Genetics and Molecular Biology, 34, 4, 587-591 (2011)

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Short Communication

Comparative analysis of human and bovine protein kinases reveals unique relationship and functional diversity

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Abstract

Reversible protein phosphorylation by protein kinases and phosphatases is a common event in various cellular processes. The eukaryotic protein kinase superfamily, which is one of the largest superfamilies of eukaryotic proteins, plays several roles in cell signaling and diseases. We identified 482 eukaryotic protein kinases and 39 atypical protein kinases in the bovine genome, by searching publicly accessible genetic-sequence databases. Bovines have 512 putative protein kinases, each orthologous to a human kinase. Whereas orthologous kinase pairs are, on an average, 90.6% identical, orthologous kinase catalytic domain pairs are, on an average, 95.9% identical at the amino acid level. This bioinformatic study of bovine protein kinases provides a suitable framework for further characterization of their functional and structural properties.

Key words: ePK, kinome, aPK, bovine.

Received: September 25, 2010; Accepted: June 1, 2011.

The protein kinase family is one of the largest families of proteins. Protein kinases play important roles in many intracellular or intercellular signaling pathways, resulting in cell proliferation, gene expression, metabolism, motility, membrane transport, apoptosis and differentiation. Furthermore, they modulate the activity of their substrate proteins by phosphorylating serine, threonine or tyrosine residues that mediate the activation, inhibition, translocation or degradation of substrate proteins (Brognard and Hunter, 2011).

Protein kinases are subdivided into two distinct superfamilies, referred to as eukaryotic protein kinases (ePKs) and atypical protein kinases (aPKs) (Hanks and Hunter, 1995). ePKs contain a conserved catalytic domain of approximately 250 amino acids. This domain is divided into 12 subdomains with highly conserved individual amino acids and motifs (Hanks *et al.*, 1988). Within this domain, three motifs, 'VAIK', 'HRD' and 'DFG', are critical for the catalytic function, even though any residue from this region is fully conserved in all family members (Manning *et al.*, 2002b). Conservation of these typical motifs is thought to be due to selection pressure for conserving important functions, such as the interaction with ATP, and the transfer of a phosphate group to the substrate. aPKs are functionally known to have kinase activity which lack significant sequence similarity to the ePK domain.

The sequencing of several vertebrate genomes has been completed. Initial estimates of the number of protein kinases in the human genome place this at around 1000 (Hunter, 1987), with later studies identifying 518 putative protein kinases (Manning *et al.*, 2002b). The mouse and rat genomes contain 540 and 555 protein kinases, respectively, with 509 human orthologs (Caenepeel *et al.*, 2004; Kazi *et al.*, 2008), thereby implying possible functional conservation across species. In the present study, and by using sensitive bioinformatics approaches we identified the near complete set of bovine protein kinases. These were further classified into groups, families and subfamilies, based on the Hanks *et al.* (1988) and Manning *et al.* (2002b) classification scheme. This classification reveals many kinases that are conserved between bovine and human, thus reflecting functional constraints of these protein kinases in the core of signaling pathway. This study provides a suitable framework for further characterization of the functional and structural properties of these protein kinases.

A search was made of bovine proteome sequences available in GenBank (Benson *et al.*, 2010) and Ensembl (Hubbard *et al.*, 2009) for bovine protein kinases, using various tools. A preliminary search for protein kinases was performed using PSI-BLAST (Altschul *et al.*, 1997), against the bovine proteome with an e-value threshold of 0.0001, and an h-value of 0.1 for five iterations. Previously published human (Manning *et al.*, 2002b), mouse (Caenepeel *et al.*, 2004) and rat (Kazi *et al.*, 2008) eukaryotic protein kinases and kinase catalytic domains, as well as

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eukaryotic protein kinase catalytic domains from a variety of organisms available at the kinase.com database were used as query sequences. A further search for protein kinases was performed using HMMER (Eddy, 1998). A Hidden Markov profile was created and validated by means of known eukaryotic protein-kinase catalytic domains. A further search was made for atypical protein kinases, using human, mouse and rat atypical protein kinases by PSI-BLAST or HMMER. Hits identified by using the different methods were combined, and duplicate records removed. Where splice variants were encountered, the variant showing either the closest proximity to the human ortholog, or the longest protein encoding variant, was recorded. All protein kinases were then evaluated for the presence of a conserved eukaryotic protein kinase domain (Hanks *et al.*, 1988; Manning *et al.*, 2002b). Catalytic domains were defined using RPS-BLAST in the BLAST package (Altschul *et al.*, 1997) against the Pfam database (Finn *et al.*, 2010), and sequence alignments carried out with AlinX implemented in the Vector-NTI package (Lu and Moriyama, 2004). Alignments were then manually edited, and all the kinases manually evaluated. Finally, 482 eukaryotic protein kinases and 39 atypical protein kinases were identified (Table S1). The primary names of the protein kinases were derived from their respective homologs in human (Manning *et al.*, 2002b), mouse (Caenepeel *et al.*, 2004) and rat (Kazi *et al.*, 2008) protein kinases. On deriving a second name and synonyms from the Entrez Gene records (Maglott *et al.*, 2005), the full protein names were retrieved thence. Representative records in Entrez Gene, corresponding to each bovine sequence, were identified, whereupon related information was included. Based upon the human protein kinases classification scheme (Manning *et al.*, 2002b), these protein kinases were further classified into 10 groups, 129 families and 81 subfamilies (Table 1 and Table S1).

Previous studies have shown that almost all human protein-kinase orthologs are present in mouse and rat genomes (Caenepeel *et al.*, 2004; Kazi *et al.*, 2008). Thus, a search among bovine kinase sequences was conducted for the orthologous kinases using BLASTP (Altschul *et al.*, 1997). The results were parsed, the symmetrically best hits being considered as orthologous kinases. The orthology relationships were further analyzed by CLUSTALW alignment (Thompson *et al.*, 1997), followed by phylogenetic analysis. The latter was carried out by phylogenetic tree option incorporated into the CLUSTALW program. The NJ clustering algorithm was used for drawing bootstrap trees. As almost all bovine and human protein kinases exist as orthologous pairs (Figure S1), the similar functions in both organisms give to understand their evolutionary conservation. Human and bovine genomes contain 512 common protein kinase orthologs. Our search could not identify seven human protein kinase orthologs, likely due to the incomplete nature of bovine genome sequencing data (Table 2). In these seven human protein kinases, only TAF1L is absent in the chimpanzee genome. All are present in various higher eukaryotes, such as of orangutans and monkeys. Ten protein kinases were absent in the human genome, eight of which being bovine specific and the other two, PLK5 and TSSK5 found in other genomes (Table 2). EphB1L might be a retrotransposed copy of the EphB1 gene, with 89.2% of amino acid sequence identity with the EphB1 protein.

Several proteins, such as ErbB3, SCYL1 and KSR1, have an inactive catalytic domain (Citri *et al.*, 2003; Manning *et al.*, 2002a). These inactive kinases, besides acting mainly as adaptor proteins, or dimerizing with active kinases, have also been shown to be involved in various cellular functions (Salerno *et al.*, 2005; Schmidt *et al.*, 2007; Sergina *et al.*, 2007). Three conserved motifs, ‘VAIK’, ‘HRD’ and ‘DFG’, are important for catalytic activities. Inactive kinases lack at least one of these three conserved motifs. Fifty catalytic domains and 45 protein kinases in the human genome were predicted as catalytically inactive due to the lack of at least one of the three conserved residues (Manning *et al.*, 2002b). The bovine complement of inactive kinases is equivalent to that of the human (Table S1).

All the human and bovine orthologous protein kinase pairs and orthologous catalytic domain pairs were analyzed for the percentage of identity by AlignX incorporated into Vector-NTI (Lu and Moriyama, 2004). In protein sequence alignments of orthologous kinase pairs we observed a wide variation in local sequence conservation (Figure 1A). These were, on an average, 90.6% identical (amino acid se-

Table 1 - Protein-kinases and their distribution by groups in different genomes.

Species	AGC	CAMK	CK1	CMGC	Other	RGC	STE	TK	TKL	Atypical	Total
Human	63	74	12	61	83	5	47	90	43	40	518
Bovine	62	75	12	61	85	5	47	91	44	39	521
Rat	60	112	11	61	84	7	46	91	43	40	555
Mouse	60	97	11	60	84	7	47	90	43	39	538
Drosophila melanogaster	30	32	10	33	45	6	18	32	17	17	240
Caenorhabditis elegans	30	46	85	49	67	27	25	90	15	20	454
Saccharomyces cerevisiae	17	21	4	21	38	0	14	0	0	15	130

Table 2 - Lineage-specific protein kinases.

Found in	Gene Name	Introns	Paralog	Other orthologs
Human and bovine			512 genes	
Human	CK1a2	No	CK1a1 (91%)	Chimpanzee, Orangutan, Monkey
	TAF1L	No	TAF1 (94%)	Orangutan, Monkey
	PKACg	No	PKACa (83%)	Chimpanzee, Orangutan
	LTK	Yes	-	Chimpanzee, Orangutan, Rat, Mouse, Horse, Chicken
	ROS	Yes	-	
	PSKH2	Yes	-	Chimpanzee, Monkey, Dog, Orangutan, Rabbit, Horse
	PRKY	Yes	PRKX (92%)	Chimpanzee, Gorilla, Monkey
Bovine	AURL	Yes	AurB (61%)	-
	CK1b	Yes	CK1a (81%)	-
	EphB1L	No	EphB1 (89.2%)	-
	FERL	Yes	FER (82%)	-
	MARKL	Yes	-	-
	MASTL2	Yes	-	-
	Par-1L	Yes	-	-
	PLK5	Yes	-	Orangutan, Monkey, Mouse, Rat
	RYKL	Yes	-	-
	TSSK5	Yes	-	Dog, Horse, Mouse, Rat

In 'Paralog' parentheses show % of identity (amino acid) with respective paralog.

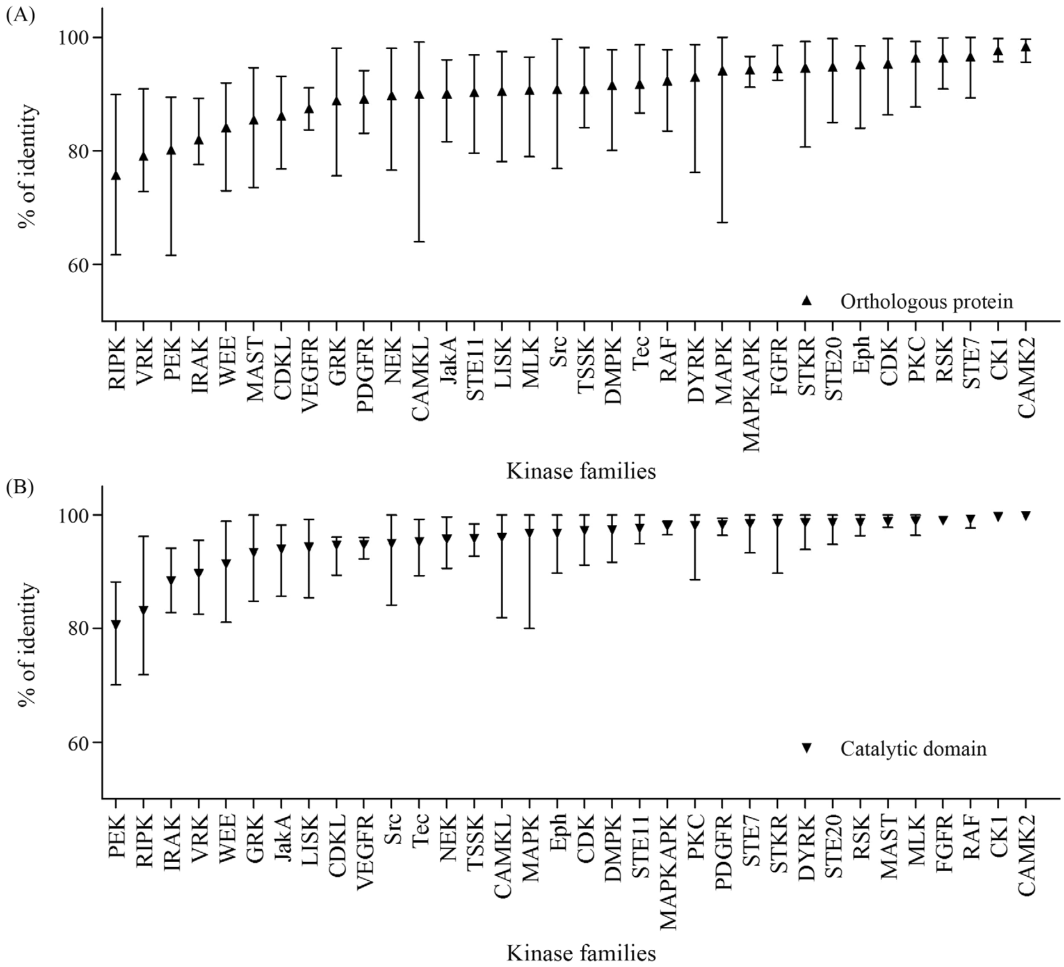

Figure 1 - Conservation within orthologous kinases (A) and catalytic domains (B) is family-dependent. Triangles indicate mean identity within selected families, and bars indicate the range.

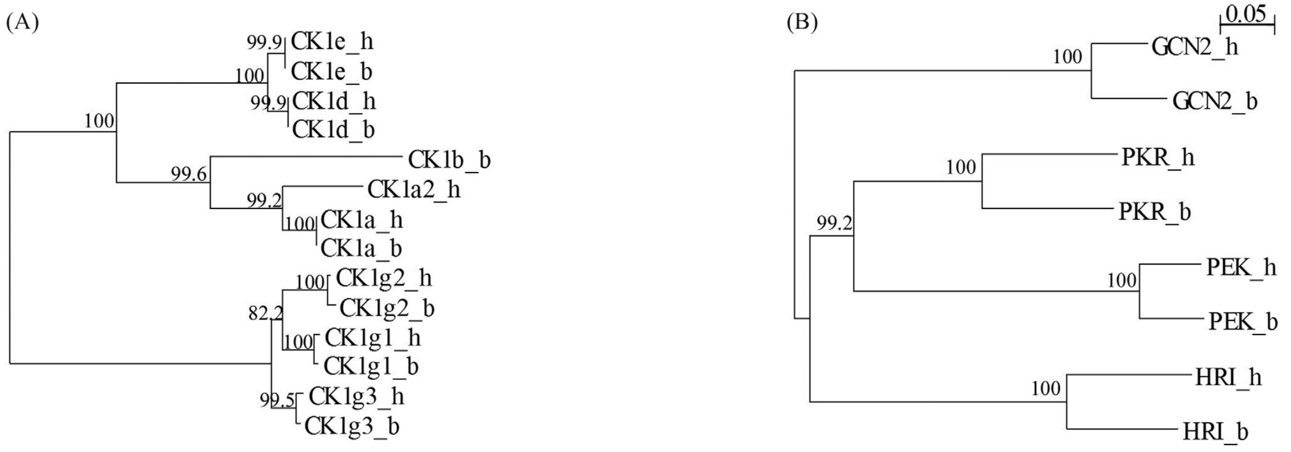

Figure 2 - Catalytic domain conservation is family-dependent. (A) The CK1 family is highly conserved, with zero to two amino acid changes between bovine and human orthologs. (B) Catalytic domains of the PEK family are poorly conserved between human and bovine. h, Human; b, Bovine.

quence), although some were as low as 47.7%, with four pairs presenting high levels of sequence identity throughout the protein (Table S1). Although most differences between orthologs are due to amino acid substitution, many proteins contained substantial insertions or deletions (indels) between orthologs, which may account for many of the functional differences between species. Several proteins contained insertions or deletions (indels), as shown by sequence alignment (Table S1). These comparisons are also informative within the conserved domains. Although orthologous catalytic domains were, on an average, 95.9% identical, some were as low as 63.8%. Sixty two pairs were identical across the full domain, whereas 48 differed by only one amino acid (Table S1), thus indicative of strong conservative pressure throughout the catalytic domain. Catalytic domain pairs showed clearly family-dependent variability (Figure 1B). For example, of the six casein kinase 1 (CK1) family domain pairs, three were identical, and the other three differed by two residues, an average difference of only 0.4%, thereby indicating that changes in almost any amino acid within the domain destroyed some function, and thus have been eliminated by evolution (Figure 2A). At the other extreme, PEK family catalytic domain pairs are 70-88% identical, thereby implying that the core functions of this family of kinases do not greatly constrain the domain sequence (Figure 2B).

Our study presents a bioinformatic overview and evolutionary insight into the kinases within the bovine genome. Comparison with the human kinome revealed the evolutionary conservation of the protein kinase function. The curated kinase dataset from the bovine genome, presented here, could serve as a framework for further investigation of this important gene family.

Acknowledgments

This work was supported by a KN Biomedical Research Grant. We are grateful to Nadid Ahnaf Kazi.

References

Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, Miller W and Lipman DJ (1997) Gapped BLAST and PSI-BLAST: A new generation of protein database search programs. Nucleic Acids Res 25:3389-3402.

Benson DA, Karsch-Mizrachi I, Lipman DJ, Ostell J and Sayers EW (2010) GenBank. Nucleic Acids Res 38:D46-51.

Brognard J and Hunter T (2011) Protein kinase signaling networks in cancer. Curr Opin Genet Dev 21:4-11.

Caenepeel S, Charydczak G, Sudarsanam S, Hunter T and Manning G (2004) The mouse kinome: Discovery and comparative genomics of all mouse protein kinases. Proc Natl Acad Sci USA 101:11707-11712.

Citri A, Skaria KB and Yarden Y (2003) The deaf and the dumb: The biology of ErbB-2 and ErbB-3. Exp Cell Res 284:54-65.

