

Supplementary Information S1

Alignment of eight **SKF** sequences by ClustalW analysis. Phosphorylation site by CSK and autophosphorylation site in kinase domain are shown in bold.

P12931 SRC_HUMAN	-----MGSNKS KP-KDASQRRRSLEPAENVHGAG	28
P07947 YES_HUMAN	-----MGCIKSKENKSPAICYRPENTPEPVSTSV	29
P09769 FGR_HUMAN	-----MGCVFCKKLEPVATAKEDAGLEGDFRSYG	29
P06241 FYN_HUMAN	-----MGCVCQCKDEATKLTEERDGS LNQSSGY-	28
P08631 HCK_HUMAN	MGGRSSCEDPGCPRDEERAPRMGCMKSFKLQVGGN--TFSKTETSASPHC	48
P07948 LYN_HUMAN	-----MGCIKSKGKDSLSDGVDLKTQPVNRTER	29
P06239 LCK_HUMAN	-----MGC GCS----SHPEDDWMENIDVCENCHY	25
P51451 BLK_HUMAN	-----MGLVSSK---KPDKEKPIKEKDKGQWSPL	26
P12931 SRC_HUMAN	G--GAFPASQTSPKSPASADGHRG--PSAAFAPAAAEF--KLFGGFNSSDT	72
P07947 YES_HUMAN	SHYGAEPTTVSPCPSSSAKGTAVNFSSLSMTPFGGSSGVTFFGGASSSFS	79
P09769 FGR_HUMAN	A---ADHYGPDPT-KARPASSFAHIPNYSNFSSQ-----AINPGFLDS--	68
P06241 FYN_HUMAN	-----RYGTDPTPQHYPSTFGVTSIPNYNFHAAGGQGLTVFGGVNSSSH	72
P08631 HCK_HUMAN	P----VYVPDPTSTIKPGPNSH-----NSNTPG	72
P07948 LYN_HUMAN	T----IYVRDPTSNKQRPVPE-----SQLLP	53
P06239 LCK_HUMAN	P----IVPLDGKGTLLIRNGSE-----VRDPLV	49
P51451 BLK_HUMAN	K----VSAQDKDAPPLPPLVVF-----NHLTPP	50
P12931 SRC_HUMAN	VTSPQRAGPLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNTEGDWW	122
P07947 YES_HUMAN	VVPSSYPAGLTGGVTIFVALYDYEARTEDLSFKKGERFQIINNTEGDWW	129
P09769 FGR_HUMAN	-GTIRGVSGIG--VTLFIALYDYEARTEDDLTFTKGKGFHILNTEGDWW	115
P06241 FYN_HUMAN	TGTLRTRGGTG--VTLFVALYDYEARTEDDLSFKKGERFQILNSSEGDWW	120
P08631 HCK_HUMAN	----IREAGS--EDIIVVALYDYEAIHHEDLSFQKGDQMVVLEES-GEWW	115
P07948 LYN_HUMAN	QRFQTKDPEE--QGDIVVALYPYDGIHPDDLSTFKKGEKMKVLEEH-GEWW	100
P06239 LCK_HUMAN	TYEGSNPPASPLQDNLVIALHSYEPSHDGDLGFKEGQRLRILEQS-GEWW	98
P51451 BLK_HUMAN	PPDEHLEDK---HFVVALYDYTAMNDRDLQMLKGEKLQVLKGT-GDWW	95
P12931 SRC_HUMAN	LAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNAENPR	172
P07947 YES_HUMAN	EARSIAATGKNGYIPSNYVAPADSIQAEWYFGKMGKDAERLLLNPQNQR	179
P09769 FGR_HUMAN	EARSLSSGKTGCIPSNYVAPVDSIQAEWYFGKIGRKDAERQLLSPGNPQ	165
P06241 FYN_HUMAN	EARSLTTGETGYIPSNYVAPVDSIQAEWYFGKLRKDAERQLLSFGNPR	170
P08631 HCK_HUMAN	KARSLATRKEGYIPSNYVARVDSLETEEWFFKGISRKDAERQLLAPGNML	165
P07948 LYN_HUMAN	KAKSLLTKEGFIIPSNYVAKLNTLETEEWFFKIDTRKDAERQLLAPGNSA	150
P06239 LCK_HUMAN	KAQSLTTGQEGFIPNFVAKANSLEPEPWFKNLSRKDAERQLLAPGNTH	148
P51451 BLK_HUMAN	LARSLVTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKA	145
P12931 SRC_HUMAN	GTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSGGFYITSRTQ	222
P07947 YES_HUMAN	GIFLVRESETTKGAYSLIRDWDEIRGDNVHYKIRKLDNGGGYITTRAQ	229
