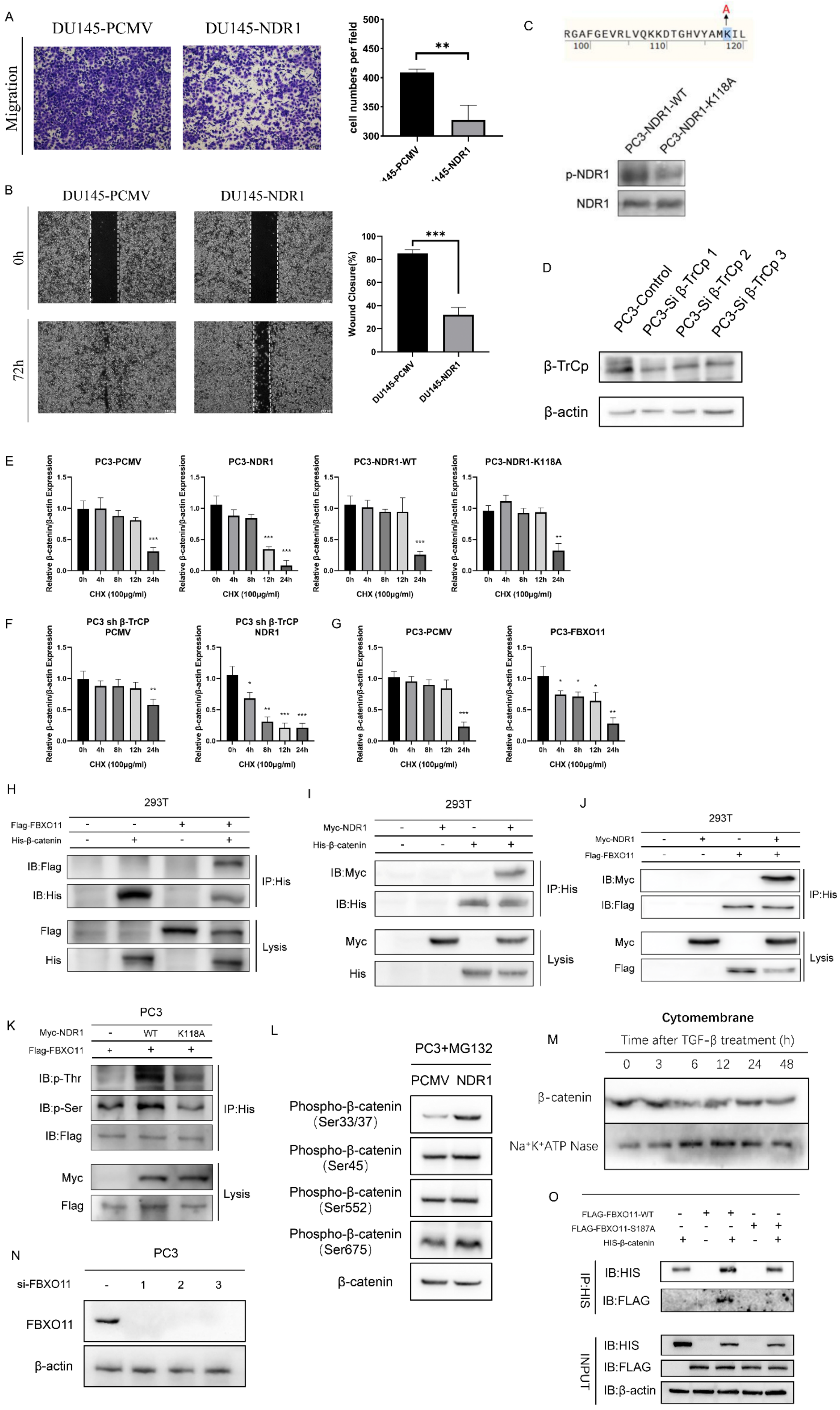
Supplementary Figure S1. Experimental analysis of NDR1-mediated regulation of EMT and β-catenin pathway in prostate cancer cells. A, B: Migration and scratch assays demonstrate that NDR1 inhibits epithelial-mesenchymal transition (EMT) in prostate cancer cells (DU145) by reducing cell migration and wound closure. C: Mutation of the NDR1 ATP-binding site (K118A) significantly reduces the phosphorylation rate of NDR1. D: Efficiency verification of β-TrCP knockout, confirming successful elimination of β-TrCP protein. E-G: The gray value quantification for protein half-life experiments. H: Immunoprecipitation (IP) with exogenous proteins confirms the direct interaction between FBXO11 and β-Catenin. I: IP with exogenous proteins confirms the direct interaction between NDR1 and β-Catenin. J: IP with exogenous proteins confirms the direct interaction between NDR1 and FBXO11. K: Measurement of panphosphorylation levels of IP-enriched FBXO11 reveals significant promotion of FBXO11 phosphorylation by NDR1. L: NDR1 promotes phosphorylation of β-Catenin at residues S33/37. M: Changes in membrane expression of β-catenin after stimulation with TGF-β. N: Efficiency verification of FBXO11 knockout, confirming successful down-expression of the FBXO11 protein. O: IP binding assay demonstrates that mutation of FBXO11 at residue S187A affects its interaction with β-catenin.



