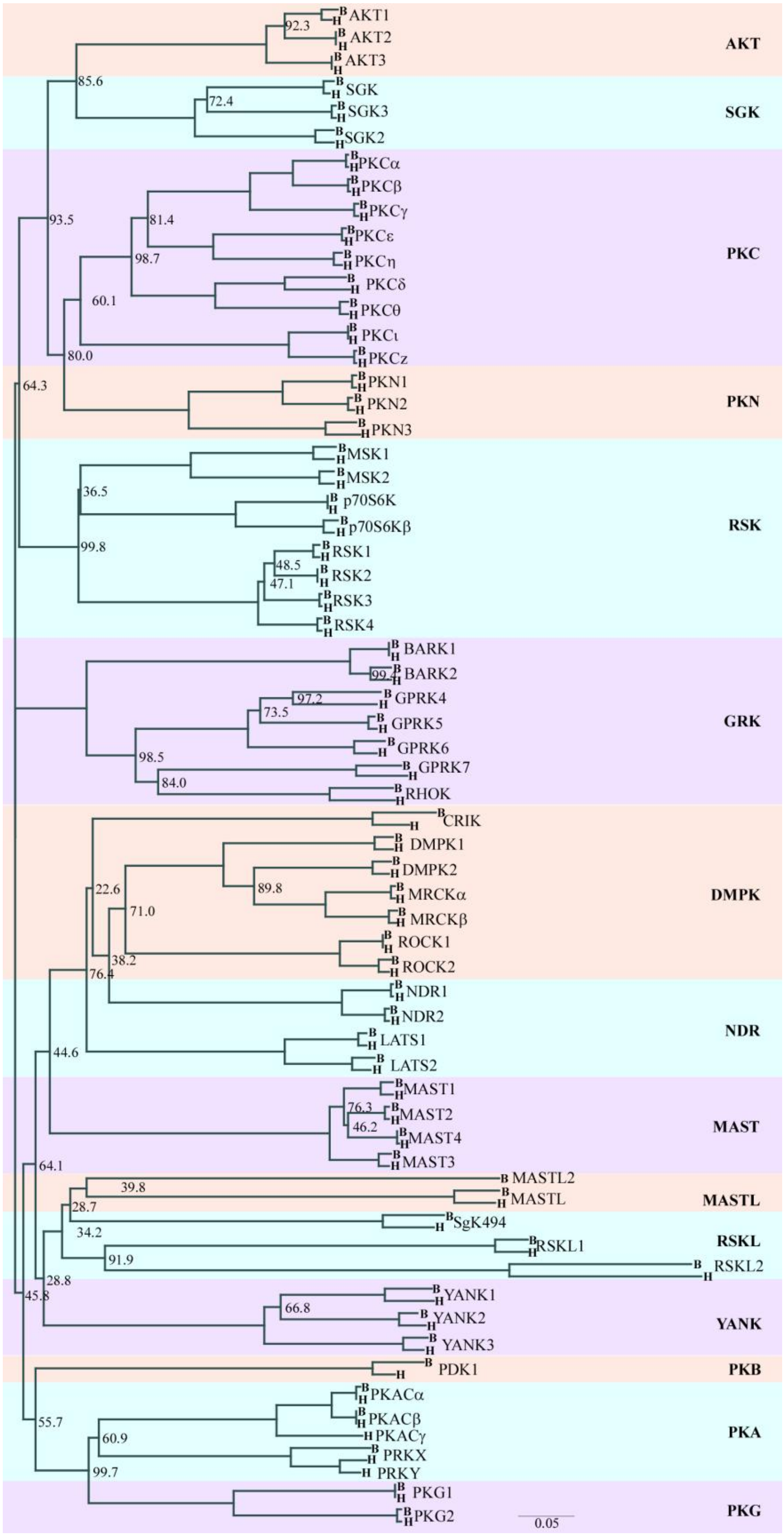
Figure Legend

Figure S1.

Phylogenetic trees of bovine and human protein kinases. The phylogenetic trees were created by aligning the catalytic domain sequences of human and bovine protein kinases using the NJ method. Each empty node has a bootstrap value of 100. H, Human; B, Bovine.