P09769 FGR_HUMAN	GAFLIRESSETTKGAYSLIRDWQTRGDHVKHYKIRKLDMGGGYITTRVQ	215
P06241 FYN_HUMAN	GTFLIRESSETTKGAYSLIRDWDMDKGDHVKHYKIRKLDNGGGYITTRAQ	220
P08631 HCK_HUMAN	GSFMIRDSETTKGSYSLVRDYPDPRQDQTVKHYKIRKLDNGGGYISPRST	215
P07948 LYN_HUMAN	GAFLIRESSETLKGFSLSVRDFDPVHGDVIKHYKIRKLDNGGGYISPRIT	200
P06239 LCK_HUMAN	GSFLIRESESTAGSFSLSVRDFDQNGQEVVHYKIRKLDNGGGYISPRIT	198
P51451 BLK_HUMAN	GSFLIRESETNKGAFSLVKDVT-TQGELIKHYKIRCLDEGGYISPRIT	194
P12931 SRC_HUMAN	FNSLQQLVAYYSKHADGLCHRLTTVCPTSKPQTQGL---AKDAWEIPRES	269
P07947 YES_HUMAN	FDTLQKLVKHYTEHADGLCHRLTTVCPTVKPQTQGL---AKDAWEIPRES	276
P09769 FGR_HUMAN	FNSVQELVQHYMEVNDGLCNLLIAPCTIMKPQTGL---AKDAWEISRSS	262
P06241 FYN_HUMAN	FETLQQLVQHYSERAGLCCRLVVPCHKGMPRLTDLVSKTKDVWEIPRES	270
P08631 HCK_HUMAN	FSTLQELVDHYKKGNDGLCQKLSVPCMSKPKQKPWE---KDAWEIPRES	261
P07948 LYN_HUMAN	FPCISDMIKHYQKQADGLCRRLEKACISPKPKQKPDW---KDAWEIPRES	246
P06239 LCK_HUMAN	FPGLHELVRHYTNASDGLCTRLSRPCQTQKPKQKPDW---EDEWEVPRET	244
P51451 BLK_HUMAN	FPSLQALVQHYSKKGDGLCQRLTLPCVRPAPQNPWA---QDEWEIPRQS	240

P12931 SRC_HUMAN	LRLEVKLGGQCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLEAEQVMKK	319	
P07947 YES_HUMAN	LRLEVKLGGQCFGEVWMGTWNGTTKVAIKTLKPGTMMPEAFLEAEQIMKK	326	
P09769 FGR_HUMAN	ITLEERRLGTGCFGDVWLGTWNGSTKVAVKTLKPGTMSPKAFLEAEQVMKL	312	
P06241 FYN_HUMAN	LQLIKRLNGQCFGEVWMGTWNGNTKVAIKTLKPGTMSPEAFLEAEQIMKK	320	
P08631 HCK_HUMAN	LKLEKKLGAGQCFGEVWMATYNNKHTKVAVKTMKPGSMSVEAFLEAEANVMKT	311	
P07948 LYN_HUMAN	IKLVKRLGAGQCFGEVWMGYNNSTKVAVKTLKPGTMSVQAFLEAEANLMT	296	
P06239 LCK_HUMAN	LKLVRLGAGQCFGEVWMGYNGHTKVAVKSLKQGSMSPDFALEAEANLMKQ	294	
P51451 BLK_HUMAN	LRLVRKLGSQCFGEVWMGYKNNMKVAIKTLKEGTMSPEAFLEAEANVMA	290	
P12931 SRC_HUMAN	LRHEKLVQLYAVVSE-EPIYIVTEYMSKGSLLDFLKGETGKYLRPLQLVD	368	
P07947 YES_HUMAN	LRHDKLVPLYAVVSE-EPIYIVTEFMSKGSLLDFLKEGDKYLRPLQLVD	375	
P09769 FGR_HUMAN	LRHDKLVQLYAVVSE-EPIYIVTEFMCHGSLLDFLKNPEGQDLRLPLQLVD	361	
P06241 FYN_HUMAN	LKHKLVQLYAVVSE-EPIYIVTEYMNKGSLLDFLKDEGRALKLPNLVD	369	
P08631 HCK_HUMAN	LQHDKLVKLHAVVTK-EPIYIITEFMAKGSLLDFLKSDEGSKQPLPKLID	360	
P07948 LYN_HUMAN	LQHDKLVRLYAVVTREPIYIITEYMAKGSLLDFLKSDEGGKVLLPKLID	346	
P06239 LCK_HUMAN	LQHQRVRLYAVVTQ-EPIYIITEYMENGLVDFLKTSGIKLTINKLLD	343	
P51451 BLK_HUMAN	LQHERLVRLYAVVTK-EPIYIVTEYMARGCLLDLFLKTDEGSRLSLPLID	339	
P12931 SRC_HUMAN	MAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIEDNE	418	
P07947 YES_HUMAN	MAAQIADGMAYIERMNYIHRDLRAANILVGENLVCKIADFGLARLIEDNE	425	
P09769 FGR_HUMAN	MAAQVAEGMAYMERMNYIHRDLRAANILVGERLACKIADFGLARLIKDE	411	
P06241 FYN_HUMAN	MAAQVAAGMAYIERMNYIHRDLRSANILVGNGLICKIADFGLARLIEDNE	419	