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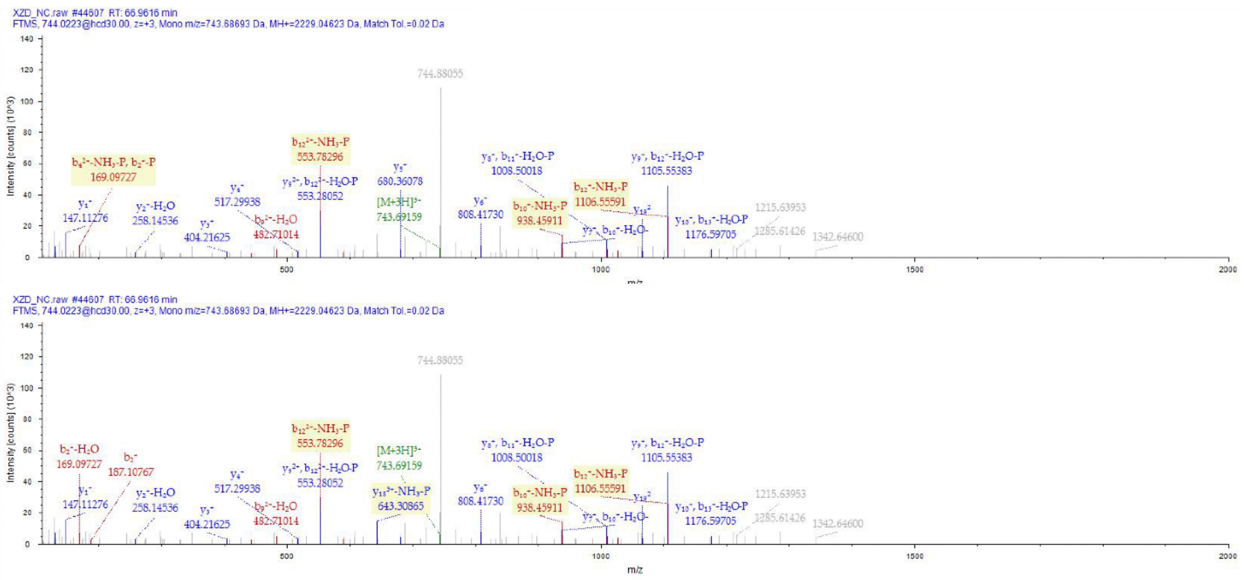
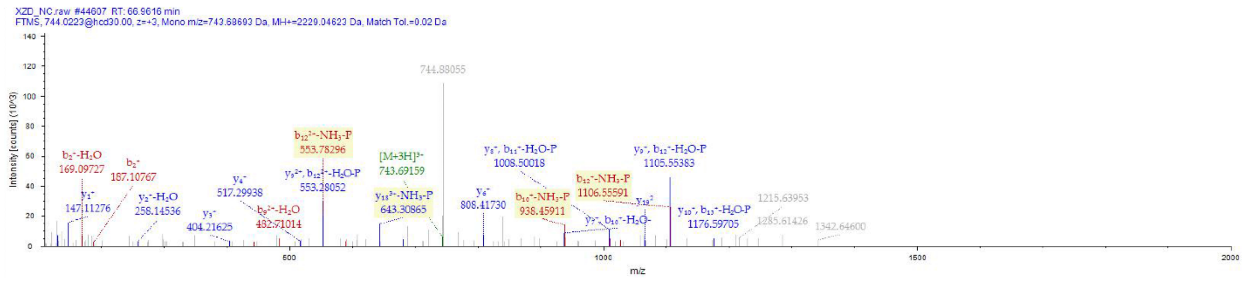
Supplementary Figure S2. Secondary mass spectrometry (MS/MS) spectrum of phosphorylated FBXO11 peptide. Control Spectrum of Phosphorylated FBXO11 Peptide at (A) Serine 140 and 143, (B) Serine 147, (C) Serine 542, and (D) Serine 841.

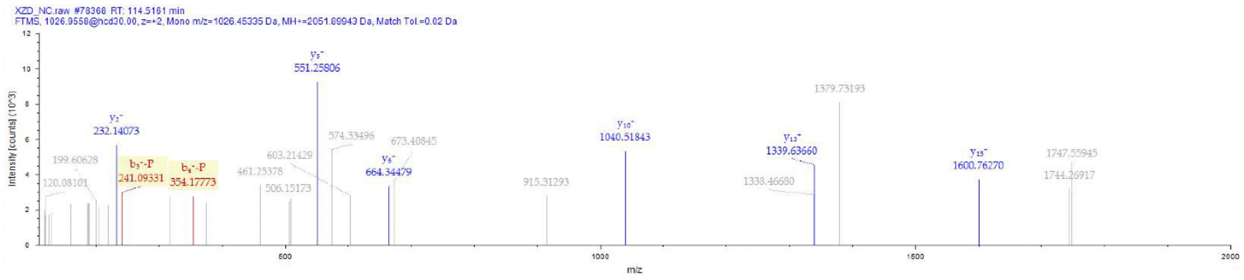
A FBXO11 Ser140 Ser143 :VSGKSQDLSAAPAEQYLQEK (NC-FBXO11-293T)



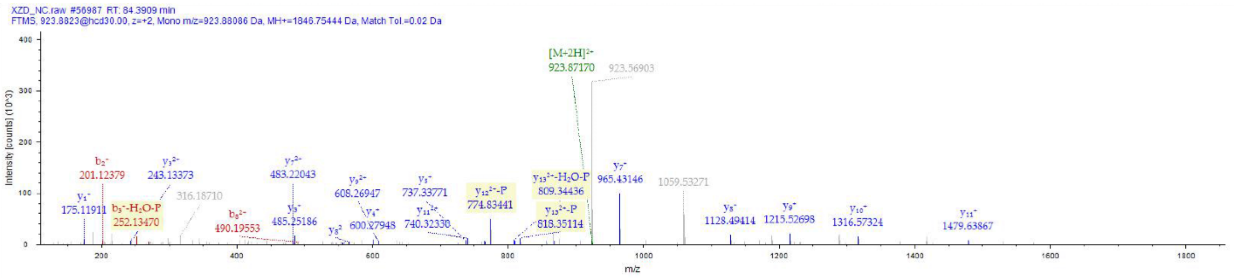
B FBXO11 Ser147:VSGKSQDLSAAPAEQYLQEK (NC-FBXO11-293T)



C FBXO11 Ser542: GNSIFNGNQGGVYIFGDGR (NC-FBXO11-293T)

