

SUPPLEMENTAL INFORMATION

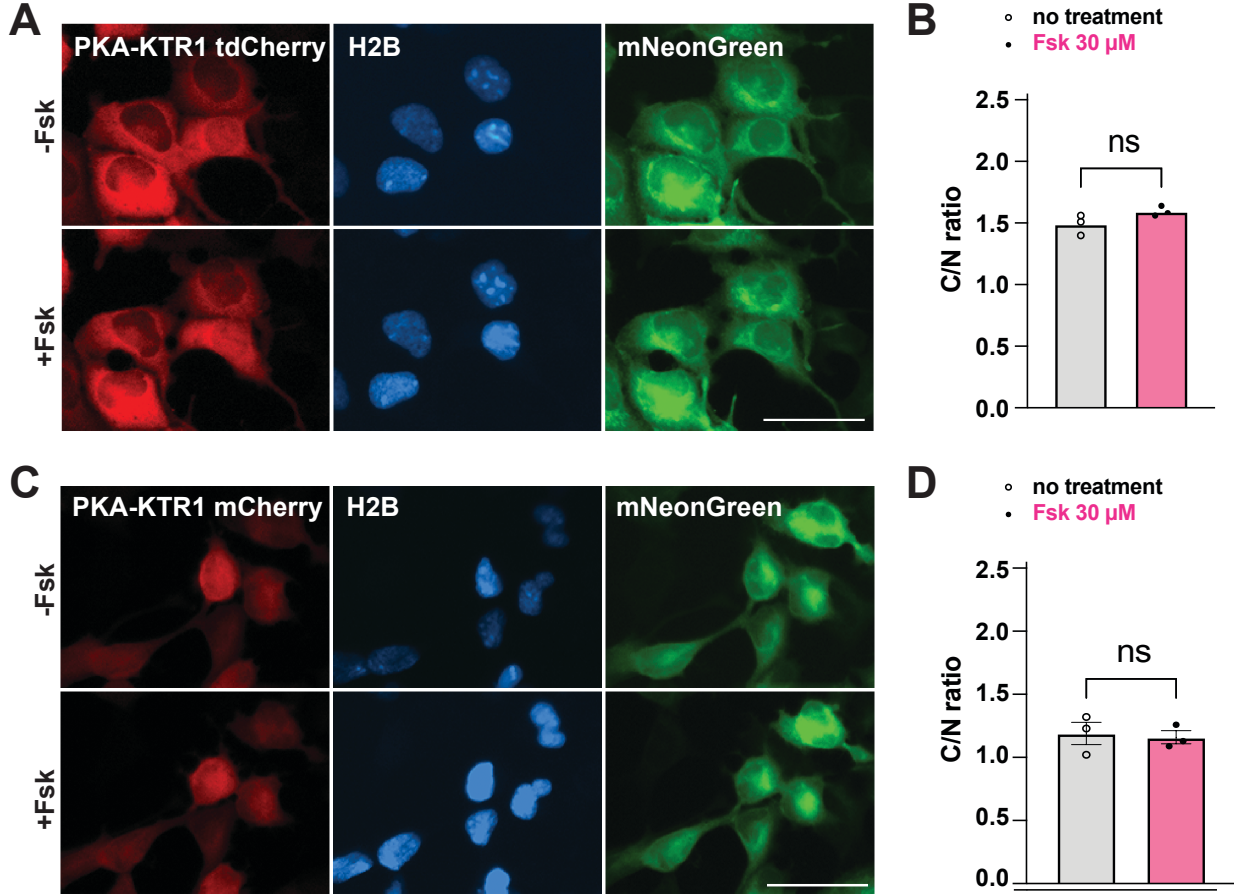


Figure S1. The PKA-KTR1 sensor domain does not drive Fsk-induced protein translocation to the cytoplasm. HEK293 cells were transfected with plasmids designed to co-express H2B-mTagBFP2, mNeonGreen, and (A, B) PKA-KTR1/tdCherry (~64 kDa), or (C, D) PKA-KTR1-mCherry (~32 kDa). (A) Fluorescence micrographs of HEK293 expressing cells expressing PKA-KTR1/tdCherry before and after 30 minutes incubation in 30 μ M Fsk. Bar, 50 μ M. (B) Bar plot of PKA-KTR1/tdCherry C/N ratio before and after addition of after 30 minutes incubation in 30 μ M Fsk. (C) Fluorescence micrographs of HEK293 expressing cells expressing PKA-KTR1/mCherry before and after 30 minutes incubation in 30 μ M Fsk. Bar, 50 μ M. (D) Bar plot of PKA-KTR1/mCherry C/N ratio before and after addition of after 30 minutes incubation in 30 μ M Fsk. Data are from a minimum of three independent biological replicates.

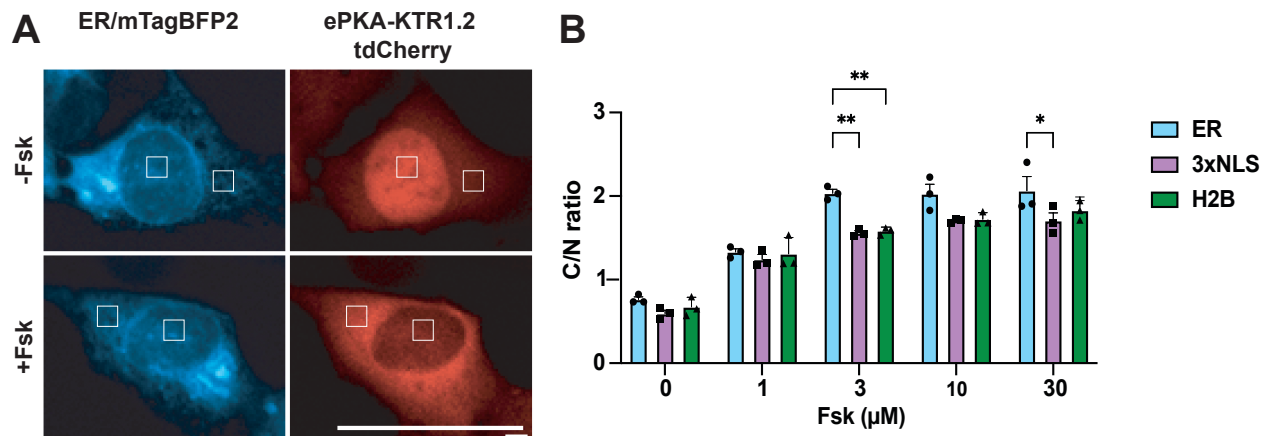


Figure S2. Marking nucleus and cytoplasm with ER-mTagBFP2. (A) Fluorescence micrographs of HEK293 cells co-expressing ER-mTagBFP2 and ePKA-KTR1.2/tdCherry. The distribution of ER-mTagBFP2 determines the positioning of ‘counting areas’ (white boxes) that are then used to count the relative fluorescence intensity of KTR proteins in the nucleus and cytoplasm, with the C/N ratio determined from the average fluorescence brightness of all pixels within each counting area. (B) C/N ratios of ePKA-KTR1.2 in HEK293 cells co-expressing (blue bars) the ER-mTagBFP2 marker (ER), (purple bars) the 3xNLS-mTagBFP2 marker (3xNLS), or (green bars) the H2B-mTagBFP2 marker (H2B). Cells were exposed to 0, 1, 3, 10, or 30 μM Fsk for 30 minutes, imaged by fluorescence microscopy, and C/N ratios were calculated from digital images. Data are from a minimum of three independent biological replicates. ANOVA p values are denoted by * <0.05 , and ** <0.01 .