P08631 HCK_HUMAN	FSAQIAEGMAFIEQRNYIHRDLRAANILVSASLVCKIADFGLARVIEDNE	410	
P07948 LYN_HUMAN	FSAQIAEGMAYIERKNYIHRDLRAANLVSESLMCKIADFGLARVIEDNE	396	
P06239 LCK_HUMAN	MAAQIAEGMAFIEERNYIHRDLRAANILVSDTLSCKIADFGLARLIEDNE	393	
P51451 BLK_HUMAN	MSAQIAEGMAYIERMNSIHRDLRAANILVSEALCCKIADFGLARIIDS-E	388	
P12931 SRC_HUMAN	<u>Y</u> TARQGAQKFIKWTAPEAALYGRFTIKSDVWSFGILLTELTTKGRVPYPG	468	Y419 (autophosphorylation)
P07947 YES_HUMAN	<u>Y</u> TARQGAQKFIKWTAPEAALYGRFTIKSDVWSFGILQTELVTKGRVPYPG	475	Y426 (autophosphorylation)
P09769 FGR_HUMAN	<u>Y</u> NPQQGSFKFIKWTAPEAALFGRFTIKSDVWSFGILLTELITKGRIPYPG	461	Y412 (autophosphorylation)
P06241 FYN_HUMAN	<u>Y</u> TARQGAQKFIKWTAPEAALYGRFTIKSDVWSFGILLTELVTKGRVPYPG	469	Y420 (autophosphorylation)
P08631 HCK_HUMAN	<u>Y</u> TAREGAQKFIKWTAPEAINFGSFTIKSDVWSFGILLMEIVTYGRIPYPG	460	Y411 (autophosphorylation)
P07948 LYN_HUMAN	<u>Y</u> TAREGAQKFIKWTAPEAINFGCFTIKSDVWSFGILLYEIVTYGKIPYPG	446	Y397 (autophosphorylation)
P06239 LCK_HUMAN	<u>Y</u> TAREGAQKFIKWTAPEAINYGTFTIKSDVWSFGILLTEIVTHGRIPYPG	443	Y394 (autophosphorylation)
P51451 BLK_HUMAN	<u>Y</u> TAQEGAKFIKWTAPEAIHFVFTIKADVWSFGVLLMEVVTYGRVPYPG	438	Y389 (autophosphorylation)
P12931 SRC_HUMAN	MVNREVLDQVERGYRMPCCPPECPESLHD-LMCQCWRKEPEERPTFEYLQA	517	
P07947 YES_HUMAN	MVNREVLEQVERGYRMPCCPGCPESLHE-LMNLCKWKDPDERPTFEYIQS	524	
P09769 FGR_HUMAN	MNKREVLEQVEQGYHMPCCPGCPASLYE-AMEQTWRLDPEERPTFEYLQS	510	
P06241 FYN_HUMAN	MNNREVLEQVERGYRMPCCQDCPISLHE-LMIHCWKDPPEERPTFEYLQS	518	
P08631 HCK_HUMAN	MSNPEVIRALERGYRMPRENCPEELYN-IMMRCWKNRPEERPTFEYIQS	509	
P07948 LYN_HUMAN	RTNADVMTALSQGYRMPRVENCPEELYD-IMKMCWKEKAEERPTFDYLQS	495	
P06239 LCK_HUMAN	MTNPEVIQNLERGYRMPVDPNCPEELYQ-LMRLCWKERPEDRPTFDYLRS	492	
P51451 BLK_HUMAN	MSNPEVIRNLERGYRMPRPTCPPELYRGVIAECWRSRPEERPTFEFLQS	488	
P12931 SRC_HUMAN	FLEDYFTSTEPQ <u>Y</u> QPGENL	536	Y530 (Phosphorulated by CSK)
P07947 YES_HUMAN	FLEDYFTATEPQ <u>Y</u> QPGENL	543	Y537 (Phosphorulated by CSK)
P09769 FGR_HUMAN	FLEDYFTSAEPQ <u>Y</u> QPGDQT	529	Y523 (Phosphorulated by CSK)
P06241 FYN_HUMAN	FLEDYFTATEPQ <u>Y</u> QPGENL	537	Y531 (Phosphorulated by CSK)
P08631 HCK_HUMAN	VLDDFYTATESQ <u>Y</u> QQQP--	526	Y522 (Phosphorulated by CSK)
P07948 LYN_HUMAN	VLDDFYTATEGQ <u>Y</u> QQQP--	512	Y508 (Phosphorulated by CSK)
P06239 LCK_HUMAN	VLEDDFTATEGQ <u>Y</u> QQQP--	509	Y505 (Phosphorulated by CSK)
P51451 BLK_HUMAN	VLEDDFYTATERQ <u>Y</u> ELQP--	505	Y501 (Phosphorulated by CSK)

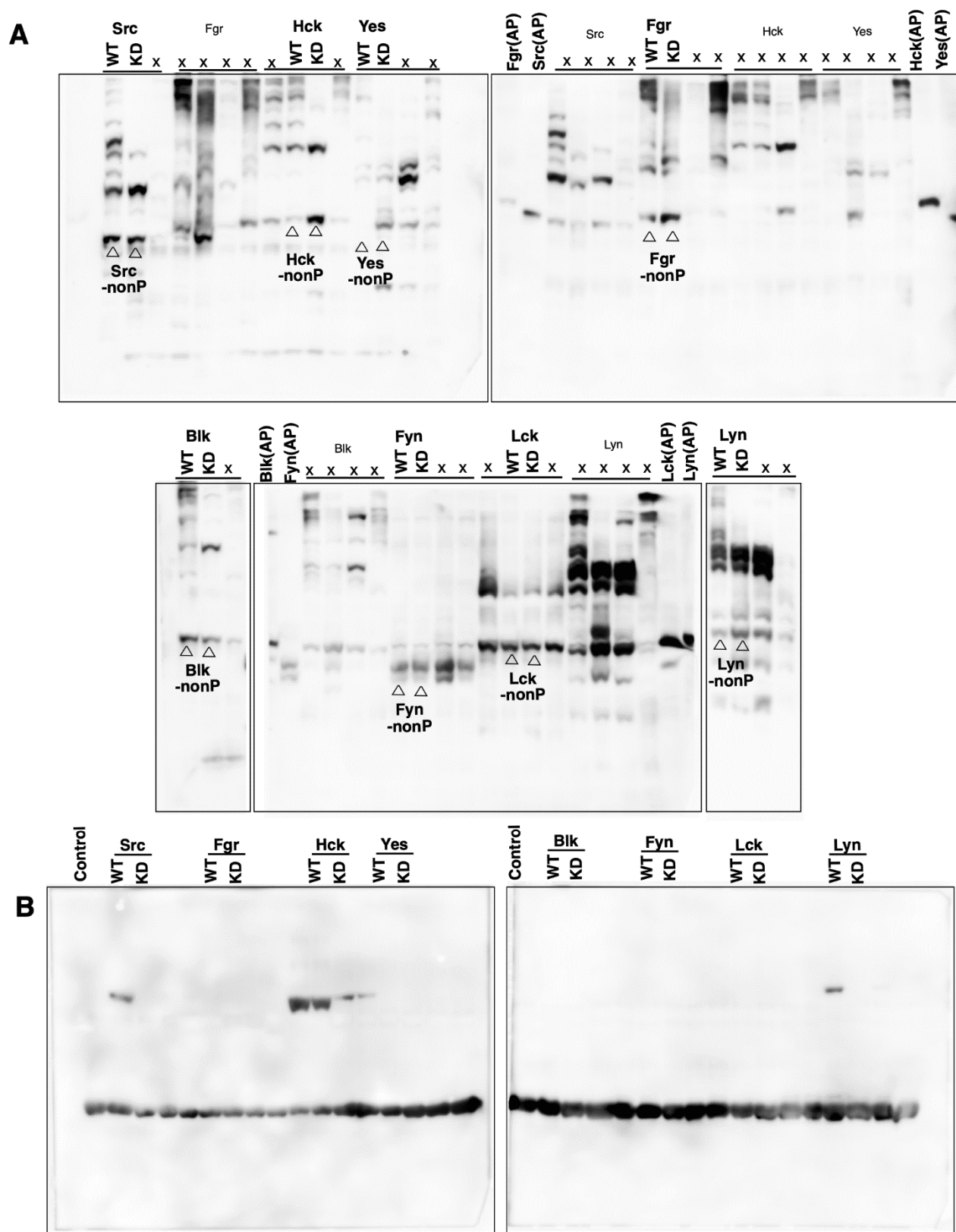
Supplementary Table S1. DNA oligomers used for plasmid construction.