AGC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AKT2
AKT3
92.3
85.6
AKT
SGK
SGK3
SGK2
72.4
SGK
PKCα
PKCβ
PKCγ
PKCε
PKCη
PKCδ
PKCθ
PKCι
PKCz
93.5
81.4
98.7
60.1
80.0
PKC
PKN1
PKN2
PKN3
64.3
PKN
MSK1
MSK2
p70S6K
p70S6Kβ
RSK1
RSK2
RSK3
RSK4
36.5
99.8
48.5
47.1
RSK
BARK1
BARK2
GPRK4
GPRK5
GPRK6
GPRK7
RHOK
99.7
97.2
73.5
98.5
84.0
GRK
CRIK
DMPK1
DMPK2
MRCKα
MRCKβ
ROCK1
ROCK2
22.6
71.0
89.8
38.2
76.4
DMPK
NDR1
NDR2
LATS1
LATS2
44.6
NDR
MAST1
MAST2
MAST4
MAST3
76.3
46.2
MAST
MASTL2
MASTL
64.1
39.8
28.7
MASTL
SgK494
RSKL1
RSKL2
34.2
91.9
RSKL
YANK1
YANK2
YANK3
28.8
45.8
66.8
YANK
PDK1
PKB
PKACα
PKACβ
PKACγ
PRKX
PRKY
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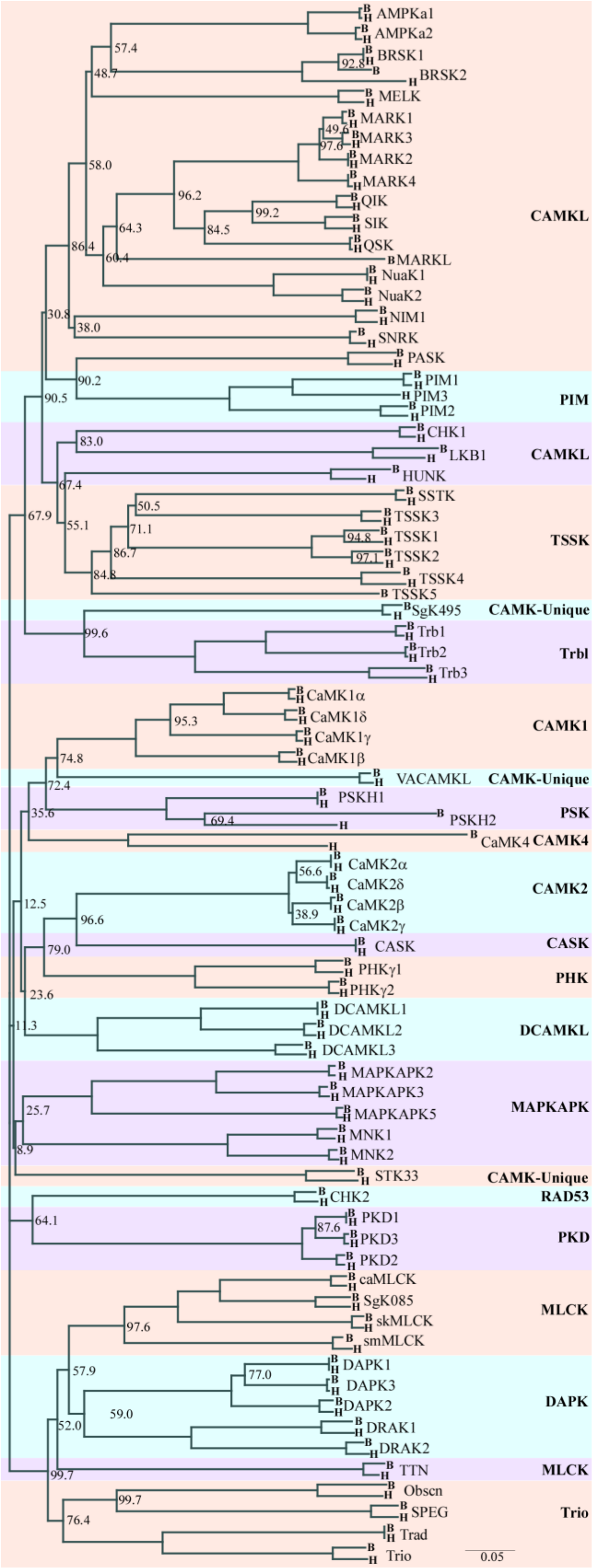
60.9
99.7
PKA
PKG1
PKG2
PKG
0.05
B
H

CAMK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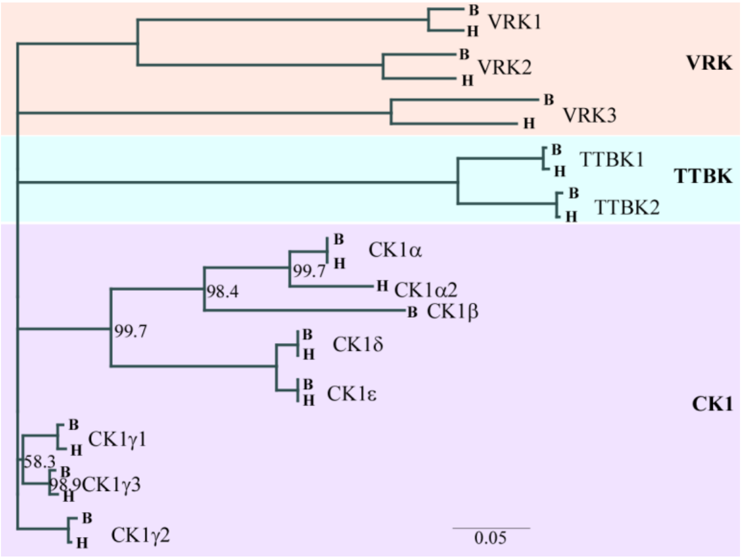