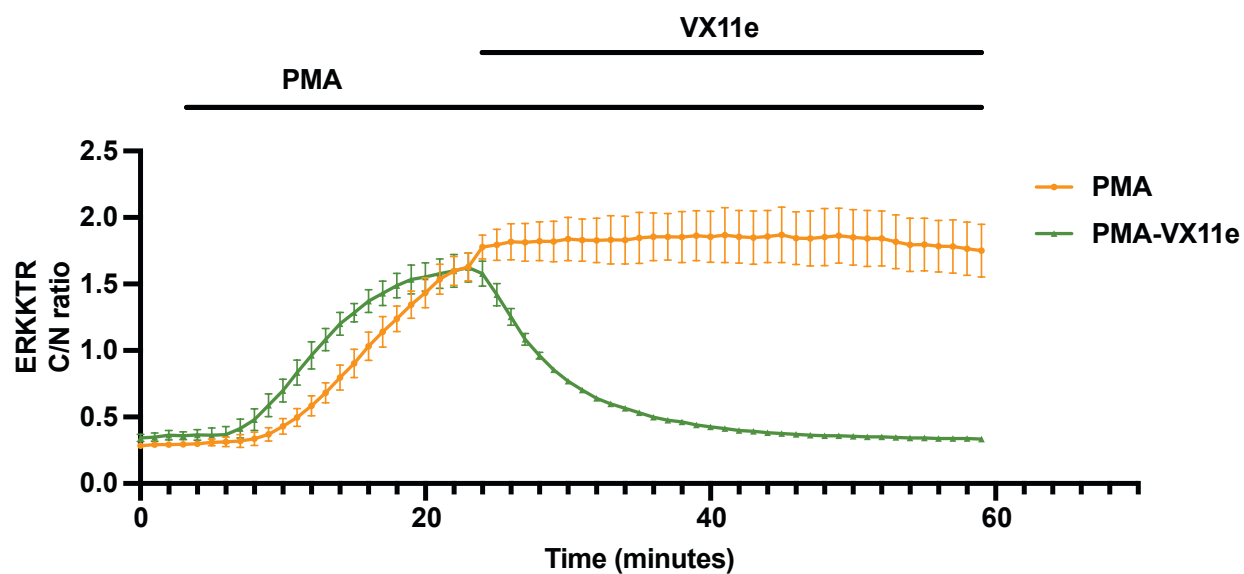


Figure S3. Response of eERK-KTR1.2/emiRFP670 to PMA, and to PMA then VX11e. HEK293 cells expressing eERK-KTR1.2/emiRFP670 were imaged every 60 sec (orange) in response to PMA alone or (green) in response to PMA, followed 20 min later by addition of VX11e. Data are from a minimum of three independent biological replicates.

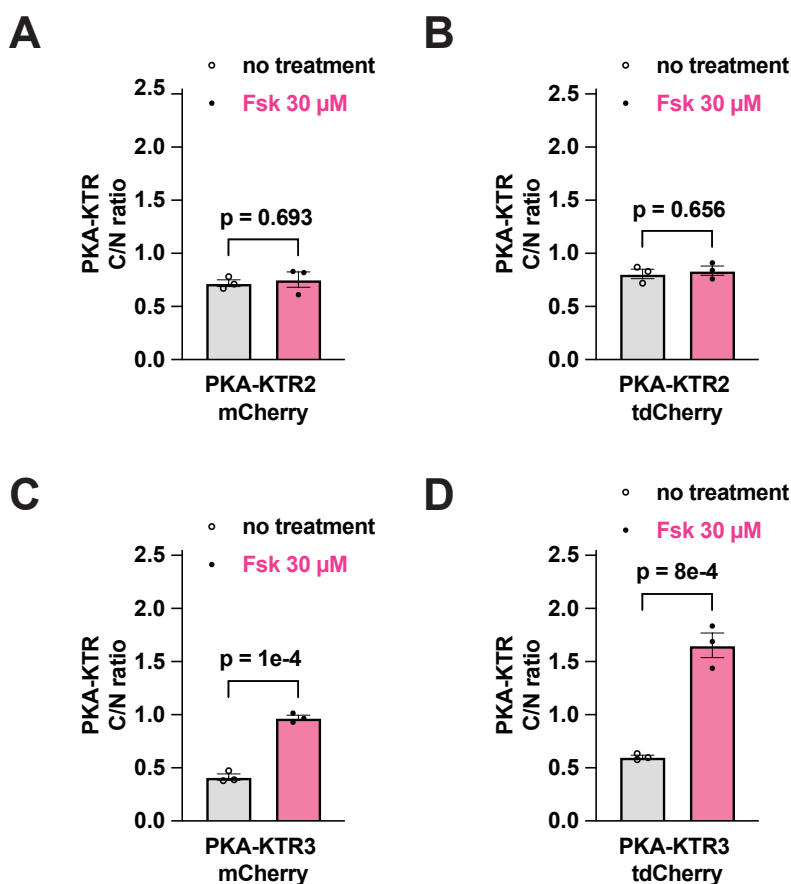


Figure S4. Increasing KTR size triples the dynamic range of PKA-KTR3. HEK293 cells were transfected with plasmid vectors designed to express fusion proteins comprised of the sensor domains of PKA-KTR2(28) or PKA-KTR3(29) appended to the N-terminus of either mCherry, tdCherry. Two days later, cells were imaged by fluorescence microscopy prior to or after a 30 min. incubation in 30 mM Fsk, followed by calculation of C/N ratios in 10 cells in independent regions of interest (ROIs) from three biological replicates, shown here in bar graph form. (A, B) Both PKA-KTR2/mCherry, a ~34 kDa proteins, and PKA-KTR2/tdCherry, a ~64 kDa protein, had resting C/N ratios <1, and neither showed a Fsk-induced translocation to the cytoplasm. (C) PKA-KTR3/mCherry, a ~34 kDa protein, displayed a low resting C/N ratio and moved to the cytoplasm in response to Fsk, confirming that the PKA-KTR3 sensor domain is a useful reporter of PKA activity. However, Fsk-induced C/N ratio of PKA-KTR3/mCherry remained <1, and its dynamic range was relatively narrow, only ~2-fold. (D) In contrast, we found that PKA-KTR3/tdCherry, ~64 kDa, had a broader dynamic range, ~3-fold, showing once again that increasing KTR size can be sufficient to improve KTR performance characteristics. Data are from a minimum of three independent biological replicates. ANOVA *p* values are denoted by *** <0.001.