Oligomer name	Sequence (5'-3')
Srctide_F	gggatccccggaattcggcgaagaaccgctgtattggagcttccggcgaaaaaaataa tcgagcgccgcgc (EcoRI, <u>Srctide</u> , <u>stop codon</u> , <u>ΔXhoI</u>)
Srctide_R	gatcgcgccgctcga ttatTTTTTTTcgccggaagctcaatacagcggttcttcgccaattccggggatccc (<u>ΔXhoI</u> , <u>stop codon</u> , <u>Srctide</u> , EcoRI)
pGEX-6P-1_EcoRI	gaattccggggatcccaggg (EcoRI)
pGEX-6P-1_ΔXhoI	tcgagcgccgcgcgcgtgac (ΔXhoI)
GST Srctide_pCDF1b_F	caagagtcggatccatgcccctatactaggta (BamHI, GST)
GSTSrctide_pCDF1b_R	ttctttaccagactcttattTTTTTTTggcgaacg (XhoI, Srctide)
pCDF1b_BamHI	ggatccggactctgtgctc (BamHI)
pCDF1b_XhoI	gagctctgtaagaacacgc (XhoI)
pET21a_Src_F	atgggtcgcggatccatgggtagcaacaagagc (BamHI, <u>start codon</u>)
pET21a_Src_R	gtggtggtgctcgaggaggttctccccgggctg (XhoI)
pET21a_Fgr_F	atgggtcgcggatccatgggctgtgtgtctgc (BamHI, <u>start codon</u>)
pET21a_Fgr_R	gtggtggtgctcgagtgctgatccccgggctg (XhoI)
pET21a_Hck F	atgggtcgcggatccatgggctgtgtgtctgc (BamHI, <u>start codon</u>)
pET21a_Hck R	gtggtggtgctcgagtggtgctgtgtgtgactg (XhoI)
pET21a_Yes_F	atgggtcgcggatccatgggctgcattaaaagt (BamHI, <u>start codon</u>)
pET21a_Yes_R	gtggtggtgctcgagtaaatttctctggctg (XhoI)
pET21a_Blκ_F	atgggtcgcggatccatgggctggttaagtagc (BamHI, <u>start codon</u>)
pET21a_Blκ_R	gtggtggtgctcgaggggctgcagctgtactg (XhoI)
pET21a_Fyn_F	atgggtcgcggatccatgggctgtgtgcaatgt (BamHI, <u>start codon</u>)
pET21a_Fyn_R	gtggtggtgctcgagcaggtttcaccaggttg (XhoI)
pET21a_Lck_F	atgggtcgcggatccatgggctgtgtgtgcagc (BamHI, <u>start codon</u>)
pET21a_Lck_R	gtggtggtgctcgagaggctgaggctgtactg (XhoI)
pET21a_Lyn_F	atgggtcgcggatccatgggatgtataaaatca (BamHI, <u>start codon</u>)
pET21a_Lyn_R	gtggtggtgctcgagaggctgctgtgtgtattg (XhoI)
pET21a_BamHI	ggatccgcgacccatttgct (BamHI)
pET21a_XhoI	ctcgagcaccaccaccacca (XhoI)
pcDNA3.1_Src_F	gctggatatctgcagaattcatgggtagcaacaagagcaag (EcoRI, <u>start codon</u>)
pcDNA3.1_Src_R	ttggtaccgagctcgatcctcacttatcgtcgtcatccttgtaatcagggttctccccgggctg (BamHI, <u>stop codon</u> , FLAG)
pcDNA3.1_Lck_F	gctggatatctgcagaattcatgggctgtggctgcagctca (EcoRI, <u>start codon</u>)
pcDNA3.1_Lck_R	ttggtaccgagctcgatcctcacttatcgtcgtcatccttgtaatcagggtgaggctgtgtactg (BamHI, <u>stop codon</u> , FLAG)