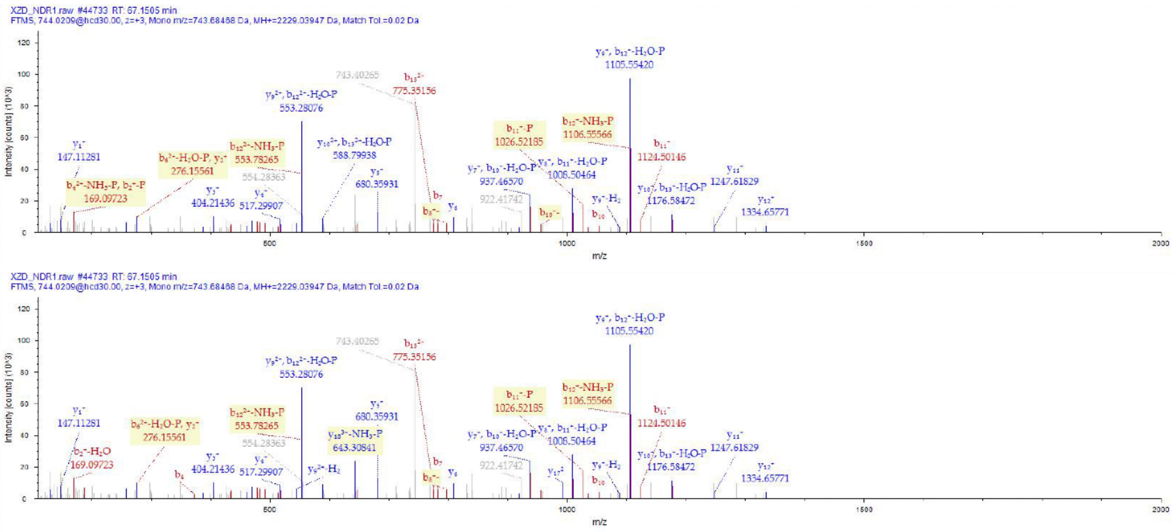


D FBXO11 Ser841: ISSYTSYPMHDFYR (NC-FBXO11-293T)

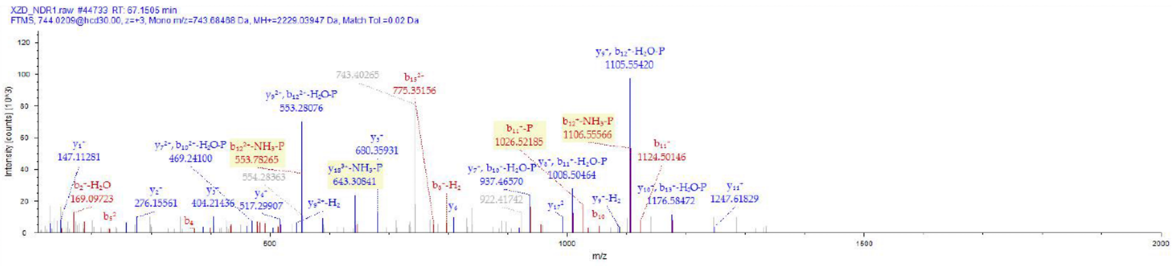


Supplementary Figure S3. Secondary mass spectrometry (MS/MS) spectrum of phosphorylated FBXO11 peptide with NDR1 co-expression. Spectrum of phosphorylated FBXO11 peptide at (A) Serine 140 and 143, (B) Serine 147, (C) Serine 542, and (D) Serine 841 with NDR1 co-expression.

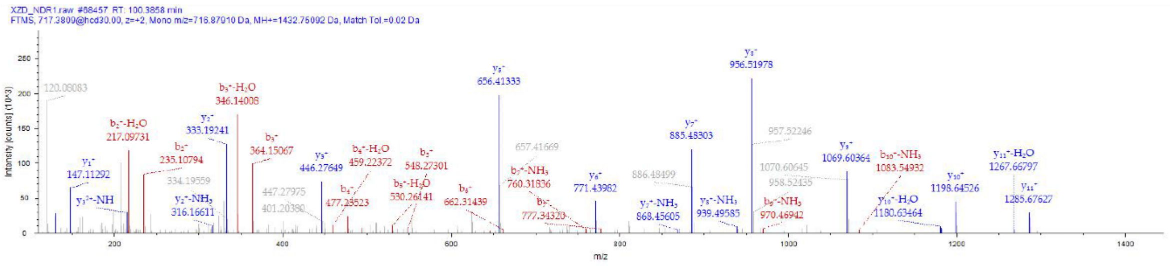
A FBXO11 Ser140 Ser143 :VSGKSQDLSAAPAEQYLQEK (NDR1-FBXO11-293T)



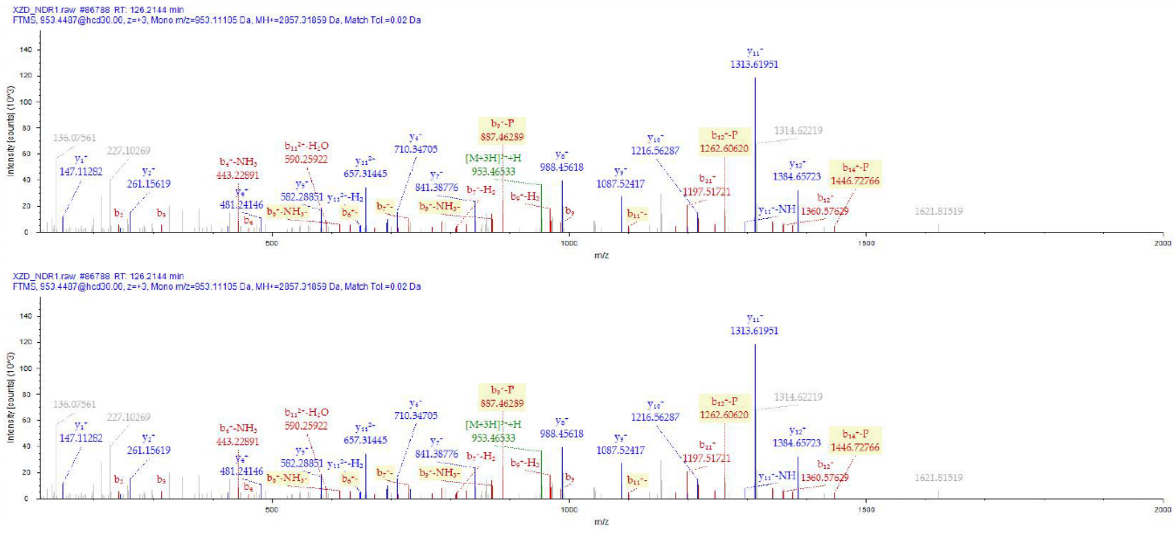
B FBXO11 Ser147:VSGKSQDLSAAPAEQYLQEK (NDR1-FBXO11-293T)