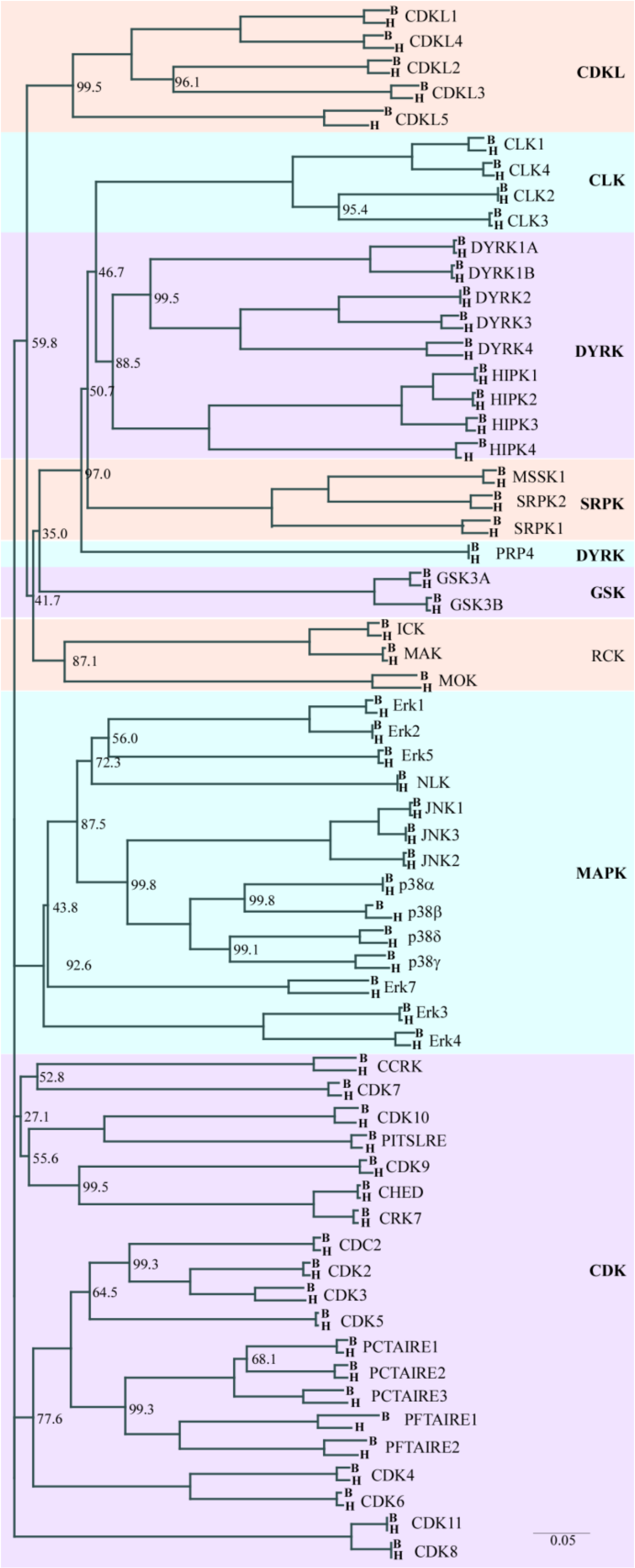
92.8
48.7
BRSK2
MELK
MARK1
49.2
MARK3
97.6
MARK2
58.0
MARK4
96.2
QIK
99.2
SIK
64.3
84.5
QSK
86.4
60.4
MARKL
NuaK1
NuaK2
30.8
NIM1
38.0
SNRK
PASK
CAMKL
90.2
PIM1
PIM3
90.5
PIM2
PIM
CHK1
83.0
LKB1
CAMKL
HUNK
67.4
SSTK
50.5
TSSK3
67.9
55.1
71.1
TSSK1
94.8
86.7
TSSK2
97.1
84.8
TSSK4
TSSK5
TSSK
SgK495
CAMK-Unique
Trb1
99.6
Trb2
Trb3
Trbl
CaMK1α
95.3
CaMK1δ
CaMK1γ
74.8
CaMK1β
CAMK1
VACAMKL
CAMK-Unique
72.4
PSKH1
35.6
PSKH2
69.4
PSK
CaMK4
CAMK4
CaMK2α
56.6
CaMK2δ
12.5
CaMK2β
38.9
96.6
CaMK2γ
CAMK2
CASK
CASK
79.0
PHKγ1
23.6
PHKγ2
PHK
DCAMKL1
11.3
DCAMKL2
DCAMKL3
DCAMKL
MAPKAPK2
MAPKAPK3
25.7
MAPKAPK5
MNK1
8.9
MNK2
MAPKAPK
STK33
CAMK-Unique
CHK2
RAD53
64.1
PKD1
87.6
PKD3
PKD2
PKD
caMLCK
SgK085
97.6
skMLCK
smMLCK
MLCK
DAPK1
57.9
77.0
DAPK3
59.0
DAPK2
DRAK1
52.0
DRAK2
DAPK
TTN
99.7
MLCK
Obscn
99.7
SPEG
76.4
