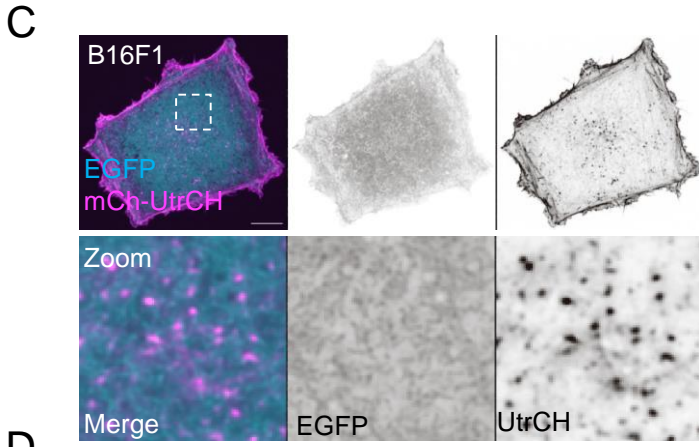
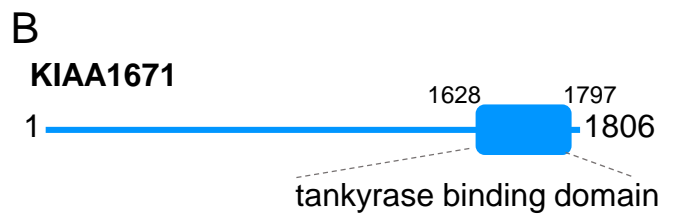
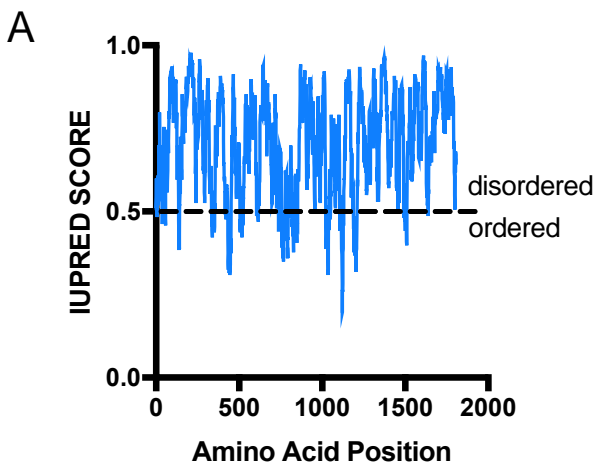


Supplementary Materials
Molecular Biology of the Cell
Gaeta and Tyska



D

KIAA1671	1617	PPDACPEKRVDDFSFI	DQTSVLDS	SALKTRVQLSKRSRR	RAPI---SHSL	1663
TNKS1BP1	1543	PPARS	PSQ---DFSFI	EDTEILD	SAMYRSRANLGRKRGR	RAPVIRPGGTL 1594
KIAA1671	1664	RRSRFSE	SESRSPLEDET	DNTWFMFKD	STEEKSPRKEESDE---EETASKA	1710
TNKS1BP1	1595	GLSEAAD	SDAH-----L	FQDSTE	PRASRVVPS	SDEEVVEEPQSR 1633
KIAA1671	1711	ER				
TNKS1BP1	1634	TR				

identical
similar
not similar

E

KIAA1671	1013	PAVKQ	GSPVEPKATFFAVTYQI	PNTQKAKGVVLSGAESL	LEHSRKITP-	1060
CARMIL1	959	PSLRQ	----EKRSSGF--	ISELPS	EEGKK-----LEHFTKLRPKR	992
KIAA1671	1061	-----P	SSPHSLTSTLVSLGHEEA	LEMAGSKNWMK	GREHENASILKTLKP	1105
CARMIL1	993	NKKQQP	PTQAAVCAANI	VS-----QDGEQ	NGLMGRVDE	EGVDEFFTKKV 1034
KIAA1671	1106	TDRP	SSLGAWSLDPFN	GRIIDVDAL	WSHRGSE	1137
CARMIL1	1035	TKMDSK	-----KW	STRGSE		1048

identical
similar
not similar

CPI consensus motif: LxHxTxxRPKx6P

Supplemental Figure 1.

(A) Prediction of sequence disorder using IUPRED2A. IUPRED scores over 0.5 predict disorder while values under 0.5 predict ordered residues. **(B)** Domain diagram of KIAA1671 highlighting its annotated tankyrase binding domain. **(C)** B16F1 melanoma cell expressing EGFP and mCherry-UtrCH. Zoom indicates region with UtrCH puncta. **(D)** EMBOSS Water local sequence alignment of human KIAA1671 (NP_001138678.1) and human TNKS1BP1 (Accession NP_203754.2) using a BLOSUM62 matrix. Identical residues are highlighted in magenta, similar residues are highlighted in black, and not similar amino acids are shown in light gray. **(D)** EMBOSS Water local sequence alignment of human KIAA1671 (NP_001138678.1) and human CARMIL1 (also known as F-actin-uncapping protein LRRC16A; NP_060110.4) using a BLOSUM62 matrix. The CARMIL annotated CPI consensus motif is highlighted in the red box. Identical residues are highlighted in magenta, similar residues are highlighted in black, and not similar amino acids are shown in light gray.