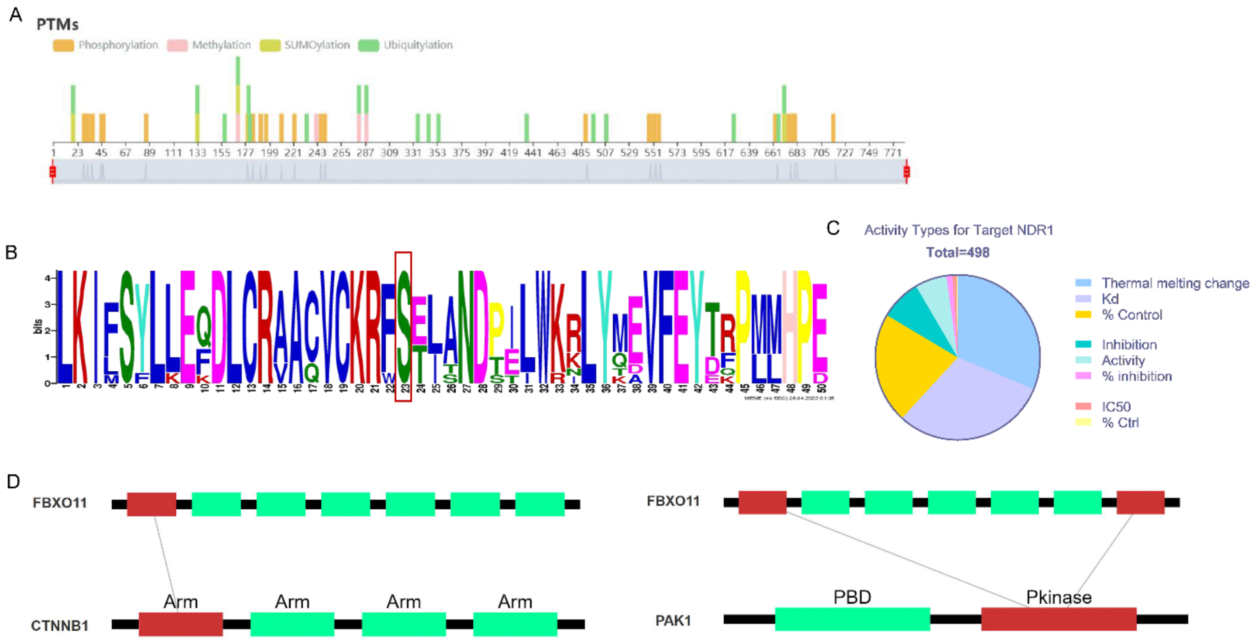
C FBXO11 Ser542: FSELANDPILWK (NDR1-FBXO11-293T)



D NDR1 Ser281: QLAFSTVGTPDYIAPEVFMQTGYNK



Supplementary Figure S4. Bioinformatics and experimental analyses of β-catenin and FBXO11 regulatory pathways. A: Predicted post-translational modification sites of β-catenin. B: Conservation analysis of FBXO11 protein sequence across different species. C: Screening of small molecule activators for NDR1, showing the process of identifying compounds that enhance NDR1 activity as potential therapeutic agents. D: Prediction of FBXO11-mediated ubiquitination of β-catenin and PAK1, indicating the computational modeling of the interaction between FBXO11 and its substrates for ubiquitination, β-catenin, and PAK1.



Supplementary Table S1. Sequences of primers used in RT-qPCR assay.

Gene Name		Primer sequences (5' to 3')
GAPDH	Forward primer	GAGTCAACGGATTTGGTCGT
	Reverse primer	GACAAGCTTCCCGTTCTCAG
STK38	Forward primer	TCAGCACATGCTCGGAAGG
	Reverse primer	ACAAGCCGTACCTCACCAAAT
CTNNB1	Forward primer	CTTGGACTGAGACTGCTGATCTTG
	Reverse primer	CACCAGAGTGAAAAGAACGATAGCTA
STK38-K118A	Forward primer	TGTATGCAATGGCTATACTCCGTAAAGCAGATATG
	Reverse primer	GAGTATAGCCATTGCATACACATGTCCCGTATCTT
FBXO11	Forward primer	TGGACGTGATGTTGGTGTGTTCACA
	Reverse primer	TCCTCCAGTCTGCCCATGGTGA
c-Myc	Forward primer	GGCTCCTGGCAAAAGGTCA
	Reverse primer	CTGCGTAGTTGTGCTGATGT
Cyclin D1	Forward primer	GCTGCGAAGTGGAAACCATC
	Reverse primer	CCTCCTTCTGCACACATTTGAA
CTNNB1	Forward primer	GCGGTACCATGGCTACTCAAGCT
	Reverse primer	CGGCCGCTCTAGACTCGAGTTTA
CTNNB1 S33A	Forward primer	CAGCAACAGTCTTACCTGGACGCTGGAATCCATTCT
	Reverse primer	AGTGGCACCAGAATGGATTCCAGCGTCCAGGTAAGA
CTNNB1 S37A	Forward primer	TACCTGGACTCTGGAATCCATGCTGGTGCCACTACC
	Reverse primer	AGGAGCTGTGGTAGTGGCACCAGCATGGATTCCAGA

CTNNB1 S33A-S37A	Forward primer	TACCTGGACGCTGGAATCCATGCTGGTGCCACTACC
	Reverse primer	AGGAGCTGTGGTAGTGGCACCAGCATGGATTCCAGC
CTNNB1 S1	Forward primer	GCGTCGACAAAAAGCGGCTGTT
	Reverse primer	GCGTCTAGATTATGTGGCAAGTTCTGC
CTNNB1 S2	Forward primer	CGTCGACAACGTGCAATCCCTGAA
	Reverse primer	CGCGCGTCTAGATTAACTAGCCAGTATG
CTNNB1 S3	Forward primer	CGTCGACAAGGTGGACCCCAAG
	Reverse primer	CGCGCGTCTAGATTATAGTCCTCTGATAAC
CTNNB1 S4	Forward primer	GCGGCGTCGACAAAATACCATTCCATT
	Reverse primer	GGCGCGTCTAGATTACAGGTCAGTATCA

Supplementary Table S2. Correlation of NDR1 expression with prostate cancer characteristics.

