Supplementary information for:

Mapping the virome in wild-caught *Aedes aegypti* from Cairns and Bangkok

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Running title: Mapping the *Aedes aegypti* virome

Key words: *Aedes aegypti*, insect-specific virus, Phasi Charoen-like virus, Humaita-Tubiacanga virus, Cell fusing agent virus.

Figure S1. (**a**) Read based mapping (using data from Cairns mosquitoes) to PCLV genome segments using BWA mem (colour coding represents percent nucleotide identity). (**b**) Single nucleotide polymorphisms (SNPs) in reads mapping PCLV. SNPs with at least 100 reads and an allele frequency of at least 20% are shown. Cairns 698,434 reads and Bangkok 2,080,162 reads.

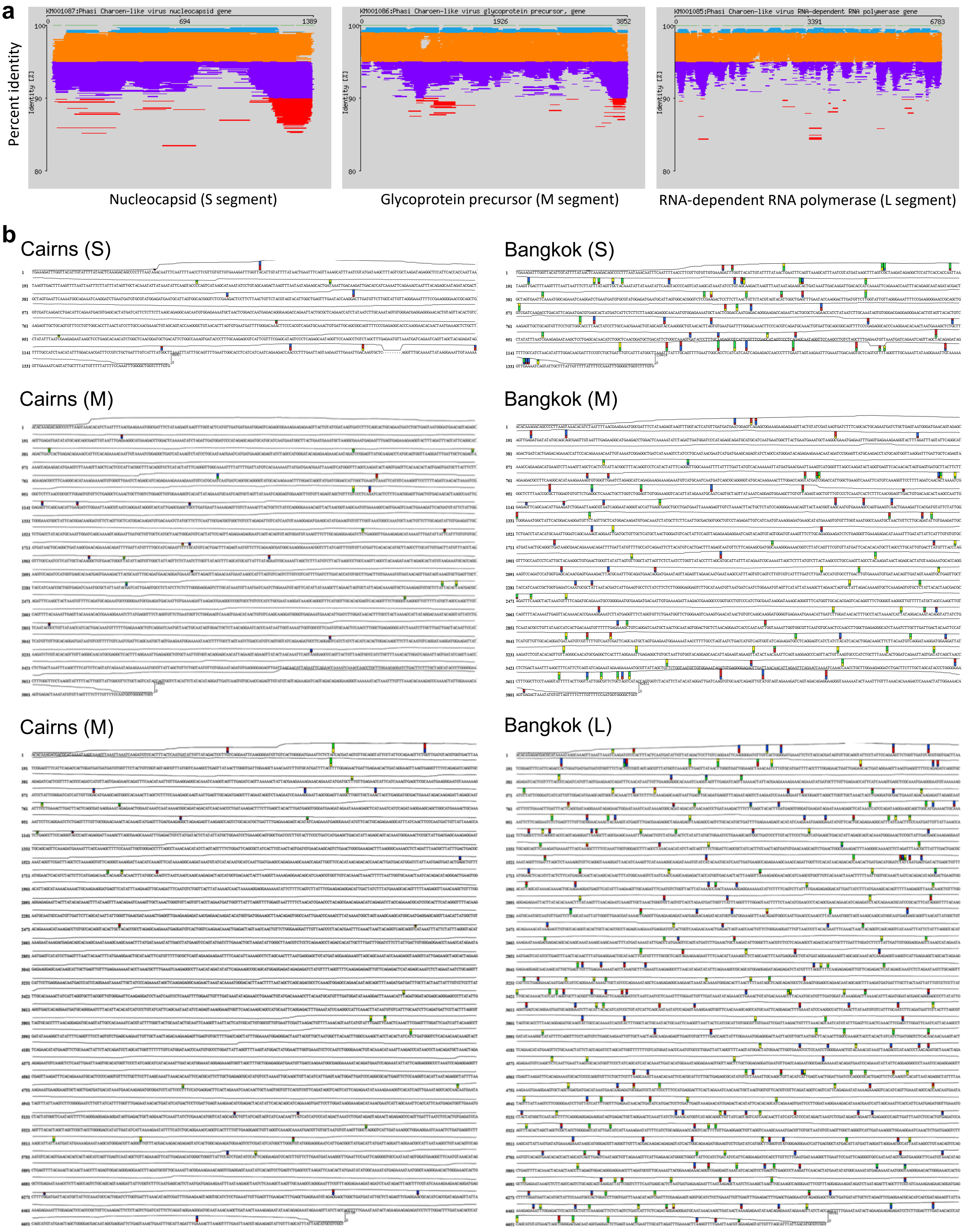
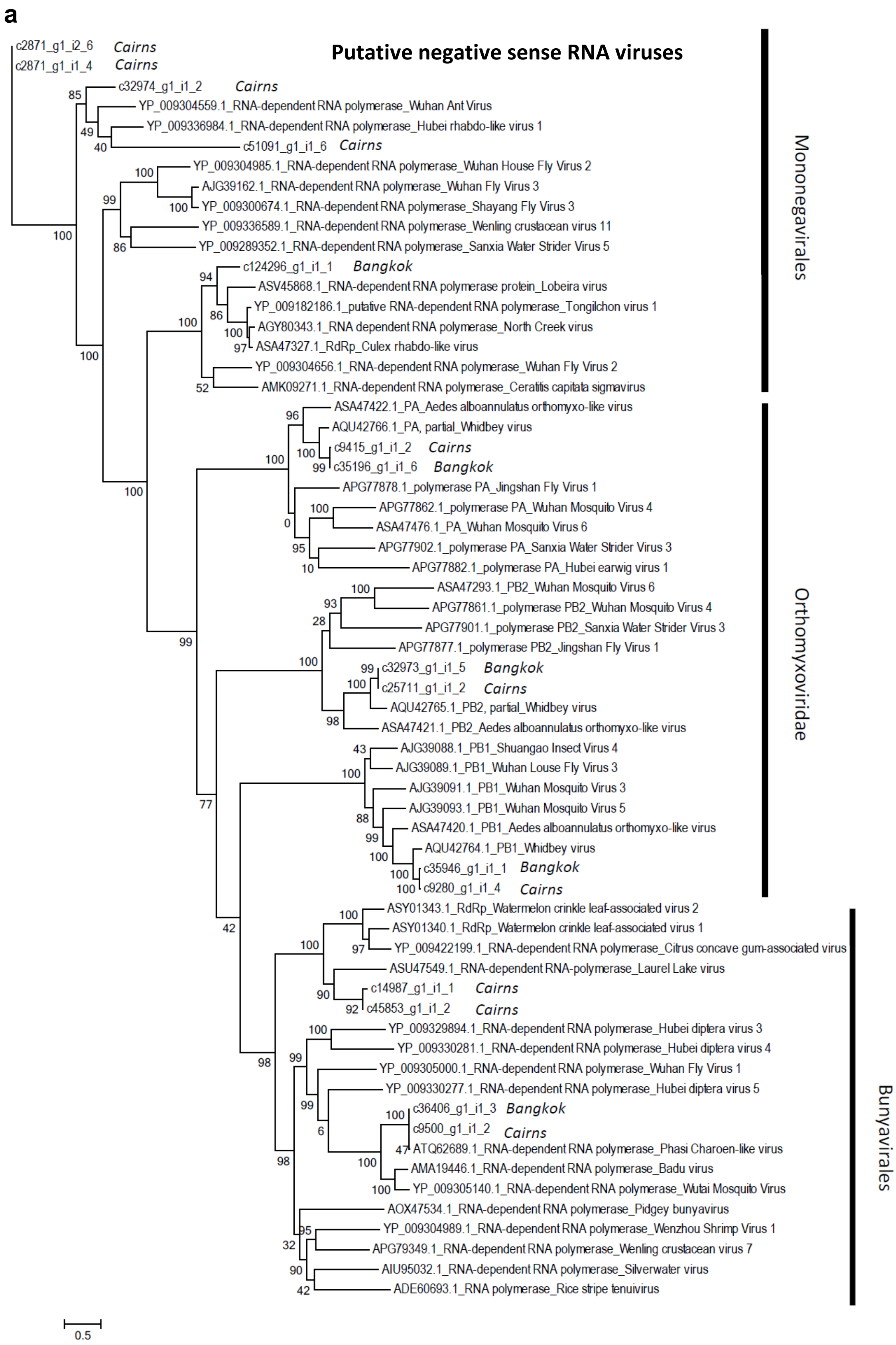
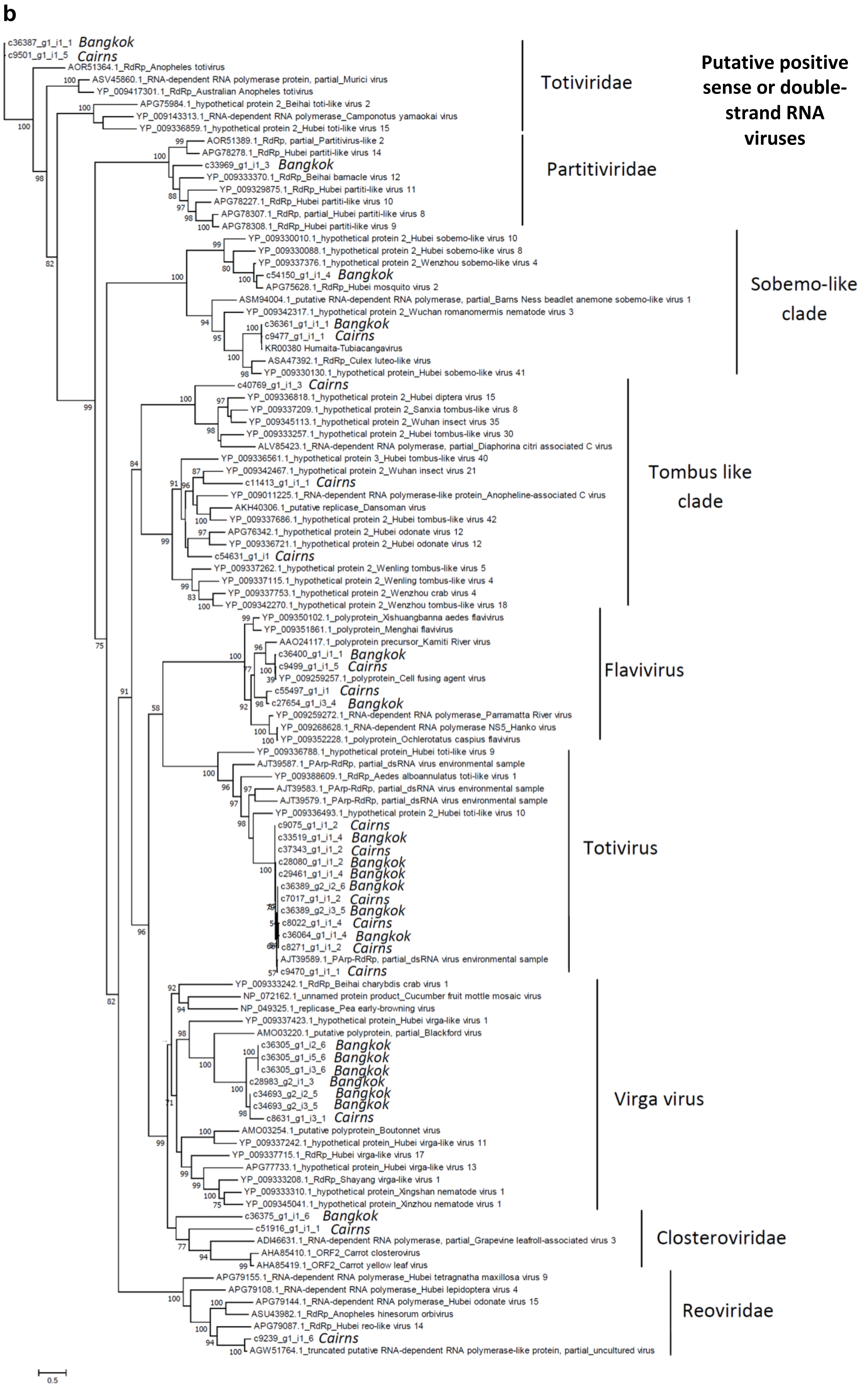