Trad
Trio
0.05
Trio

CK1


B
H
VRK1
B
VRK2
H
B
H
VRK3
VRK
B
TTBK1
H
TTBK
B
TTBK2
H
B
CK1α
H
99.7
H
CK1α2
98.4
B
CK1β
99.7
B
CK1δ
H
B
CK1ε
H
CK1
B
CK1γ1
H
58.3
B
98.9
CK1γ3
H
B
CK1γ2
H
0.05

CMGC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CDKL4
CDKL2
CDKL3
CDKL5
99.5
96.1
CDKL
CLK1
CLK4
CLK2
CLK3
95.4
CLK
DYRK1A
DYRK1B
DYRK2
DYRK3
DYRK4
HIPK1
HIPK2
HIPK3
HIPK4
46.7
99.5
59.8
88.5
50.7
DYRK
MSSK1
SRPK2
SRPK1
97.0
SRPK
35.0
PRP4
DYRK
GSK3A
GSK3B
41.7
GSK
ICK
MAK
MOK
87.1
RCK
Erk1
Erk2
Erk5
NLK
56.0
72.3
JNK1
JNK3
JNK2
87.5
p38α
p38β
p38δ
p38γ
99.8
99.8
99.1
43.8
92.6
Erk7
Erk3
Erk4
MAPK
CCRK
CDK7
52.8
CDK10
PITSLRE
27.1
CDK9
CHED
CRK7
55.6
99.5
CDC2
CDK2
CDK3
CDK5
99.3
64.5
PCTAIRE1
PCTAIRE2
PCTAIRE3
68.1
PFTAIRE1
PFTAIRE2
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77.6
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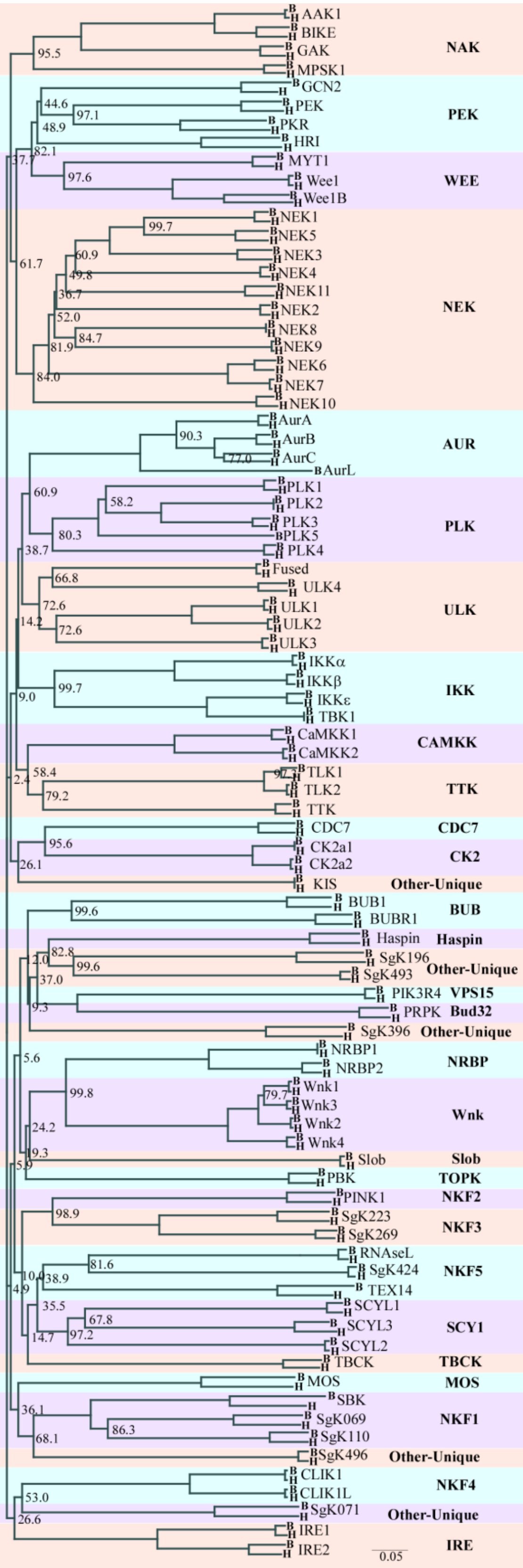