Characteristics	Low expression of NDR1	High expression of NDR1	p value
n	249	250	
T stage，n (%)			0.023
T2	109 (22.2%)	80 (16.3%)	
T3	133 (27%)	159 (32.3%)	
T4	4 (0.8%)	7 (1.4%)	
N stage，n (%)			0.047
N0	173 (40.6%)	174 (40.8%)	
N1	29 (6.8%)	50 (11.7%)	
M stage，n (%)			1.000
M0	221 (48.3%)	234 (51.1%)	
M1	1 (0.2%)	2 (0.4%)	
PSA (ng/ml)，n (%)			0.136
＜4	208 (47.1%)	207 (46.8%)	
≥4	9 (2%)	18 (4.1%)	
Gleason score，n (%)			0.012
6	27 (5.4%)	19 (3.8%)	
7	132 (26.5%)	115 (23%)	
8	35 (7%)	29 (5.8%)	
9	55 (11%)	83 (16.6%)	
10	0 (0%)	4 (0.8%)	

Supplementary Table 3. NetPhos3.1 predicts phosphorylation sites on FBXO11 by NDR1 (Score > 0.5).

```
>AAV87312.1        927 amino acids
#
# netphos-3.1b prediction results
#
# Sequence                 # x   Context     Score   Kinase    Answer
# AAV87312.1                3 S   --MNSVRAA   0.799   PKC       YES
#
# AAV87312.1               15 S   PRRVSRPRP   0.998   unsp      YES
# AAV87312.1               15 S   PRRVSRPRP   0.834   PKB       YES
# AAV87312.1               15 S   PRRVSRPRP   0.788   PKA       YES
# AAV87312.1               15 S   PRRVSRPRP   0.530   PKC       YES
# AAV87312.1               15 S   PRRVSRPRP   0.510   RSK       YES
#
# AAV87312.1               90 S   VAEESGPGA   0.573   CKI       YES
#
# AAV87312.1               97 S   GAQNSPYQL   0.837   unsp      YES
# AAV87312.1               97 S   GAQNSPYQL   0.583   cdk5      YES
# AAV87312.1               97 S   GAQNSPYQL   0.510   p38MAPK   YES
#
# AAV87312.1              105 T   LRRKTLLPK   0.895   unsp      YES
# AAV87312.1              105 T   LRRKTLLPK   0.769   PKA       YES
# AAV87312.1              105 T   LRRKTLLPK   0.664   PKG       YES
#
# AAV87312.1              111 T   LPKRTACPT   0.670   PKG       YES
# AAV87312.1              111 T   LPKRTACPT   0.536   unsp      YES
#
# AAV87312.1              115 T   TACPTKNSM   0.608   PKC       YES
#
# AAV87312.1              118 S   PTKNSMEGA   0.758   unsp      YES
# AAV87312.1              118 S   PTKNSMEGA   0.577   cdc2      YES
#
# AAV87312.1              123 S   MEGASTSTT   0.954   unsp      YES
#
# AAV87312.1              124 T   EGASTSTTE   0.548   CKII      YES
#
# AAV87312.1              125 S   GASTSTTEN   0.977   unsp      YES
# AAV87312.1              125 S   GASTSTTEN   0.537   CKI       YES
# AAV87312.1              125 S   GASTSTTEN   0.510   CKII      YES
#
# AAV87312.1              140 S   RARVSGKSQ   0.998   unsp      YES
# AAV87312.1              140 S   RARVSGKSQ   0.849   PKC       YES
# AAV87312.1              140 S   RARVSGKSQ   0.738   PKA       YES
#
# AAV87312.1              143 S   VSGKSQDLS   0.915   unsp      YES
#
# AAV87312.1              147 S   SQDLSAAPA   0.626   unsp      YES
#
# AAV87312.1              154 Y   PAEQYLQEK   0.667   unsp      YES
#
# AAV87312.1              187 S   CKRFSELAN   0.956   unsp      YES
# AAV87312.1              187 S   CKRFSELAN   0.565   PKA       YES
#
# AAV87312.1              200 Y   WKRLYMEVF   0.520   EGFR      YES
#
# AAV87312.1              206 Y   EVFEYTRPM   0.502   unsp      YES
#
# AAV87312.1              226 Y   NPEEYEHPN   0.962   unsp      YES
# AAV87312.1              226 Y   NPEEYEHPN   0.553   EGFR      YES
#
# AAV87312.1              254 Y   AEHFYSNPA   0.950   unsp      YES
# AAV87312.1              254 Y   AEHFYSNPA   0.536   EGFR      YES
#
# AAV87312.1              269 Y   NMLYYDTIE   0.566   unsp      YES
```

```
#
# AAV87312.1          271 T   LYYDTIEDA    0.708   unsp      YES
#
# AAV87312.1          295 Y   HSGIYTDEW    0.546   unsp      YES
#
# AAV87312.1          296 T   SGIYTDEWI    0.582   CKII      YES
#
# AAV87312.1          301 Y   DEWIYIESP    0.973   unsp      YES
# AAV87312.1          301 Y   DEWIYIESP    0.531   EGFR      YES
# AAV87312.1          301 Y   DEWIYIESP    0.519   SRC       YES
#
# AAV87312.1          325 T   IIENTRDST    0.792   unsp      YES
#
# AAV87312.1          328 S   NTRDSTFVF    0.902   unsp      YES
# AAV87312.1          328 S   NTRDSTFVF    0.573   PKA       YES
#
# AAV87312.1          336 S   FMEGSEDAY    0.526   CKII      YES
#
# AAV87312.1          340 Y   SEDAYVGYM    0.984   unsp      YES
#
# AAV87312.1          345 T   VGYMTIRFN    0.717   PKC       YES
# AAV87312.1          345 T   VGYMTIRFN    0.601   unsp      YES
#
# AAV87312.1          382 T   IIRSTCTVG    0.558   PKC       YES
#
# AAV87312.1          384 T   RSTCTVGSA    0.783   PKC       YES
#
# AAV87312.1          399 T   GACPTIKHC    0.681   PKC       YES
#
# AAV87312.1          406 S   HCNISDCEN    0.937   unsp      YES
# AAV87312.1          406 S   HCNISDCEN    0.562   CKII      YES
# AAV87312.1          406 S   HCNISDCEN    0.558   PKA       YES
#
# AAV87312.1          423 Y   AQGIYEDNE    0.931   unsp      YES
#
# AAV87312.1          487 Y   EVKAYANPT    0.808   unsp      YES
#
# AAV87312.1          491 T   YANPTVVRC    0.626   PKC       YES
#
# AAV87312.1          521 Y   ENKIYANNF    0.929   unsp      YES
# AAV87312.1          521 Y   ENKIYANNF    0.518   INSR      YES
#
# AAV87312.1          532 S   VWITSNSDP    0.813   unsp      YES
#
# AAV87312.1          537 T   NSDPTIRGN    0.765   unsp      YES
# AAV87312.1          537 T   NSDPTIRGN    0.672   PKC       YES
#
# AAV87312.1          542 S   IRGNSIFNG    0.893   unsp      YES
# AAV87312.1          542 S   IRGNSIFNG    0.777   PKA       YES
#
# AAV87312.1          567 Y   GNDIYGNAL    0.939   unsp      YES
# AAV87312.1          567 Y   GNDIYGNAL    0.587   INSR      YES
# AAV87312.1          567 Y   GNDIYGNAL    0.548   EGFR      YES
#
# AAV87312.1          580 S   IRTNSCPIV    0.732   PKA       YES
#
# AAV87312.1          613 Y   ENEVYSNTL    0.974   unsp      YES
# AAV87312.1          613 Y   ENEVYSNTL    0.518   INSR      YES
#
# AAV87312.1          616 T   VYSNTLAGV    0.533   CKI       YES
#
# AAV87312.1          623 T   GVWVTTGST    0.747   PKC       YES
#
# AAV87312.1          627 T   TTGSTPVLR    0.647   cdk5      YES
# AAV87312.1          627 T   TTGSTPVLR    0.536   p38MAPK   YES
#
```