Figure S2: Maximum likelihood phylogeny of (**a)** putative negative-sense RNA viruses and (**b**) putative positive-sense and double-stranded RNA viruses. Phylogentic trees of the viral RdRp protein sequences encoded on Cairns and Bangkok contigs and reference sequences from GenBank. Viruses shared between Cairns and Bangkok cluster closely within a clade. Some viruses were unique to each geographic location.



b
Putative positive sense or double-strand RNA viruses
c36387_g1_i1_1 Bangkok
c9501_g1_i1_5 Cairns
AOR51364.1_RdRp_Anopheles totivirus
ASV45860.1_RNA-dependent RNA polymerase protein, partial_Murici virus
YP_009417301.1_RdRp_Australian Anopheles totivirus
APG75984.1_hypothetical protein 2_Beihai toti-like virus 2
YP_009143313.1_RNA-dependent RNA polymerase_Camponotus yamaokai virus
YP_009336859.1_hypothetical protein 2_Hubei toti-like virus 15
Totiviridae
AOR51389.1_RdRp, partial_Partitivirus-like 2
APG78278.1_RdRp_Hubei partiti-like virus 14
c33969_g1_i1_3 Bangkok
YP_009333370.1_RdRp_Beihai barnacle virus 12
YP_009329875.1_RdRp_Hubei partiti-like virus 11
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APG78307.1_RdRp, partial_Hubei partiti-like virus 8
APG78308.1_RdRp_Hubei partiti-like virus 9
Partitiviridae
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c54150_g1_i1_4 Bangkok
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ASM94004.1_putative RNA-dependent RNA polymerase, partial_Barns Ness beadlet anemone sobemo-like virus 1
YP_009342317.1_hypothetical protein 2_Wuchan romanomermis nematode virus 3
c36361_g1_i1_1 Bangkok
c9477_g1_i1_1 Cairns
KR00380 Humaita-Tubiacangavirus
ASA47392.1_RdRp_Culex luteo-like virus
YP_009330130.1_hypothetical protein_Hubei sobemo-like virus 41
Sobemo-like clade
c40769_g1_i1_3 Cairns
YP_009336818.1_hypothetical protein 2_Hubei diptera virus 15
YP_009337209.1_hypothetical protein 2_Sanxia tombus-like virus 8
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YP_009333257.1_hypothetical protein 2_Hubei tombus-like virus 30
ALV85423.1_RNA-dependent RNA polymerase, partial_Diaphorina citri associated C virus
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YP_009342467.1_hypothetical protein 2_Wuhan insect virus 21
c11413_g1_i1_1 Cairns
YP_009011225.1_RNA-dependent RNA polymerase-like protein_Anopheline-associated C virus
AKH40306.1_putative replicase_Dansoman virus
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YP_009336721.1_hypothetical protein 2_Hubei odonate virus 12
c54631_g1_i1 Cairns
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YP_009337753.1_hypothetical protein 2_Wenzhou crab virus 4
YP_009342270.1_hypothetical protein 2_Wenzhou tombus-like virus 18
Tombus like clade
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YP_009351861.1_polyprotein_Menghai flavivirus
AAO24117.1_polyprotein precursor_Kamiti River virus
c36400_g1_i1_1 Bangkok
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c55497_g1_i1 Cairns
c27654_g1_i3_4 Bangkok
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YP_009268628.1_RNA-dependent RNA polymerase NS5_Hanko virus
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Flavivirus
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Totivirus
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NP_049325.1_replicase_Pea early-browning virus
YP_009337423.1_hypothetical protein_Hubei virga-like virus 1
AMO03220.1_putative polyprotein, partial_Blackford virus
c36305_g1_i2_6 Bangkok
c36305_g1_i5_6 Bangkok
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c34693_g2_i2_5 Bangkok
c34693_g2_i3_5 Bangkok
c8631_g1_i3_1 Cairns
AMO03254.1_putative polyprotein_Boutonnet virus
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YP_009337715.1_RdRp_Hubei virga-like virus 17
APG77733.1_hypothetical protein_Hubei virga-like virus 13
YP_009333208.1_RdRp_Shayang virga-like virus 1
YP_009333310.1_hypothetical protein_Xingshan nematode virus 1
YP_009345041.1_hypothetical protein_Xinzhou nematode virus 1
Virga virus
c36375_g1_i1_6 Bangkok
c51916_g1_i1_1 Cairns
ADI46631.1_RNA-dependent RNA polymerase, partial_Grapevine leafroll-associated virus 3
AHA85410.1_ORF2_Carrot closterovirus
AHA85419.1_ORF2_Carrot yellow leaf virus
Closteroviridae
APG79155.1_RNA-dependent RNA polymerase_Hubei tetragnatha maxillosa virus 9
APG79108.1_RNA-dependent RNA polymerase_Hubei lepidoptera virus 4
APG79144.1_RNA-dependent RNA polymerase_Hubei odonate virus 15
ASU43982.1_RdRp_Anopheles hinesorum orbivirus
APG79087.1_RdRp_Hubei reo-like virus 14
c9239_g1_i1_6 Cairns
AGW51764.1_truncated putative RNA-dependent RNA polymerase-like protein, partial_uncultured virus
Reoviridae
0.5

Table S1. Contig nucleotide sequences (len = nucleotide length).

Cairns contigs

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Table S2a. Contig based virus identification of viruses in Cairns *Ae. aegypti*. Contigs were assembled from reads obtained from sequencing Cairns *Ae. aegypti* and were used for virus identification using the NCBI protein and nucleic data bases. Percentage amino acid identity is shown with the number in brackets the percentage of the contig length aligned in the BLAST hit; this was added as the reference sequence was often only a partial sequence. Underlining highlights viruses (or phage) or nearest relatives (italics), which appear to be unique to Cairns mosquitoes, with no reads from Bangkok aligning with the indicated Cairns contig(s) and/or no Cairns contigs overlapping with Bangkok contigs. Grey shading in the **Contig id** column represents contigs that overlap with contigs identified from Bangkok *Ae. aegypti*. [1]Similar match to *Ochlerotatus caspius* flavivirus, Hanko virus, and Parramatta River virus. [2]c50692_g1_i1 is possibly derived from an EVE (see Table S2). [3] Similar match to Blacklegged tick phlebovirus.

Classification	Virus or *nearest match*	Contig id	Amino acid identity	Gene	Length (nucleo-tides)	Mean read depth	E Data ncbi protein	Host	Refs
Known viruses of *Ae aegypti*									
Genus; *Phlebovirus* ssRNA(-)	Phasi Charoen-like virus	c9421_g1_i1 c9498_g1_i1 c9500_g1_i1	98.5(60) 97(97) 99(99)	Nucleocapsid, glycoprotein, RNA polymerase	1339 3842 6697	62661 28142 18605	6.49E-175 0 0	*Ae aegypti*	[1,2]
Genus; *Flavivirus* ssRNA(+)	Cell fusing agent virus	c9499_g1_i1	99(94)	Polyprotein	10684	664	0	*Ae aegypti*	[3]
Unclassified ssRNA(+)	Humaita-Tubiacanga virus	c9445_g1_i1 c9477_g1_i1	98(80) 97(51)	Capsid Replicase	1618 2761	16949 19494	0 0	*Ae aegypti*	[2]
Unclassified dsRNA (probably a Totivirus)	Unnamed	c7017_g1_i1 c8022_g1_i1 c8271_g1_i1 c9075_g1_i1 c9470_g1_i1 c37343_g1_i1	96(99) 90(99) 95(99) 97(99) 98(41) 95(99)	PArp-RdRp, partial (Contig 5425)	238 265 892 619 6772 253	140 437 465 389 1081 298	4.85E-43 3.79E-50 0 1.14E-138 0 1.14E-47	*Ae aegypti* Thailand	[4] AJT39589.1, KP642128.1
Mosquito-associated viruses									
Genus; *Flavivirus*	*Xishuangbanna flavivirus*	c55497_g1_i1[1]	60(79)	RNA polymerase Polyprotein	239	27	3.29E-22	*Ae albopictus*	[5]
Genus: *Orthomyxovirus* ssRNA(-)	*Whidbey virus*	c9280_g1_i1 c9415_g1_i1 c25711_g1_i1	85(92) 79(90) 76(92)	PB1 PA PB2	2438 2203 2417	285 299 288	0 0 0	*Aedes dorsalis*	AQU42764.1
Unclassified. Order; *Mononegavirales* ssRNA(-)	*Xincheng mosquito virus*	c4670_g1_i2 c4670_g1_i1	37(77) 59(81)	Glycoprotein	212 251	2 17	2.34E-9 6E-17	*Anopheles sinensis*	[6]
Family; *Bunyaviridae* Phasmavirus like. ssRNA(-)	*Wuhan mosquito virus 2*	c7211_g1_i1 c8461_g1_i1 c8461_g2_i1	34(96) 44(96) 39(82)	Glycoprotein precursor	447 308 809	18 23 12	4.05E-21 7.49E-24 7.87E-47	*Culex, Anopheles, Aedes sp*	[6]
Unclassified; *Rhabdoviridae* ssRNA(-)	*Wuhan nosquito virus 9*	c33645_g1_i1 c50692_g1_i1[2]	28(60) 37(83)	Glycoprotein ORF1	930 383	8.59 8.7	1.5E-015 1.28E-12	*Culex, Aedes sp*	[6]
Genus; *Totivirus* dsRNA	*Anopheles totivirus*	c9501_g1_i1 c9501_g1_i1	45(37) 27(42)	RdRp Putative capsid	6086 6086	1106 1106	0 4.00E-82	*Anopheles gambiae*	[7]
Unclassified	*Kaiowa virus*	c32637_g1_i1	75(99)	Putative glycoprotein	214	11	3.9e-192	*Brazilian mosquitoes*	[8]
Unclassified	*Hubei toti-like virus10*	c8605_g1_i1 c48383_g1_i1	39(96) 46(93)	Hypothetical protein 1	410 229	268 232	1.50E-16 2.8E-15	Mosquito	[9]
Unclassified	*dsRNA virus environmental sample*	c2748_g1_i1	37(98)	Proline-alanine-rich protein	373	235	1.3E-13	*Ochlero-tatus sierrensis*	[4]
Oribivirus	*Unnamed*	c9239_g1_i1	87(60)	RdRp AGW51764.1	4038	3543	0	*Ochlerotatus caspius & detritus*	[10]
Other insect-associated viruses									
Unclassified	*Blackford virus*	c177_g1_i1 c8631_g1_i2	45(75) 44(64)	Putative polyprotein	240 333	19 37	3.6E-6 1.1E-12 6.5E-7	*D. tristis*	[11]