pcDNA3.1_Hck_F	gctggatatctgcagaattcatggggggcgctcaagctgc (EcoRI, <u>start codon</u>)
pcDNA3.1_Hck_R	ttggtaccgagctcgatcctcacttatcgtcgtcatccttgtaatcagggtgctgtgtgtactg

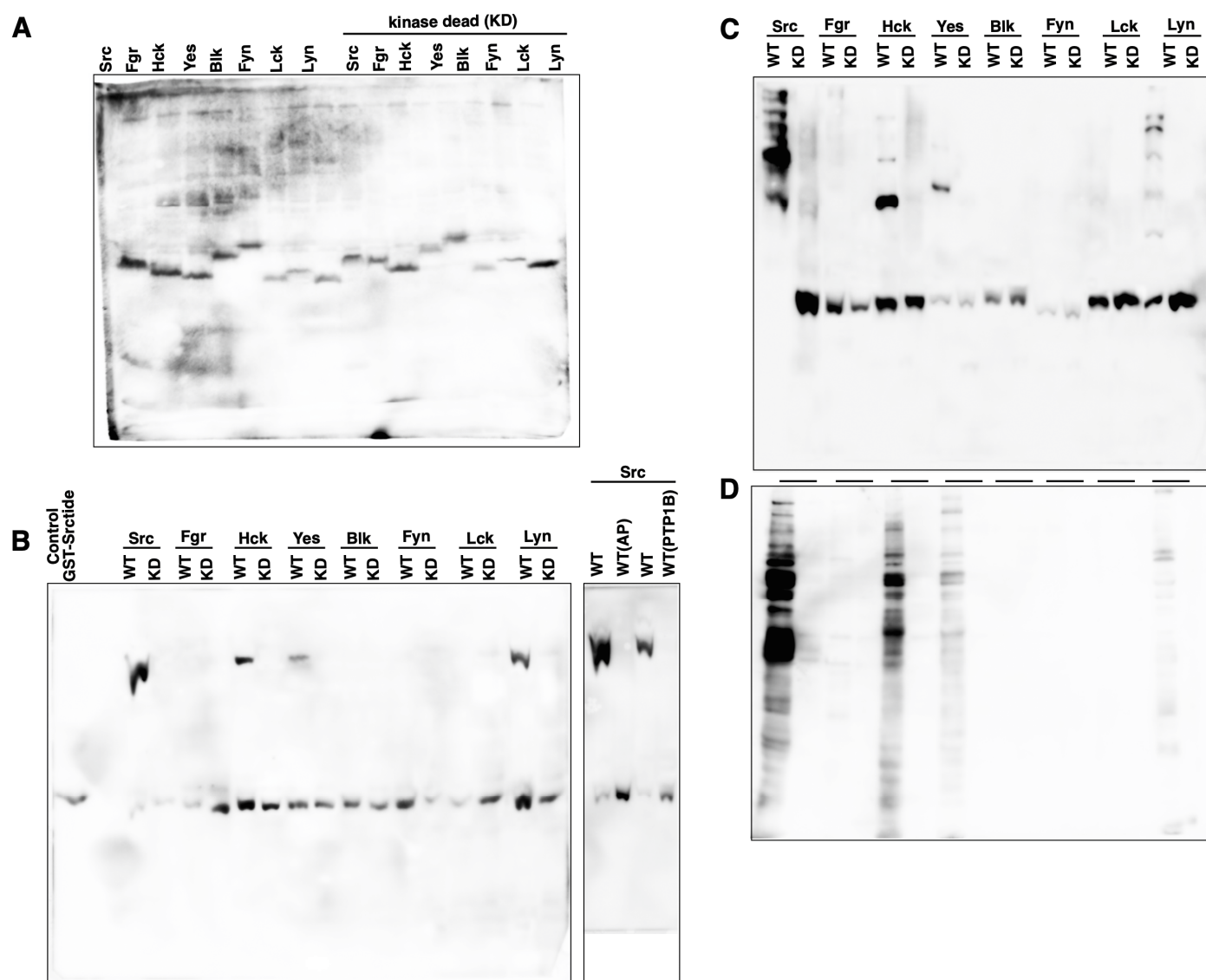
	(<u>BamHI</u> , <u>stop codon</u> , <u>FLAG</u>)
pcDNA3.1_Black_F	<u>gctggatattcgcagaattcatgggctggaagtagcaaa</u> (<u>EcoRI</u> , <u>start codon</u>)
pcDNA3.1_Black_R	<u>ttggtagcagctcggatcctcattatcgctgcatccttgaatcgggctgcagctcgtactg</u> (<u>BamHI</u> , <u>stop codon</u> , <u>FLAG</u>)
pcDNA3.1_BamHI	<u>ggatccgagctcggtaccaa</u> (<u>BamHI</u>)
pcDNA3.1_EcoRI	<u>gaattctgcagatattccagc</u> (<u>EcoRI</u>)
pHEK293_Yes_F	<u>ctccccgggctcgaggatccatgggctgcataaaagtaaa</u> (<u>BamHI</u> , <u>start codon</u>)
pHEK293_Yes_R	<u>tgctgcaggtcgactctagattactatcgctgcatccttgaatcctaaatttctcctggctg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pHEK293_Fyn_F	<u>ctccccgggctcgaggatccatgggctgtgtgcaatgaag</u> (<u>BamHI</u> , <u>start codon</u>)
pHEK293_Fyn_R	<u>tgctgcaggtcgactctagattactatcgctgcatccttgaatccagggtttcaccagggtg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pHEK293_Lyn_F	<u>ctccccgggctcgaggatccatgggctgtataaaatcaaaa</u> (<u>BamHI</u> , <u>start codon</u>)
pHEK293_Lyn_R	<u>tgctgcaggtcgactctagattactatcgctgcatccttgaatcaggctgctgctggtattg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pHEK293_Fgr_F	<u>ctccccgggctcgaggatccatgggctgtgtgtctgaag</u> (<u>BamHI</u> , <u>start codon</u>)
pHEK293_Fgr_R	<u>tgctgcaggtcgactctagattactatcgctgcatccttgaatcgtctgatccccgggctg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pHEK293_BamHI	<u>ggatccctcgagcccgaggag</u> (<u>BamHI</u>)
pHEK293_XbaI	<u>tctagagtcgacctgcaggca</u> (<u>XbaI</u>)
pSP64 poly(A)_Src_F	<u>aagcttgggctgcagatgggtagcaacaagagc</u> (<u>PstI</u> , <u>start codon</u>)
pSP64 poly(A)_Src_R	<u>cggggatcctctagattactatcgctgcatccttgaatcggagttctccccgggctg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pSP64 poly(A)_Fgr_F	<u>aagcttgggctgcagatgggctgtgtgtctgc</u> (<u>PstI</u> , <u>start codon</u>)
pSP64 poly(A)_Fgr_R	<u>cggggatcctctagattactatcgctgcatccttgaatcgtctgatccccgggctg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pSP64 poly(A)_Hck_F	<u>aagcttgggctgcagatgaagccaagtctc</u> (<u>PstI</u> , <u>start codon</u>)