Eddy SR (1998) Profile hidden Markov models. Bioinformatics 14:755-763.

Finn RD, Mistry J, Tate J, Coggill P, Heger A, Pollington JE, Gavin OL, Gunasekaran P, Ceric G, Forslund K, *et al.* (2010) The Pfam protein families database. Nucleic Acids Res 38:D211-222.

Hanks SK and Hunter T (1995) Protein kinases 6. The eukaryotic protein kinase superfamily: Kinase (catalytic) domain structure and classification. FASEB J 9:576-596.

Hanks SK, Quinn AM and Hunter T (1988) The protein kinase family: Conserved features and deduced phylogeny of the catalytic domains. Science 241:42-52.

Hubbard TJ, Aken BL, Ayling S, Ballester B, Beal K, Bragin E, Brent S, Chen Y, Clapham P, Clarke L, *et al.* (2009) Ensembl 2009. Nucleic Acids Res 37:D690-697.

Hunter T (1987) A thousand and one protein kinases. Cell 50:823-829.

Kazi JU, Kabir NN and Soh JW (2008) Bioinformatic prediction and analysis of eukaryotic protein kinases in the rat genome. Gene 410:147-153.

Lu G and Moriyama EN (2004) Vector NTI, a balanced all-in-one sequence analysis suite. Brief Bioinform 5:378-388.

Maglott D, Ostell J, Pruitt KD and Tatusova T (2005) Entrez gene: Gene-centered information at NCBI. Nucleic Acids Res 33:D54-58.

Manning G, Plowman GD, Hunter T and Sudarsanam S (2002a) Evolution of protein kinase signaling from yeast to man. Trends Biochem Sci 27:514-520.

Manning G, Whyte DB, Martinez R, Hunter T and Sudarsanam S (2002b) The protein kinase complement of the human genome. Science 298:1912-1934.

Salerno M, Palmieri D, Bouadis A, Halverson D and Steeg PS (2005) Nm23-H1 metastasis suppressor expression level influences the binding properties, stability, and function of the kinase suppressor of Ras1 (KSR1) Erk scaffold in breast carcinoma cells. Mol Cell Biol 25:1379-1388.

Schmidt WM, Kraus C, Hoger H, Hochmeister S, Oberndorfer F, Branka M, Bingemann S, Lassmann H, Muller M, Macedo-Souza LI, *et al.* (2007) Mutation in the Scyl1 gene encoding amino-terminal kinase-like protein causes a recessive form of spinocerebellar neurodegeneration. EMBO Rep 8:691-697.

Sergina NV, Rausch M, Wang D, Blair J, Hann B, Shokat KM and Moasser MM (2007) Escape from HER-family tyrosine kinase inhibitor therapy by the kinase-inactive HER3. Nature 445:437-441.

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F and Higgins DG (1997) The CLUSTAL_X windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25:4876-4882.

Internet Resources

Kinase.com database, Genomics, evolution and function of protein kinases, http://kinase.com/kinbase/FastaFiles/.

Supplementary Material

The following online material is available for this article:

Table S1 - List of bovine kinases with sequences.

Figure S1 - Phylogenetic trees for human and bovine kinases.

This material is available as part of the online article from http://www.scielo.br/gmb.

Associate Editor: Alexandre Rodrigues Caetano

Line #	Name	Symbol	Group	Family	Subfamily	GeneID
1	AKT1	AKT1	AGC	AKT		280991
2	AKT2	AKT2	AGC	AKT		534923
3	AKT3	AKT3	AGC	AKT		100137872
4	DMPK1		AGC	DMPK	GEK	
5	DMPK2	CDC42BPG	AGC	DMPK	GEK	518121
6	MRCKa	CDC42BPA	AGC	DMPK	GEK	538392
7	MRCKb		AGC	DMPK	GEK	
8	ROCK1	ROCK1	AGC	DMPK	ROCK	785911
9	ROCK2	ROCK2	AGC	DMPK	ROCK	282041
10	CRIK		AGC	DMPK		
11	BARK1	ADRBK1	AGC	GRK	BARK	282682
12	BARK2	ADRBK2	AGC	GRK	BARK	282136
13	GPRK4	GRK4	AGC	GRK	GRK	512489
14	GPRK5	GRK5	AGC	GRK	GRK	281801
15	GPRK6		AGC	GRK	GRK	
16	GPRK7	GRK7	AGC	GRK	GRK	281802
17	RHOK	GRK1	AGC	GRK	GRK	281457
18	MAST1	MAST1	AGC	MAST		539825
19	MAST2		AGC	MAST		
20	MAST3	MAST3	AGC	MAST		534230
21	MAST4		AGC	MAST		
22	MASTL	MASTL	AGC	MASTL		540206
23	MASTL2		AGC	MASTL		
24	LATS1	LATS1	AGC	NDR		535935
25	LATS2	LATS2	AGC	NDR		508208
26	NDR1	STK38	AGC	NDR		533677
27	NDR2	STK38L	AGC	NDR		514787
28	PKACa	PRKACA	AGC	PKA		282322
29	PKACb	PRKACB	AGC	PKA		282323
30	PRKX	PRKX	AGC	PKA		505773
31	PDK1	PDK1	AGC	PKB		100138102
32	PKCi	PRKCI	AGC	PKC	Atypical	528478
33	PKCz	PRKCZ	AGC	PKC	Atypical	286877
34	PKCa	PRKCA	AGC	PKC	Classical	282001
35	PKCb	PRKCB1	AGC	PKC	Classical	282325
36	PKCg	PRKCG	AGC	PKC	Classical	282002
37	PKCd	PRKCD	AGC	PKC	Nobel	505708
38	PKCe	PRKCE	AGC	PKC	Nobel	507041
39	PKCh	PRKCH	AGC	PKC	Nobel	518542
40	PKCt	PRKCQ	AGC	PKC	Nobel	505901
41	PKG1	PRKG1	AGC	PKG		282004
42	PKG2	PRKG2	AGC	PKG		533330
43	PKN1	PKN1	AGC	PKN		509080
44	PKN2	PKN2	AGC	PKN		519754
45	PKN3	PKN3	AGC	PKN		505353
46	MSK1	RPS6KA5	AGC	RSK	MSK	504408
47	MSK2		AGC	RSK	MSK	523746
48	p70S6K	RPS6KB1	AGC	RSK	p70	404181
49	p70S6Kb	RPS6KB2	AGC	RSK	p70	506083

50	RSK1	RPS6KA2	AGC	RSK	RSK	517953
51	RSK2	RPS6KA3	AGC	RSK	RSK	511190
52	RSK3	RPS6KA1	AGC	RSK	RSK	533908
53	RSK4	RPS6KA6	AGC	RSK	RSK	526227
54	RSKL1	RPS6KC1	AGC	RSKL		533192
55	RSKL2	RPS6KL1	AGC	RSKL		530047
56	SgK494	SGK494	AGC	RSKL		527796
57	SGK	SGK1	AGC	SGK		515854
58	SGK2	SGK2	AGC	SGK		517909
59	SGK3	SGK3	AGC	SGK		504480
60	YANK1	STK32A	AGC	YANK		100125774
61	YANK2	STK32B	AGC	YANK		529134
62	YANK3	STK32C	AGC	YANK		524218
63	A6	TWF1	Atypical	A6		506683
64	A6r	TWF2	Atypical	A6		282024
65	ADCK3	CABC1	Atypical	ABC1	ABC1-A	536925
66	ADCK4	ADCK4	Atypical	ABC1	ABC1-A	514322
67	ADCK1	ADCK1	Atypical	ABC1	ABC1-B	533372
68	ADCK5	ADCK5	Atypical	ABC1	ABC1-B	522614
69	ADCK2	ADCK2	Atypical	ABC1	ABC1-C	539345
70	ChaK1	TRPM7	Atypical	Alpha	ChaK	514642
71	ChaK2	TRPM6	Atypical	Alpha	ChaK	527597
72	eEF2K	EEF2K	Atypical	Alpha	eEF2K	521730
73	AlphaK1	ALPK3	Atypical	Alpha		
74	AlphaK2	ALPK2	Atypical	Alpha		510218
75	AlphaK3	ALPK1	Atypical	Alpha		524375
76	BCR	BCR	Atypical	BCR		789892
77	BRD2	BRD2	Atypical	BRD		505358
78	BRD3	BRD3	Atypical	BRD		525051
79	BRD4	BRD4	Atypical	BRD		614048
80	BRDT	BRDT	Atypical	BRD		523971
81	FASTK	FASTK	Atypical	FAST		509781
82	G11	STK19	Atypical	G11		508320
83	H11	HSPB8	Atypical	H11		539524
84	BCKDK	BCKDK	Atypical	PDHK		505005
85	PDHK1	PDK1	Atypical	PDHK		528655
86	PDHK2	PDK2	Atypical	PDHK		524075
87	PDHK3	PDK3	Atypical	PDHK		510841
88	PDHK4	PDK4	Atypical	PDHK		507367
89	ATM	ATM	Atypical	PIKK	ATM	526824
90	ATR	ATR	Atypical	PIKK	ATR	504869
91	DNAPK	PRKDC	Atypical	PIKK	DNAPK	512740
92	FRAP	MTOR	Atypical	PIKK	FRAP	100139219
93	SMG1	SMG1	Atypical	PIKK	SMG1	525143
94	TRRAP	TRRAP	Atypical	PIKK	TRRAP	507169
95	RIOK1	RIOK1	Atypical	RIO	RIO1	516289
96	RIOK2	RIOK2	Atypical	RIO	RIO2	540772
97	RIOK3	RIOK3	Atypical	RIO	RIO3	522917
98	TAF1	TAF1	Atypical	TAF1		504792
99	TIF1a	TRIM33	Atypical	TIF1		533296

100	TIF1b		Atypical	TIF1		
101	TIF1g	TRIM24	Atypical	TIF1		537246
102	CaMK1a	CAMK1	CAMK	CAMK1		520498
103	CaMK1b	PNCK	CAMK	CAMK1		614251
104	CaMK1d	CAMK1D	CAMK	CAMK1		526873
105	CaMK1g	CAMK1G	CAMK	CAMK1		511504
106	CaMK2a	CAMK2A	CAMK	CAMK2		530719
107	CaMK2b	CAMK2B	CAMK	CAMK2		525416
108	CaMK2d	CAMK2D	CAMK	CAMK2		532713
109	CaMK2g	CAMK2G	CAMK	CAMK2		282162
110	CaMK4	OC10033708	CAMK	CAMK4		100337083
111	AMPKa1	PRKAA1	CAMK	CAMKL	AMPK	540404
112	AMPKa2	PRKAA2	CAMK	CAMKL	AMPK	538954
113	BRSK1	BRSK1	CAMK	CAMKL	BRSK	538009
114	BRSK2	BRSK2	CAMK	CAMKL	BRSK	535868
115	CHK1	CHEK1	CAMK	CAMKL	CHK1	513678
116	HUNK	HUNK	CAMK	CAMKL	HUNK	537640
117	LKB1	STK11	CAMK	CAMKL	LKB	515245
118	MARK1	MARK1	CAMK	CAMKL	MARK	539563
119	MARK2	MARK2	CAMK	CAMKL	MARK	535197
120	MARK3	MARK3	CAMK	CAMKL	MARK	534872
121	MARK4	MARK4	CAMK	CAMKL	MARK	525675
122	MARKL	LOC618482	CAMK	CAMKL	MARK	618482
123	MELK	MELK	CAMK	CAMKL	MELK	520088
124	NIM1	LOC530210	CAMK	CAMKL	NIM1	530210
125	NuaK1	NUAK1	CAMK	CAMKL	NuaK	519892
126	NuaK2	NUAK2	CAMK	CAMKL	NuaK	518632
127	PASK	PASK	CAMK	CAMKL	PASK	512154
128	QIK	SNF1LK2	CAMK	CAMKL	QIK	539570
129	QSK	SIK3	CAMK	CAMKL	QIK	506539
130	SIK	SIK	CAMK	CAMKL	QIK	
131	SNRK	SNRK	CAMK	CAMKL	SNRK	536909
132	SgK495	STK40	CAMK	CAMK-Unique		515723
133	STK33	STK33	CAMK	CAMK-Unique		528309
134	VACAMKL	CAMKV	CAMK	CAMK-Unique		525741
135	CASK	CASK	CAMK	CASK		404149
136	DAPK1	DAPK1	CAMK	DAPK		540873
137	DAPK2	DAPK2	CAMK	DAPK		529131
138	DAPK3	DAPK3	CAMK	DAPK		525506
139	DRAK1	STK17A	CAMK	DAPK		513665
140	DRAK2	STK17B	CAMK	DAPK		511373
141	DCAMKL1		CAMK	DCAMKL		
142	DCAMKL2	DCLK2	CAMK	DCAMKL		536110
143	DCAMKL3	DCLK3	CAMK	DCAMKL		507205
144	MAPKAPK2	MAPKAPK2	CAMK	MAPKAPK	MAPKAPK	788091
145	MAPKAPK3	MAPKAPK3	CAMK	MAPKAPK	MAPKAPK	615215
146	MAPKAPK5	MAPKAPK5	CAMK	MAPKAPK	MAPKAPK	535625
147	MNK1	MKNK1	CAMK	MAPKAPK	MNK	525647
148	MNK2	MKNK2	CAMK	MAPKAPK	MNK	538519
149	caMLCK	MYLK3	CAMK	MLCK		526379

150	SgK085	MYLK4	CAMK	MLCK		518025
151	skMLCK	MYLK2	CAMK	MLCK		533378
152	smMLCK	MYLK	CAMK	MLCK		338037
153	TTN	TTN	CAMK	MLCK		540561
154	PHKg1	PHKG1	CAMK	PHK		540682
155	PHKg2	PHKG2	CAMK	PHK		512670
156	PIM1	PIM1	CAMK	PIM		281402
157	PIM2	PIM2	CAMK	PIM		508424
158	PIM3	OC10033665	CAMK	PIM		100336651
159	PKD1	PRKD1	CAMK	PKD		533270
160	PKD2	PRKD2	CAMK	PKD		782793
161	PKD3	PRKD3	CAMK	PKD		538447
162	PSKH1	PSKH1	CAMK	PSK		509656
163	CHK2	CHEK2	CAMK	RAD53		518897
164	Trb1	TRIB1	CAMK	Trbl		521857
165	Trb2	TRIB2	CAMK	Trbl		352960
166	Trb3	TRIB3	CAMK	Trbl		538465
167	Obscn	OBSCN	CAMK	Trio		508247
168	SPEG	SPEG	CAMK	Trio		523490
169	Trad	KALRN	CAMK	Trio		540675
170	Trio	TRIO	CAMK	Trio		538292
171	SSTK	TSSK6	CAMK	TSSK		539707
172	TSSK1	TSSK1B	CAMK	TSSK		529193
173	TSSK2	TSSK2	CAMK	TSSK		
174	TSSK3	TSSK3	CAMK	TSSK		538659
175	TSSK4	TSSK4	CAMK	TSSK		539477
176	TSSK5	LOC523023	CAMK	TSSK		523023
177	CK1a	CSNK1A1	CK1	CK1		282684
178	CK1b	CSNK1B	CK1	CK1		785423
179	CK1d	CSNK1D	CK1	CK1		523542
180	CK1e	CSNK1E	CK1	CK1		768234
181	CK1g1	CSNK1G1	CK1	CK1		527889
182	CK1g2	CSNK1G2	CK1	CK1		506060
183	CK1g3		CK1	CK1		
184	TTBK1		CK1	TTBK		
185	TTBK2	TTBK2	CK1	TTBK		541215
186	VRK1	VRK1	CK1	VRK		618880
187	VRK2	VRK2	CK1	VRK		523902
188	VRK3	VRK3	CK1	VRK		520302
189	CDC2	CDC2	CMGC	CDK	CDC2	281061
190	CDK2	CDK2	CMGC	CDK	CDC2	519217
191	CDK3	CDK3	CMGC	CDK	CDC2	618631
192	CDK10	CDK10	CMGC	CDK	CDK10	615171
193	CDK4	CDK4	CMGC	CDK	CDK4	510618
194	CDK6	CDK6	CMGC	CDK	CDK4	511754
195	CDK5	CDK5	CMGC	CDK	CDK5	281066
196	CDK7	CDK7	CMGC	CDK	CDK7	515462
197	CDK11	CDC2L6	CMGC	CDK	CDK8	511802
198	CDK8	CDK8	CMGC	CDK	CDK8	507149
199	CDK9	CDK9	CMGC	CDK	CDK9	520580