		c8631_g1_i3	47(93)		203	12	3.9E-4		
		c9229_g1_i1	48(55)		1131	67			
Unclassified RNA virus	*Hubei tombus-like virus 40*	c54631_g1_i1	51(96)	Hypothetical proteins	221	5.5	2.3E-13	*Coleoptera*	9
		c11413_g1_i1	51(91)		693	5.6	1.2E-51		
Unclassified	*Diaphorina citri associated C virus*	c40769_g1_i1	34(86)	RdRp	1259	7.4	6.07E-48	Psyllid	12
Family: *Rhabdoviridae* ssRNA(-)	*Wuhan ant virus*	c2871_g1_i1	32(92)	RdRp	2961	7.9	9.5E-140	*Camponotus japonicus*	6
		c2871_g1_i2	35(98)		2057	4.7	5.9E-125		
		c32974_g1_i1	53(99)		2318	10.6	0		
		c51091_g1_i1	32(91)		640	11	1E-23		
Family; *Baculoviridae* dsDNA	*Autographa californica nucleo-polyhedrovirus*	c35321_g1_i1	69(72)	ORF B	563	6.6	5.59E-46	*Autographa californica*	13
Plant viruses									
Unclassified phlebovirus-like	*Citrus concave gum-associated virus*	c14987_g1_i1	45(99)	RNA-dependent RNA polymerase	548	5.8	8.1E-46	*Citrus sinensis*	14
Genus: *Closterovirus*	*Carrot closterovirus*	c51916_g1_i1	36(95)	ORF2	482	6.6	2.71E-18	Carrot	15
Phenuiviridae ssRNA(-)	*Watermelon crinkle leaf-associated virus 2*	c18669_g1_i1	35(82)	Nucleocapsid	952	9.8	7.5E-31	*Citrullus lanatus*	16
		c45853_g1_i1	49(99)	Polymerase	203	12	5.8E-13		
Phage									
	Enterobacteria phage SP6	c18294_g1_i1	100(53)	Protein 45	339	158	7.4E-36	Entero-bacteria	AAR90038

Table S2b. Contig based virus identification of viruses in Bangkok *Ae aegypti*. Contigs were assembled from reads obtained from sequencing of Bangkok *Ae. aegypti* and were used for virus identification as in Table 1. Underlining as for Table 1 except for Bangkok contigs. Grey shading in the **Contig id** column represents contigs that overlap with contigs identified from Cairns *Ae. aegypti*. [1] Similar match to *Culex pipiens pallens* densovirus. [2] Similar match to Menghai flavivirus. [3] Similar match to Hubei virga-like virus 17.

Classification	Virus or *nearest match*	Contig id	Amino acid identity	Gene	Length (nucleo-tide)	Mean reac depth	E Data ncbi protein	Host	Refs
Known viruses of *Ae aegypti*									
Genus; *Phlebovirus* ssRNA(-)	Phasi Charoen-like virus	c125955_g1_i1	81(54)		320	4.0	1.22E-22	*Ae aegypti*	1,2
		c33559_g1_i2	69(56)	Nucleocapsid	374	461	3.8E-23		
		c36351_g1_i2	99.6(61)		1327	96046	7.1E-178		
		c38870_g1_i1	54(100)		246	5.0	2.1E-28		
		c36369_g1_i1	99(94)	Glycoprotein	1239	48052	0		
		c36405_g1_i1	99(96)		2738	51100	0		
		c36406_g1_i1	99.6(99)	RdRp	6400	28145	0		
Genus; *Flavivirus* ssRNA(+)	Cell fusing agent virus	c36400_g1_i1	98(94)	Polyprotein	10659	4396	0	*Ae aegypti*	17
Unclassified ssRNA(+)	Humaita-Tubiacanga virus	c36290_g1_i1	98(78)	Capsid	1668	19454	0	*Ae aegypti*	2
		c36361_g1_i1	97(49)	Replicase	2839	18407	0		
Unclassified dsRNA	Unnamed	c36064_g1_i1	91(99)	PArp-RdRp, partial (Contig 5425)	887	266	0	*Ae aegypti Thailand*	[4] AJT39589.1, KP642128.1
		c36389_g2_i2	99(99)		456	305	2E-97		
		c29461_g1_i1	96(100)		238	238	5E-45		
		c33519_g1_i1	97(99)		502	261	2.3E-108		
		c28080_g1_i1	97(37)		284	319	8E-55		
		c36389_g2_i3	96(44)		677	276	1.2E-42		
Subfamily: *Densovirinae* ssDNA	*Aedes aegypti densovirus 2*	c30446_g1_i1[1]	98(61)	Non-structural protein 1 & capsid	3790	106	0	*Ae aegypti*	18
Mosquito-associated viruses									
Genus; *Flavivirus*	*Xishuangbanna flavivirus*	c27654_g1_i3	67(57)	RdRp	368	38	4.94E-35	*Ae albopictus*	5,19
		c14012_g1_i1[2]	59(73)	Polyprotein	320	18	7.42E-40		
Genus: *Orthomyxovirus* ssRNA(-)	*Whidbey virus*	c35946_g1_i1	85(92)	PB1	2434	104	0	*Ae dorsalis*	20
		c35196_g1_i1	79(90)	PA, partial	2187	115	0		
		c32973_g1_i1	76(93)	PB2	2402	131	0		
Unclassified. Order; *Mononegavirales* ssRNA(-)	*Xincheng mosquito virus*	c32243_g1_i1	39(72)	Glycoprotein	318	12	3.4E-15	*Anopheles sinensis*	6
		c32243_g1_i2	42(74)		356	43	1.7E-19		
Family; *Bunyaviridae* Phasmavirus like. ssRNA(-)	*Wuhan mosquito virus 2*	c35613_g1_i1	42(78)	Glycoprotein precursor	2049	80	4.2E-118	*Culex, Anopheles, Aedes sp*	6
Family *Rhabdoviridae* ssRNA(-)	*Tongilchon virus 1*	c124296_g1_i1	57(98)	Putative RdRp	280	4.2	2E-26	*Culex bitaeniorhynchus*	21
Unclassified; *Rhabdoviridae* ssRNA(-)	*Wuhan mosquito virus 9*	c64714_g1_i1	30(80)	Glycoprotein	477	3.3	6E-7	*Culex, Aedes sp*	6
		c1882_g1_i2	37(79)	ORF1	472	10.8	2E-11		
Genus; *Totivirus* dsRNA	*Anopheles totivirus*	c36387_g1_i1	45(36) 28(41)	RdRp & Putative capsid	6125	1509	0 2.E-107	*Anopheles gambiae*	7
Unclassified	*Kaiowa virus*	c15947_g1_i1	73(72)	Putative glycoprotein	1115	5.6	1e-146	*Brazilian mosquitoes*	ASV45863.1
Unclassified virus	*Croada virus*	c32738_g1_i1	68(36)	Putative glycoprotein	529	52	5E-23	*Psorophora pools*	ASV45861.1
		c32738_g1_i3	68(29)		664	31	1.8E-22		
Unclassified RNA virus	*Wenzhou sobemo-like virus 4*	c54150_g1_i1	84(43)	Hypothetical protein	3099	1137	1.6E-48	Mosquito	9
Unclassified virus	*Hubei mosquito virus 2*	c70842_g1_i1	48(83)	Hypothetical protein	1639	1491	8E-142	Mosquito	22
Family; *Chuviridae* ssRNA(-)	*Chuvirus Mos8Chu0*	c914_g1_i1	63(86)	Putative nucleoprotein	836	9.6	6.9E-75	*Culiseta minnesotae*	API61889.1
Other insect-associated viruses									
Unclassified	*Blackford virus*	c34693_g2_i2	46(46)	Putative polyprotein	880	44	6.9E-30	*D. tristis*	11
		c34693_g2_i3	46(39)		853	26	5.1E-23		