pSP64 poly(A)_Hck_R	<u>cggggatcctctagattactatcgctgcatccttgaatcggctgctgttggtactg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pSP64 poly(A)_Yes_F	<u>aagcttgggctgcagatgggctgcataaaagt</u> (<u>PstI</u> , <u>start codon</u>)
pSP64 poly(A)_Yes_R	<u>cggggatcctctagattactatcgctgcatccttgaatcctaaatttctcctggctg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pSP64 poly(A)_Black_F	<u>aagcttgggctgcagatgggctggaagtagc</u> (<u>PstI</u> , <u>start codon</u>)
pSP64 poly(A)_Black_R	<u>cggggatcctctagattactatcgctgcatccttgaatcgggctgcagctcgtactg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pSP64 poly(A)_Fyn_F	<u>aagcttgggctgcagatgggctgtgtgcaatgt</u> (<u>PstI</u> , <u>start codon</u>)
pSP64 poly(A)_Fyn_R	<u>cggggatcctctagattactatcgctgcatccttgaatccagggtttcaccagggtg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pSP64 poly(A)_Lck_F	<u>aagcttgggctgcagatgggctgtggctgcagc</u> (<u>PstI</u> , <u>start codon</u>)
pSP64 poly(A)_Lck_R	<u>cggggatcctctagattactatcgctgcatccttgaatcaggctgaggctggtactg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pSP64 poly(A)_Lyn_F	<u>aagcttgggctgcagatgggctgtataaaatca</u> (<u>PstI</u> , <u>start codon</u>)
pSP64 poly(A)_Lyn_R	<u>cggggatcctctagattactatcgctgcatccttgaatcaggctgctgctggtattg</u> (<u>XbaI</u> , <u>stop codon</u> , <u>FLAG</u>)
pSP64 poly(A)_PstI	<u>ctgcagcccaagctgtattc</u> (<u>PstI</u>)
pSP64 poly(A)_XbaI	<u>tctagaggatccccgggcag</u> (<u>XbaI</u>)
pF25A ICE T7_Src_F	<u>tataaagcgatcgccatgggtagcaacaagagc</u> (<u>SgfI</u> , <u>start codon</u>)
pF25A ICE T7_Src_R	<u>ccgaattcgttttaaacctatcgctgcatccttgaatcggagttctccccgggctg</u> (<u>PmeI</u> , <u>stop codon</u> , <u>FLAG</u>)
pF25A ICE T7_Fgr_F	<u>tataaagcgatcgccatgggctgtgtgtctgc</u> (<u>SgfI</u> , <u>start codon</u>)

pF25A ICE T7_ Fgr_R	ccgaattcgtttaaaccttatcgtcgtcatccttgtaatctgtctgatccccgggctg (PmeI, stop codon,FLAG)
pF25A ICE T7_Hck F	tataaagcgatcgccatgaagtccaagttcctc (SgfI, start codon)
pF25A ICE T7_Hck R	ccgaattcgtttaaaccttatcgtcgtcatccttgtaatctggctgctgttggtactg (PmeI, stop codon,FLAG)
pF25A ICE T7_ Yes_F	tataaagcgatcgccatgggctgcattaaaagt (SgfI, start codon)