200	CHED	CDC2L5	CMGC	CDK	CRK7	511147
201	CRK7	CRKRS	CMGC	CDK	CRK7	511513
202	PITSLRE	CDC2L1	CMGC	CDK	PITSLRE	493708
203	PCTAIRE1	PCTK1	CMGC	CDK	TAIRE	613810
204	PCTAIRE2	PCTK2	CMGC	CDK	TAIRE	539655
205	PCTAIRE3	PCTK3	CMGC	CDK	TAIRE	534048
206	PFTAIRE1	CDK14	CMGC	CDK	TAIRE	784403
207	PFTAIRE2	CDK15	CMGC	CDK	TAIRE	616118
208	CCRK	CCRK	CMGC	CDK		510920
209	CDKL1	CDKL1	CMGC	CDKL		523900
210	CDKL2	CDKL2	CMGC	CDKL		533114
211	CDKL3	CDKL3	CMGC	CDKL		541279
212	CDKL4	CDKL4	CMGC	CDKL		517478
213	CDKL5	CDKL5	CMGC	CDKL		538337
214	CLK1	CLK1	CMGC	CLK		613808
215	CLK2	CLK2	CMGC	CLK		512737
216	CLK3	CLK3	CMGC	CLK		505499
217	CLK4	CLK4	CMGC	CLK		529633
218	DYRK1A	DYRK1A	CMGC	DYRK	Dyrk1	532989
219	DYRK1B	DYRK1B	CMGC	DYRK	Dyrk1	507571
220	DYRK2	DYRK2	CMGC	DYRK	Dyrk2	514916
221	DYRK3	DYRK3	CMGC	DYRK	Dyrk2	505149
222	DYRK4	LOC531276	CMGC	DYRK	Dyrk2	531276
223	HIPK1	HIPK1	CMGC	DYRK	HIPK	512233
224	HIPK2	HIPK2	CMGC	DYRK	HIPK	510158
225	HIPK3	HIPK3	CMGC	DYRK	HIPK	538866
226	HIPK4	HIPK4	CMGC	DYRK	HIPK	520157
227	PRP4	PRPF4B	CMGC	DYRK	PRP4	512236
228	GSK3A	GSK3A	CMGC	GSK		536561
229	GSK3B	GSK3B	CMGC	GSK		790875
230	Erk1	MAPK3	CMGC	MAPK	ERK	531391
231	Erk2	MAPK1	CMGC	MAPK	ERK	327672
232	Erk3	MAPK6	CMGC	MAPK	ERK	538094
233	Erk4	MAPK4	CMGC	MAPK	ERK	529183
234	Erk5	MAPK7	CMGC	MAPK	ERK	537703
235	Erk7	MAPK15	CMGC	MAPK	Erk7	512125
236	JNK1	MAPK8	CMGC	MAPK	JNK	539941
237	JNK2	MAPK9	CMGC	MAPK	JNK	534125
238	JNK3	MAPK10	CMGC	MAPK	JNK	537631
239	NLK	NLK	CMGC	MAPK	nmo	507204
240	p38a	MAPK14	CMGC	MAPK	p38	534492
241	p38b	MAPK11	CMGC	MAPK	p38	618906
242	p38d	MAPK13	CMGC	MAPK	p38	535327
243	p38g	MAPK12	CMGC	MAPK	p38	512943
244	ICK	ICK	CMGC	RCK		506286
245	MAK	MAK	CMGC	RCK		536048
246	MOK	RAGE	CMGC	RCK		616277
247	MSSK1	SRPK3	CMGC	SRPK		508325
248	SRPK1	SRPK1	CMGC	SRPK		512631
249	SRPK2	SRPK2	CMGC	SRPK		505945

250	AurA	AURKA	Other	AUR		504437
251	AurB	AURKB	Other	AUR		360192
252	AurC	AURKC	Other	AUR		618599
253	AurL		Other	AUR		
254	BUB1	BUB1	Other	BUB		514777
255	BUBR1	BUB1B	Other	BUB		537027
256	PRPK	TP53RK	Other	Bud32		619100
257	CaMKK1	CAMKK1	Other	CAMKK	Meta	510260
258	CaMKK2	CAMKK2	Other	CAMKK	Meta	509084
259	CDC7	CDC7	Other	CDC7		516094
260	CK2a1	CSNK2A1	Other	CK2		282419
261	CK2a2	CSNK2A2	Other	CK2		282420
262	Haspin	GSG2	Other	Haspin		767819
263	IKKa	CHUK	Other	IKK		281073
264	IKKb	IKBKB	Other	IKK		281854
265	IKKe	IKBKE	Other	IKK		533216
266	TBK1	TBK1	Other	IKK		533141
267	IRE1	IRE1	Other	IRE		
268	IRE2	IRE2	Other	IRE		
269	MOS	MOS	Other	MOS		444869
270	AAK1	AAK1	Other	NAK		532546
271	BIKE	BIKE	Other	NAK		505766
272	GAK	GAK	Other	NAK		511296
273	MPSK1	STK16	Other	NAK		521237
274	NEK1		Other	NEK		
275	NEK10	NEK10	Other	NEK		522335
276	NEK11	NEK11	Other	NEK		614924
277	NEK2	NEK2	Other	NEK		523998
278	NEK3	NEK3	Other	NEK		505876
279	NEK4	NEK4	Other	NEK		511455
280	NEK5	NEK5	Other	NEK		100138147
281	NEK6	NEK6	Other	NEK		515816
282	NEK7	NEK7	Other	NEK		781355
283	NEK8	NEK8	Other	NEK		532332
284	NEK9	NEK9	Other	NEK		534652
285	SBK	LOC614815	Other	NKF1		614815
286	SgK069	SBK2	Other	NKF1		615123
287	SgK110	LOC789661	Other	NKF1		789661
288	PINK1	PINK1	Other	NKF2		510683
289	SgK223	SgK223	Other	NKF3		
290	SgK269	SgK269	Other	NKF3		
291	CLIK1	STK35	Other	NKF4		540979
292	CLIK1L	PDIK1L	Other	NKF4		510253
293	SgK424	LOC785881	Other	NKF5		785881
294	TEX14	TEX14	Other	NKF5		522810
295	NRBP1	NRBP1	Other	NRBP		532919
296	NRBP2	NRBP2	Other	NRBP		504664
297	KIS	UHMK1	Other	Other-Unique		538770
298	RNAseL	RNASEL	Other	Other-Unique		100048947
299	SgK071	LOC614899	Other	Other-Unique		614899

300	SgK196	MGC151666	Other	Other-Unique		514490
301	SgK396	STK31	Other	Other-Unique		781749
302	SgK493	PKDCC	Other	Other-Unique		539467
303	SgK496	RIPK5	Other	Other-Unique		534684
304	GCN2	GCN2	Other	PEK	GCN2	
305	PEK	EIF2AK3	Other	PEK	PEK	535820
306	HRI	EIF2AK1	Other	PEK		507689
307	PKR	EIF2AK2	Other	PEK		347700
308	PLK1	PLK1	Other	PLK		538238
309	PLK2	PLK2	Other	PLK		539449
310	PLK3	PLK3	Other	PLK		504282
311	PLK4	PLK4	Other	PLK		514405
312	PLK5	LOC511891	Other	PLK		511891
313	SCYL1	SCYL1	Other	SCY1		515247
314	SCYL2	SCYL2	Other	SCY1		782059
315	SCYL3	SCYL3	Other	SCY1		506600
316	Slob	PXK	Other	Slob		614093
317	TBCK	TBCK	Other	TBCK		528650
318	TLK1	TLK1	Other	TLK		537517
319	TLK2	TLK2	Other	TLK		534705
320	PBK	PBK	Other	TOPK		534781
321	TTK	TTK	Other	TTK		524925
322	Fused	STK36	Other	ULK		508408
323	ULK1	ULK1	Other	ULK		526310
324	ULK2	ULK2	Other	ULK		618601
325	ULK3	ULK3	Other	ULK		506063
326	ULK4	ULK4	Other	ULK		531267
327	PIK3R4	PIK3R4	Other	VPS15		507414
328	MYT1	PKMYT1	Other	WEE		522613
329	Wee1	WEE1	Other	WEE		540322
330	Wee1B	WEE2	Other	WEE		520049
331	Wnk1	WNK1	Other	Wnk		506433
332	Wnk2	WNK2	Other	Wnk		506520
333	Wnk3	WNK3	Other	Wnk		533409
334	Wnk4	WNK4	Other	Wnk		
335	ANPa	NPR1	RGC	RGC		533048
336	ANPb	NPR2	RGC	RGC		281357
337	CYGD	GUCY2D	RGC	RGC		282245
338	CYGF	GUCY2F	RGC	RGC		282246
339	HSER	GUCY2C	RGC	RGC		282244
340	MAP3K1	MAP3K1	STE	STE11		523962
341	MAP3K2	MAP3K2	STE	STE11		504592
342	MAP3K3	MAP3K3	STE	STE11		508943
343	MAP3K4	MAP3K4	STE	STE11		511779
344	MAP3K5	MAP3K5	STE	STE11		537380
345	MAP3K6	MAP3K6	STE	STE11		614598
346	MAP3K7	MAP3K15	STE	STE11		529335
347	MAP3K8	YSK4	STE	STE11		538897
348	OSR1	OSR1	STE	STE20	FRAY	
349	STLK3	STK39	STE	STE20	FRAY	522103

350	GCK	MAP4K2	STE	STE20	KHS	520058
351	HPK1	MAP4K1	STE	STE20	KHS	522002
352	KHS1	MAP4K5	STE	STE20	KHS	781335
353	KHS2	MAP4K3	STE	STE20	KHS	507624
354	ZC1	ZC1	STE	STE20	MSN	
355	ZC2	TNIK	STE	STE20	MSN	539627
356	ZC3	MINK1	STE	STE20	MSN	519558
357	ZC4	NRK	STE	STE20	MSN	783774
358	MST1	STK4	STE	STE20	MST	514886
359	MST2	STK3	STE	STE20	MST	533815
360	MYO3A	MYO3A	STE	STE20	NinaC	535824
361	MYO3B	MYO3B	STE	STE20	NinaC	536123
362	PAK1	PAK1	STE	STE20	PAKA	533729
363	PAK2	LOC513673	STE	STE20	PAKA	513673
364	PAK3	PAK3	STE	STE20	PAKA	534526
365	PAK4	PAK4	STE	STE20	PAKB	539742
366	PAK5	PAK7	STE	STE20	PAKB	513432
367	PAK6	PAK6	STE	STE20	PAKB	539224
368	LOK	STK10	STE	STE20	SLK	526376
369	SLK	SLK	STE	STE20	SLK	535342
370	STLK5	LYK5	STE	STE20	STLK	515024
371	STLK6	STRADB	STE	STE20	STLK	506029
372	TAO1	TAOK1	STE	STE20	TAO	536532
373	TAO2	TAOK2	STE	STE20	TAO	533897
374	TAO3	TAOK3	STE	STE20	TAO	534620
375	MST3	STK24-LIKE	STE	STE20	YSK	532455
376	MST4	MST4	STE	STE20	YSK	539445
377	YSK1	STK25	STE	STE20	YSK	373543
378	MAP2K1	MAP2K1	STE	STE7		533199
379	MAP2K2	MAP2K2	STE	STE7		510434
380	MAP2K3	MAP2K3	STE	STE7		516039
381	MAP2K4	MAP2K4	STE	STE7		526469
382	MAP2K5	MAP2K5	STE	STE7		100295732
383	MAP2K6	MAP2K6	STE	STE7		286883
384	MAP2K7	MAP2K7	STE	STE7		787278
385	COT	MAP3K8	STE	STE-Unique		535622
386	NIK	MAP3K14	STE	STE-Unique		508367
387	ABL	ABL1	TK	Abl		540876
388	ARG	ABL2	TK	Abl		511845
389	ACK	ACK1	TK	Ack		280710
390	TNK1	TNK1	TK	Ack		510356
391	ALK	ALK	TK	Alk		536642
392	AXL	AXL	TK	Axl		516598
393	MER	MERTK	TK	Axl		504429
394	TYRO3	TYRO3	TK	Axl		788224
395	CCK4	PTK7	TK	CCK4		514819
396	CSK	CSK	TK	Csk		509246
397	CTK	MATK	TK	Csk		504668
398	DDR1	DDR1	TK	DDR		534092
399	DDR2	DDR2	TK	DDR		533523

400	EGFR	EGFR	TK	EGFR		407217
401	ErbB2	ERBB2	TK	EGFR		
402	ErbB3	ERBB3	TK	EGFR		785655
403	ErbB4	ERBB4	TK	EGFR		522419
404	EphA1	EPHA1	TK	Eph		525946
405	EphA10	EPHA10	TK	Eph		540439
406	EphA2	EPHA2	TK	Eph		512798
407	EphA3	EPHA3	TK	Eph		537951
408	EphA4	EPHA4	TK	Eph		520192
409	EphA5	EPHA5	TK	Eph		538224
410	EphA6	EPHA6	TK	Eph		616165
411	EphA7	EPHA7	TK	Eph		538797
412	EphA8	EPHA8	TK	Eph		517368
413	EphB1	EPHB1	TK	Eph		534731
414	EphB1L	LOC618263	TK	Eph		618263
415	EphB2	EPHB2	TK	Eph		535137
416	EphB3	EPHB3	TK	Eph		540907
417	EphB4	EPHB4	TK	Eph		515756
418	EphB6	EPHB6	TK	Eph		529800
419	FAK	PTK2	TK	Fak		506270
420	PYK2	PTK2B	TK	Fak		541008
421	FER	FER	TK	Fer		536759
422	FERL		TK	Fer		
423	FES	FES	TK	Fer		507304
424	FGFR1	FGFR1	TK	FGFR		281768
425	FGFR2	FGFR2	TK	FGFR		404193
426	FGFR3	FGFR3	TK	FGFR		281769
427	FGFR4	FGFR4	TK	FGFR		317696
428	IGF1R	IGF1R	TK	InsR		281848
429	INSR	INSR	TK	InsR		408017
430	IRR	INSRR	TK	InsR		787068
431	JAK1	JAK1	TK	JakA		537201
432	JAK2	JAK2	TK	JakA		525246
433	JAK3	JAK3	TK	JakA		538276
434	TYK2	TYK2	TK	JakA		512484
435	LMR1	AATK	TK	Lmr		511515
436	LMR2	LMTK2	TK	Lmr		512290
437	LMR3	LMR3	TK	Lmr		
438	MET	MET	TK	Met		280855
439	RON	MST1R	TK	Met		525504
440	MUSK	MUSK	TK	Musk		540052
441	FLT3	FLT3	TK	PDGFR		512700
442	FMS	FMS	TK	PDGFR		
443	KIT	KIT	TK	PDGFR		280832
444	PDGFRa	PDGFRA	TK	PDGFR		282301
445	PDGFRb	PDGFRB	TK	PDGFR		527165
446	RET	RET	TK	Ret		515924
447	ROR1	ROR1	TK	Ror		783965
448	ROR2	ROR2	TK	Ror		785924
449	RYK	RYK	TK	Ryk		781353

450	RYKL		TK	Ryk		
451	BLK	BLK	TK	Src		532587
452	BRK	PTK6	TK	Src		529814
453	FGR	FGR	TK	Src		516133
454	FRK	FRK	TK	Src		509227
455	FYN	FYN	TK	Src		527263
456	HCK	HCK	TK	Src		280814
457	LCK	LCK	TK	Src		508890
458	LYN	LYN	TK	Src		534996
459	SRC	SRC	TK	Src		535742
460	SRM	SRMS	TK	Src		521816
461	YES	YES1	TK	Src		507632
462	SYK	SYK	TK	Syk		515515
463	ZAP70	ZAP70	TK	Syk		504509
464	BMX	BMX	TK	Tec		531514
465	BTK	BTK	TK	Tec		533459
466	ITK	ITK	TK	Tec		522311
467	TEC	TEC	TK	Tec		504733
468	TXK	TXK	TK	Tec		504782
469	TIE1	TIE1	TK	Tie		280941
470	TIE2	TEK	TK	Tie		280939
471	SuRTK106	STYK1	TK	TK-Unique		513920
472	TRKA	NTRK1	TK	Trk		353111
473	TRKB	TRKB	TK	Trk		
474	TRKC	NTRK3	TK	Trk		539126
475	FLT1	FLT1	TK	VEGFR		503620
476	FLT4	FLT4	TK	VEGFR		338031
477	KDR	KDR	TK	VEGFR		407170
478	IRAK1	IRAK1	TKL	IRAK		533953
479	IRAK2	IRAK2	TKL	IRAK		515034
480	IRAK3	IRAK3	TKL	IRAK		510342
481	IRAK4	IRAK4	TKL	IRAK		533692
482	LIMK1	LIMK1	TKL	LISK	LIMK	535225
483	LIMK2	LIMK2	TKL	LISK	LIMK	513539
484	TESK1	TESK1	TKL	LISK	TESK	527643
485	TESK2	TESK2	TKL	LISK	TESK	539979
486	LRRK1	LRRK1	TKL	LRRK		513994
487	LRRK2	LRRK2	TKL	LRRK		535652
488	HH498	TNNI3K	TKL	MLK	HH498	535940
489	DLK	DLK	TKL	MLK	LZK	
490	LZK	MAP3K13	TKL	MLK	LZK	505369
491	MLK1	LOC538340	TKL	MLK	MLK	538340
492	MLK2	MAP3K10	TKL	MLK	MLK	781037
493	MLK3	MAP3K11	TKL	MLK	MLK	514210
494	MLK4	LOC616014	TKL	MLK	MLK	616014
495	ZAK	ZAK	TKL	MLK	MLK	519251
496	TAK1	MAP3K7	TKL	MLK	TAK1	529146
497	ARAF	ARAF	TKL	RAF		540421
498	BRAF	BRAF	TKL	RAF		536051
499	KSR1	KSR1	TKL	RAF		100138565

500	KSR2	KSR2	TKL	RAF		617325
501	RAF1	RAF1	TKL	RAF		521196
502	ANKRD3	RIPK4	TKL	RIPK		508668
503	RIPK1	RIPK1	TKL	RIPK		504727
504	RIPK2	RIPK2	TKL	RIPK		534407
505	RIPK3	RIPK3	TKL	RIPK		507427
506	SgK288	SgK288	TKL	RIPK		
507	ALK1	ACVRL1	TKL	STKR	Type1	534536
508	ALK2	ACVR1	TKL	STKR	Type1	338068
509	ALK4	ACVR1B	TKL	STKR	Type1	539315
510	ALK7	ACVR1C	TKL	STKR	Type1	536380
511	BMPR1A	BMPR1A	TKL	STKR	Type1	404101
512	BMPR1B	BMPR1B	TKL	STKR	Type1	407128
513	TGFbR1	TGFBR1	TKL	STKR	Type1	282382
514	ACTR2	ACVR2A	TKL	STKR	Type2	281598
515	ACTR2B	ACVR2B	TKL	STKR	Type2	282131
516	BMPR2	BMPR2	TKL	STKR	Type2	407127
517	MISR2		TKL	STKR	Type2	
518	TGFbR2	TGFBR2	TKL	STKR	Type2	535376
519	ILK	ILK	TKL	TKL-Unique	ILK	540207
520	MLKL	MLKL	TKL	TKL-Unique		790225
521	Par-1L		TKL	TKL-Unique		