		c36305_g1_i2	47(36)		1763	45	1.2E-49		
		c36305_g1_i3	47(36)		1757	56	1.1E-49		
		c36305_g1_i5	47(50)		1256	40	2.4E-51		
		c46271_g1_i1	45(52)		538	9.0	2.3E-14		
		c28983_g2_i1	46(33)		4421	409	1.1E-124		
Unclassified	*Chaq virus*	c123170_g1_i1	38(97)	Orf1	521	7.6	9.7E-32	Pachypsylla psyllid	23
		c27006_g1_i1	59(61)		1437	8068	2.8E-111		
Unclassified RNA	*Hubei virga-like virus 12*	c70967_g1_i1	31(88)	Hypothetical protein	511	4.8	1.4E-07	*Dipteria*	24
Family*;* *Baculoviridae* dsDNA	*Autographa californica nucleo-polyhedrovirus*	c39646_g1_i1	56(70)	ORF B	1084	7.0	2E-91	*Spodoptera frugiperda*	25
		c76297_g1_i1	75(99)	ORF B	529	3.7	2E-88		
		c55859_g1_i1	100(48)	AcOrf-4 peptide	395	2.8	3.1E-38		
		c82294_g1_i1	99(99)	AcOrf-5 peptide	206	3	1.10E-41		
Other									
Unclassified RNA viruses	*Beihai barnacle virus 12*	c33969_g1_i1	44(91)	RdRp	1727	4527	4.4-163	*Barnacle*	7
Plant virus									
Genus *Tobamovirus* ssRNA(+)	*Cucumber fruit mottle mosaic virus*	c36375_g1_i1[3]	28(47)	Unnamed protein	6510	108	5.41E-58	Cucumber	NP_072162.1
Phage									
	Spiroplasma phage 4	c40444_g1_i1	36(84)	Hypothetical protein Sp-4p1	345	5.1	4.9E-6		26

References

1. Chandler, J. A. *et al.* Metagenomic shotgun sequencing of a Bunyavirus in wild-caught Aedes aegypti from Thailand informs the evolutionary and genomic history of the Phleboviruses. *Virology* **464-465**, 312-319 (2014).
2. Aguiar, E. R. *et al.* Sequence-independent characterization of viruses based on the pattern of viral small RNAs produced by the host. *Nucleic Acids Res* **43**, 6191-6206 (2015).
3. Yamanaka, A., Thongrungkiat, S., Ramasoota, P. & Konishi, E. Genetic and evolutionary analysis of cell-fusing agent virus based on Thai strains isolated in 2008 and 2012. *Infect Genet Evol* **19**, 188-194 (2013).
4. Chandler, J. A., Liu, R. M. & Bennett, S. N. RNA shotgun metagenomic sequencing of northern California (USA) mosquitoes uncovers viruses, bacteria, and fungi. *Front Microbiol* **6**, 185 (2015).
5. Fan, H. *et al.* Complete genome sequence of Xishuangbanna flavivirus, a novel mosquito-specific flavivirus from China. *Arch Virol* **161**, 1723-1727 (2016).
6. Li, C. X. *et al.* Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. *Elife* **4**, e05378 (2015).
7. Fauver, J. R. *et al.* West African Anopheles gambiae mosquitoes harbor a taxonomically diverse virome including new insect-specific flaviviruses, mononegaviruses, and totiviruses. *Virology* **498**, 288-299 (2016).
8. Pauvolid-Correa, A. *et al.* Novel Viruses Isolated from Mosquitoes in Pantanal, Brazil. *Genome Announc* **4**, e01195-01116 (2016).
9. Shi, M. *et al.* Redefining the invertebrate RNA virosphere. *Nature* **540**, 539–543 (2016).
10. Cook, S. *et al.* Novel virus discovery and genome reconstruction from field RNA samples reveals highly divergent viruses in dipteran hosts. *PLoS One* **8**, e80720 (2013).
11. Webster, C. L., Longdon, B., Lewis, S. H. & Obbard, D. J. Twenty-Five New Viruses Associated with the Drosophilidae (Diptera). *Evol Bioinform Online* **12**, 13-25 (2016).
12. Nouri, S., Salem, N. & Falk, B. W. Complete Genome Sequence of Diaphorina citri-associated C virus, a Novel Putative RNA Virus of the Asian Citrus Psyllid, Diaphorina citri. *Genome Announc* **4**, e00639-00616 (2016).
13. Friesen, P. D. & Nissen, M. S. Gene organization and transcription of TED, a lepidopteran retrotransposon integrated within the baculovirus genome. *Mol Cell Biol* **10**, 3067-3077 (1990).
14. Navarro, B. *et al.* The first phlebo-like virus infecting plants: a case study on the adaptation of negative-stranded RNA viruses to new hosts. *Mol Plant Pathol* (2017).
15. Menzel, W., Goetz, R., Lesemann, D. E. & Vetten, H. J. Molecular characterization of a closterovirus from carrot and its identification as a German isolate of Carrot yellow leaf virus. *Arch Virol* **154**, 1343-1347 (2009).
16. Xin, M. *et al.* Two Negative-Strand RNA Viruses Identified in Watermelon Represent a Novel Clade in the Order Bunyavirales. *Front Microbiol* **8**, 1514 (2017).
17. Bolling, B. G. *et al.* Insect-specific viruses detected in laboratory mosquito colonies and their potential implications for experiments evaluating arbovirus vector competence. *Am J Trop Med Hyg* **92**, 422-428 (2015).
18. Sivaram, A. *et al.* Isolation and characterization of densonucleosis virus from Aedes aegypti mosquitoes and its distribution in India. *Intervirology* **52**, 1-7 (2009).
19. Blitvich, B. J. & Firth, A. E. Insect-specific flaviviruses: a systematic review of their discovery, host range, mode of transmission, superinfection exclusion potential and genomic organization. *Viruses* **7**, 1927-1959 (2015).
20. Makhsous, N. *et al.* Isolation and characterization of the fall Chinook aquareovirus. *Virol J* **14**, 170 (2017).
21. Hang, J. *et al.* Genome Sequences of Five Arboviruses in Field-Captured Mosquitoes in a Unique Rural Environment of South Korea. *Genome Announc* **4**, e01644-01615 (2016).
22. Shi, M. *et al.* High-Resolution Metatranscriptomics Reveals the Ecological Dynamics of Mosquito-Associated RNA Viruses in Western Australia. *J Virol* **91**, e00680-00617 (2017).
23. Webster, C. L. *et al.* The Discovery, Distribution, and Evolution of Viruses Associated with Drosophila melanogaster. *PLoS Biol* **13**, e1002210 (2015).
24. Shi, M. *et al.* Divergent Viruses Discovered in Arthropods and Vertebrates Revise the Evolutionary History of the Flaviviridae and Related Viruses. *J Virol* **90**, 659-669 (2015).
25. Ayres, M. D., Howard, S. C., Kuzio, J., Lopez-Ferber, M. & Possee, R. D. The complete DNA sequence of Autographa californica nuclear polyhedrosis virus. *Virology* **202**, 586-605 (1994).
26. Renaudin, J., Pascarel, M. C. & Bove, J. M. Spiroplasma virus 4: nucleotide sequence of the viral DNA, regulatory signals, and proposed genome organization. *J Bacteriol* **169**, 4950-4961 (1987).