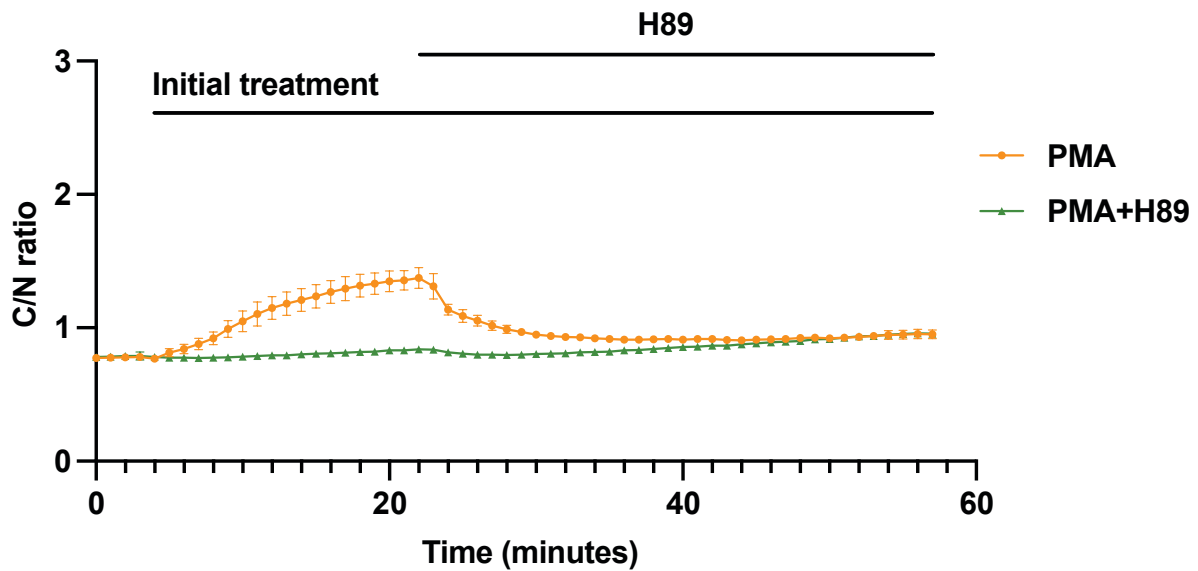


Figure S5. PMA induces a mild activation of PKA. Plot of C/N ratios for ePKA-KTR1.2/tdTomato C/N at every minute in ePKA-KTR1.2/tdTomato-expressing HEK293 cells exposed to (orange) PMA at t = 3 min, followed by the addition of the PKA inhibitor H89 at t = 23, or (green) PMA and H89 at t = 3, followed by addition of H89 again at t = 23 min.

	<p>TLYPADGGLEGRNDMALKLVGGSHLIANAKTYYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDL PSKLGHLKNGMDELYKGRSPGLNGSGATNFSLLKQAGDVEENPG</p>		
ePKA-KTR1.3 /tdCherry.2a .H2B-mTagBF P2	<p>MEMPEEPANSGHSLPPVYIYSPEYVSI CDSLKVKPKRASMVNEDEAPAKRRASLVGSSRLERLTLQSSGAPVSKGEEDN MAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDY KLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMPEDGALKGEIK QRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYKARGSGATSAT MVSKGEEDNMAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVK HPADIPDYKLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMP EDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYK ASGSGATNFSLLKQAGDVEENPG < . . . > PSPAMPEPAKSAPAPKKGSKAVTKAQKGGKRRKRSRKEYSISYVYKV LKQVHPDTGISKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGLAKHAVSEGTKAITKYTS AKDPGGSSSRVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGS KTFINHTQGI P DFFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDQDGLIYNVKIRGVNFTSNGPVMQKKTGWAEAFTE TLYPADGGLEGRNDMALKLVGGSHLIANAKTYYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDL PSKLGHLKNGMDELYKGRSPGLNGSGATNFSLLKQAGDVEENPG</p>	P C	S 5 1 4
ePKA-KTR1.4 /tdCherry.2a .H2B-mTagBF P2	<p>MEMPEEPANSGHSLPPVYIYSPEYVSI CDSLKVKPKRASMVNEDEAPAKRRASLVGSSRLERLTLQSSGAPVSKGEED NMAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDY KLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMPEDGALKGEIK QRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYKARGSGATSAT TMVSKGEEDNMAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYV KHPADIPDYKLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMP EDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYK ASGSGATNFSLLKQAGDVEENPG < . . . > PSPAMPEPAKSAPAPKKGSKAVTKAQKGGKRRKRSRKEYSISYVYKV VLKQVHPDTGISKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGLAKHAVSEGTKAITKYTS SAKDPGGSSSRVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGS SKTFINHTQGI P DFFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDQDGLIYNVKIRGVNFTSNGPVMQKKTGWAEAFTE ETLYPADGGLEGRNDMALKLVGGSHLIANAKTYYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDL LPSKLGHLKNGMDELYKGRSPGLNGSGATNFSLLKQAGDVEENPG</p>	P C	S 5 1 5
ePKA-KTR1.5 /tdCherry.2a .H2B-mTagBF P2	<p>MEMPEEPANSGHSLPPVYIYSPEYVSI CDSLKVKPKRASMVNEDEAPSKRRASLVGSSRLERLTLQSSGAPVSKGEED NMAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDY KLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMPEDGALKGEIK QRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYKARGSGATSAT TMVSKGEEDNMAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYV KHPADIPDYKLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMP EDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYK ASGSGATNFSLLKQAGDVEENPG < . . . > PSPAMPEPAKSAPAPKKGSKAVTKAQKGGKRRKRSRKEYSISYVYKV VLKQVHPDTGISKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGLAKHAVSEGTKAITKYTS SAKDPGGSSSRVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGS SKTFINHTQGI P DFFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDQDGLIYNVKIRGVNFTSNGPVMQKKTGWAEAFTE ETLYPADGGLEGRNDMALKLVGGSHLIANAKTYYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDL LPSKLGHLKNGMDELYKGRSPGLNGSGATNFSLLKQAGDVEENPG</p>	P C	S 7 4 2
ePKA-KTR1.2 /mCherry.2a .ER-mTagBF P2	<p>MEMPEEPANSGHSLPPVYIYSPEYVSI CDSLKVKPKRASMVNEDEAPSKRRASLVGSSRLERLTLQSSGAPVSKGEEDN MAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDY KLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMPEDGALKGEIK QRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYKARGSGATNFS LLKQAGDVEENPG < . . . > PMKLSLVAAMLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYE GTQTMRIKVVVEGGPLPFAFDILATSFLYGSKTFINHTQGI P DFFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDQDGLI YNVKIRGVNFTSNGPVMQKKTGWAEAFTE TLYPADGGLEGRNDMALKLVGGSHLIANAKTYYRSKPKAKNLKMPGVVY VDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLKNDDEL</p>	P L e n t i	Y G 6 1
ePKA-KTR1.4 /mCherry.2a .ER-mTagBF P2	<p>MEMPEEPANSGHSLPPVYIYSPEYVSI CDSLKVKPKRASMVNEDEAPAKRRASLVGSSRLERLTLQSSGAPVSKGEED NMAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDY KLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMPEDGALKGEIK QRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYKARGSGATNFS LLKQAGDVEENPG < . . . > PMKLSLVAAMLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYE GTQTMRIKVVVEGGPLPFAFDILATSFLYGSKTFINHTQGI P DFFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDQDGLI YNVKIRGVNFTSNGPVMQKKTGWAEAFTE TLYPADGGLEGRNDMALKLVGGSHLIANAKTYYRSKPKAKNLKMPGVVY VDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLKNDDEL</p>	P L e n t i	Y G 6 5
ePKA-KTR1.4 /tdCherry.2a .ER-mTagBF P2	<p>MEMPEEPANSGHSLPPVYIYSPEYVSI CDSLKVKPKRASMVNEDEAPAKRRASLVGSSRLERLTLQSSGAPVSKGEED NMAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDY KLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMPEDGALKGEIK QRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYKARGSGATSAT TMVSKGEEDNMAI I KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYV KHPADIPDYKLSFPFEGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMP EDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTI VEQYERAEGRHSTGGMDELYK ASGSGATNFSLLKQAGDVEENPG < . . . > PMKLSLVAAMLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKC TSEGEKPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGSKTFINHTQGI P DFFKQSFPEGFTWERVTTYEDGGVLTAT QDTSLDQDGLIYNVKIRGVNFTSNGPVMQKKTGWAEAFTE TLYPADGGLEGRNDMALKLVGGSHLIANAKTYYRSKPKA KNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLKNDDEL</p>	P L e n t i	Y G 6 7
ePKA-KTR1.2 /mScar	<p>MEMPEEPANSGHSLPPVYIYSPEYVSI CDSLKVKPKRASMVNEDEAPSKRRASLVGSSRLERLTLQSSGAPVSKGEAVI KEFMRFKVHMEGSVNGHEFE I BEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFP FEGFKWERVMNFEDGGAVTVTQDTSLEDGLTIYKVKLRGTNFPDGPVPMQKKTMGWEASSERMPEDGVLKGDIKMALR</p>	p L e	Y G 8