Protein Acc	RNA acc	Synonyms
NP_776411.1	NM_173986.2	-
XP_870006.1	XM_864913.2	-
NP_001178238.1	NM_001191309.1	
NP_001095972.1	NM_001102502.1	MGC155045
XP_618596.3	XM_618596.3	-
XP_001253770.1	XM_001253769.1	-
NP_776877.1	NM_174452.2	-
NP_777135.1	NM_174710.2	GRK2
NP_776925.1	NM_174500.2	-
XP_590012.3	XM_590012.3	-
NP_776756.1	NM_174331.2	GPRK5
NP_776757.1	NM_174332.3	GPRK7
NP_776598.1	NM_174173.2	RHOK
XP_002704808.1	XM_002704762.1	
XP_613922.3	XM_613922.3	-
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XP_616050.3	XM_616050.3	-
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XP_001249767.1	XM_001249766.1	-

NP_001069436.1	NM_001075968.1	MGC142356
XP_608273.2	XM_608273.2	-
NP_001092461.1	NM_001098991.1	MGC159776
XP_586141.3	XM_586141.3	-
NP_001071440.1	NM_001077972.1	-
NP_001103664.1	NM_001110194.1	-
NP_001029506.1	NM_001034334.1	MGC126900
XP_614963.2	XM_614963.3	-
NP_001104274.1	NM_001110804.1	-
XP_600086.3	XM_600086.3	-
NP_001094530.1	NM_001101060.1	-
NP_001032542.1	NM_001037465.1	MGC127145
XP_870655.1	XM_865562.2	-
NP_001179636.1	NM_001192707.1	-
NP_001029761.1	NM_001034589.1	MGC126902
NP_001098858.1	NM_001105388.1	MGC165932
XP_580898.3	XM_580898.3	-
XP_870050.2	XM_864957.2	-
NP_776390.1	NM_173965.2	TIE
NP_776389.1	NM_173964.2	MGC139569
XP_591681.3	XM_591681.3	SYTK1
XP_613650.2	XM_613650.3	TRKA
XP_002696558.1	XM_002696512.1	-
NP_001178061.1	NM_001191132.1	VEGFR1
NP_001178273.1	NM_001191344.1	
NP_001103470.1	NM_001110000.1	VEGFR2|flk-1
NP_001035645.1	NM_001040555.1	-
NP_001069164.1	NM_001075696.1	IRAK-2
XP_587469.2	XM_587469.3	-
NP_001069466.1	NM_001075998.1	IRAK-4|MGC137816
XP_002698230.1	XM_002698184.1	
NP_001033187.1	NM_001038098.1	MGC134164
XP_606040.2	XM_606040.3	-
XP_590674.3	XM_590674.3	-
XP_591774.3	XM_591774.3	-
XP_615760.3	XM_615760.3	-
XP_001250856.1	XM_001250855.1	MGC152244
NP_001095323.1	NM_001101853.1	MGC179376
XP_002691037.1	XM_002690991.1	-
XP_001249388.1	XM_001249387.1	-
NP_001095461.1	NM_001101991.1	MGC165851
XP_873070.2	XM_867977.2	-
XP_870499.1	XM_865406.2	-
NP_001075064.1	NM_001081595.1	MGC154981
NP_001014964.1	NM_001014964.1	MGC128775
XP_002687048.1	XM_002687002.1	-
XP_001788801.1	XM_001788749.1	

XP_874651.2	XM_869558.2	-
NP_001095975.1	NM_001102505.1	MGC165882
NP_001093797.1	NM_001100327.1	-
NP_001030184.1	NM_001035012.1	MGC127532
NP_001029782.1	NM_001034610.1	MGC127456
NP_001095354.1	NM_001101884.1	MGC152488
NP_001076948.1	NM_001083479.1	MGC139457
NP_788836.2	NM_176663.3	ActR-IA
XP_586402.3	XM_586402.3	-
XP_616508.3	XM_616508.3	-
NP_001070268.1	NM_001076800.1	BMPR-IA
NP_001098798.1	NM_001105328.1	ALK6|BMP15|BMPR-IB|BMPRIB
NP_777046.1	NM_174621.2	-
NP_776652.1	NM_174227.3	ACVR2
NP_776920.1	NM_174495.2	ActR-IIB|ActRIIB
XP_617592.3	XM_617592.3	bmprii
XP_615445.2	XM_615445.3	-
NP_001029865.1	NM_001034693.1	MGC129022
XP_001256760.1	XM_001256759.1	-

Description
v-akt murine thymoma viral oncogene homolog 1
v-akt murine thymoma viral oncogene homolog 2
v-akt murine thymoma viral oncogene homolog 3
CDC42 binding protein kinase gamma
CDC42 binding protein kinase alpha (DMPK-like)
Rho-associated, coiled-coil containing protein kinase 1
Rho-associated, coiled-coil containing protein kinase 2
adrenergic, beta, receptor kinase 1
adrenergic, beta, receptor kinase 2
G protein-coupled receptor kinase 4
G protein-coupled receptor kinase 5
G protein-coupled receptor kinase 7
G protein-coupled receptor kinase 1
microtubule associated serine/threonine kinase 1
microtubule associated serine/threonine kinase 3
microtubule associated serine/threonine kinase-like
LATS, large tumor suppressor, homolog 1 (Drosophila)
LATS, large tumor suppressor, homolog 2 (Drosophila)
serine/threonine kinase 38
serine/threonine kinase 38 like
protein kinase, cAMP-dependent, catalytic, alpha
protein kinase, cAMP-dependent, catalytic, beta
protein kinase, X-linked
3-phosphoinositide dependent protein kinase-1
protein kinase C, iota
protein kinase C, zeta
protein kinase C, alpha
protein kinase C, beta 1
protein kinase C, gamma
protein kinase C, delta
protein kinase C, epsilon
protein kinase C, eta
protein kinase C, theta
protein kinase, cGMP-dependent, type I
protein kinase, cGMP-dependent, type II
protein kinase N1
protein kinase N2
protein kinase N3
ribosomal protein S6 kinase, 90kDa, polypeptide 5
ribosomal protein S6 kinase, 90kDa, polypeptide 4
ribosomal protein S6 kinase, 70kDa, polypeptide 1
ribosomal protein S6 kinase, 70kDa, polypeptide 2

ribosomal protein S6 kinase, 90kDa, polypeptide 2
ribosomal protein S6 kinase, 90kDa, polypeptide 3
ribosomal protein S6 kinase, 90kDa, polypeptide 1
ribosomal protein S6 kinase, 90kDa, polypeptide 6
ribosomal protein S6 kinase, 52kDa, polypeptide 1
ribosomal protein S6 kinase-like 1
similar to Putative serine/threonine-protein kinase F31E3.2
serum/glucocorticoid regulated kinase 1
serum/glucocorticoid regulated kinase 2
serum/glucocorticoid regulated kinase family, member 3
serine/threonine kinase 32A
serine/threonine kinase 32B
serine/threonine kinase 32C
twinfilin, actin-binding protein, homolog 1 (Drosophila)
twinfilin, actin-binding protein, homolog 2 (Drosophila)
chaperone, ABC1 activity of bc1 complex homolog (S. pombe)
aarF domain containing kinase 4
aarF domain containing kinase 1
aarF domain containing kinase 5
aarF domain containing kinase 2
transient receptor potential cation channel, subfamily M, member 7
transient receptor potential cation channel, subfamily M, member 6
eukaryotic elongation factor-2 kinase
alpha-kinase 2
alpha-kinase 1
breakpoint cluster region
bromodomain containing 2
bromodomain containing 3
bromodomain containing 4
bromodomain, testis-specific
Fas-activated serine/threonine kinase
serine/threonine kinase 19
heat shock 22kDa protein 8
branched chain ketoacid dehydrogenase kinase
pyruvate dehydrogenase kinase, isozyme 1
pyruvate dehydrogenase kinase, isozyme 2
pyruvate dehydrogenase kinase, isozyme 3
pyruvate dehydrogenase kinase, isozyme 4
ataxia telangiectasia mutated
ataxia telangiectasia and Rad3 related
protein kinase, DNA-activated, catalytic polypeptide
mechanistic target of rapamycin (serine/threonine kinase)
SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)
transformation/transcription domain-associated protein
RIO kinase 1 (yeast)
RIO kinase 2 (yeast)
RIO kinase 3 (yeast)
TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa
tripartite motif-containing 33

tripartite motif-containing 24
calcium/calmodulin-dependent protein kinase I
pregnancy upregulated non-ubiquitously expressed CaM kinase
similar to Calcium/calmodulin-dependent protein kinase ID
calcium/calmodulin-dependent protein kinase IG
calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha
calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
calcium/calmodulin-dependent protein kinase (CaM kinase) II delta
calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
similar to Calcium/calmodulin-dependent protein kinase type IV (CAM kinase-GR) (CaMK IV)
protein kinase, AMP-activated, alpha 1 catalytic subunit
protein kinase, AMP-activated, alpha 2 catalytic subunit
BR serine/threonine kinase 1
BR serine/threonine kinase 2
CHK1 checkpoint homolog (S. pombe)
hormonally upregulated Neu-associated kinase
serine/threonine kinase 11
MAP/microtubule affinity-regulating kinase 1
MAP/microtubule affinity-regulating kinase 2
MAP/microtubule affinity-regulating kinase 3
MAP/microtubule affinity-regulating kinase 4
hypothetical LOC618482
maternal embryonic leucine zipper kinase
hypothetical LOC530210
NUAK family, SNF1-like kinase, 1
NUAK family, SNF1-like kinase, 2
PAS domain containing serine/threonine kinase
SNF1-like kinase 2
similar to KIAA0999 protein
SNF related kinase
serine/threonine kinase 40
serine/threonine kinase 33
CaM kinase-like vesicle-associated
calcium/calmodulin-dependent serine protein kinase (MAGUK family)
death-associated protein kinase 1
death-associated protein kinase 2
death-associated protein kinase 3
serine/threonine kinase 17a
serine/threonine kinase 17b
doublecortin-like kinase 2
doublecortin-like kinase 3
mitogen-activated protein kinase-activated protein kinase 2
mitogen-activated protein kinase-activated protein kinase 3
mitogen-activated protein kinase-activated protein kinase 5
MAP kinase interacting serine/threonine kinase 1
MAP kinase interacting serine/threonine kinase 2
myosin light chain kinase 3

myosin light chain kinase family, member 4
myosin light chain kinase 2
myosin light chain kinase
titin
phosphorylase kinase, gamma 1 (muscle)
phosphorylase kinase, gamma 2 (testis)
pim-1 oncogene
pim-2 oncogene
serine/threonine protein kinase pim-3-like
protein kinase D1
protein kinase D2
protein kinase D3
protein serine kinase H1
CHK2 checkpoint homolog (S. pombe)
tribbles homolog 1 (Drosophila)
tribbles homolog 2 (Drosophila)
tribbles homolog 3 (Drosophila)
obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
SPEG complex locus
kalirin, RhoGEF kinase
triple functional domain (PTPRF interacting)
testis-specific serine kinase 6
testis-specific serine kinase 2
testis-specific serine kinase 3
testis-specific serine kinase 4
similar to testis-specific serine kinase 5
casein kinase 1, alpha 1
casein kinase I beta
casein kinase 1, delta
casein kinase 1, epsilon
casein kinase 1, gamma 1
casein kinase 1, gamma 2
tau tubulin kinase 2
vaccinia related kinase 1
vaccinia related kinase 2
vaccinia related kinase 3
cell division cycle 2, G1 to S and G2 to M
cyclin-dependent kinase 2
cyclin-dependent kinase 3
cyclin-dependent kinase 10
cyclin-dependent kinase 4
cyclin-dependent kinase 6
cyclin-dependent kinase 5
cyclin-dependent kinase 7
cell division cycle 2-like 6 (CDK8-like)
cyclin-dependent kinase 8
cyclin-dependent kinase 9

cell division cycle 2-like 5 (cholinesterase-related cell division controller)
Cdc2-related kinase, arginine/serine-rich
cell division cycle 2-like 1 (PITSLRE proteins)
PCTAIRE protein kinase 1
PCTAIRE protein kinase 2
PCTAIRE protein kinase 3
cyclin-dependent kinase 14
cyclin-dependent kinase 15
cell cycle related kinase
cyclin-dependent kinase-like 1 (CDC2-related kinase)
cyclin-dependent kinase-like 2 (CDC2-related kinase)
cyclin-dependent kinase-like 3
cyclin-dependent kinase-like 4
CDC-like kinase 1
CDC-like kinase 2
CDC-like kinase 3
CDC-like kinase 4
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B
similar to Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
ual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3
hypothetical LOC531276
homeodomain interacting protein kinase 1
homeodomain interacting protein kinase 2
homeodomain interacting protein kinase 3
homeodomain interacting protein kinase 4
PRP4 pre-mRNA processing factor 4 homolog B (yeast)
glycogen synthase kinase 3 alpha
glycogen synthase kinase 3 beta
mitogen-activated protein kinase 3
mitogen-activated protein kinase 1
mitogen-activated protein kinase 6
mitogen-activated protein kinase 4
mitogen-activated protein kinase 7
mitogen-activated protein kinase 15
mitogen-activated protein kinase 8
mitogen-activated protein kinase 9
mitogen-activated protein kinase 10
nemo-like kinase
mitogen-activated protein kinase 14
mitogen-activated protein kinase 11
mitogen-activated protein kinase 13
mitogen-activated protein kinase 12
intestinal cell (MAK-like) kinase
male germ cell-associated kinase
renal tumor antigen
SFRS protein kinase 3
SFRS protein kinase 1
SFRS protein kinase 2

aurora kinase A
aurora kinase B
aurora kinase C
BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)
BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)
TP53 regulating kinase
calcium/calmodulin-dependent protein kinase kinase 1, alpha
calcium/calmodulin-dependent protein kinase kinase 2, beta
cell division cycle 7 homolog (S. cerevisiae)
casein kinase 2, alpha 1 polypeptide
casein kinase 2, alpha prime polypeptide
germ cell associated 2 (haspin)
conserved helix-loop-helix ubiquitous kinase
inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon
TANK-binding kinase 1
v-mos Moloney murine sarcoma viral oncogene homolog
AP2 associated kinase 1
cyclin G associated kinase
serine/threonine kinase 16
NIMA (never in mitosis gene a)- related kinase 10
NIMA (never in mitosis gene a)- related kinase 11
NIMA (never in mitosis gene a)-related kinase 2
NIMA (never in mitosis gene a)-related kinase 3
NIMA (never in mitosis gene a)-related kinase 4
NIMA (never in mitosis gene a)-related kinase 5
NIMA (never in mitosis gene a)-related kinase 6
NIMA (never in mitosis gene a)-related kinase 7
NIMA (never in mitosis gene a)- related kinase 8
NIMA (never in mitosis gene a)- related kinase 9
similar to SH3-binding kinase
SH3-binding domain kinase family, member 2
similar to protein kinase
PTEN induced putative kinase 1
serine/threonine kinase 35
PDLIM1 interacting kinase 1 like
similar to Gene model 1082, (NCBI)
testis expressed 14
nuclear receptor binding protein 1
nuclear receptor binding protein 2
U2AF homology motif (UHM) kinase 1
ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)
hypothetical LOC614899

hypothetical LOC514490
serine/threonine kinase 31
protein kinase domain containing, cytoplasmic homolog (mouse)
receptor interacting protein kinase 5
eukaryotic translation initiation factor 2-alpha kinase 3
eukaryotic translation initiation factor 2-alpha kinase 1
eukaryotic translation initiation factor 2-alpha kinase 2
polo-like kinase 1 (Drosophila)
polo-like kinase 2 (Drosophila)
polo-like kinase 3 (Drosophila)
polo-like kinase 4
similar to Serine/threonine-protein kinase PLK5 (Polo-like kinase 5) (PLK-5)
SCY1-like 1 (S. cerevisiae)
SCY1-like 2 (S. cerevisiae)
SCY1-like 3 (S. cerevisiae)
PX domain containing serine/threonine kinase
TBC1 domain containing kinase
tousled-like kinase 1
tousled-like kinase 2
PDZ binding kinase
TTK protein kinase
serine/threonine kinase 36, fused homolog (Drosophila)
unc-51-like kinase 1 (C. elegans)
unc-51-like kinase 2 (C. elegans)
unc-51-like kinase 3 (C. elegans)
unc-51-like kinase 4 (C. elegans)
phosphoinositide-3-kinase, regulatory subunit 4
protein kinase, membrane associated tyrosine/threonine 1
WEE1 homolog (S. pombe)
WEE1 homolog 2 (S. pombe)
WNK lysine deficient protein kinase 1
WNK lysine deficient protein kinase 2
WNK lysine deficient protein kinase 3
natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)
natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)
guanylate cyclase 2D, membrane (retina-specific)
guanylate cyclase 2F, retinal
guanylate cyclase 2C (heat stable enterotoxin receptor)
mitogen-activated protein kinase kinase kinase 1
mitogen-activated protein kinase kinase kinase 2
mitogen-activated protein kinase kinase kinase 3
mitogen-activated protein kinase kinase kinase 4
mitogen-activated protein kinase kinase kinase 5
mitogen-activated protein kinase kinase kinase 6
mitogen-activated protein kinase kinase kinase 15
yeast Sps1/Ste20-related kinase 4 (S. cerevisiae)
serine threonine kinase 39 (STE20/SPS1 homolog, yeast)