Table S3. Contigs showing homology to EVEs. *c50692 might be derived from a relative of Wuhan mosquito virus 9 (Table 1). ** Closest match was to a reverse transcriptase-like enzyme in a transposable genetic element in *Drosophila melanogaster*. ***EVE based on presence of multiple stop codons.

Contig id from Cairns	Nucleotide identity	Gene	Length (nucleo-tides)	Mean read depth	E Data ncbi protein	Refs
c9237_g1_i1	95	PREDICTED: *Aedes aegypti* uncharacterized LOC110677206	382	16	1.1E-26	1
c25880_g1_i1	99	Uncharacterized protein LOC110677205	513	5.9	2.2E-30	1
c50692_g1_i1*	88	PREDICTED: uncharacterized protein LOC109422677 [*Aedes albopictus*]	383	8.7	2E-40	2
c7681_g1_i1	85	Uncharacterized protein LOC110677235	734	7.9	8.3E-102	1
c49221_g1_i1	84	Uncharacterized protein LOC110677235	303	4.5	2.7E-49	1
c7681_g1_i1	85	Uncharacterized protein LOC110677235	734	7.9	8.3E-102	1
c23353_g1_i1	88	Uncharacterized protein LOC110677235	208	3.2	4.2E-07	1
c118388_g1_i1**	58	Retrovirus-related pol polyprotein	208	2.7	4.3E-06	3
c47288_g1_i1***	69	Polyprotein	272	5.1	1.21E-14	4

Contig id from Bangkok	Nucleotide identity	Gene	Length (nucleo-tides)	Mean read depth	E Data ncbi protein	Refs
c35604_g1_i3	89	uncharacterized protein LOC110677205	633	35	3.5E-67	1
c35604_g1_i6	89	uncharacterized protein LOC110677205	804	16	6.3E-68	1
c15103_g1_i1	97	uncharacterized protein LOC110677205	433	15	7.5E-11	1
c36162_g1_i2	98	uncharacterized protein LOC110677205	677	195	7.6E-24	1
c18481_g1_i1	98	uncharacterized protein LOC110677235	324	7.1	5.1E-59	1
c25987_g1_i1	83	uncharacterized protein LOC110677235	1033	17	5.7E-165	1
c36378_g1_i1	89	uncharacterized protein LOC110677235	12872	665	0	1
c36378_g1_i2	89	uncharacterized protein LOC110677235	10372	599	0	1
c36378_g1_i1	89	uncharacterized protein LOC110677235	12872	665	0	1
c54922_g1_i1	99	Subfamily of reverse transcriptases	1698	26.3	0	5
c36237_g2_i1^	74	Polyprotein	240	91	3.8E-8	4
c27654_g1_i1^	59	Polyprotein	368	38	1.1E-39	6
c35778_g3_i1^	83	Polyprotein	473	27	1.68E-24	4

References

1 Matthews, B. J., McBride, C. S., DeGennaro, M., Despo, O. & Vosshall, L. B. The neurotranscriptome of the Aedes aegypti mosquito. *BMC Genomics* **17**, 32 (2016).

2 Chuang, C. K., Yang, T. H., Chen, T. H., Yang, C. F. & Chen, W. J. Heat shock cognate protein 70 isoform D is required for clathrin-dependent endocytosis of Japanese encephalitis virus in C6/36 cells. *J Gen Virol* **96**, 793-803 (2015).

3 Saigo, K. *et al.* Identification of the coding sequence for a reverse transcriptase-like enzyme in a transposable genetic element in Drosophila melanogaster. *Nature* **312**, 659-661 (1984).

4 Fan, H. *et al.* Complete genome sequence of Xishuangbanna flavivirus, a novel mosquito-specific flavivirus from China. *Arch Virol* **161**, 1723-1727 (2016).

5 Shinnick, T. M., Lerner, R. A. & Sutcliffe, J. G. Nucleotide sequence of Moloney murine leukaemia virus. *Nature* **293**, 543-548 (1981).

6 Cholleti, H. *et al.* Discovery of Novel Viruses in Mosquitoes from the Zambezi Valley of Mozambique. *PLoS One* **11**, e0162751 (2016).

Table S4. Contig based virus identification of mycoviruses. Contigs assembled from *Ae aegypti* reads were used for mycovirus identification using the NCBI protein data base. Underlining in the **Classification** column indicates viruses or nearest relatives that appear to be unique to Cairns or Bangkok *Ae. aegypti*.