let- I.2a.E R- mTagBF P2	LKDGGRYLADFKTTYKAKKPVQMPGAYNVDRKLDITSHNEDYTVVEQYERSEGRHSTGGMDELYKASGSGATNFSLLKQAGDVEENPG <...> PMKLSLVAAMLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTRIKVVEGGPLFFAFDILATSFLYGSKTFINHTQGI PDDFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDGCLLYNVKIRGVNFTSNGPVMQKKTGWAEFTETLYPADGGLEGRNDMALKLVGGSHLIANAKT TYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLNKDEL	n t i	
ePKA- KTR1.2 /mScar let- I/BCR. 2a.E- mTagBF P2	MEMPEEPANSGHSLPVIYISPEYVSI CDSLVKVPKRASMVNEDEAPSKRRASLGVSRLERLTLQSSGAPVSKGEAVIKFEMRFKVMHEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFSWDILSPQFMYGSAF IKHPADIPDYKQSFPEGFKWERVMNFDGGAVTVTQDTSLEDGTLIYKVKLRGTFNFPDGPVVMQKKTMGWEAS TERLYRLEKIDKMALRLKDGGRYLADFKTTYKAKKPVQMPGAYNVDRKLDITSHNEDYTVVEQYERSEGRHSTGGMDELYKSGSAGGSAGGSDIEQELEERAKASIRRLEQEVNQERSRMAYLQTL LAKGGSAGGSASGSGATNFSLLKQAGDVEENPG <...> PMKLSLVAAMLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTRIKVVEGGPLFFAFDILATSFLYGSKTFINHTQGI PDDFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDGCLLYNVKIRGVNFTSNGPVMQKKTGWAEFTETLYPADGGLEGRNDMALKLVGGSHLIANAKT TYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLNKDEL	P l e n t i	Y G 1 8
ERK- KTR1/t dCherry. 2a.H 2B- mTagBF P2	MKGRKPRDLELPLSPSLLGGQGPERTPGSGTSSGLQAPGALSPSKRSGLEDPATPSKKPRTPSVSSRLERLTLQSSFQFPPSAPVSKGEEDNMAI I KEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPEGFKWERVMNFDGGVTVTQDSSLQDGEFIYKVKLRGTFNFPDGPVVMQKKTMGWEASSE RMYPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTVVEQYERAEGRHSTGGMD ELYKARGSAGSATM VSKGEEDNMAI I KEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPEGFKWERVMNFDGGVTVTQDSSLQDGEFIYKVKLRGTFNFPDGPVVMQKKTMGWEASSE RMYPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTVVEQYERAEGRHSTGGMDELYKASGSGATNFSLLKQAGDVEENPG <...> PSPAMPEPAKSAPAPKKGSKKAVTKAQKGGKRRRSRRESYSIYVYKVLKQVHPDGTGISSKAMGIMNSFVNDIFER IAGEASRLAHYNKRSTITSREIQTA VRLLLPGLLAKH AVSEGTKAITKYTS AKDPGGSSRVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTRIKVVEGGPLFFAFDILATSFLYGSKTFINHTQGI PDDFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDGCLLYNVKIRGVNFTSNGPVMQKKTGWAEFTETLYPADGGLEGRNDMALKLVGGSHLIANAKT TYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLNGMDELYKGRSPGLNGGSGATNFSLLKQAGDVEENPG	P C	S 4 6 8
eERK- KTR1.1 /tdCher rry.2a .H2B- mTagBF P2	MKGRKPRDLELPLSPSLLGGQGPERTPGSGTSSGLQAPGALSPSKRSGLEDPATPSKKPRTPSVSSRLERLTLQSSFQFPPSAPVSKGEEDNMAI I KEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPEGFKWERVMNFDGGVTVTQDSSLQDGEFIYKVKLRGTFNFPDGPVVMQKKTMGWEASSE RMYPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTVVEQYERAEGRHSTGGMD ELYKARGSAGSATM VSKGEEDNMAI I KEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPEGFKWERVMNFDGGVTVTQDSSLQDGEFIYKVKLRGTFNFPDGPVVMQKKTMGWEASSE RMYPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTVVEQYERAEGRHSTGGMDELYKASGSGATNFSLLKQAGDVEENPG <...> PSPAMPEPAKSAPAPKKGSKKAVTKAQKGGKRRRSRRESYSIYVYKVLKQVHPDGTGISSKAMGIMNSFVNDIFER IAGEASRLAHYNKRSTITSREIQTA VRLLLPGLLAKH AVSEGTKAITKYTS AKDPGGSSRVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTRIKVVEGGPLFFAFDILATSFLYGSKTFINHTQGI PDDFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDGCLLYNVKIRGVNFTSNGPVMQKKTGWAEFTETLYPADGGLEGRNDMALKLVGGSHLIANAKT TYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLNGMDELYKGRSPGLNGGSGATNFSLLKQAGDVEENPG	P C	S 7 1 2
eERK- KTR1.2 /tdCher rry.2a .H2B- mTagBF P2	MKGRKPRDLELPLSPSLLGGQGPERTPGSGTSSGLQAPGALSPSKRSGLEDPATPSKKPRTPSVSSRLERLTLQSSFQFPPSAPVSKGEEDNMAI I KEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPEGFKWERVMNFDGGVTVTQDSSLQDGEFIYKVKLRGTFNFPDGPVVMQKKTMGWEASSE RMYPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTVVEQYERAEGRHSTGGMD ELYKARGSAGSATM VSKGEEDNMAI I KEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPEGFKWERVMNFDGGVTVTQDSSLQDGEFIYKVKLRGTFNFPDGPVVMQKKTMGWEASSE RMYPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTVVEQYERAEGRHSTGGMDELYKASGSGATNFSLLKQAGDVEENPG <...> PSPAMPEPAKSAPAPKKGSKKAVTKAQKGGKRRRSRRESYSIYVYKVLKQVHPDGTGISSKAMGIMNSFVNDIFER IAGEASRLAHYNKRSTITSREIQTA VRLLLPGLLAKH AVSEGTKAITKYTS AKDPGGSSRVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTRIKVVEGGPLFFAFDILATSFLYGSKTFINHTQGI PDDFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDGCLLYNVKIRGVNFTSNGPVMQKKTGWAEFTETLYPADGGLEGRNDMALKLVGGSHLIANAKT TYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLNGMDELYKGRSPGLNGGSGATNFSLLKQAGDVEENPG	P C	S 7 1 3
eERK- KTR1.3 /tdCher rry.2a .H2B- mTagBF P2	MKGRKPRDLELPLSPSLLGGQGPERTPGSGTSSGLQAPGALSPSKRSGLEDPATPSKKPRTPSVSSRLERLTLQSSFQFPPSAPVSKGEEDNMAI I KEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPEGFKWERVMNFDGGVTVTQDSSLQDGEFIYKVKLRGTFNFPDGPVVMQKKTMGWEASSE RMYPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTVVEQYERAEGRHSTGGMD ELYKARGSAGSATM VSKGEEDNMAI I KEFMRFKVHMEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPEGFKWERVMNFDGGVTVTQDSSLQDGEFIYKVKLRGTFNFPDGPVVMQKKTMGWEASSE RMYPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNLIKLDITSHNEDYTVVEQYERAEGRHSTGGMDELYKASGSGATNFSLLKQAGDVEENPG <...> PSPAMPEPAKSAPAPKKGSKKAVTKAQKGGKRRRSRRESYSIYVYKVLKQVHPDGTGISSKAMGIMNSFVNDIFER IAGEASRLAHYNKRSTITSREIQTA VRLLLPGLLAKH AVSEGTKAITKYTS AKDPGGSSRVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTRIKVVEGGPLFFAFDILATSFLYGSKTFINHTQGI PDDFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDGCLLYNVKIRGVNFTSNGPVMQKKTGWAEFTETLYPADGGLEGRNDMALKLVGGSHLIANAKT TYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLNGMDELYKGRSPGLNGGSGATNFSLLKQAGDVEENPG	P C	S 7 6 5
eERK- KTR1.2 /mScar let- I.2a.E	MKGRKPRDLELPLSPSLLGGQGPERTPGSGTSSGLQAPGALSPSKRSGLEDPATPSKKPRTPSVSSRLERLTLQSSFQFPPSAPVSKGEAVIKFEMRFKVMHEGSMNGHEFEIEGEGEGRPYEGTQAKLVTKGGPLPFSWDILSPQFMYGSAF IKHPADIPDYKQSFPEGFKWERVMNFDGGAVTVTQDTSLEDGTLIYKVKLRGTFNFPDGPVVMQKKTMGWEAS TERLYRLEKIDKMALRLKDGGRYLADFKTTYKAKKPVQMPGAYNVDRKLDITSHNEDYTVVEQYERSEGRHSTGGMDELYKASGSGATNFSLLKQAGDVEENPG <...> PMKLSLVAAMLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTRIKVVEGGPLFFAFDILATSFLYGSKTFINHTQGI PDDFKQSFPEGFTWERVTTYEDGGVLTATQDTSLDGCLLYNVKIRGVNFTSNGPVMQKKTGWAEFTETLYPADGGLEGRNDMALKLVGGSHLIANAKT TYRSKPKAKNLKMPGVVYVDYRLERIKEANNETYVEQHEVAVARYCDLPSKLGHLNKDEL	P l e n	S 9 4 0