mitogen-activated protein kinase kinase kinase kinase 2
mitogen-activated protein kinase kinase kinase kinase 1
mitogen-activated protein kinase kinase kinase kinase 5
mitogen-activated protein kinase kinase kinase kinase 3
TRAF2 and NCK interacting kinase
misshapen-like kinase 1 (zebrafish)
Nik related kinase
serine/threonine kinase 4
serine/threonine kinase 3 (STE20 homolog, yeast)
myosin IIIA
myosin IIIB
p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)
similar to serine/threonine kinase
p21 (CDKN1A)-activated kinase 3
p21(CDKN1A)-activated kinase 4
p21(CDKN1A)-activated kinase 7
p21(CDKN1A)-activated kinase 6
serine/threonine kinase 10
STE20-like kinase (yeast)
protein kinase LYK5
STE20-related kinase adaptor beta
TAO kinase 1
TAO kinase 2
TAO kinase 3
serine/threonine kinase 24 (STE20 homolog, yeast)-like
serine/threonine protein kinase MST4
serine/threonine kinase 25 (STE20 homolog, yeast)
mitogen-activated protein kinase kinase 1
mitogen-activated protein kinase kinase 2
mitogen-activated protein kinase kinase 3
mitogen-activated protein kinase kinase 4
mitogen-activated protein kinase kinase 5
mitogen-activated protein kinase kinase 6
mitogen-activated protein kinase kinase 7
mitogen-activated protein kinase kinase kinase 8
mitogen-activated protein kinase kinase kinase 14
c-abl oncogene 1, receptor tyrosine kinase
v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)
activated p21cdc42Hs kinase
tyrosine kinase, non-receptor, 1
anaplastic lymphoma receptor tyrosine kinase
AXL receptor tyrosine kinase
c-mer proto-oncogene tyrosine kinase
TYRO3 protein tyrosine kinase
PTK7 protein tyrosine kinase 7
c-src tyrosine kinase
megakaryocyte-associated tyrosine kinase
discoidin domain receptor tyrosine kinase 1
discoidin domain receptor tyrosine kinase 2

epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
v-erb-a erythroblastic leukemia viral oncogene homolog 4
EPH receptor A1
EPH receptor A10
EPH receptor A2
EPH receptor A3
EPH receptor A4
EPH receptor A5
EPH receptor A6
EPH receptor A7
EPH receptor A8
EPH receptor B1
similar to protein tyrosine kinase
EPH receptor B2
EPH receptor B3
EPH receptor B4
EPH receptor B6
PTK2 protein tyrosine kinase 2
PTK2B protein tyrosine kinase 2 beta
fer (fps/fes related) tyrosine kinase
feline sarcoma oncogene
fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
acteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer
fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
fibroblast growth factor receptor 4
insulin-like growth factor 1 receptor
insulin receptor
insulin receptor-related receptor
Janus kinase 1
Janus kinase 2 (a protein tyrosine kinase)
similar to Janus kinase 3
tyrosine kinase 2
apoptosis-associated tyrosine kinase
lemur tyrosine kinase 2
met proto-oncogene (hepatocyte growth factor receptor)
macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
muscle, skeletal, receptor tyrosine kinase
fms-related tyrosine kinase 3
v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
platelet-derived growth factor receptor, alpha polypeptide
platelet-derived growth factor receptor, beta polypeptide
ret proto-oncogene
receptor tyrosine kinase-like orphan receptor 1
receptor tyrosine kinase-like orphan receptor 2
RYK receptor-like tyrosine kinase

B lymphoid tyrosine kinase
PTK6 protein tyrosine kinase 6
Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
fyn-related kinase
FYN oncogene related to SRC, FGR, YES
hemopoietic cell kinase
lymphocyte-specific protein tyrosine kinase
v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites
v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
spleen tyrosine kinase
zeta-chain (TCR) associated protein kinase 70kDa
BMX non-receptor tyrosine kinase
Bruton agammaglobulinemia tyrosine kinase
IL2-inducible T-cell kinase
tec protein tyrosine kinase
TXK tyrosine kinase
tyrosine kinase with immunoglobulin-like and EGF-like domains 1
TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)
serine/threonine/tyrosine kinase 1
neurotrophic tyrosine kinase, receptor, type 1
neurotrophic tyrosine kinase, receptor, type 3
fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
fms-related tyrosine kinase 4
kinase insert domain receptor (a type III receptor tyrosine kinase)
interleukin-1 receptor-associated kinase 1
interleukin-1 receptor-associated kinase 2
interleukin-1 receptor-associated kinase 3
interleukin-1 receptor-associated kinase 4
LIM domain kinase 1
LIM domain kinase 2
testis-specific kinase 1
testis-specific kinase 2
leucine-rich repeat kinase 1
leucine-rich repeat kinase 2
TNNI3 interacting kinase
mitogen-activated protein kinase kinase kinase 13
mitogen-activated protein kinase kinase kinase 9
mitogen-activated protein kinase kinase kinase 10
mitogen-activated protein kinase kinase kinase 11
similar to mixed lineage kinase 4 (KIAA1804)
sterile alpha motif and leucine zipper containing kinase AZK
mitogen-activated protein kinase kinase kinase 7
v-raf murine sarcoma 3611 viral oncogene homolog
v-raf murine sarcoma viral oncogene homolog B1
kinase suppressor of ras 1

kinase suppressor of ras 2
v-raf-1 murine leukemia viral oncogene homolog 1
receptor-interacting serine-threonine kinase 4
receptor (TNFRSF)-interacting serine-threonine kinase 1
receptor-interacting serine-threonine kinase 2
receptor-interacting serine-threonine kinase 3
activin A receptor type II-like 1
activin A receptor, type I
activin A receptor, type IB
activin A receptor, type IC
bone morphogenetic protein receptor, type IA
bone morphogenetic protein receptor, type IB
transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)
activin A receptor, type IIA
activin A receptor, type IIB
bone morphogenetic protein receptor, type II (serine/threonine kinase)
transforming growth factor, beta receptor II (70/80kDa)
integrin-linked kinase
mixed lineage kinase domain-like

Chr	**cDNA lenght**	**ORF length**	**Protein size**	**kinase domain (KD)n size**
21	1691	1443	480	259
18	3460	1446	481	258
16	1776	1440	479	258
18	2434	1857	618	269
29	5018	4632	1543	266
16	5265	5265	1754	267
21	6560	5271	1756	267
24	4793	4104	1367	263
11	5053	4167	1388	263
17	5837	NA	1820	110
29	2520	2070	689	263
17	2791	2067	688	263
6	1752	1752	583	263
26	2539	1773	590	263
7	2853	1725	574	259
1	2227	1659	552	264
12	2898	1686	561	266
7	4719	4719	1572	274
3	5414	5136	1711	274
7	5651	4101	1366	274
20	7677	7302	2433	274
13	2736	2643	880	276
3	795	795	264	161
9	7537	3372	1123	306
12	4733	3048	1015	305
23	3545	1398	465	294
5	4209	1395	464	294
7	2522	1056	351	255
3	1750	1056	351	255
X	1139	957	318	255
25	1820	1605	534	265
1	2813	1791	596	269
16	2240	1785	594	267
19	2324	2019	672	259
25	2955	2022	673	259
18	3032	2094	697	264
22	3019	2031	676	255
11	5491	2214	737	261
10	2389	2049	682	260
13	3181	2121	706	255
26	2775	2016	671	260
6	2289	2289	762	259
7	3059	2835	944	260
3	3226	2946	981	260
11	3386	2661	886	260
10	4103	2346	781	270
29	3061	2316	771	269
19	1585	1584	527	262
29	1791	1560	519	262

9	3605	2202	733	260
X	2927	2223	740	260
2	3157	2208	735	260
X	2635	2235	744	258
16	4415	3186	1061	232
10	3608	1326	441	283
19	1628	819	272	171
9	2382	1296	431	258
13	1755	1104	367	258
14	3363	1473	490	258
7	1852	1101	366	259
6	1479	1479	492	261
26	3409	2889	962	261
5	1242	1053	350	NA
22	1614	1050	349	NA
16	2903	1947	648	NA
18	2149	1578	525	NA
10	2274	1572	523	NA
14	1927	1743	580	NA
4	2160	1878	625	NA
10	7214	5601	1866	NA
8	6756	6480	2159	NA
25	5774	2172	723	NA
21	5352	NA	1783	NA
24	6916	6360	2119	NA
6	4289	3774	1257	NA
17	3127	2967	988	NA
23	2412	2412	803	NA
11	3093	2169	722	NA
7	5608	4107	1368	NA
3	2936	2808	935	NA
4	1829	1632	543	NA
23	2416	510	169	NA
17	1906	591	196	NA
25	1872	1239	412	NA
2	3859	1317	438	NA
19	2277	1032	343	NA
X	2082	1248	415	NA
4	3805	1224	407	NA
15	9406	9165	3054	NA
1	8268	7935	2644	NA
14	12953	12375	4124	NA
16	8303	7656	2551	NA
25	15784	10977	3658	NA
25	12190	11496	3831	NA
23	1952	NA	544	NA
7	1871	1656	551	NA
24	4335	1560	519	NA
X	7765	6090	2029	NA
3	3622	3330	1109	NA

18	2934	2202	733	NA
4	3365	2808	935	NA
22	1456	1113	370	257
X	1410	1029	342	256
13	1510	1140	379	272
16	2357	1425	474	255
7	3032	1437	478	259
4	1912	1629	542	259
6	1537	1500	499	259
28	1780	1488	495	259
10	1532	1392	463	255
20	1698	1698	565	268
3	2153	1659	552	253
18	3018	2481	826	252
29	2175	2175	724	265
29	2276	1431	476	257
1	2028	2028	675	261
7	1623	1326	441	264
16	2681	2388	795	252
29	2274	2274	757	252
21	2995	2379	792	252
18	1947	1329	442	252
14	1518	1518	505	250
8	2445	1953	650	253
20	2122	1311	436	252
5	2227	1989	662	252
16	1476	1476	491	251
3	4495	4128	1375	253
15	3639	2721	906	252
15	6891	3945	1314	252
1	1797	NA	599	255
22	5000	2085	694	254
3	1749	1311	436	195
15	2228	1461	486	266
22	2932	1515	504	263
X	3302	2727	908	265
8	2519	4293	1430	263
10	1579	1452	483	263
7	3120	1365	454	263
4	1760	1245	414	261
2	1577	1119	372	260
12	1296	NA	431	258
17	2304	2304	767	258
22	2607	2607	868	258
16	1747	1212	403	262
22	2654	1155	384	261
17	1751	1419	472	285
3	2553	1263	420	286
7	1504	1395	464	286
18	2457	2361	786	256

23	1206	1206	401	256
13	2249	1872	623	256
1	3983	3531	1176	256
2	5	NA	NA	255
25	2042	1164	387	269
25	1717	1221	406	268
23	2753	942	313	253
X	2155	1233	410	255
5	1888	981	326	254
21	3323	2553	850	257
18	2894	2652	883	257
11	5173	2673	890	257
18	3390	1275	424	258
17	1992	1605	534	267
14	3504	1119	372	245
11	3047	1032	343	245
13	1988	1074	357	245
7	5737	5643	1880	254
2	10000	9846	3281	254
1	8961	8961	2986	255
20	4672	4212	1403	255
7	1350	822	273	256
17	1459	1104	367	261
17	1548	1077	358	261
2	1240	810	269	256
10	1220	1017	338	281
14	1639	1188	395	277
7	1429	978	325	261
X	1903	1011	336	261
19	3533	1230	409	261
5	2133	1401	466	261
10	1924	1314	437	264
7	2383	1245	414	263
7	4603	1341	446	262
23	3834	3834	1277	254
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5	1525	1191	396	267
11	2106	1296	431	264
18	1956	1356	451	240
28	1258	894	297	284
5	1369	897	298	283
19	1576	918	305	283
18	1644	1086	361	285
5	1369	912	303	290
4	1619	981	326	288
4	1100	879	292	283
20	1376	1041	346	284
9	2895	1503	500	316
12	2484	1332	443	293
11	1747	1119	372	297

4	7268	4539	1512	294
19	5981	4473	1490	294
16	2916	2316	771	286
X	3105	1491	496	282
5	3625	1572	523	282
16	2847	1416	471	282
4	1605	1486	494	285
2	1305	1305	434	285
8	2119	1041	346	285
10	1889	1059	352	284
6	2549	1710	569	284
7	1776	1776	591	283
11	1216	948	315	283
X	2949	2949	982	285
2	1831	1458	485	317
3	2131	1500	499	317
21	1901	1473	490	317
7	2081	1446	481	316
1	5114	2292	763	321
18	2567	2067	688	321
5	1800	1800	599	314
16	2180	1764	587	314
5	1914	1914	637	297
3	3645	3645	1214	331
4	3606	3573	1190	329
15	4874	3651	1216	329
18	3360	1851	616	337
23	4163	3027	1008	313
18	2506	1488	495	285
1	1861	1299	432	298
25	2135	1089	362	289
17	1272	1083	360	289
10	3901	2169	722	297
24	1755	1080	359	265
19	3054	2346	781	293
14	1959	1611	536	292
28	3047	1284	427	296
7	4602	1275	424	296
6	2913	1281	426	296
19	4073	1584	527	290
23	4284	1083	360	285
5	2290	1056	351	272
23	1402	1101	366	284
5	1727	1104	367	285
23	4005	1887	628	281
23	2257	1872	623	281
21	1731	1302	433	282
X	2100	1698	565	486
23	4291	1968	655	574
4	5185	2133	710	606

13	2000	1209	402	251
19	2164	1035	344	251
18	1071	915	304	251
20	1053	1053	350	233
11	3750	3237	1078	269
10	4018	3189	1062	265
13	1406	762	253	220
19	2043	1518	505	285
17	1957	1740	579	282
3	3466	1731	576	514
13	2328	1176	391	285
18	1529	1053	350	286
19	2999	2346	781	314
26	3442	2223	740	274
27	3490	2271	756	275
16	3106	2157	718	318
5	3348	2190	729	296
19	2955	2931	976	262
25	2937	2778	925	262
14	1130	1023	340	272
11	3195	2877	958	275
6	3437	3375	1124	291
6	4394	3807	1268	274
2	1482	918	305	271
8	1272	NA	424	255
22	2505	2505	834	246
1	1731	1731	576	259
16	2142	1338	445	264
12	2089	1488	495	254
22	3480	2364	787	256
12	1644	1644	547	256
11	2550	942	313	261
16	1680	912	303	262
19	2147	2097	698	255
10	5508	2934	977	257
25	1077	1077	358	265
18	1503	1503	500	264
18	1095	1095	364	262
2	2971	1767	588	352
27	4155	NA	1384	313
21	4647	4647	1548	337
13	1540	1209	402	329
2	1394	1290	429	333
18	2025	2025	674	111
19	4808	4482	1493	305
11	2165	1608	535	264
14	3298	1500	499	270
3	2115	1260	419	282
16	2779	2172	723	110
11	1965	1965	654	266

27	3345	1053	350	251
4	2922	2922	973	237
11	2142	1482	493	228
16	5138	2787	928	264
10	5179	4956	1651	412
11	4607	3348	1115	484
25	2860	1899	632	418
11	2267	1602	533	256
25	2187	1809	602	253
20	2903	2058	685	253
3	2371	1944	647	253
17	3583	2682	893	254
7	1941	1941	646	255
29	2644	2424	807	231
5	5581	2790	929	296
16	2907	2259	752	221
22	2927	1740	579	248
6	2931	2931	976	256
2	3897	2289	762	279
19	3037	2313	770	280
8	1972	975	324	288
9	2971	2571	856	266
2	4460	3948	1315	251
17	3805	3168	1055	263
19	3522	3114	1037	264
21	2562	1419	472	257
22	3788	3678	1225	277
1	4994	4077	1358	284
25	2579	1494	497	250
15	2561	1269	422	271
4	1701	1701	566	275
5	8732	NA	2118	226
8	6855	6681	2226	259
Un	2460	NA	700	259
19	4010	3660	1219	259
3	3818	3195	1064	269
8	3276	3144	1047	270
19	4594	3333	1110	274
X	5956	3312	1103	280
5	3772	3219	1072	273
20	4881	4530	1509	268
2	3025	1863	620	261
19	2187	1851	616	261
9	5630	4662	1553	259
9	5283	4101	1366	261
2	4109	3888	1295	254
X	5876	4473	1490	256
2	3984	3984	1327	264
22	1833	1584	527	275
2	3229	1614	537	275

29	2885	2466	821	258
18	2653	2463	820	258
10	4458	2541	846	258
11	4184	2685	894	258
11	4312	3999	1332	267
1	6668	3918	1305	248
19	4916	3933	1310	265
X	5847	4761	1586	289
13	1911	1464	487	252
14	3034	1830	609	252
13	4908	4908	1635	267
2	2985	2985	994	267
29	3079	1635	544	252
9	4292	1038	345	252
X	2336	1635	544	252
18	2616	1782	593	252
13	2511	2160	719	252
10	3868	2046	681	252
20	5256	2904	967	259
26	3176	2967	988	259
19	2294	1122	373	311
2	2001	1299	432	312
19	6255	3006	1001	254
25	4145	3150	1049	254
17	4101	2697	898	254
12	1744	1302	433	251
X	1743	1365	454	251
3	1618	1284	427	251
10	2376	1182	393	294
7	1633	1203	400	298
19	2233	1044	347	262
19	3848	1239	412	266
10	1311	1311	436	253
19	1527	1005	334	262
7	3524	1407	468	261
13	2553	1407	468	253
19	4323	2862	953	267
11	3952	3456	1151	252
16	3539	3441	1146	252
1	4276	3216	1071	260
19	2611	1992	663	262
11	4866	4866	1621	270
18	4510	3012	1003	269
11	3474	2928	975	266
10	3746	2670	889	262
23	4281	3450	1149	266
21	2105	1353	450	246
7	1895	1458	485	244
23	3770	2748	915	295
3	3105	2568	855	287