Mycoviruses from Cairns *Ae. aegypti*

Classification	Virus or *nearest match*	Contig id	Amino acid identity	Gene	Length (nucleo-tide)	Mean read depth	E Data ncbi protein	Host	Refs
Mycoviruses									
Family: *Partitiviridae* dsRNA	*Botryosphaeria dothidea partitivirus 1*	c7547_g1_i1	62	RdRp Coat protein	544	10	5E-54	*Botryosphaeria dothidea*	1
		c35315_g1_i1	85		396	5.7	2E-72		
		c27686_g1_i1	41		615	3.8	2E-39		
		c28765_g1_i1	66		401	5.6	3E-33		
		c43767_g1_i1	69		338	7.3	7.9E-13		
Family: *Partitiviridae*	*Ustilaginoidea virens partitivirus*	c9031_g1_i1	79	RdRp Coat protein	699	14	3.30E-110	*Ustilaginoidea virens*	2
		c5575_g1_i1	88		446	14	9.32E-92		
		c5783_g1_i1	70		733	16	1.99E-95		
		c6217_g1_i1	61		886	15	5.46E-82		
Family: *Partitiviridae*	*Botryotinia fuckeliana partitivirus 1*	c3606_g1_i1	78	RdRp	492	8.9	3.59E-88	*Botryotinia fuckeliana*	NC_010349.1
Family: *Partitiviridae*	Unnamed	c8342_g1_i1	45	RdRp AGW51759.1	1509	55341	1.38E-109	*Fusarium solani*	3
Family: *Chrysoviridae* (clade I) dsRNA	*Tolypocladium cylindrosporum virus 2*	c16223_g1_i1	74	RdRp	254	10	6.02E-35	*Tolypocladium cylindrosporum*	4
		c26707_g1_i1	42		500	17	2.98E-15		
		c35080_g1_i1	49		257	7.9	3.53E-16		
Genus: *Chrysovirus* (clade II) dsRNA	*Magnaporthe oryzae chrysovirus 3*	c10259_g1_i1	35	Hypothetical proteins	1503	9.5	4.47E-62	*Magnaporthe oryzae*	US20140037586 A1
		c18623_g1_i1	45		378	4.4	3.31E-26		
		c18803_g1_i1	63		293	7.5	2.83E-18		
		c28520_g1_i1	52		232	9.3	1.62E-13		
		c31892_g1_i1	51		286	5.9	2.36E-15		
		c35229_g1_i1	36		493	5.4	9.70E-18		
		c45206_g1_i1	47		581	6.7	6.35E-33		
Genus: *Chrysovirus*	*Magnaporthe oryzae chrysovirus 1*	c11895_g1_i1	69	RdRp. Hypothetical protein	515	3.9	8.42E-77	*Magnaporthe oryzae*	5
		c17275_g1_i1	66		561	5.2	5.98E-81		
		c54876_g1_i1	39		513	5.2	2.69E-35		
		c18610_g1_i1	40		1073	11	5.12E-30		
Genus: *Chrysovirus*	*Penicillium chrysogenum virus*	c16117_g1_i1	83	RdRp	424	4.3	2.77E-79	*Penicillium*	6
		c34127_g1_i1	93		361	4.9	1.06E-72		
		c43319_g1_i1	79		505	3.6	2.43E-92		
		c49342_g1_i1	78		1296	7.9	0		
		c16636_g1_i1	60	Major capsid protein	213	6.0	7.35E-9		
		c18833_g1_i1	59		466	5.5	6.04E-30		
		c19064_g1_i1	73		553	12	1.18E-56		
		c33782_g1_i1	68		204	6	1.62E-16		
		c35317_g1_i1	83		276	8.7	4.18E-45		
		c45192_g1_i1	44		938	5.4	2.70E-73		
		c45834_g1_i1	72		494	5.2	1.70E-53		
		c48065_g1_i1	82		289	5.3	1.94E-47		
		c51680_g1_i1	84		860	5.6	1.30E-173		
		c45395_g1_i1	35		228	4	0.00002		
		c9510_g1_i1	54	Hypothetical protein	536	5.3	1.73E-56		
		c27061_g1_i1	54		719	3.8	4.59E-82		
		c29121_g1_i1	59		631	4.9	1.97E-66		
		c32979_g1_i1	40		449	12	2.44E-22		
		c39328_g1_i1	80		266	4.3	2.71E-21		
		c19508_g1_i1	66	Hypothetical protein	293	5.5	5.11E-33		
		c27836_g1_i1	77		245	4.8	2.11E-36		
		c29554_g1_i1	80		383	4.7	1.34E-69		
		c31457_g1_i1	81		393	11	2.26E-43		
		c37624_g1_i1	86		614	7.3	2.63E-127		
		c45358_g1_i1	74		208	8.0	3.77E-28		
		c48709_g1_i1	77		393	6.0	1.08E-65		
		c53047_g1_i1	81		243	4.0	4.49E-41		
		c53928_g1_i1	78		458	4.2	2.66E-82		

Genus; *Totivirus* dsRNA	*Scheffersomyces segobiensis virus L*	c24059_g1_i1	52	Capsid	313	6.0	2.53E-27	*Scheffersomyces segobiensis*	7
		c50237_g1_i1	59		391	4.4	1.73E-45		
		c42138_g1_i1	61	Polyprotein	440	4.2	4.50E-62		
		c45664_g1_i1	51		401	4.4	2.66E-36		
		c28122_g1_i1	53	Polyprotein	369	5.0	3.30E-32		
		c31620_g1_i1	52		321	4.9	7.69E-34		
		c32294_g1_i1	52		309	4.9	2.54E-28		
		c33879_g1_i1	42		403	4.8	1.34E-26		
Genus; *Totivirus* dsRNA	*Ustilago maydis virus H1*	c37453_g1_i1	33	Cap-pol fusion protein	594	5.1	3.31E-6	*Ustilago maydis*	8
		c42393_g1_i1	72		205	6.0	3.62E-29		
		c43689_g1_i1	80		402	4.7	3.25E-69		
		c51753_g1_i1	57	Polyprotein	404	6.8	4.79E-50		
Unclassified ourmia-like virus	*Rhizoctonia solani ourmia-like virus 1 RNA 1*	c6975_g1_i1	36	RdRp	1806	23	1.18E-53	*Rhizoctonia solani*	KP900922.1KP900921
		c13763_g1_i1	33		747	23	2.04E-14		
		c2560_g1_i1	38		2481	189	1.21E-84		
		c45380_g1_i1	56		320	10	1.20E-18		
Unclassified ourmia-like virus	*Botrytis ourmia-like virus*	c17358_g1_i1	30	RdRp	983	8.8	2.82E-16	Botrytis	9
Family *Bunyaviridae* ssRNA(-)	*Fusarium poae negative-stranded virus 2*	c8881_g1_i1	46	RdRp	6498	37	8e-58	*Fusarium poae*	10
Genus: *Victorivirus* dsRNA	*Ustilaginoidea virens RNA virus M*	c25256_g1_i1	35	RdRp	1070	7.1	2.69E-49	*Ustilaginoidea virens*	11
		c51155_g1_i1	44		357	12	3.80E-23		

Mycoviruses from Bangkok *Ae aegypti*

Classification	Virus or *nearest match*	Contig id	Amino acid identity	Gene	Length (nucleo-tide)	Mean read depth	E Data ncbi protein	Host	Refs
Mycoiruses									
Family: Ophioviridae ssRNA(-)	*Rhizoctonia solani negative-stranded virus 1*	c31623_g1_i1	31	RdRp	3076	55	9.88E-76	*Rhizoctonia solani*	12
Family: Ophioviridae	*Rhizoctonia solani negative-stranded virus 3*	c26658_g1_i1	29	RdRp	2239	54	8.66E-11	*Rhizoctonia solani*	12
Family *Bunyaviridae* ssRNA(-)	*Fusarium poae negative-stranded virus 2*	c35704_g1_i1	26	RdRp	7947	103	3.35E-118	*Fusarium poae*	10
		c12670_g1_i1	25		1492	39	2.47E-13		

References

1 Wang, L. *et al.* Hypovirulence of the phytopathogenic fungus Botryosphaeria dothidea: association with a coinfecting chrysovirus and a partitivirus. *J Virol* **88**, 7517-7527 (2014).

2 Zhong, J. *et al.* Complete genome sequence and organization of a novel virus from the rice false smut fungus Ustilaginoidea virens. *Virus Genes* **48**, 329-333 (2014).

3 Cook, S. *et al.* Novel virus discovery and genome reconstruction from field RNA samples reveals highly divergent viruses in dipteran hosts. *PLoS One* **8**, e80720 (2013).

4 Herrero, N. & Zabalgogeazcoa, I. Mycoviruses infecting the endophytic and entomopathogenic fungus Tolypocladium cylindrosporum. *Virus Res* **160**, 409-413 (2011).

5 Urayama, S. *et al.* A dsRNA mycovirus, Magnaporthe oryzae chrysovirus 1-B, suppresses vegetative growth and development of the rice blast fungus. *Virology* **448**, 265-273 (2014).

6 Jiang, D. & Ghabrial, S. A. Molecular characterization of Penicillium chrysogenum virus: reconsideration of the taxonomy of the genus Chrysovirus. *J Gen Virol* **85**, 2111-2121 (2004).

7 Taylor, D. J., Ballinger, M. J., Bowman, S. M. & Bruenn, J. A. Virus-host co-evolution under a modified nuclear genetic code. *PeerJ* **1**, e50 (2013).

8 Voth, P. D., Mairura, L., Lockhart, B. E. & May, G. Phylogeography of Ustilago maydis virus H1 in the USA and Mexico. *J Gen Virol* **87**, 3433-3441 (2006).