```
# AAV87312.1          637 S   NRIHSGKQV   0.994   unsp     YES
# AAV87312.1          637 S   NRIHSGKQV   0.848   PKC      YES
# AAV87312.1          637 S   NRIHSGKQV   0.626   PKA      YES
# AAV87312.1          637 S   NRIHSGKQV   0.600   PKB      YES
#
# AAV87312.1          659 Y   DNDIYNHMY   0.953   unsp     YES
# AAV87312.1          659 Y   DNDIYNHMY   0.560   EGFR     YES
# AAV87312.1          659 Y   DNDIYNHMY   0.554   INSR     YES
# AAV87312.1          659 Y   DNDIYNHMY   0.536   SRC      YES
#
# AAV87312.1          672 S   IRTGSNPKI   0.597   PKC      YES
# AAV87312.1          672 S   IRTGSNPKI   0.567   RSK      YES
#
# AAV87312.1          721 T   DSNPTLRRN   0.902   PKC      YES
# AAV87312.1          721 T   DSNPTLRRN   0.570   unsp     YES
#
# AAV87312.1          761 S   GVLISTNSH   0.673   PKC      YES
#
# AAV87312.1          790 T   HATATLEGN   0.822   PKC      YES
#
# AAV87312.1          813 T   GVNVTMKDN   0.853   PKC      YES
#
# AAV87312.1          831 S   EKAVSRGQC   0.787   unsp     YES
#
# AAV87312.1          840 S   LYKISSYTS   0.556   PKG      YES
#
# AAV87312.1          841 S   YKISSYTSY   0.764   PKC      YES
# AAV87312.1          841 S   YKISSYTSY   0.548   DNAPK    YES
#
# AAV87312.1          844 S   SSYTSYPMH   0.990   unsp     YES
#
# AAV87312.1          845 Y   SYTSYPMHD   0.506   unsp     YES
#
# AAV87312.1          858 T   HTCNTTDRN   0.715   PKC      YES
# AAV87312.1          858 T   HTCNTTDRN   0.519   unsp     YES
#
# AAV87312.1          896 S   AGTLSNPCT   0.569   cdc2     YES
# AAV87312.1          896 S   AGTLSNPCT   0.509   PKA      YES
#
# AAV87312.1          900 T   SNPCTLASE   0.512   CKI      YES
#
# AAV87312.1          903 S   CTLASEPTH   0.510   cdc2     YES
#
# AAV87312.1          906 T   ASEPTHDTD   0.553   CKI      YES
#
# AAV87312.1          911 T   HDTDTLYDS   0.866   unsp     YES
#
# AAV87312.1          913 Y   TDTLYDSAP   0.941   unsp     YES
# AAV87312.1          913 Y   TDTLYDSAP   0.561   SRC      YES
#
# AAV87312.1          915 S   TLYDSAPPI   0.517   cdc2     YES
```

```
MNSVRAANRRPRRVSRPRPVQQQQQQPPQQPPPQPPQQQPPQQQPPPPPQ      #   50
    QQQQQQPPPPPPPPPPLPQERNNVGERDDDVPADMVAEESGPGAQNSPYQ  #  100
    LRRKTLLPKRTACPTKNSMEGASTSTTENFGHRAKRARVSGKSQDLSAAP  #  150
    AEQYLQEKLPDEVVLKIFSYLLEQDLCRAACVCKRFSELANDPILWKRLY  #  200
    MEVFEYTRPMMHPEPGKFYQINPEEYEHPNPWKESFQQLYKGAHVKPGFA  #  250
    EHFYSNPARYKGRENMLYYDTIEDALGGVQEAHFDGLIFVHSGIYTDEWI  #  300
    YIESPITMIGAAPGKVADKVIIENTRDSTFVFMEGSEDAYVGYMTIRFNP  #  350
    DDKSAQHHNAHHCLEITVNCSPIIDHCIIRSTCTVGSAVCVSGQGACPTI  #  400
    KHCNISDCENVGLYITDHAQGIYEDNEISNNALAGIWVKNHGNPIIRRNH  #  450
    IHHGRDVGVFTFDHGMGYFESCNIHRNRIAGFEVKAYANPTVVRCEIHHG  #  500
    QTGGIYVHEKGRGQFIENKIYANNFAGVWITSNSDPTIRGNSIFNGNQGG  #  550
    VYIFGDGRGLIEGNDIYGNALAGIQIRTNSCPIVRHNKIHDGQHGGIYVH  #  600
    EKGQGVIEENEVYSNTLAGVWVTTGSTPVLRRNRIHSGKQVGVYFYDNGH  #  650
    GVLEDNDIYNHMYSGVQIRTGSNPKIRRNKIWGGQNGGILVYNSGLGCIE  #  700
```

```
        DNEIFDNAMAGVWIKTDSNPTLRRNKIHDGRDGGICIFNGGRGLLEENDI        #    750
        FRNAQAGVLISTNSHPILRKNRIFDGFAAGIEITNHATATLEGNQIFNNR        #    800
        FGGLFLASGVNVTMKDNKIMNNQDAIEKAVSRGQCLYKISSYTSYPMHDF        #    850
        YRCHTCNTTDRNAICVNCIKKCHQGHDVEFIRHDRFFCDCGAGTLSNPCT        #    900
        LASEPTHDTDTLYDSAPPIESNTLQHN                               #    950
```

```
%1   ..S...........S...................................      #     50
%1   .......................................S......S...      #    100
%1   ....T.....T...T..S....STS..............S..S...S...      # 150
%1   ...Y................................S............Y      #    200
%1   .....Y...................Y........................      #    250
%1   ...Y..............Y.T.......................YT....      #    300
%1   Y.......................T..S......S...Y....T.....       #    350
%1   ...............................T.T..............T.     #    400
%1   .....S................Y...........................      #    450
%1   ....................................Y...T.........     #    500
%1   ....................Y..........S....T....S........      #    550
%1   ................Y............S....................      #    600
%1   ............Y..T......T...T.........S.............      #    650
%1   ........Y............S............................      #    700
%1   ....................T.............................      #    750
%1   ..........S............................T..........      #    800
%1   ............T.................S........SS..SY.....      #    850
%1   .......T.....................................S...T      #    900
%1   ..S..T....T.Y.S............
```