CDK6
CDK11
CDK8
CDK
B
H
0.05

Other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MPSK1
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NAK
GCN2
PEK
PKR
HRI
44.6
97.1
48.9
82.1
37.7
PEK
MYT1
Wee1
Wee1B
97.6
WEE
NEK1
NEK5
NEK3
NEK4
NEK11
NEK2
NEK8
NEK9
NEK6
NEK7
NEK10
99.7
60.9
49.8
36.7
52.0
84.7
81.9
84.0
61.7
NEK
AurA
AurB
AurC
AurL
90.3
77.0
AUR
PLK1
PLK2
PLK3
PLK5
PLK4
60.9
58.2
80.3
38.7
PLK
Fused
ULK4
ULK1
ULK2
ULK3
66.8
72.6
14.2
72.6
ULK
IKKα
IKKβ
IKKε
TBK1
99.7
9.0
IKK
CaMKK1
CaMKK2
CAMKK
TLK1
TLK2
TTK
58.4
97.3
2.4
79.2
TTK
CDC7
CDC7
CK2a1
CK2a2
95.6
26.1
CK2
KIS
Other-Unique
BUB1
BUBR1
99.6
BUB
Haspin
Haspin
SgK196
SgK493
82.8
12.0
99.6
37.0
Other-Unique
PIK3R4
VPS15
PRPK
Bud32
9.3
SgK396
Other-Unique
NRBP1
NRBP2
5.6
NRBP
Wnk1
Wnk3
Wnk2
Wnk4
99.8
79.7
24.2
Wnk
Slob
19.3
Slob
5.9