pF25A ICE T7_ Yes_R	ccgaattcgtttaaaccttatcgtcgtcatccttgtaatctaaatttctctggctg (PmeI, stop codon,FLAG)
pF25A ICE T7_Bl k_F	tataaagcgatcgccatgggctggtaagtagc (SgfI, start codon)
pF25A ICE T7_Bl k_R	ccgaattcgtttaaaccttatcgtcgtcatccttgtaatcgggctgcagctcgtactg (PmeI, stop codon,FLAG)
pF25A ICE T7_ Fyn_F	tataaagcgatcgccatgggctgtgtgcaatgt (SgfI, start codon)
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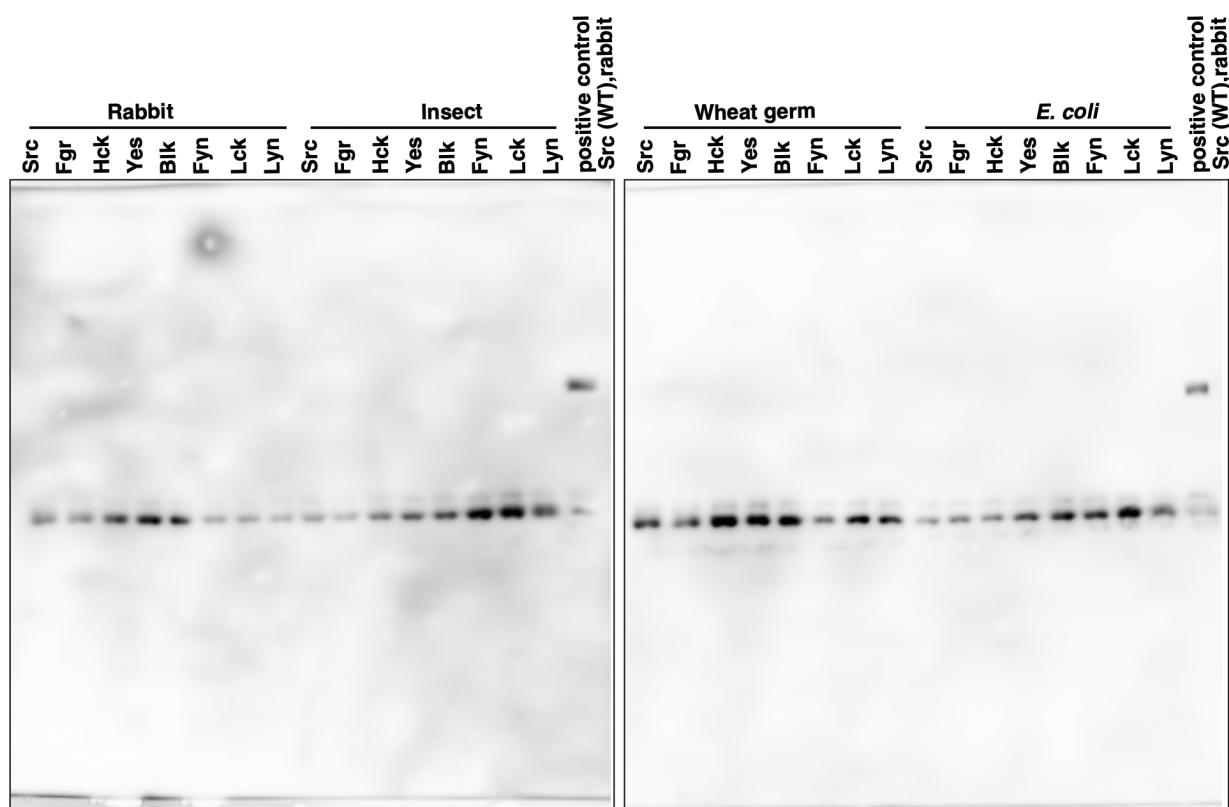
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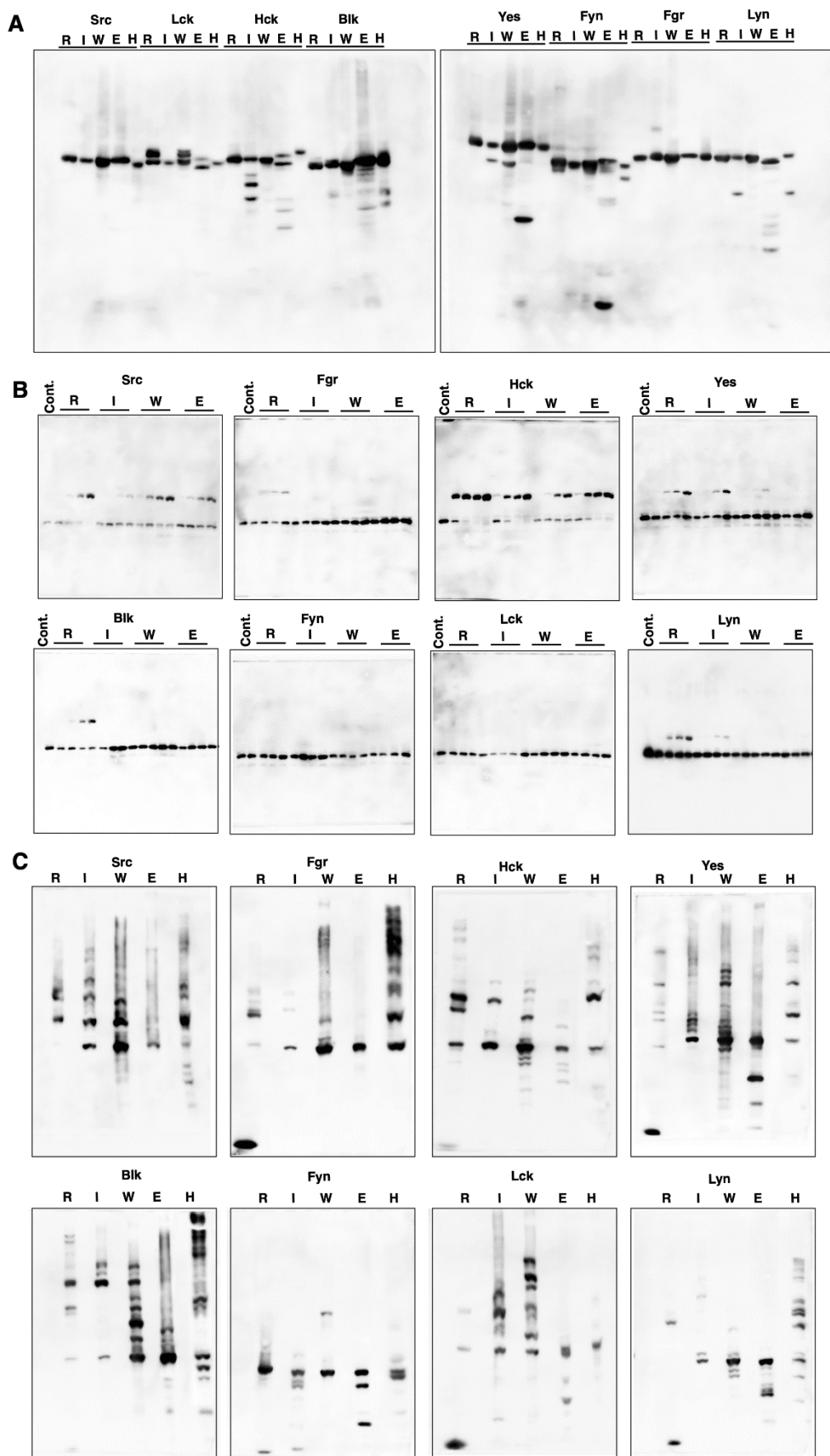
Supplementary Figure S1. Raw images used for Fig. 2. The band position of the unphosphorylated form of the kinase was assigned by the banding pattern of alkaline phosphatase (AP)-treated lysates shown in Fig. S1A. For AP treatment, 293 cells expressing the kinase were lysed with cell lysis buffer [50 mM Tris-HCl (pH8.0), 150 mM NaCl, 0.5%(w/v) sodium deoxycholate, 1.0%(v/v) Nonidet P40] and the soluble fraction of the lysate was incubated with AP in 50 mM Tris-HCl (pH 9.0) and 1 mM MgCl₂ for 3 h at 37 °C. The reactions were terminated by adding a half volume of sample-loading buffer for SDS-PAGE, consisting of 195 mM Tris-HCl (pH 6.8), 3.0% w/v SDS, 30% v/v glycerol, 15% v/v 2-sulfanylethanol, and 0.10% w/v bromophenol blue.



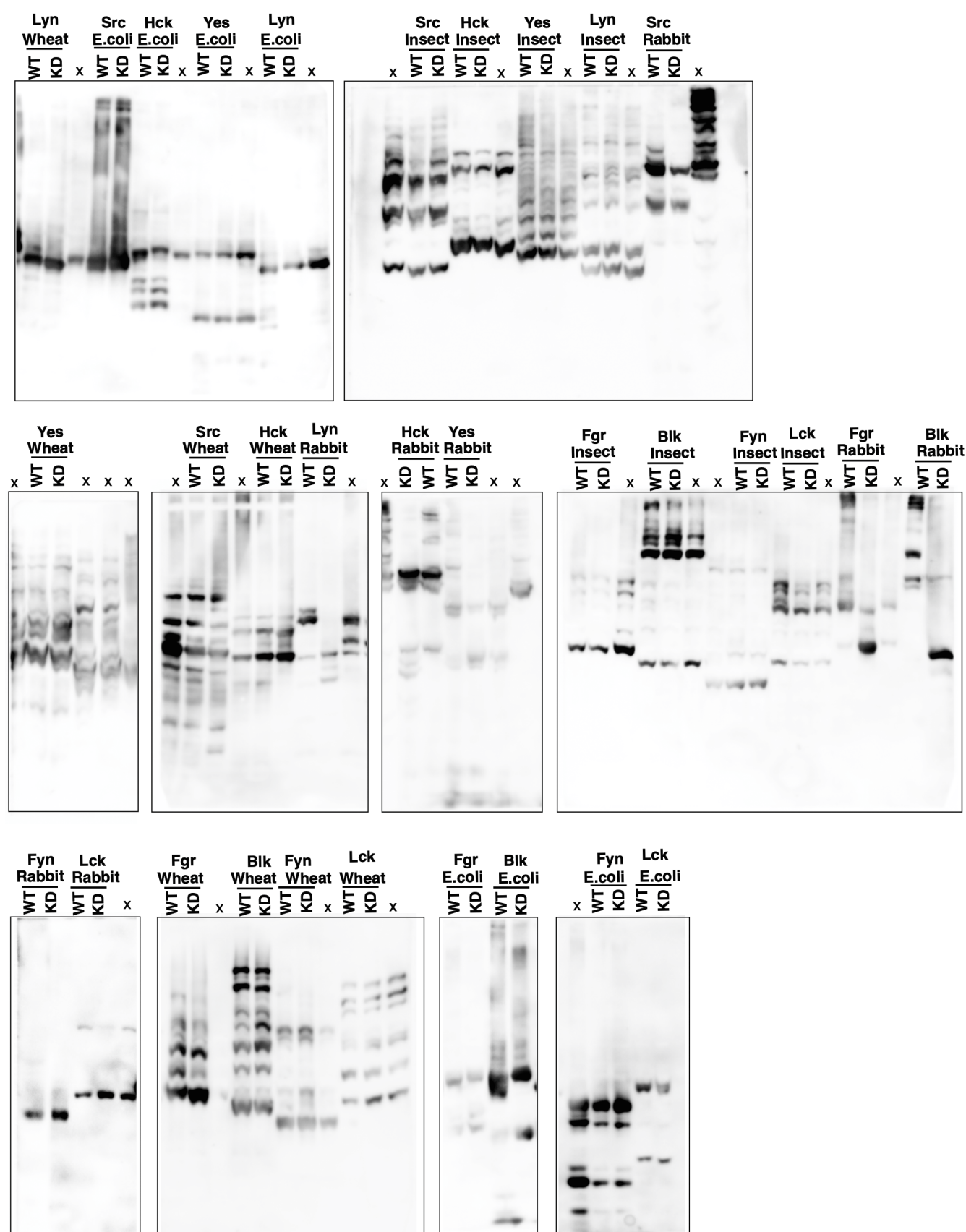
Supplementary Figure S2. Raw images used for Fig. 3. The right panel of Fig. S2B shows alkaline phosphatase (AP) and tyrosine phosphatase (PTP 1B) assays of the Src-expressed lysate. For the AP assay, the lysate was incubated with AP in 50 mM Tris-HCl (pH 9.0) and 1 mM MgCl₂ for 3 h at 37 °C. For the PTP 1B assay, the lysate was incubated with PTP1B in 10 mM Tris-HCl (pH 8.0) and 50 mM NaCl, 1 mM dithiothreitol, and 1 mM MnCl₂ for 3 h at 37 °C. The reactions were terminated by adding a half volume of sample-loading buffer for SDS-PAGE, consisting of 195 mM Tris-HCl (pH 6.8), 3.0% w/v SDS, 30% v/v glycerol, 15% v/v 2-sulfanylethanol, and 0.10% w/v bromophenol blue. The reactions were analyzed by Phos-tag SDS-PAGE (10% w/v polyacrylamide, 20 μM Zn²⁺-Phos-tag), followed by Western blotting with anti-GST antibody.