22	3633	3633	1210	258
19	3786	3786	1261	258
5	5448	4011	1336	257
2	3459	2190	1152	258
4	3207	2952	983	260
3	3027	3027	1008	255
2	3264	2928	975	257
1	3050	2955	984	257
2	3313	2973	990	257
6	1712	NA	569	257
1	3182	NA	1059	300
9	3321	2997	998	257
2	3156	3156	1051	258
1	3830	2889	962	260
3	504	504	167	85
2	3886	2898	965	260
1	3784	2994	997	260
25	3975	3021	1006	285
4	3175	2979	992	247
14	4541	3186	1061	264
8	4131	3030	1009	260
7	2636	2469	822	254
X	516	NA	172	138
21	2739	2469	822	256
27	3400	2463	820	277
26	3944	2469	822	277
6	2562	2409	802	277
7	2974	2403	800	277
21	4483	3615	1204	270
7	4770	3876	1291	268
3	3906	3906	1301	270
3	4331	3477	1158	278
8	4695	3399	1132	278
7	3775	3318	1105	283
7	5781	3558	1185	266
19	4706	4104	1367	274
25	4751	NA	1422	275
18	4631	NA	1431	320
4	4823	4155	1384	261
22	4489	4206	1401	253
8	3259	2610	869	281
12	3416	2925	974	334
7	3825	2895	964	330
6	5078	2967	988	336
6	3270	3270	1089	358
7	4452	3312	1103	359
28	3541	3342	1113	284
3	3299	2727	908	307
8	4006	2823	940	307
1	2593	1617	538	267

8	660	660	219	218
8	2114	1506	501	251
13	1353	1353	450	253
2	2195	1584	527	250
9	3436	1545	514	258
9	2409	1614	537	250
13	2046	1512	503	251
2	2080	1530	509	251
14	2750	1539	512	252
13	1697	1629	542	249
13	1485	1485	494	251
24	4997	1626	541	250
8	2532	1818	605	249
11	3947	1854	617	249
X	1965	1965	654	252
X	2577	1980	659	252
7	4393	1863	620	250
6	2538	1956	651	250
6	2312	1584	527	252
3	3631	3411	1136	269
8	4625	3378	1125	269
5	1592	1269	422	269
3	2603	2388	795	275
8	3538	2514	837	273
21	3380	2478	825	272
12	4080	4080	1359	328
7	4383	4068	1355	325
6	5998	4071	1356	327
X	2215	2157	718	310
22	2823	1866	621	268
5	2177	1743	580	279
5	2590	1386	461	269
25	3086	1944	647	266
17	2274	1917	638	271
8	2192	1893	630	258
3	1569	1569	522	260
21	6561	6048	2015	283
5	7871	7608	2535	246
3	3020	2508	835	261
5	3332	2685	894	239
1	3425	2901	966	240
10	3312	3312	1103	260
18	1077	1077	358	193
29	3595	2595	864	260
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2	2778	2403	800	244
9	3388	1740	579	248
X	2355	1821	606	258
4	2492	2298	765	260
19	2913	2334	777	264

17	1836	1836	611	262
22	3209	2007	668	260
1	3794	2358	785	264
23	2403	1998	665	269
14	1688	1623	540	267
10	1802	1512	503	261
15	1884	NA	628	215
5	2494	1512	503	288
2	2808	1530	509	288
5	2578	1518	505	288
2	1662	1479	492	288
28	4059	1599	532	288
6	3498	1509	502	288
8	2060	1500	499	288
2	4428	1542	513	281
22	1833	1539	512	291
2	3823	2745	914	307
5	1716	1716	571	312
22	4280	1704	567	295
15	1701	1359	452	257
18	2323	1407	468	263
14	759	759	252	177

VAIK	**HRD**	**DFG**	**Catalytic activity**
YAMK	YRD	DFG	Active
YAMK	YRD	DFG	Active
YAMK	YRD	DFG	Active
YAMK	HRD	DFG	Active
FAMK	HRD	DFG	Active
FAMK	HRD	DFG	Active
YAMK	HRD	DFG	Active
YAMK	HRD	DFD	Active
YAMK	HRD	DFD	Active
			partial
YAMK	YRD	DLG	Active
YAMK	YRD	DLG	Active
YACK	YRD	DLG	Active
YACK	YRD	DLG	Active
YACK	YRD	DLG	Active
YACK	YRD	DLG	Active
YACK	YRD	DLG	Active
FAMK	HRD	DFG	Active
FAMK	HRD	DFG	Active
FAIK	HRD	DFG	Active
FAMK	HRD	DFG	Active
YAVK	HRD	DFG	Active
---	HRD	DFG	Inactive
YATK	HRD	DFG	Active
YAMK	HRD	DFG	Active
YAMK	HRD	DFG	Active
YAMK	HRD	DFG	Active
YAMK	YRD	DFG	Active
YAMK	YRD	DFG	Active
FALK	YRD	DFG	Active
YAIK	HRD	DFG	Active
YAMK	YRD	DYG	Active
YAMK	YRD	DYG	Active
YAIK	YRD	DFG	Active
YAVK	YRD	DFG	Active
YAIK	YRD	DFG	Active
FAIK	YRD	DFG	Active
YAVK	YRD	DFG	Active
YAVK	YRD	DFG	Active
FAIK	YRD	DFG	Active
FAMK	YRD	DFG	Active
FAMK	YRD	DFG	Active
FAIK	YRD	DFG	Active
FAIK	YRD	DFG	Active
YAIK	YRD	DFG	Active
YAMK	YRD	DFG	Active
YAMK	YRD	DFG	Active
FAMK	YRD	DFG	Active
YAMK	YRD	DFG	Active

YAMK	YRD	DFG	Active
YAMK	YRD	DFG	Active
YAMK	YRD	DFG	Active
YAMK	YRD	DFG	Active
LKTE	CRD	**YFS**	Inactive
LHLE	CRD	**YFG**	Inactive
FAVK	HRD	DFG	Active
YAVK	YRD	DFG	Active
YAVK	YRD	DFG	Active
YAVK	YRD	DFG	Active
YMNK	HRD	DFN	Active
YAMK	HRD	DFN	Active
YAMK	HRD	DFN	Active
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FLVK	IGDRH	DFG	Active
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			Atypical
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			Atypical

			Atypical
			Atypical
VAIK	HRD	DFG	Active
VALK	HRD	DFG	Active
FAVK	HRD	DFG	Active
FALK	HRD	DFG	Active
YAAK	HRD	DFG	Active
YAAK	HRD	DFG	Active
YAAK	HRD	DFG	Active
YAAK	HRD	DFG	Active
YALK	HRD	DRG	Active
VAVK	HRD	DFG	Active
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VAIK	HRD	DFG	Active
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VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
RAVK	HKD	DLG	Active
VAVK	HRD	DFG	Active
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VAIK	HRD	DFG	Active
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VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
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VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VVVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
YVIK	FYD	DGR	Active
WAIK	HRD	DFG	Active
HTCK	HRN	DFH	Inactive
FAVK	HRD	GFG	Inactive
YAAK	HFD	DFG	Active
YAAK	HFD	DFG	Active
YAAK	HFD	DFG	Active
FAAK	HLD	DFG	Active
YAAK	HLD	DFG	Active
YALK	HRD	DFG	Active
FALK	HRD	DFG	Active
YAMK	HRD	DFG	Active
FALK	HRD	DFG	Active
CALK	HRD	DFG	Active
FALK	HRD	DFG	Active
YAVK	HRD	DLG	Active
YAVK	HRD	DLG	Active
LAAK	HLD	DFG	Active

LAAK	HLD	DFG	Active
LAAK	HLD	DFG	Active
WAGK	HLD	DFG	Active
YMAK	HFD	**EFG**	Inactive
YAVK	HRD	DFG	Active
FAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HCD	DFG	Active
VAVK	HCD	DFG	Active
VAIK	HCD	DFG	Active
YAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
LRCK	LGD	**SLE**	Inactive
LVCK	LRD	**SLE**	Inactive
YICK	LRD	**NLE**	Inactive
CAAK	HLD	DFG	Active
FAAK	HLD	DFG	Active
VAVK	HLD	DLE	Active
VATK	HLD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	GRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	YRD	DFG	Active
VAIK	YRD	DFG	Active
VAIK	YRD	DFG	Active
VALK	HRD	DFG	Active
VALK	HRD	DFG	Active
CVVK	HGD	DYG	Active
HVIK	HGD	DYG	Active
HQDK	HGN	**GYG**	Inactive
VAMK	HRD	DFG	Active
VALK	HRD	DFG	Active
VALK	HRD	DFG	Active
VALK	HRD	DFG	Active
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VALK	HRD	DFG	Active
VALK	HRD	DFG	Active
VAIK	HRD	DFG	Active
YALK	HRD	DMG	Active
YALK	HRD	DMG	Active
VALK	HRD	DFG	Active

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VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VELK	HRD	DFG	Active
VAVK	HTD	DFG	Active
VALK	HTD	DWD	Active
VALK	HTD	DFG	Active
VAVK	HTD	DFG	Active
VAIK	HCD	DFG	Active
VAIK	HCD	DFG	Active
VALK	HCD	DFG	Active
VALK	HCD	DFG	Active
VALK	HCD	DFG	Active
VAIK	HAD	DFG	Active
VAIK	HAD	DFG	Active
VAIK	HAD	DFG	Active
VAIK	HAD	DFG	Active
VAVK	HAD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VALK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
IAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
YACK	HRD	DFG	Active
VALK	HTD	DLG	Active
VAMK	HTD	DLG	Active
VAMK	HTD	DLG	Active

LALK	HRD	DFG	Active
VALK	HRD	DFG	Active
VALK	HRD	DFG	Active
VTLK	**RRD**	**LIS**	Inactive
FALK	HGD	DLG	Active
TIIK	HGD	DFS	Active
AVVK	HGD	DFG	Active
YAMK	HRD	DFG	Active
YAMK	HRD	DFG	Active
IALK	HRD	DFG	Active
VVVK	HRD	DWG	Active
VVVK	HRD	DWG	Active
VALK	HRD	**TLN**	Inactive
IAIK	HRD	DLG	Active
IAIK	HRD	DLG	Active
VAVK	HRD	DFG	Active
FAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HLD	DFG	Active
CALK	HRD	DFG	Active
YALK	HRD	DFG	Active
YALK	HRD	DFG	Active
YALK	HRD	DLG	Active
YVIK	HRD	DFG	Active
LAMK	HRD	DFG	Active
KVLK	HRD	DFG	Active
LVWK	HRD	DFG	Active
FAMK	HRD	DFG	Active
YVIK	HRD	DLG	Active
CVIK	HRD	DFG	Active
VALK	HRD	DLG	Active
VALK	HRD	DLG	Active
VIIK	HRD	DFG	Active
VVWK	HRD	DYG	Active
MALK	HRD	DFG	Active
LALK	YRD	DFG	Active
VALK	HAD	DLG	Active
LAIK	HRD	DFG	Active
YAVK	HRD	**NFL**	Inactive
YAVK	HCD	**NFS**	Inactive
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VKAK			partial
VTVK	**HRS**	**NLE**	Inactive
VVWN	**HGN**	**VAP**	Inactive
VVWN	**HGN**	**VWH**	Inactive
GALK	HAD	DFG	Active
VAVK	HQD	DFD	Active
TKVK	***HRN***	DLS	Inactive

VALS	**TRV**	**NFS**	Inactive
ILLK	**HGS**	DFD	Inactive
VALK	LLD	DLD	Active
CALK	HRD	DLG	Active
YAVK	HRD	DFG	Active
YAIK	HRD	DFG	Active
YAIK	HRD	DFG	Active
YVIK	HRD	DFG	Active
FAGK	HRD	DFG	Active
YAAK	HRD	DFG	Active
YAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
FALK	HRD	DLG	Active
VSIF	**HNN**	GLD	Inactive
VAVF	HGN	GFD	Inactive
ASVF	ARD	**GME**	Inactive
LVLS	**YGH**	DLE	Inactive
LTPN	**HRA**	**KFG**	Inactive
AAVK	HYD	DFG	Active
VAVK	HYD	DFG	Active
WAVK	HGD	DVG	Active
HAIK	HSD	DFG	Active
VALK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HLD	DFG	Active
VAIL	FCD	**NFC**	Inactive
VVVK	HGD	DFA	Active
YAVK	HLD	DFG	Active
YAIK	HMD	DLG	Active
YAIK	HLD	DLG	Active
VAWC	HRD	DLG	Active
VAWC	HRD	DLG	Active
VAWC	HRD	DLG	Active
VAWC	HRD	DLG	Active
VAVK	**HGN**	DYG	Inactive
VAIK	HGS	DYG	Inactive
VWLK	**HGR**	DHG	Inactive
VWLK	**HGR**	DYG	Inactive
VILK	**HGR**	DFG	Inactive
MAVK	HRD	DFG	Active
LAVK	HRD	DFG	Active
LASK	HRD	DFG	Active
MAMK	HRD	DFG	Active
IAIK	HRD	DFG	Active
IAIK	HRD	DFG	Active
IAIK	HRD	DFG	Active
IAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active

AAVK	HRD	DFG	Active
VALK	HRD	DFG	Active
AAVK	HRD	DFG	Active
AAIK	HRD	DFG	Active
AAIK	HRD	DFG	Active
AAIK	HRD	DFG	Active
AAIK	HRD	DFG	Active
TAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
AAVK	HRD	DFG	Active
AAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
AAAK	HRD	DFG	Active
AAAK	HRD	DFG	Active
VTVR	**HRS**	**GLR**	Inactive
VTIK	**HRS**	**GLS**	Inactive
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
MARK	HRD	DFG	Active
MARK	HRD	DFG	Active
MAVK	HRD	DFG	Active
MAVK	HRD	DFG	Active
LAVK	HRD	DFG	Active
MAVK	HRD	DFG	Active
IAVK	HRD	DFG	Active
MACK	HHD	DFG	Active
CAVK	HGD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VLVK	HKD	**ALG**	Inactive
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active

VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VCIK	**HRN**	DFG	Inactive
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVH	**HRG**	**GFG**	Inactive
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
			partial
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIQ	**HRS**	**RLG**	Inactive
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
	HRD	DFG	partial
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VALK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VVVK	HSD	DYG	Active
VIVK	HSD	DYG	Active
VVVK	HSD	DYG	Active
CAVK	HRD	DFG	Active
CAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HKD	DLG	Active
VAIK	HKD	DLG	Active
AFVK	HKD	DNA	Active

AFVK	HQD	DNA	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAIK	HRD	DFG	Active
AAIK	HRD	DFG	Active
AAIK	HRD	DFG	Active
VTLK	HGD	**GLG**	Inactive
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
YAVK	HGD	DFG	Active
FVFK	HSN	HSM	Inactive
YAIK	**CGS**	DFA	Inactive
VAVK	HRD	DFG	Active
QAIK	HRD	DFG	Active
QAIK	HRD	DFG	Active
MVLK	HRD	DFG	Active
NVHK	HRD	DFG	Active
VAVK	FCD	DYG	Active
VAVK	YRD	DYG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
TVLK	EID	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIR	HKD	DFG	Inactive

VAIR	HKD	DFG	Inactive
VAVK	HRD	DFG	Active
LAIK	HLD	DFG	Active
VILK	HRD	DLG	Active
VAVK	HHD	DFG	Active
VAVK	HRD	DFG	Active
EAAK	HLD	DFG	Active
VAVK	HRD	DLG	Active
VAVK	HRD	DLG	Active
VAVK	HRD	DLG	Active
VAVK	HRD	DLG	Active
VAVK	HRD	DLG	Active
VAVK	HRD	DLG	Active
VAVK	HRD	DLG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAVK	HRD	DFG	Active
VAIK	HRD	DLG	Active
VAVK	HRD	DFG	Active
IVVK	**RHA**	**---**	Inactive
VAIK	**HRN**	**ELS**	Inactive
			partial

Ensemble Pep	Gene	Transcript	% identity in KD
			97,7
			100
			100
			96,7
ENSBTAP00000015459	ENSBTAG00000011639	ENSBTAT00000015459	96,6
			99,3
			98,5
			100
			98,1
			91,7
			100
			96,6
			84,8
ENSBTAP00000001500	ENSBTAG00000001126	ENSBTAT00000001500	98,9
			93,2
			91,3
			88,7
ENSBTAP00000007991			97,8
			99,3
			97,8
			100
ENSBTAP00000018430	ENSBTAG00000013876	ENSBTAT00000018430	92,4
			98,7
			96,4
			99,7
			99,3
			99,6
			100
			89,9
			98,8
			100
ENSBTAP00000024029	ENSBTAG00000018049	ENSBTAT00000024029	99,6
ENSBTAP00000023654	ENSBTAG00000017788	ENSBTAT00000023654	99,2
			99,6
			99,2
			88,6
			99,6
			98,5
			98,4
			100
			99,2
			99,2
ENSBTAP00000045293	ENSBTAG00000033983	ENSBTAT00000048212	99,2
			94,2
			96,3
ENSBTAP00000020910			97,4
			100
ENSBTAP00000043326	ENSBTAG00000014351	ENSBTAT00000045990	98,1

			98,8
			99,6
			99,6
			99,2
			93,2
			63,8
			87,9
			98,4
			96,9
			99,2
			91,5
			95,8
			96,2
ENSBTAP00000019684	ENSBTAG00000014794	ENSBTAT00000019684	