R- mTagBF P2	KCTSEGEKPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGSKTFINHTQGI P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N K D E L	t i	
eERK- KTR1.2 /mScar let- I/BCR. 2a. ER- mTagBF P2	MKGRKPRDLEPLSPSLLGGQPPERTPGSGTSSGLQAPGPALSPSKRSGLLEDDEPATPSKPKRTPPSVSSRLERLTLQSS FQFPGSAPVSKGEAVIKEFMRFKVHMEGSMNGHEFEIEEGEGRPEYEGTQAKLKVTKGGPLPFSWDILSPQFMYGSRA FIKHPADIPDYKQSFPEGFKWERVMNFEDGGAVTVDQTSLEDGTLIYKVKLRGTNFPDPGPMQKKTMGWEAS TERLYPEDGVLKGDIKMALRLKDGGRYLADFKTTYKAKKPVQMPGAYNVDRKLDITSHNEDYTVVEQYERSEGRHSTGGMDEL YKSGSAGGSAGSDIEQELERAKASIRRLQEVNQERSRMAYLQTLTLLAKGGSAGGSASGSGATNFSLLKQAGDVEENP G <...> PMKLSLVAAMLLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTMRIKVVVEG GPLPFAFDILATSFLYGSKTFINHTQGI P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N K D E L	P l e n t i	Y G 2 1
ePKA- KTR1.2 /tdChe rry.2a .3xNLS - mTagBF P2	MEMPEEPANSGHSLPPVYIYSPEYVSI C D S L V K V P K R A S M V N E D E A P S K R R A S L G V S S R L E R L T L Q S S G A P V S K G E E D N MAIKEFMRFKVHMEGSMNGHEFEIEEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDY KLSFPFGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVMQKKTMGWEASSERMPEDGALKGEIK QRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIIVEQYERAEGRHSTGGMDELYKARGSAGSATT MVSKGEEDNMAIKEFMRFKVHMEGSMNGHEFEIEEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVK HPADIPDYKLSFPFGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVMQKKTMGWEASSERMP DALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIIVEQYERAEGRHSTGGMDELYK SGSGATNFSLLKQAGDVEENPG <...> PSPAPKKRKRKVGDDGCPKKRKRKVGDDGCPKKRKRKVGDDGCPKKRKRKVGDDSSRVSKGEE LKENMHMKLYMEGTVDNHHFKCTSEGEKPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGSKTFINHTQGI P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N G M D E L Y K G R S P G L N G S G A T N F S L L K Q A G D V E E N P G	P C	S 3 8 1
ePKA- KTR1.2 /tdChe rry.2a .ER- mTagBF P2	MEMPEEPANSGHSLPPVYIYSPEYVSI C D S L V K V P K R A S M V N E D E A P S K R R A S L G V S S R L E R L T L Q S S G A P V S K G E E D N MAIKEFMRFKVHMEGSMNGHEFEIEEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDY KLSFPFGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVMQKKTMGWEASSERMPEDGALKGEIK QRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIIVEQYERAEGRHSTGGMDELYKARGSAGSATT MVSKGEEDNMAIKEFMRFKVHMEGSMNGHEFEIEEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVK HPADIPDYKLSFPFGFKWERVMNFEDGGVVTVDQSSLDQGEFIYKVKLRGTNFPDGPVMQKKTMGWEASSERMP DALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIIVEQYERAEGRHSTGGMDELYK SGSGATNFSLLKQAGDVEENPG <...> PMKLSLVAAMLLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKCT SEGEKPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGSKTFINHTQGI P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N K D E L	P l e n t i	Y G 6 3
ePKA- KTR1.2 /tdTom ato.2a .ER- mTagBF P2	MEMPEEPANSGHSLPPVYIYSPEYVSI C D S L V K V P K R A S M V N E D E A P S K R R A S L G V S S R L E R L T L Q S S G A P V S K G E E V I KEFMRFKVHMEGSMNGHEFEIEEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLS FPEGFKWERVMNFEDGGLVTVTQDSSLQDGTLYIYKVKMRGTNFPDGPVMQKKTMGWEASTERLYPRDGLKGEIHQAL LKDGGHYLVFVKTIYMAKKPVQLPGYVVDTKLDITSHNEDYTIIVEQYERSEGRHHLFLGHGTGSGSGTASSEDN NMAVIKEFMRFKVHMEGSMNGHEFEIEEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIP DYKLSFPFGFKWERVMNFEDGGLVTVTQDSSLHDTLYIYKVKMRGTNFPDGPVMQKKTMGWEASTERLYPRDGLK GEIHQALKLDGGHYLVFVKTIYMAKKPVQLPGYVVDTKLDITSHNEDYTIIVEQYERSEGRHHLFLYGMDELYKASG SGATNFSLLKQAGDVEENPG <...> PMKLSLVAAMLLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKCT SEGEKPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGSKTFINHTQGI P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N K D E L	P l e n t i	Y G 5 0
eERK- KTR1.2 /emiRF P670.2 a.ER- mTagBF P2	MKGRKPRDLEPLSPSLLGGQPPERTPGSGTSSGLQAPGPALSPSKRSGLLEDDEPATPSKPKRTPPSVSSRLERLTLQSS FQFPGSAPMAEGSVARQPDLLTCEHEEIHLAGSIQPHGALLVVEHSHRVIQASANAEEFLNLGSLVGLPAIEIDGDL L I K I L P H L D P T A E G M P V A V R C R I G N P S T E Y C G L M H R P E G G L I E L E R A G P S I D L S G T L A P A L E R I N T A G S L R A L C D D T V L L F Q Q C T G Y D R V M V Y R F D E Q G H L V F S E C H V P G L E S Y F G N R Y P S S T V P Q M A R Q L Y V R Q R V R V L V D V T Y Q V P L E P R L S P L T G R D L D M S G C F L R S M S P C H L Q F L K D M G V R A T L A V S L V V G G K L W L G V V C H H Y L P R F I R F E L R A I C K R L A E R I A T R I T A L E S L Y K A S G S G A T N F S L L K Q A G D V E E N P G < . . . > P M K L S L V A A M L L L L S A A R A V S K G E E L I K E N M H M K L Y M E G T V D N H H F K C T S E G E K P Y E G T Q T M R I K V V E G G P L P F A F D I L A T S F L Y G S K T F I N H T Q G I P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N K D E L	P l e n t i	Y G 6
ePKA- KTR1.4 /tdTom ato.2a .ER- mTagBF P2	MEMPEEPANSGHSLPPVYIYSPEYVSI C D S L V K V P K R A S M V N E D E A P A K R R A S L G V S S R L E R L T L Q S S G A P V S K G E E V I IKEFMRFKVHMEGSMNGHEFEIEEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLS FPEGFKWERVMNFEDGGLVTVTQDSSLQDGTLYIYKVKMRGTNFPDGPVMQKKTMGWEASTERLYPRDGLKGEIHQAL KLKDGGHYLVFVKTIYMAKKPVQLPGYVVDTKLDITSHNEDYTIIVEQYERSEGRHHLFLGHGTGSGSGTASSED NNMAVIKEFMRFKVHMEGSMNGHEFEIEEGEGRPEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIP DYKLSFPFGFKWERVMNFEDGGLVTVTQDSSLHDTLYIYKVKMRGTNFPDGPVMQKKTMGWEASTERLYPRDGLK GEIHQALKLDGGHYLVFVKTIYMAKKPVQLPGYVVDTKLDITSHNEDYTIIVEQYERSEGRHHLFLYGMDELYKASG SGATNFSLLKQAGDVEENPG <...> PMKLSLVAAMLLLLSAARAVSKGEELIKENMHMKLYMEGTVDNHHFKCTSEGE KPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGSKTFINHTQGI P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N K D E L	P l e n t i	Y G 1 1 5
PKA- KTR2/m Cherry .2a.H2 B-	MVLRASLGKRRASLGKRRASLGVDQLRLERLQIDE GAPVSKGEEDNMAIKEFMRFKVHMEGSMNGHEFEIEEGEGR PEYEGTQAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPFGFKWERVMNFEDGGVVTVDQSSLDQ GEFIYKVKLRGTNFPDGPVMQKKTMGWEASSERMPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAY NVNIKLDITSHNEDYTIIVEQYERAEGRHSTGGMDELYKASGATNFSLLKQAGDVEENPG <...> PSPAMPEAKS GAPAPKKGSKAVTKAQKGGKRRKRKRKESYSIYVYKVLQVHPDGTGISSKAMGIMNSFVNDIFERIAGEASRLAHYK	P C	S 7 3 7