PBK
TOPK
PINK1
NKF2
SgK223
SgK269
98.9
NKF3
RNAseL
SgK424
TEX14
81.6
10.0
38.9
4.9
NKF5
SCYL1
SCYL3
SCYL2
35.5
67.8
14.7
97.2
SCY1
TBCK
TBCK
MOS
MOS
SBK
SgK069
SgK110
36.1
86.3
68.1
NKF1
SgK496
Other-Unique
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CLIK1L
NKF4
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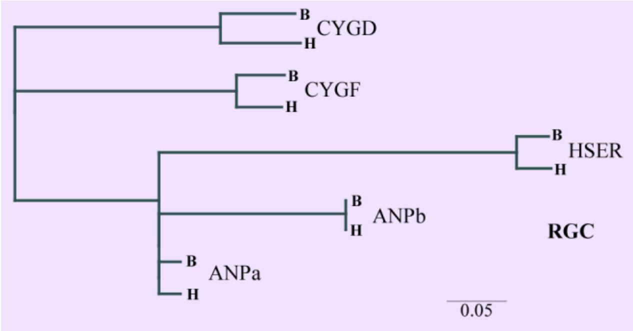
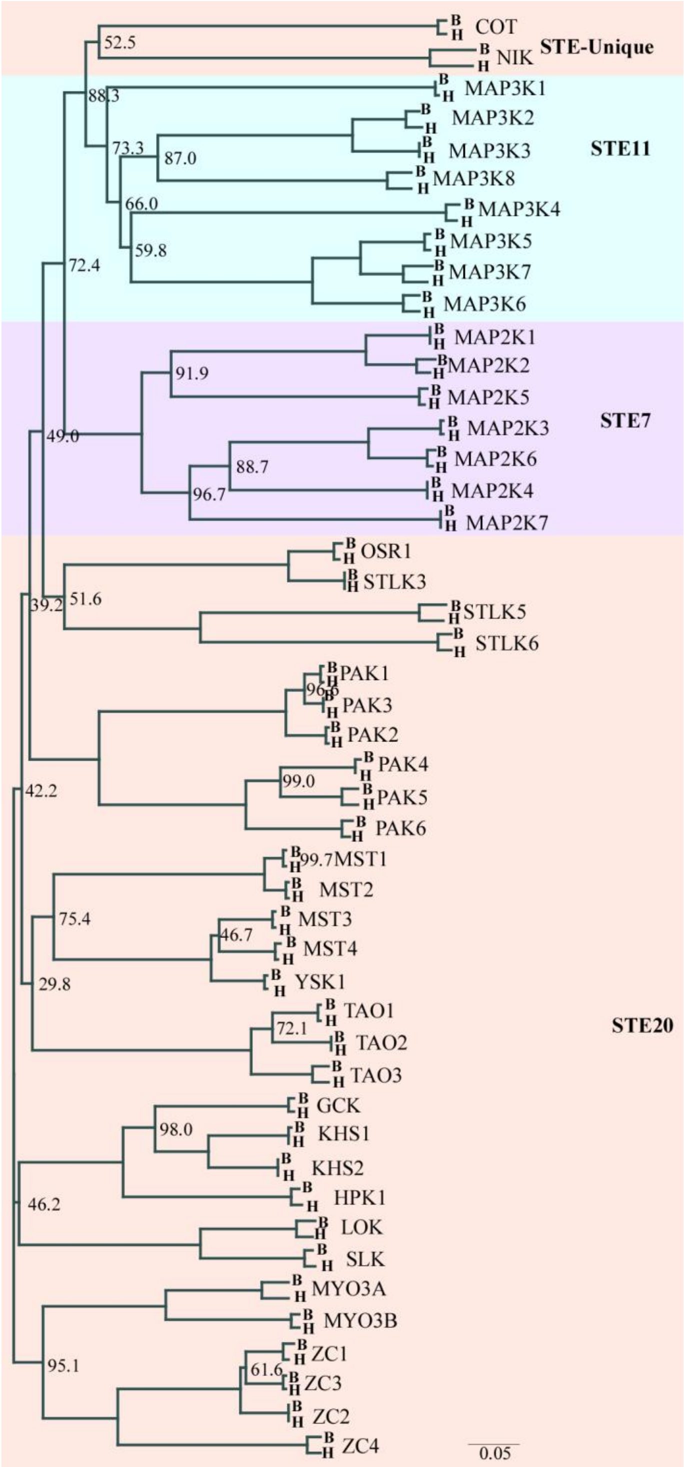
SgK071
26.6
Other-Unique
IRE1
IRE2
0.05
IRE

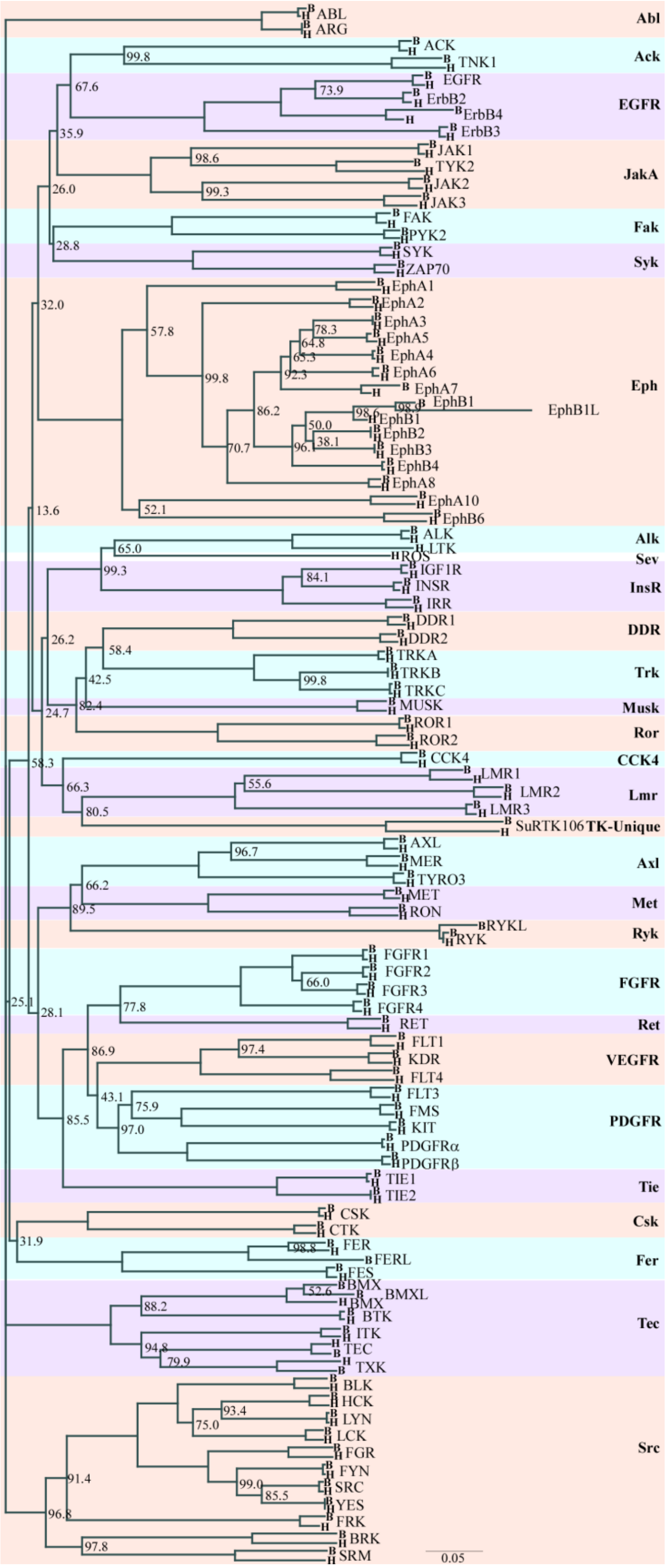
RGC



STE


STE-Unique
STE11
STE7
STE20
COT
NIK
MAP3K1
MAP3K2
MAP3K3
MAP3K8
MAP3K4
MAP3K5
MAP3K7
MAP3K6
MAP2K1
MAP2K2
MAP2K5
MAP2K3
MAP2K6
MAP2K4
MAP2K7
OSR1
STLK3
STLK5
STLK6
PAK1
PAK3
PAK2
PAK4
PAK5
PAK6
MST1
MST2
MST3
MST4
YSK1
TAO1
TAO2
TAO3
GCK
KHS1
KHS2
HPK1
LOK
SLK
MYO3A
MYO3B
ZC1
ZC3
ZC2
ZC4
B
H
52.5
88.3
73.3
87.0
66.0
59.8
72.4
91.9
49.0
88.7