			98,8
			96,9
ENSBTAP00000029173	ENSBTAG00000022777	ENSBTAT00000029173	100
			98,8
			100
ENSBTAP00000039020	ENSBTAG00000034436	ENSBTAT00000039220	99,6
			99,6
			100
			100
			94
			99,2
			100
ENSBTAP00000019220	ENSBTAG00000014456	ENSBTAT00000019220	81,9
			96,9
			97,9
			86,1
			99,2
			100
			98,4
			99,6
			95,3
			95,6
ENSBTAP00000013805			100
			95,6
			90,9
			97,2
			99,6
			93,7
			98
			98,8
			90,2
			89
			100
			99,2
			97,6
			99,6
ENSBTAP00000010716	ENSBTAG00000008151	ENSBTAT00000010716	93,9
			95,8
ENSBTAP00000032957			100
			98,1
			94,2
ENSBTAP00000018325	ENSBTAG00000013790	ENSBTAT00000018325	98,9
			98,1
			98,2
			96,5
			98,2
ENSBTAP00000015445	ENSBTAG00000011628	ENSBTAT00000015445	96,9

ENSBTAP00000008354	ENSBTAG00000006359	ENSBTAT00000008354	93,4
			97,7
ENSBTAP00000007991	ENSBTAG00000006080	ENSBTAT00000007991	98,9
			96,5
			94,8
			98,1
			98,8
ENSBTAP00000009545	ENSBTAG00000007256	ENSBTAT00000009545	94,5
			96,9
			100
			98,4
ENSBTAP00000009942	ENSBTAG00000007556	ENSBTAT00000009942	99,6
			100
			95,5
			98,3
			99,6
ENSBTAP00000008672	ENSBTAG00000006601	ENSBTAT00000008672	88,9
ENSBTAP00000001378	ENSBTAG00000001037	ENSBTAT00000001378	86,8
			94,9
ENSBTAP00000010653	ENSBTAG00000008098	ENSBTAT00000010653	100
			93,3
			98,4
			92,7
			93,9
			96,1
			97,9
ENSBTAP00000015986	ENSBTAG00000012047	ENSBTAT00000015986	100
ENSBTAP00000027857	ENSBTAG00000020904	ENSBTAT00000027857	
			100
			100
ENSBTAP00000024657	ENSBTAG00000018524	ENSBTAT00000024657	99,2
			99,2
			99,2
			99,6
			99,6
			95,5
			90,9
			82,5
			98,9
			98,6
			91,2
			96,1
			97,9
			99
			99,6
			97,9
			100
			94,3
			98,3

			99,7
			99,3
			97,9
			98,6
			97,9
			92,6
			100
			93
			92,6
			96,1
			96,1
			95,8
			95,8
			89,4
			97,2
			100
ENSBTAP00000000016	ENSBTAG00000000013	ENSBTAT00000000016	99,7
			98,4
ENSBTAP00000026195	ENSBTAG00000032234	ENSBTAT00000026195	99,7
ENSBTAP00000026189	ENSBTAG00000019652	ENSBTAT00000026189	99,7
			100
			96,8
			93,9
			99,1
			99,7
			98,2
			98,3
			100
ENSBTAP00000015200	ENSBTAG00000011437	ENSBTAT00000015200	98,2
			95,6
			98,6
			100
			99,7
			97
			99
			80
			99,7
ENSBTAP00000000744	ENSBTAG00000000570	ENSBTAT00000000744	99,7
			100
			100
			100
			89,8
			95,4
			94,7
			98,2
			99,3
ENSBTAP00000032957	ENSBTAG00000012114	ENSBTAT00000033031	91,8
			91,4
			95,3
			96,5

			97,2
			96
			86,9
			87,4
ENSBTAP00000023740	ENSBTAG00000017860	ENSBTAT00000023740	89,8
			91,8
			89,7
			98,9
			89,7
			100
			99,3
			85,7
			98,5
			97,8
ENSBTAP00000009441	ENSBTAG00000007173	ENSBTAT00000009441	95,3
			100
			97,3
			90,5
			71,5
			99,6
ENSBTAP00000017759	ENSBTAG00000013347	ENSBTAT00000017759	86,3
			93,5
ENSBTAP00000020910	ENSBTAG00000016551	ENSBTAT00000020910	94,1
ENSBTAP00000018430			96,1
			94,7
			91,5
			97,3
			90,6
ENSBTAP00000002122	ENSBTAG00000001618	ENSBTAT00000002122	97,7
ENSBTAP00000025471			91
			98,8
			98,4
			96,9
			99,6
ENSBTAP00000029056	ENSBTAG00000021798	ENSBTAT00000029056	98,9
			80,7
			89,3
ENSBTAP00000013238	ENSBTAG00000010030	ENSBTAT00000013238	85,8
			83,1
			78,3
			99,7
			99,4
ENSBTAP00000018603	ENSBTAG00000014000	ENSBTAT00000018603	84,4
			100
			100
			92,4
ENSBTAP00000035173	ENSBTAG00000010979	ENSBTAT00000035295	99,6
			69,3
			76

			80,9
			89,9
			97,4
			97,3
			86
			88,2
			77,8
			70,1
			96
			100
			95,3
ENSBTAP00000038069	ENSBTAG00000003819	ENSBTAT00000038254	97,2
			95,7
ENSBTAP00000038339	ENSBTAG00000020758	ENSBTAT00000038526	99
			84,2
			98,8
			89,5
ENSBTAP00000042949	ENSBTAG00000014409	ENSBTAT00000045570	98,2
ENSBTAP00000040258	ENSBTAG00000000785	ENSBTAT00000042622	99,6
			91,7
			95,1
			98,8
			98,9
			97,7
			98,4
			85,9
			97,5
			94
			98,9
			81,1
ENSBTAP00000012303	ENSBTAG00000009346	ENSBTAT00000012303	100
ENSBTAP00000019230	ENSBTAG00000014463	ENSBTAT00000019230	99,6
			99,2
			98,1
			96,3
			99,6
			87,2
			92,1
ENSBTAP00000000463	ENSBTAG00000000357	ENSBTAT00000000463	94,5
ENSBTAP00000012605	ENSBTAG00000009578	ENSBTAT00000012605	99,3
ENSBTAP00000026780	ENSBTAG00000020102	ENSBTAT00000026780	96,9
			100
ENSBTAP00000016792	ENSBTAG00000012647	ENSBTAT00000016792	98,1
			99,2
			96,9
			94,9
			95,5
			98,9
			100

			99,2
			98,1
			99,6
			100
			97,4
			100
ENSBTAP00000013549	ENSBTAG00000010254	ENSBTAT00000013549	99,6
ENSBTAP00000015051	ENSBTAG00000011322	ENSBTAT00000015051	97,6
			99,2
			99,6
ENSBTAP00000042917	ENSBTAG00000010639	ENSBTAT00000045536	94,8
			98,1
ENSBTAP00000019139	ENSBTAG00000014393	ENSBTAT00000019139	99,6
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			95,2
			97,4
			99,6
ENSBTAP00000046377	ENSBTAG00000035028	ENSBTAT00000049489	100
			97,2
			99,6
			99,2
			99,2
			100
			97
			99,2
			100
			93,3
			98,9
			100
			98,4
			91,8
			99,2
			100
ENSBTAP00000040257	ENSBTAG00000030201	ENSBTAT00000042621	98,5
			90,1
ENSBTAP00000018713	ENSBTAG00000014064	ENSBTAT00000018713	98,5
			97,8
ENSBTAP00000020866	ENSBTAG00000015713	ENSBTAT00000020866	94,7
			98,1
			97,4
			99,2
ENSBTAP00000021631	ENSBTAG00000016260	ENSBTAT00000021631	96,3
			96,6
ENSBTAP00000013808	ENSBTAG00000010460	ENSBTAT00000013808	97,2

			98,1
			98,8
			98,8
			94,6
ENSBTAP00000013805	ENSBTAG00000010457	ENSBTAT00000013805	93,1
			92,2
			95,7
			100
ENSBTAP00000013238			99,6
ENSBTAP00000025471	ENSBTAG00000019134	ENSBTAT00000025471	98,8
			99,3
			95,7
			98,1
			89,7
ENSBTAP00000014411	ENSBTAG00000010855	ENSBTAT00000014411	100
ENSBTAP00000013449	ENSBTAG00000015670	ENSBTAT00000013449	100
			99,6
			92,3
			97,6
			97,3
			93,3
ENSBTAP00000018603			
			98,4
			99,3
			99,3
			98,6
			98,6
			98,9
			98,9
			95,6
			98,2
			97,8
			94
			85,7
			93,4
			94,6
ENSBTAP00000012838	ENSBTAG00000009736	ENSBTAT00000012838	98,8
			97,7
			91,7
			95
			96,4
			97,3
			99,1
			99,4
			98,6
ENSBTAP00000026519	ENSBTAG00000019907	ENSBTAT00000026519	94,4
			99,3
			94,5
			99,3

ENSBTAP00000012197	ENSBTAG00000009258	ENSBTAT00000012197	
			94,4
			85
			92,4
			96,1
			99,6
			96,8
			97,2
			99,6
ENSBTAP00000022534	ENSBTAG00000016943	ENSBTAT00000022534	99,2
			84,1
			100
			98
			96,4
ENSBTAP00000022347	ENSBTAG00000016799	ENSBTAT00000022347	94
			99,2
			96,8
			96,8
			89,3
			99,3
			100
			79,4
			98,9
			100
ENSBTAP00000015530	ENSBTAG00000010408	ENSBTAT00000015530	100
			95,7
			92,3
			96
			87,4
			82,8
			89,2
			94,1
			99,2
			95,9
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			85,4
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			99,2
			71,5

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95,5	
97,6	
86,6	Deletion in human
98	Insertion in human
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93,8	
93,7	
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98,4	

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99,4	Deletion in human
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81,3	
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87,6	
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93,1	
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86,7	
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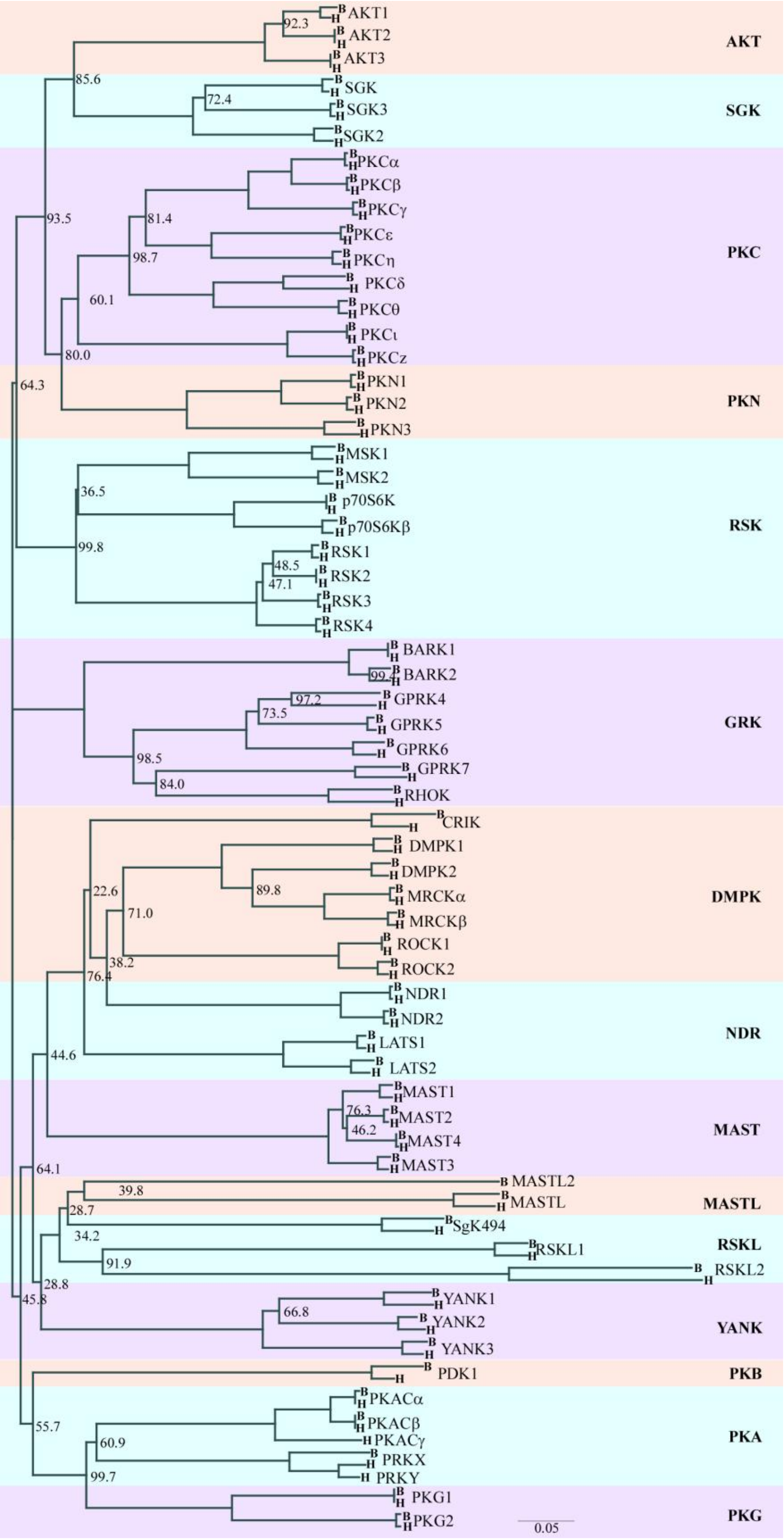
98,6	
97,9	
96,5	Insertion in human
80,7	
91,5	
99,3	
63,6	

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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PKCε
PKCη
PKCδ
PKCθ
PKCι
PKCz
93.5
81.4
98.7
60.1
80.0
PKC
64.3
PKN1
PKN2
PKN3
PKN
MSK1
MSK2
p70S6K
p70S6Kβ
36.5
99.8
RSK1
RSK2
RSK3
RSK4
48.5
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RSK
BARK1
BARK2
99.4
GPRK4
97.2
73.5
GPRK5
GPRK6
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GPRK7
84.0
RHOK
GRK
CRIK
DMPK1
DMPK2
22.6
89.8
MRCKα
71.0
MRCKβ
ROCK1
38.2
ROCK2
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NDR2
LATS1
44.6
LATS2
NDR
MAST1
76.3
MAST2
46.2
MAST4
MAST3
MAST
64.1
MASTL2
39.8
MASTL
28.7
MASTL
SgK494
34.2
RSKL1
91.9
RSKL2
RSKL
28.8
45.8
YANK1
66.8
YANK2
YANK3
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PDK1
PKB
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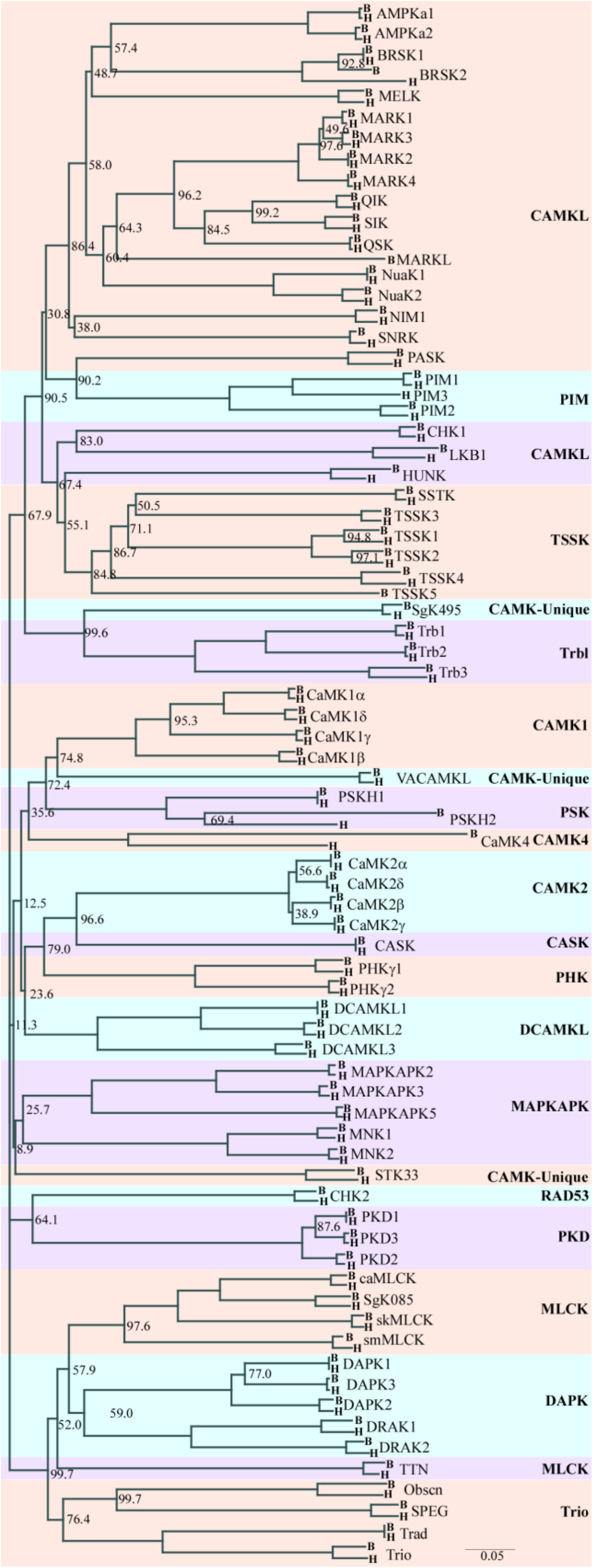
PKG