<p>mTagBF P2</p>	<p>RSTITSREIQTAVRLLLPGLAKHAVSEGTKAITKYTSAKDPGGSSRVSKGEELIKENMHMKLYMEGTVDNHHFKCTS EGEGKPYEGTQTMRIKVVVEGGPLPFAFDILATSFLYGSKTFINHTQGI P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N G M D E L Y K G R S P G L N G G S G A T N F S L L K Q A G D V E E N P G</p>		
<p>PKA-KTR2/t dCherry.2a.H 2B-mTagBF P2</p>	<p>MVLRASLGRASLGRASLGVQDLRLRLQIDEGAPVSKGEEDNMAI I K E F M R F K V H M E G S V N G H E F E I E G E G E G R P Y E G T Q T A K L K V T K G G P L P F A W D I L S P Q F M Y G S K A Y V K H P A D I P D Y L K L S F P E G F K W E R V M N F E D G G V V T V T Q D S S L Q D G E F I Y K V K L R G T N F P S D G P V M Q K K T M G W E A S S E R M Y P E D G A L K G E I K Q R L K L K D G G H Y D A E V K T T Y K A K K P V Q L P G A Y N V N I K L D I T S H N E D Y T I V E Q Y E R A E G R H S T G G M D E L Y K A R G S A G S A T T M V S K G E E D N M A I I K E F M R F K V H M E G S V N G H E F E I E G E G E G R P Y E G T Q T A K L K V T K G G P L P F A W D I L S P Q F M Y G S K A Y V K H P A D I P D Y L K L S F P E G F K W E R V M N F E D G G V V T V T Q D S S L Q D G E F I Y K V K L R G T N F P S D G P V M Q K K T M G W E A S S E R M Y P E D G A L K G E I K Q R L K L K D G G H Y D A E V K T T Y K A K K P V Q L P G A Y N V N I K L D I T S H N E D Y T I V E Q Y E R A E G R H S T G G M D E L Y K A S G S G A T N F S L L K Q A G D V E E N P G < . . . > P S P A M P E P A K S A P A P K K G S K K A V T K A Q K K G G K R K R S R K E S Y S I Y V Y K V L K Q V H P D T G I S S K A M G I M N S F V N D I F E R I A G E A S R L A H Y N K R S T I T S R E I Q T A V R L L P G L A K H A V S E G T K A I T K Y T S A K D P G G S S R V S K G E E L I K E N M H M K L Y M E G T V D N H H F K C T S E G E G K P Y E G T Q T M R I K V V E G G P L P F A F D I L A T S F L Y G S K T F I N H T Q G I P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N G M D E L Y K G R S P G L N G G S G A T N F S L L K Q A G D V E E N P G</p>	<p>P C</p>	<p>S 7 3 8</p>
<p>PKA-KTR3/m Cherry.2a.ER -mTagBF P2</p>	<p>MEMPEEPANSGHSLPPVYIYSPEYSIFDSLKVKRNPTVVNEDEAPSKRKRSLPISSRLRLTLQSSGAPVSKGEEDNM A I I K E F M R F K V H M E G S V N G H E F E I E G E G E G R P Y E G T Q T A K L K V T K G G P L P F A W D I L S P Q F M Y G S K A Y V K H P A D I P D Y L K L S F P E G F K W E R V M N F E D G G V V T V T Q D S S L Q D G E F I Y K V K L R G T N F P S D G P V M Q K K T M G W E A S S E R M Y P E D G A L K G E I K Q R L K L K D G G H Y D A E V K T T Y K A K K P V Q L P G A Y N V N I K L D I T S H N E D Y T I V E Q Y E R A E G R H S T G G M D E L Y K A S G S G A T N F S L L K Q A G D V E E N P G < . . . > P M K L S L V A A M L L L S A A R A V S K G E E L I K E N M H M K L Y M E G T V D N H H F K C T S E G E G K P Y E G T Q T M R I K V V E G G P L P F A F D I L A T S F L Y G S K T F I N H T Q G I P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N K D E L</p>	<p>P L e n t i</p>	<p>Y G 6 9</p>
<p>PKA-KTR3/t dCherry.2a.ER -mTagBF P2</p>	<p>MEMPEEPANSGHSLPPVYIYSPEYSIFDSLKVKRNPTVVNEDEAPSKRKRSLPISSRLRLTLQSSGAPVSKGEEDNM A I I K E F M R F K V H M E G S V N G H E F E I E G E G E G R P Y E G T Q T A K L K V T K G G P L P F A W D I L S P Q F M Y G S K A Y V K H P A D I P D Y L K L S F P E G F K W E R V M N F E D G G V V T V T Q D S S L Q D G E F I Y K V K L R G T N F P S D G P V M Q K K T M G W E A S S E R M Y P E D G A L K G E I K Q R L K L K D G G H Y D A E V K T T Y K A K K P V Q L P G A Y N V N I K L D I T S H N E D Y T I V E Q Y E R A E G R H S T G G M D E L Y K A R G S A G S A T T M V S K G E E D N M A I I K E F M R F K V H M E G S V N G H E F E I E G E G E G R P Y E G T Q T A K L K V T K G G P L P F A W D I L S P Q F M Y G S K A Y V K H P A D I P D Y L K L S F P E G F K W E R V M N F E D G G V V T V T Q D S S L Q D G E F I Y K V K L R G T N F P S D G P V M Q K K T M G W E A S S E R M Y P E D G A L K G E I K Q R L K L K D G G H Y D A E V K T T Y K A K K P V Q L P G A Y N V N I K L D I T S H N E D Y T I V E Q Y E R A E G R H S T G G M D E L Y K A S G S G A T N F S L L K Q A G D V E E N P G < . . . > P M K L S L V A A M L L L S A A R A V S K G E E L I K E N M H M K L Y M E G T V D N H H F K C T S E G E G K P Y E G T Q T M R I K V V E G G P L P F A F D I L A T S F L Y G S K T F I N H T Q G I P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N K D E L</p>	<p>P L e n t i</p>	<p>Y G 7 1</p>
<p>ERK-KTR1/e miRFP6 70.2a.ER -mTagBF P2</p>	<p>MKGRKPRDLELPLSPSLGGQGPERTPGSGTSSGLQAPGALSPSKRSGLEDPATPSKPRTPSVSSRLRLTLQSSFQ F P S G A P M A E G S V A R Q P D L L T C E H E E I H L A G S I Q P H G A L L V V S E H D H R V I Q A S A N A E F L N L G S V L G V P L A E I D G D L L I K I L P H L D P T A E G M P V A V R C R I G N P S T E Y C G L M H R P P E G G L I E I E L E R A G P S I D L S G T L A P A L E R I R T A G S L R A L C D D T V L L F Q Q C T G Y D R V M V Y R F D E Q G H G L V F S E C H V P G L E S Y F G N R Y P S T V P Q M A R Q L Y V R Q R V R V L V D V T Y Q P V P L E P R L S P L T G R D L D M S G C F L R S M S P C H L Q F L K D M G V R A T L A V S L V V G G K L W L V V C H H Y L P R F I R F E L R A I C K R L A E R I A T R I T A L E S L Y K A S G S G A T N F S L L K Q A G D V E E N P G < . . . > P M K L S L V A A M L L L S A A R A V S K G E E L I K E N M H M K L Y M E G T V D N H H F K C T S E G E G K P Y E G T Q T M R I K V V E G G P L P F A F D I L A T S F L Y G S K T F I N H T Q G I P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N A K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L N K D E L</p>	<p>P L e n t i</p>	<p>Y G 4 5</p>