96.7
39.2
51.6
96.6
99.0
42.2
99.7
75.4
46.7
29.8
72.1
98.0
46.2
61.6
95.1
0.05

TK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ARG
Abl
ACK
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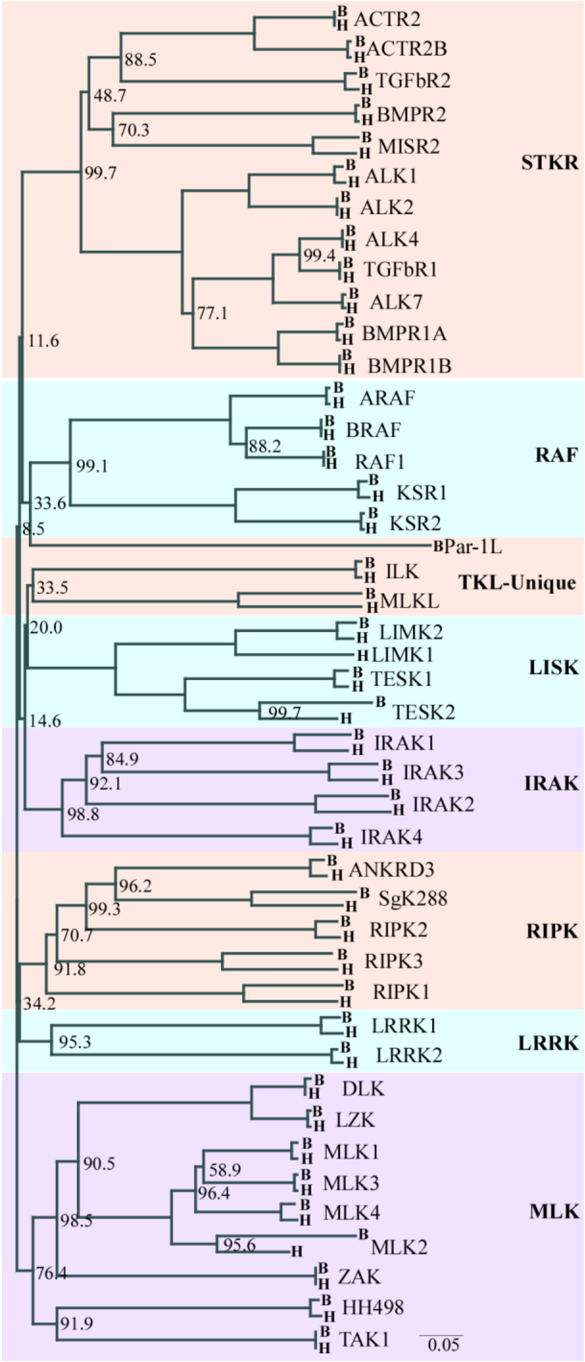
TNK1
Ack
EGFR
67.6
73.9
ErbB2
EGFR
ErbB4
35.9
ErbB3
JAK1
98.6
TYK2
JakA
JAK2
26.0
99.3
JAK3
FAK
Fak
PYK2
28.8
SYK
Syk
ZAP70
EphA1
EphA2
32.0
57.8
EphA3
78.3
EphA5
64.8
EphA4
65.3
EphA6
92.3
99.8
Eph
EphA7
EphB1
98.9
EphB1L
86.2
98.6
EphB1
50.0
EphB2
38.1
70.7
96.1
EphB3
EphB4
EphA8
EphA10
13.6
52.1
EphB6
ALK
Alk
65.0
LTK
ROS
Sev
IGF1R
99.3
84.1
INSR
InsR
IRR
DDR1
DDR
26.2
DDR2
58.4
TRKA
Trk
TRKB
42.5
99.8
TRKC
MUSK
82.4
Musk
24.7
ROR1
Ror
ROR2
CCK4
58.3
CCK4
LMR1
55.6
66.3
LMR2
Lmr
LMR3
80.5
SuRTK106
TK-Unique
AXL
96.7
MER
Axl
66.2
TYRO3
MET
Met
89.5
RON
RYKL
Ryk
RYK
FGFR1
FGFR2
FGFR
66.0
FGFR3
25.1
77.8