CAMK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99.2
SIK
CAMKL
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60.4
MARKL
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NIM1
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PIM1
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PIM
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PIM2
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LKB1
CAMKL
HUNK
67.4
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TSSK3
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55.1
71.1
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TSSK
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TSSK5
SgK495
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Trb2
Trbl
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CaMK1β
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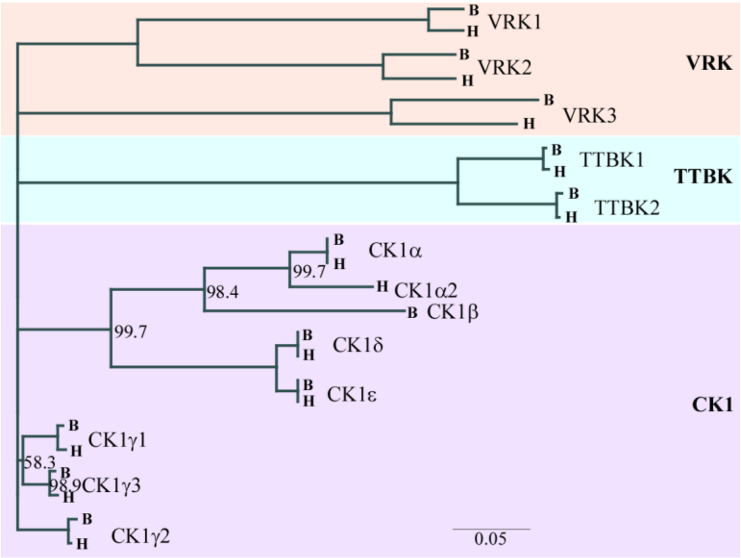
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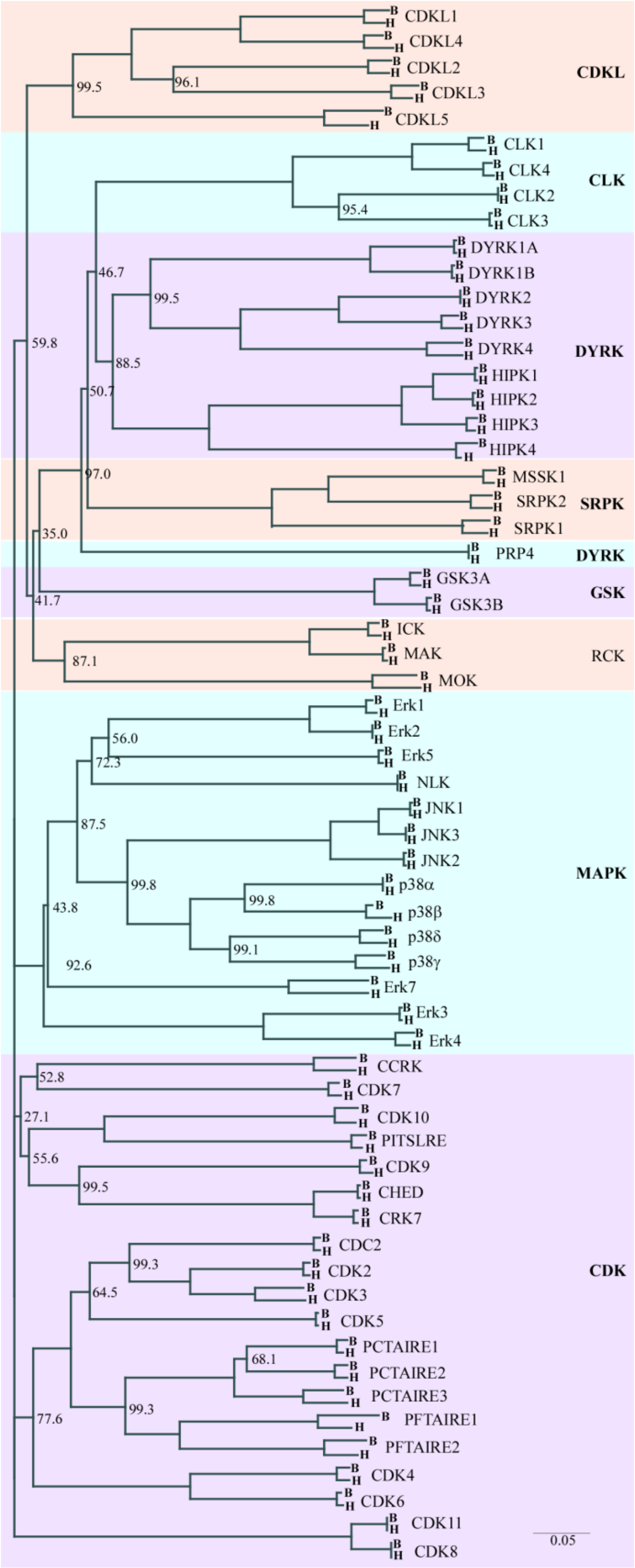
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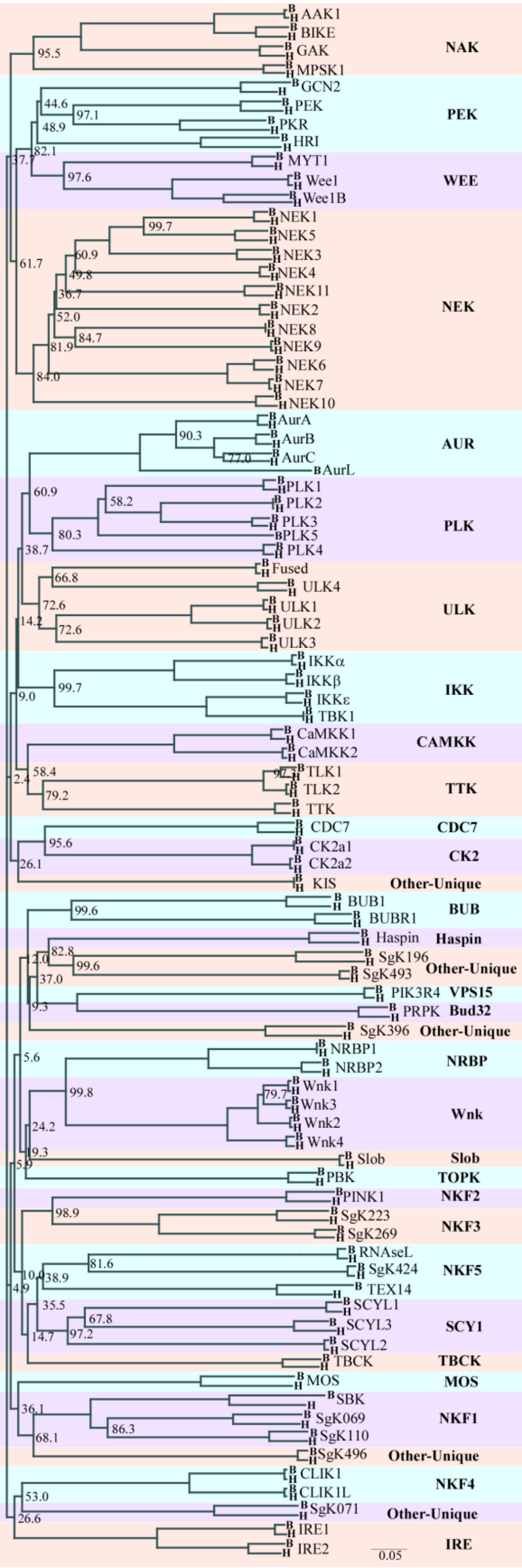
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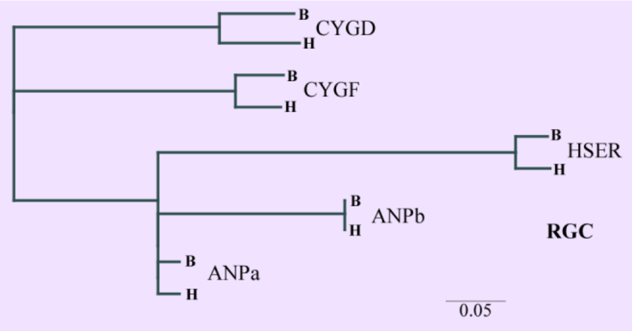

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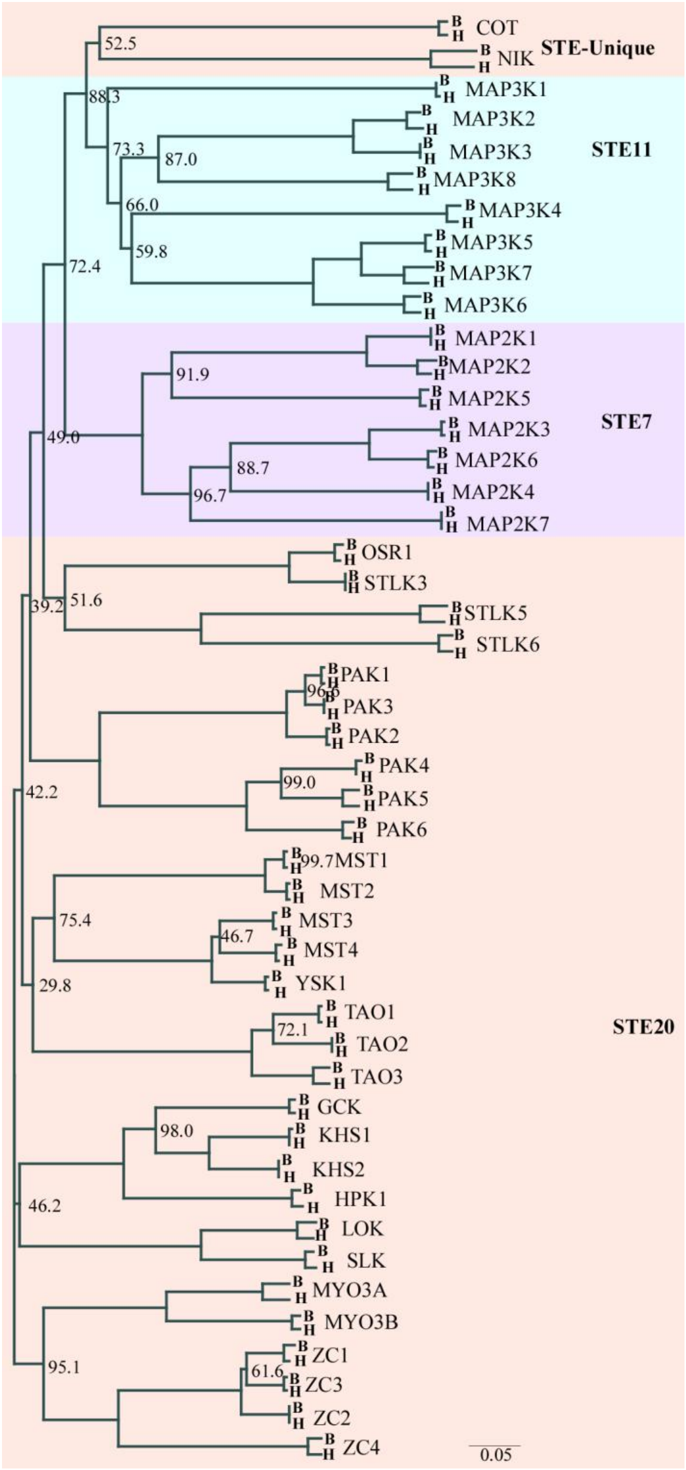
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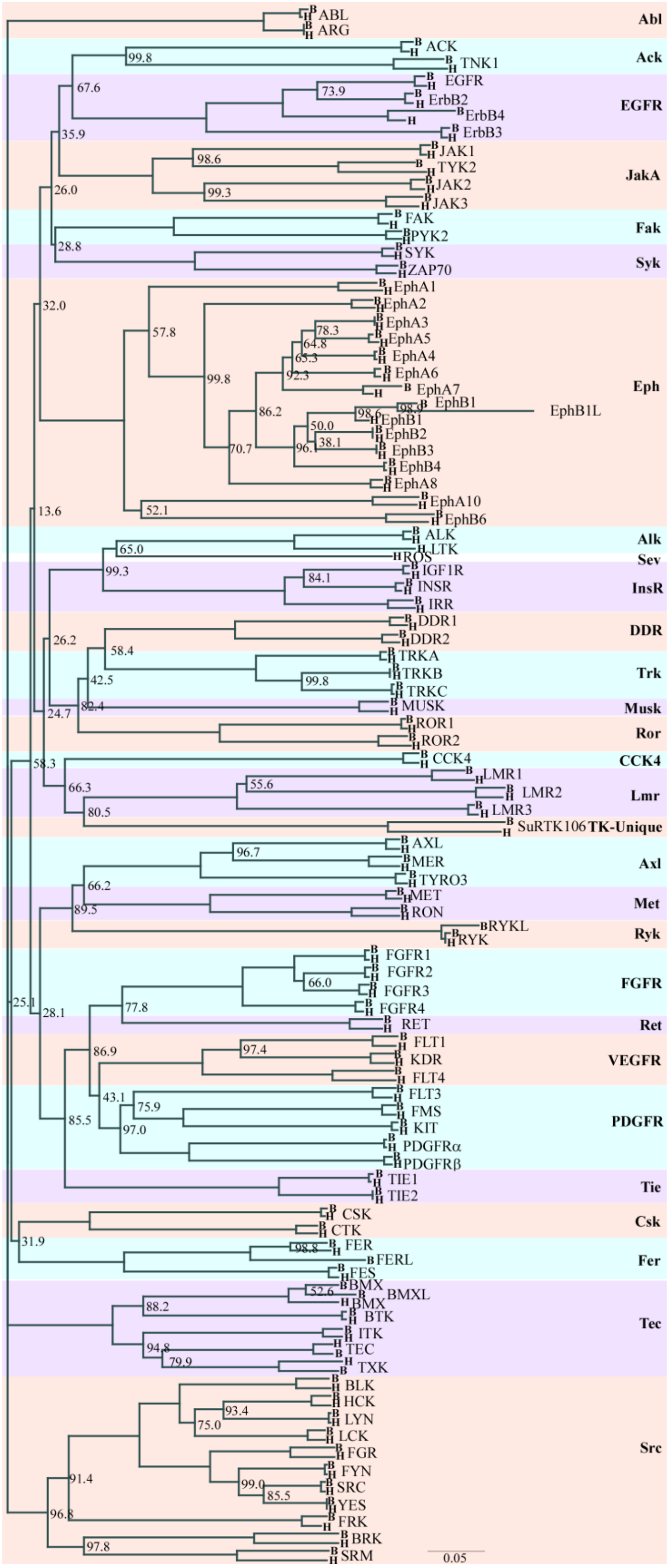
H
0.05

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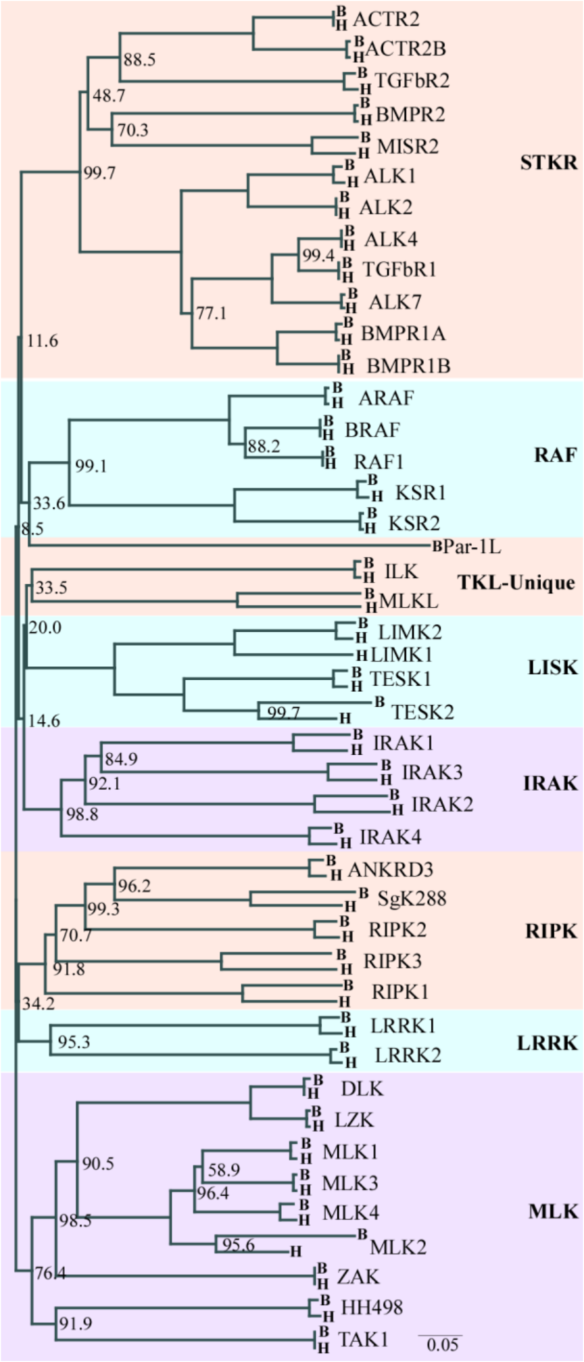
85.5
YES
96.8
FRK
BRK
97.8
SRM
Src
0.05
B
H

TKL


ACTR2
ACTR2B
TGFbR2
BMPR2
MISR2
ALK1
ALK2
ALK4
TGFbR1
ALK7
BMPR1A
BMPR1B
88.5
48.7
70.3
99.7
99.4
77.1
11.6
STKR
ARAF
BRAF
RAF1
KSR1
KSR2
88.2
99.1
33.6
8.5
RAF
Par-1L
ILK
MLKL
33.5
TKL-Unique
LIMK2
LIMK1
TESK1
TESK2
20.0
99.7
14.6
LISK
IRAK1
IRAK3
IRAK2
IRAK4
84.9
92.1
98.8
IRAK
ANKRD3
SgK288
RIPK2
RIPK3
RIPK1
96.2
99.3
70.7
91.8
34.2
RIPK
LRRK1
LRRK2
95.3
LRRK
DLK
LZK
MLK1
MLK3
MLK4
MLK2
ZAK
HH498
TAK1
90.5
58.9
96.4
98.5
95.6
76.4
91.9
MLK
0.05