Table S2. List of plasmid numbers and the ORF they express.

Name	Description (ORF expressed)	vector backbone	promoter
S739	PKA-KTR1-mCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S777	mCherry-PKA-KTR2 2a H2B-mTagBFP2	pC (plasmid)	CMV
S740	PKA-KTR1-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S738	PKA-KTR2-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S741	ePKA-KTR1.1-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S467	ePKA-KTR1.2-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S514	ePKA-KTR1.3-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S515	ePKA-KTR1.4-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S742	ePKA-KTR1.5-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
YG63	ePKA-KTR1.2-tdCherry 2a SS-mTagBFP2-KDEL	pLenti (lentiviral vector)	CMV
S381	ePKA-KTR1.2-tdCherry 2a 3xNLS-mTagBFP2	pC (plasmid)	CMV
YG61	ePKA-KTR1.2-mCherry 2a SS-mTagBFP2-KDEL	pLenti (lentiviral vector)	CMV
YG65	ePKA-KTR1.4-mCherry 2a SS-mTagBFP2-KDEL	Lentiviral	CMV
YG67	ePKA-KTR1.4-tdCherry 2a SS-mTagBFP2-KDEL	Lentiviral	CMV
YG8	ePKA-KTR1.2-mScarlet 2a SS-mTagBFP2-KDEL	Lentiviral	CMV
YG18	ePKA-KTR1.2-mScarlet-BCR 2a SS-mTagBFP2-KDEL	Lentiviral	CMV
S468	ERK-KTR1-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S712	eERK-KTR1.1-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S713	eERK-KTR1.2-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S765	eERK-KTR1.3-tdCherry 2a H2B-mTagBFP2	pC (plasmid)	CMV
S940	eERK-KTR1.2-mScarlet 2a SS-mTagBFP2-KDEL	Lentiviral	CMV
YG21	eERK-KTR1.2-mScarlet-BCR 2a SS-mTagBFP2-KDEL	Lentiviral	CMV
YG6	eERK-KTR1.2-emiRFP670 2a SS-mTagBFP2-KDEL	pLenti (lentiviral vector)	CMV
YG45	ERK-KTR1-emiRFP670 2a SS-mTagBFP2-KDEL	pLenti (lentiviral vector)	CMV
YG50	ePKA-KTR1.2-tdTomato 2a SS-mTagBFP2-KDEL	pLenti (lentiviral vector)	CMV
YG114	PKA-KTR3-tdTomato 2a SS-mTagBFP2-KDEL	pLenti (lentiviral vector)	CMV
YG115	ePKA-KTR1.4-tdTomato 2a SS-mTagBFP2-KDEL	pLenti (lentiviral vector)	CMV
S1137	jGCAMP8s	Lentiviral	CMV
YG160	eERK-KTR1.2 (mutated)-emiRFP670 2a SS-mTagBFP2-KDEL	pLenti (lentiviral vector)	CMV

Structured Methods - Reagents and Tools Table

Instructions: Please complete the relevant fields below, adding rows as needed. The following page provides an example of a completed table and additional instruction for entering your data in the table.