Supplementary Table 4. Mass spectrometry results (phosphorylation sites).

NC-FBXO11-293T					
Position	Target	Modification	Classification	Highest Peptide Confidence	Sequence Motif
140	S	Phospho	Post-translational	High	AKRARVsGKSQDL
143	S	Phospho	Post-translational	High	ARVSGKsQDLSAA
147	S	Phospho	Post-translational	High	GKSQDLsAAPAEQ
542	S	Phospho	Post-translational	High	PTIRGNsIFNGNQ
841	S	Phospho	Post-translational	High	CLYKISsYTSYPM
NDR1-FBXO11-293T					
Position	Target	Modification	Classification	Highest Peptide Confidence	Sequence Motif
140	S	Phospho	Post-translational	High	AKRARVsGKSQDL
143	S	Phospho	Post-translational	High	ARVSGKsQDLSAA
147	S	Phospho	Post-translational	High	GKSQDLsAAPAEQ
187	S	Phospho	Post-translational	High	CVCKRFsELANDP

Supplementary Table 5. NetPhos3.1 predicts phosphorylation sites on β-catenin by NDR1 (Score > 0.5).

```
>CAA61107.1        781 amino acids
#
# netphos-3.1b prediction results
#
# Sequence                 # x   Context     Score   Kinase    Answer
# CAA61107.1                3 T  --MATQADL   0.565   DNAPK     YES
#
# CAA61107.1               23 S  KAAVSHWQQ   0.749   PKC       YES
# CAA61107.1               23 S  KAAVSHWQQ   0.654   unsp      YES
#
# CAA61107.1               30 Y  QQQSYLDSG   0.815   unsp      YES
#
# CAA61107.1               33 S  SYLDSGIHS   0.564   PKC       YES
#
# CAA61107.1               37 S  SGIHSGATT   0.525   PKA       YES
#
# CAA61107.1               40 T  HSGATTTAP   0.806   PKC       YES
#
# CAA61107.1               41 T  SGATTTAPS   0.766   unsp      YES
# CAA61107.1               41 T  SGATTTAPS   0.507   PKC       YES
#
# CAA61107.1               45 S  TTAPSLSGK   0.838   unsp      YES
# CAA61107.1               45 S  TTAPSLSGK   0.600   CKI       YES
# CAA61107.1               45 S  TTAPSLSGK   0.572   PKC       YES
#
# CAA61107.1               47 S  APSLSGKGN   0.995   unsp      YES
# CAA61107.1               47 S  APSLSGKGN   0.664   PKC       YES
# CAA61107.1               47 S  APSLSGKGN   0.605   CKI       YES
#
# CAA61107.1               59 T  EDVDTSQVL   0.542   CKII      YES
#
# CAA61107.1               60 S  DVDTSQVLY   0.665   ATM       YES
# CAA61107.1               60 S  DVDTSQVLY   0.597   DNAPK     YES
# CAA61107.1               60 S  DVDTSQVLY   0.512   CKII      YES
#
# CAA61107.1               71 S  EQGFSQSFT   0.561   DNAPK     YES
# CAA61107.1               71 S  EQGFSQSFT   0.557   ATM       YES
# CAA61107.1               71 S  EQGFSQSFT   0.525   cdc2      YES
#
# CAA61107.1               73 S  GFSQSFTQE   0.504   cdc2      YES
# CAA61107.1               73 S  GFSQSFTQE   0.500   PKC       YES
#
# CAA61107.1               75 T  SQSFTQEQV   0.556   DNAPK     YES
#
# CAA61107.1               86 Y  IDGQYAMTR   0.540   unsp      YES
#
# CAA61107.1               89 T  QYAMTRAQR   0.589   PKC       YES
#
# CAA61107.1              102 T  MFPETLDEG   0.694   unsp      YES
# CAA61107.1              102 T  MFPETLDEG   0.558   CKII      YES
#
# CAA61107.1              111 S  MQIPSTQFD   0.572   cdc2      YES
#
# CAA61107.1              112 T  QIPSTQFDA   0.511   ATM       YES
#
# CAA61107.1              129 S  LAEPSQMLK   0.589   DNAPK     YES
#
# CAA61107.1              179 S  VHQLSKKEA   0.997   unsp      YES
# CAA61107.1              179 S  VHQLSKKEA   0.780   PKC       YES
#
# CAA61107.1              184 S  KKEASRHAI   0.848   unsp      YES
#
# CAA61107.1              191 S  AIMRSPQMV   0.629   cdk5      YES
#
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# CAA61107.1        205 T   TMQNTNDVE   0.515   CKII       YES
#
# CAA61107.1        210 T   NDVETARCT   0.768   unsp       YES
#
# CAA61107.1        217 T   CTAGTLHNL   0.554   PKC        YES
#
# CAA61107.1        222 S   LHNLSHHRE   0.937   unsp       YES
#
# CAA61107.1        234 S   AIFKSGGIP   0.537   PKA        YES
#
# CAA61107.1        246 S   KMLGSPVDS   0.979   unsp       YES
# CAA61107.1        246 S   KMLGSPVDS   0.534   p38MAPK    YES
# CAA61107.1        246 S   KMLGSPVDS   0.514   GSK3       YES
#
# CAA61107.1        258 T   YAITTLHNL   0.717   unsp       YES
#
# CAA61107.1        298 T   LAITTDCLQ   0.536   CKII       YES
#
# CAA61107.1        311 S   GNQESKLII   0.537   cdc2       YES
#
# CAA61107.1        330 T   NIMRTYTYE   0.636   PKC        YES
#
# CAA61107.1        339 T   KLLWTTSRV   0.558   PKC        YES
# CAA61107.1        339 T   KLLWTTSRV   0.500   cdc2       YES
#
# CAA61107.1        