FGFR4
28.1
RET
Ret
FLT1
97.4
86.9
KDR
VEGFR
FLT4
FLT3
43.1
75.9
FMS
85.5
PDGFR
KIT
97.0
PDGFRα
PDGFRβ
TIE1
Tie
TIE2
CSK
Csk
CTK
31.9
FER
98.8
FERL
Fer
FES
BMX
52.6
BMXL
88.2
BMX
BTK
Tec
ITK
TEC
94.8
79.9
TXK
BLK
HCK
93.4
LYN
75.0
LCK
Src
FGR
FYN
91.4
99.0
SRC
85.5
YES
96.8
FRK
BRK
97.8
SRM
0.05

TKL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ACTR2B
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TGFbR2
48.7
BMPR2
70.3
MISR2
STKR
99.7
ALK1
ALK2
ALK4
99.4
TGFbR1
ALK7
77.1
BMPR1A
11.6
BMPR1B
ARAF
BRAF
88.2
RAF
RAF1
99.1
KSR1
33.6
KSR2
8.5
Par-1L
ILK
TKL-Unique
33.5
MLKL
LIMK2
20.0
LIMK1
LISK
TESK1
99.7
TESK2
14.6
IRAK1
84.9
IRAK3
IRAK
92.1
IRAK2
98.8
IRAK4
ANKRD3
96.2
SgK288
99.3
RIPK2
RIPK
70.7
RIPK3
91.8
RIPK1
34.2
LRRK1
95.3
LRRK
LRRK2
DLK
LZK
MLK1
90.5
58.9
MLK3
96.4
MLK4
MLK
98.5
95.6
MLK2
76.4
ZAK
HH498
91.9
TAK1
0.05
B
H