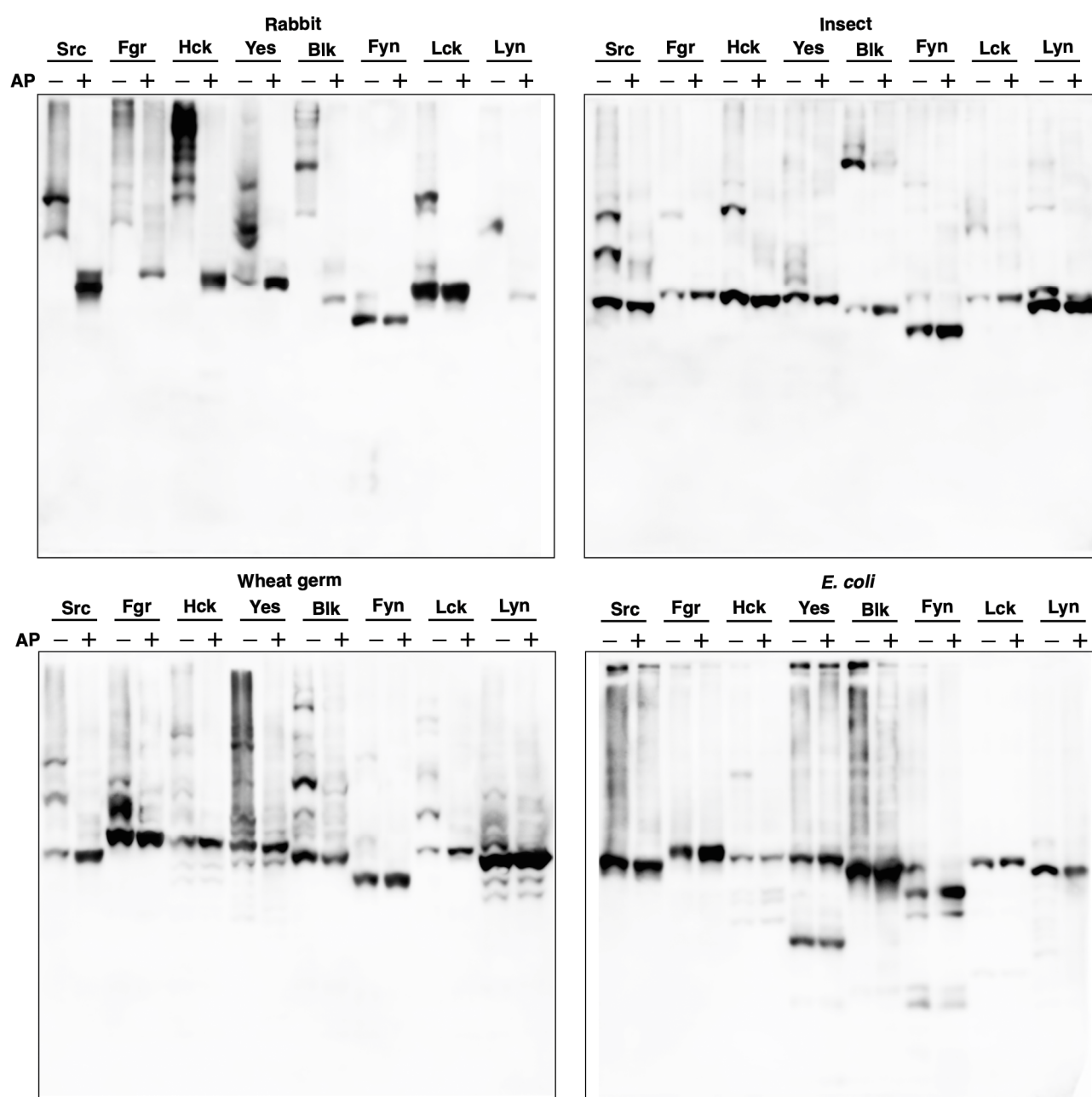
Supplementary Figure S3. In vitro GST-Srcptide phosphorylation assay of kinase-dead mutant of SFKs. Kinase-dead mutant of each SFK expressed by each cell-free protein expression system was purified by immunoprecipitation with anti-FLAG antibody-bound magnetic beads and then subjected to in vitro GST-Srcptide phosphorylation assay. Reactions were applied to Phos-tag SDS-PAGE gels (10% w/v polyacrylamide, 20 μ M Zn^{2+} -Phos-tag). The gels were analyzed by Western blotting with anti-GST antibody.



Supplementary Figure S4. Raw images used for Fig. 4.



Supplementary Figure S5. Raw images used for Fig. 5.



Supplementary Figure S6. Alkaline phosphatase (AP) assay of SFKs expressed by four types of cell-free expression systems; TnT SP6 Quick Coupled Transcription/Translation System (rabbit reticulocyte lysate system), TnT T7 Insect Cell Extract Protein Expression System, TnT SP6 High-Yield Wheat Germ Protein Expression System, S30 T7 High-Yield Protein Expression System (*E. coli* lysate system). For the AP assay, the protein expression reaction solution was incubated with AP in 50 mM Tris-HCl (pH 9.0) and 1 mM MgCl₂ for 3 h at 37 °C. The reactions were terminated by adding a half volume of sample-loading buffer for SDS-PAGE, consisting of 195 mM Tris-HCl (pH 6.8), 3.0% w/v SDS, 30% v/v glycerol, 15% v/v 2-sulfanylethanol, and 0.10% w/v bromophenol blue. The reactions were analyzed by Phos-tag SDS-PAGE (7% w/v polyacrylamide, 20 μM Zn²⁺-Phos-tag), followed by Western blotting with anti-FLAG antibody.