340 T   LLWTTSRVL   0.870   unsp       YES
# CAA61107.1        340 T   LLWTTSRVL   0.638   PKC        YES
#
# CAA61107.1        352 S   SVCSSNKPA   0.750   PKC        YES
#
# CAA61107.1        374 S   LTDPSQRLV   0.615   DNAPK      YES
# CAA61107.1        374 S   LTDPSQRLV   0.507   ATM        YES
#
# CAA61107.1        384 T   NCLWTLRNL   0.545   PKC        YES
#
# CAA61107.1        389 S   LRNLSDAAT   0.988   unsp       YES
# CAA61107.1        389 S   LRNLSDAAT   0.708   PKA        YES
#
# CAA61107.1        393 T   SDAATKQEG   0.546   CKII       YES
#
# CAA61107.1        411 S   QLLGSDDIN   0.522   cdc2       YES
#
# CAA61107.1        432 Y   TCNNYKNKM   0.549   unsp       YES
#
# CAA61107.1        472 T   LRHLTSRHQ   0.946   unsp       YES
#
# CAA61107.1        547 T   AHQDTQRRT   0.973   unsp       YES
#
# CAA61107.1        552 S   QRRTSMGGT   0.998   unsp       YES
# CAA61107.1        552 S   QRRTSMGGT   0.714   PKA        YES
#
# CAA61107.1        556 T   SMGGTQQQF   0.567   PKC        YES
# CAA61107.1        556 T   SMGGTQQQF   0.549   DNAPK      YES
#
# CAA61107.1        605 S   QLLYSPIEN   0.957   unsp       YES
# CAA61107.1        605 S   QLLYSPIEN   0.525   p38MAPK    YES
#
# CAA61107.1        646 S   ELLHSRNEG   0.991   unsp       YES
#
# CAA61107.1        653 T   EGVATYAAA   0.502   PKC        YES
#
# CAA61107.1        663 S   LFRMSEDKP   0.718   unsp       YES
#
# CAA61107.1        670 Y   KPQDYKKRL   0.527   INSR       YES
#
# CAA61107.1        675 S   KKRLSVELT   0.997   unsp       YES
```

```
# CAA61107.1              675 S    KKRLSVELT     0.718    PKA            YES
#
# CAA61107.1              681 S    ELTSSLFRT     0.514    cdc2           YES
#
# CAA61107.1              715 S    QDDPSYRSF     0.992    unsp           YES
# CAA61107.1              715 S    QDDPSYRSF     0.874    PKC            YES
#
# CAA61107.1              716 Y    DDPSYRSFH     0.904    unsp           YES
# CAA61107.1              716 Y    DDPSYRSFH     0.522    INSR           YES
#
# CAA61107.1              718 S    PSYRSFHSG     0.642    unsp           YES
#
# CAA61107.1              724 Y    HSGGYGQDA     0.504    INSR           YES
```

```
    MATQADLMELDMAMEPDRKAAVSHWQQQSYLDSGIHSGATTTAPSLSGKG    #     50
    NPEEEDVDTSQVLYEWEQGFSQSFTQEQVADIDGQYAMTRAQRVRAAMFP    #    100
    ETLDEGMQIPSTQFDAAHPTNVQRLAEPSQMLKHAVVNLINYQDDAELAT    #    150
    RAIPELTKLLNDEDQVVVNKAAVMVHQLSKKEASRHAIMRSPQMVSAIVR    #    200
    TMQNTNDVETARCTAGTLHNLSHHREGLLAIFKSGGIPALVKMLGSPVDS    #    250
    VLFYAITTLHNLLLHQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDC    #    300
    LQILAYGNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSVC    #    350
    SSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSDAATKQEGMEG    #    400
    LLGTLVQLLGSDDINVVTCAAGILSNLTCNNYKNKMMVCQVGGIEALVRT    #    450
    VLRAGDREDITEPAICALRHLTSRHQEAEMAQNAVRLHYGLPVVVKLLHP    #    500
    PSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDTQRR    #    550
    TSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRIVIRGLNTIPLFV    #    600
    QLLYSPIENIQRVAAGVLCELAQDKEAAEAIEAEGATAPLTELLHSRNEG    #    650
    VATYAAAVLFRMSEDKPQDYKKRLSVELTSSLFRTEPMAWNETADLGLDI    #    700
    GAQGEPLGYRQDDPSYRSFHSGGYGQDALGMDPMMEHEMGGHHPGADYPV    #    750
    DGLPDLGHAQDLMDGLPPGDSNQLAWFDTDL                       #    800
```

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%1   ..T...................S......Y..S...S..TT...S.S...    #    50
%1   ........TS..........S.S.T..........Y..T...........    #    100
%1   .T........ST................S.....................    #    150
%1   ............................S...S......S.........    #    200
%1   ....T....T......T....S...........S...........S....    #    250
%1   ......T........................................T..    #    300
%1   ..........S..................T........TT..........    #    350
%1   .S.....................S.........T....S...T.......    #    400
%1   ..........S....................Y..................    #    450
%1   .....................T............................    #    500
%1   ..............................................T...    #    550
%1   .S...T............................................    #    600
%1   ....S........................................S....    #    650
%1   ..T.........S......Y....S.....S...................    #    700
%1   ..............SY.S.....Y..........................    #    750
%1   ...............................
```