Reagent/Resource	Reference or Source	Identifier or Catalog Number
Experimental Models		
HEK-293 cells (H. sapiens)	ATCC	CRL-1573
Dorsal root ganglion neurons	C57BL/6 (Jackson Lab)	000664
Recombinant DNA		
psPAX2	Addgene	12260
VSV.G	Addgene	14888
PKA-KTR1/tdCherry.2a.H2B-mTagBFP2	This study	N/A
PKA-KTR1/mCherry.2a.H2B-mTagBFP2	This study	N/A
ePKA-KTR1.1/tdCherry.2a.H2B-mTagBFP2	This study	N/A
ePKA-KTR1.2/tdCherry.2a.H2B-mTagBFP2	This study	N/A
ePKA-KTR1.3/tdCherry.2a.H2B-mTagBFP2	This study	N/A
ePKA-KTR1.4/tdCherry.2a.H2B-mTagBFP2	This study	N/A
ePKA-KTR1.5/tdCherry.2a.H2B-mTagBFP2	This study	N/A
ePKA-KTR1.2/mCherry.2a.ER-mTagBFP2	This study	N/A
ePKA-KTR1.4/mCherry.2a.ER-mTagBFP2	This study	N/A
ePKA-KTR1.4/tdCherry.2a.ER-mTagBFP2	This study	N/A

ePKA-KTR1.2/mScarlet- l.2a.ER-mTagBFP2	This study	N/A
ePKA-KTR1.2/mScarlet- l/BCR.2a.ER-mTagBFP2	This study	N/A
ERK-KTR1/tdCherry.2a.H2B- mTagBFP2	This study	N/A
eERK- KTR1.1/tdCherry.2a.H2B- mTagBFP2	This study	N/A
eERK- KTR1.2/tdCherry.2a.H2B- mTagBFP2	This study	N/A
eERK- KTR1.3/tdCherry.2a.H2B- mTagBFP2	This study	N/A
eERK-KTR1.2/mScarlet- l.2a.ER-mTagBFP2	This study	N/A
eERK-KTR1.2/mScarlet- l/BCR.2a.ER-mTagBFP2	This study	N/A
ePKA- KTR1.2/tdCherry.2a.3xNLS- mTagBFP2	This study	N/A
ePKA- KTR1.2/tdCherry.2a.ER- mTagBFP2	This study	N/A
ePKA- KTR1.2/tdTomato.2a.ER- mTagBFP2	This study	N/A
eERK- KTR1.2/emiRFP670.2a.ER- mTagBFP2	This study	N/A
ePKA- KTR1.4/tdTomato.2a.ER- mTagBFP2	This study	N/A
PKA-KTR2/mCherry.2a.H2B- mTagBFP2	This study	N/A
PKA-KTR2/tdCherry.2a.H2B- mTagBFP2	This study	N/A
PKA-KTR3/mCherry.2a.ER- mTagBFP2	This study	N/A
PKA-KTR3/tdCherry.2a.ER- mTagBFP2	This study	N/A

ERK-KTR1/emiRFP670.2a.ER-mTagBFP2	This study	N/A
Additional plasmids and more information	This study	Table S1
Antibodies		
Rabbit anti-phospho-ERK1/2	Cell Signaling Technology	9101S
Rabbit anti-phospho-PKA R2 (Ser99)	Abcam	ab32390
Goat anti-rabbit Alexa488	Jackson ImmunoResearch	AB_2338046
Oligonucleotides and other sequence-based reagents		
Geneblocks and primers	Integrated DNA Technologies	Table S1
Chemicals, Enzymes and other reagents		
Phusion High-Fidelity DNA Polymerase	ThermoFisher	F530L
T4 DNA Ligase (5 U/ μ L)	ThermoFisher	EL0011
Petri Dishes	Falcon	351029
DMEM, high glucose	ThermoFisher	11965118
Trypsin-EDTA (0.25%), phenol red	ThermoFisher	25200114
Fetal Bovine Serum	ThermoFisher	16000044
24-well cell culture plates	Denville	1156F00
TC-treated Culture Dish (100 mm)	Corning	430167
Hanks' Balanced Salt Solution (HBSS)	ThermoFisher	14175103
96 Well Black Plate, Coverglass Bottom, CC2 Surface	ThermoFisher	160376
μ -Slide 8 Well high Glass Bottom	Ibidi	80807
μ -Slide 18 Well Glass Bottom	Ibidi	81817
A23187	Sigma-Aldrich	C7522
ATP	Sigma-Aldrich	A26209
Forskolin	Cayman Chemical	11018
H89	MedChemExpress	HY-15979A
EGF	Gibco	PHG0311L

VX-11e	SelleckChem	S7709
leptomycin B	Sigma-Aldrich	L2913
Phorbol 12-myristate 13-acetate	Sigma-Aldrich	P1585
Neurobasal™ Plus Medium	Gibco	A3582901
B-27™ Plus Supplement	Gibco	A3582801
Poly-L-lysine solution	Sigma-Aldrich	P8920-100ML
Laminin	Sigma-Aldrich	L2020
Papain, suspension	Worthington	LS003126
Bovine Serum Albumin	Sigma-Aldrich	A-9418
TM Liberase	Roche	5401119001
TL Liberase	Roche	5401020001
Pen/Strep (100X)	ThermoFisher	15140122
Lipofectamine™ 3000	ThermoFisher	L3000015
Open-Top Thinwall Ultra-Clear Tube	Beckman-Coulter	C14292
50 mL Luer-Lok™ Syringe	BD	309653
Syringe Filter (0.45 µm)	Millipore	SLHVR33RS
8-mm cover glasses	Electron Microscopy Sciences	7229608
QIAprep Spin Miniprep Kit	Qiagen	27106
Wizard® Plus Midipreps DNA Purification System	Promega	A7640
Ampicillin sodium salt	Sigma-Aldrich	A8351
Software		
GraphPad Prism 10	https://www.graphpad.com/	
SnapGene 7	https://www.snapgene.com/	
ImageJ (Fiji)	https://fiji.sc/	
NIS Elements Advanced Research v4.60	https://www.microscope.healthcare.nikon.com/products/software/nis-elements	
EVOS M7000 Cell Imaging System Software	https://www.thermofisher.com/us/en/home/technical-resources/software-downloads/evos-m7000-imaging-system-software-download.html	
Other		
EVOS M7000 Imaging System	ThermoFisher	AMF7000

EVOS Onstage Incubator	ThermoFisher	AMC2000
Optima L-90K ultracentrifuge	Beckman-Coulter	
SW-32 Ti rotor	Beckman-Coulter	
Sony MA900 Cell Sorter	Sony	