9 Donaire, L., Rozas, J. & Ayllon, M. A. Molecular characterization of Botrytis ourmia-like virus, a mycovirus close to the plant pathogenic genus Ourmiavirus. *Virology* **489**, 158-164 (2016).

10 Osaki, H., Sasaki, A., Nomiyama, K. & Tomioka, K. Multiple virus infection in a single strain of Fusarium poae shown by deep sequencing. *Virus Genes* (2016).

11 Zhang, T., Jiang, Y., Huang, J. & Dong, W. Complete genome sequence of a putative novel victorivirus from Ustilaginoidea virens. *Arch Virol* **158**, 1403-1406 (2013).

12 Marzano, S. Y. *et al.* Identification of Diverse Mycoviruses through Metatranscriptomics Characterization of the Viromes of Five Major Fungal Plant Pathogens. *J Virol* **90**, 6846-6863 (2016).

Table S5. Mapping of reads to the human genome. All trimmed and quality-controlled reads (before ribosomal filter) were mapped to the human reference genome (ensemble release 75) using STAR v2.5.2a. Genes were derived based on the genome coordinates. In total, 8646 reads from the Cairns and 8744 reads from the Bangkok dataset matched a human gene. Below is a table listing the number of reads matching human genes. Only genes that have at least 5 reads in both datasets (63 genes) are listed. In total, 327 genes were identified that had at least 5 reads in either of the two datasets.

Gene	**Bangkok**	**Cairns**
ENSG00000266658 RNA28S5:"RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]"	1646	4109
ENSG00000210082 MT-RNR2:mitochondrially encoded 16S RNA [Source:HGNC Symbol;Acc:7471]	118	986
ENSG00000211459 MT-RNR1:mitochondrially encoded 12S RNA [Source:HGNC Symbol;Acc:7470]	34	600
ENSG00000244734 HBB:"hemoglobin, beta [Source:HGNC Symbol;Acc:4827]"	417	126
ENSG00000188536 HBA2:"hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]"	394	85
ENSG00000206172 HBA1:"hemoglobin, alpha 1 [Source:HGNC Symbol;Acc:4823]"	351	87
ENSG00000258486 RN7SL1:"RNA, 7SL, cytoplasmic 1 [Source:HGNC Symbol;Acc:10038]"	280	60
ENSG00000150991 UBC:ubiquitin C [Source:HGNC Symbol;Acc:12468]	57	234
ENSG00000170315 UBB:ubiquitin B [Source:HGNC Symbol;Acc:12463]	111	173
ENSG00000265150 RN7SL2:"RNA, 7SL, cytoplasmic 2 [Source:HGNC Symbol;Acc:23134]"	128	18
ENSG00000226958 CTD-2328D6.1:	16	87
ENSG00000184009 ACTG1:"actin, gamma 1 [Source:HGNC Symbol;Acc:144]"	62	41
ENSG00000143632 ACTA1:"actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:129]"	49	52
ENSG00000263563 UBBP4:ubiquitin B pseudogene 4 [Source:HGNC Symbol;Acc:12467]	29	63
ENSG00000258947 TUBB3:Tubulin beta-3 chain [Source:UniProtKB/Swiss-Prot;Acc:Q13509]	16	60
ENSG00000263740 RN7SL4P:"RNA, 7SL, cytoplasmic 4, pseudogene [Source:HGNC Symbol;Acc:10039]"	54	17
ENSG00000265735 RN7SL5P:"RNA, 7SL, cytoplasmic 5, pseudogene [Source:HGNC Symbol;Acc:10040]"	46	17
ENSG00000147454 SLC25A37:"solute carrier family 25 (mitochondrial iron transporter), member 37 [Source:HGNC Symbol;Acc:29786]"	55	8
ENSG00000107796 ACTA2:"actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;Acc:130]"	22	40
ENSG00000234289 H2BFS:"H2B histone family, member S (pseudogene) [Source:HGNC Symbol;Acc:4762]"	22	34
ENSG00000265401 RP11-138I1.4:	20	33
ENSG00000132475 H3F3B:"H3 histone, family 3B (H3.3B) [Source:HGNC Symbol;Acc:4765]"	13	35
ENSG00000197409 HIST1H3D:"histone cluster 1, H3d [Source:HGNC Symbol;Acc:4767]"	12	34
ENSG00000221983 UBA52:ubiquitin A-52 residue ribosomal protein fusion product 1 [Source:HGNC Symbol;Acc:12458]	38	7
ENSG00000152234 ATP5A1:"ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle [Source:HGNC Symbol;Acc:823]"	26	18
ENSG00000075624 ACTB:"actin, beta [Source:HGNC Symbol;Acc:132]"	18	25
ENSG00000202198 RN7SK:"RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]"	37	5
ENSG00000241838 LA16c-3G11.7:	11	27
ENSG00000203852 HIST2H3A:"histone cluster 2, H3a [Source:HGNC Symbol;Acc:20505]"	9	25
ENSG00000204434 POTEKP:"POTE ankyrin domain family, member K, pseudogene [Source:HGNC Symbol;Acc:30182]"	19	15
ENSG00000180139 ACTA2-AS1:ACTA2 antisense RNA 1 [Source:HGNC Symbol;Acc:45169]	11	20
ENSG00000147403 RPL10:ribosomal protein L10 [Source:HGNC Symbol;Acc:10298]	18	13
ENSG00000197903 HIST1H2BK:"histone cluster 1, H2bk [Source:HGNC Symbol;Acc:13954]"	13	17
ENSG00000104765 BNIP3L:BCL2/adenovirus E1B 19kDa interacting protein 3-like [Source:HGNC Symbol;Acc:1085]	23	7
ENSG00000180596 HIST1H2BC:"histone cluster 1, H2bc [Source:HGNC Symbol;Acc:4757]"	8	18

ENSG00000170889 RPS9:ribosomal protein S9 [Source:HGNC Symbol;Acc:10442]	10	15
ENSG00000203811 HIST2H3C:"histone cluster 2, H3c [Source:HGNC Symbol;Acc:20503]"	8	17
ENSG00000196176 HIST1H4A:"histone cluster 1, H4a [Source:HGNC Symbol;Acc:4781]"	10	15
ENSG00000197616 MYH6:"myosin, heavy chain 6, cardiac muscle, alpha [Source:HGNC Symbol;Acc:7576]"	14	10
ENSG00000207507 RNU6-9:"RNA, U6 small nuclear 9 [Source:HGNC Symbol;Acc:34269]"	11	13
ENSG00000230037 UBBP1:ubiquitin B pseudogene 1 [Source:HGNC Symbol;Acc:12464]	6	17
ENSG00000137285 TUBB2B:"tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]"	12	10
ENSG00000188229 TUBB4B:"tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:20771]"	10	12
ENSG00000109971 HSPA8:heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:5241]	8	14
ENSG00000184779 RPS17:ribosomal protein S17 [Source:HGNC Symbol;Acc:10397]	16	5
ENSG00000104904 OAZ1:ornithine decarboxylase antizyme 1 [Source:HGNC Symbol;Acc:8095]	14	6
ENSG00000187537 POTEM:"POTE ankyrin domain family, member M [Source:HGNC Symbol;Acc:37096]"	6	14
ENSG00000083845 RPS5:ribosomal protein S5 [Source:HGNC Symbol;Acc:10426]	6	12
ENSG00000126803 HSPA2:heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235]	10	8
ENSG00000272055 RNU6-6P:"RNA, U6 small nuclear 6, pseudogene [Source:HGNC Symbol;Acc:10228]"	10	8
ENSG00000142534 RPS11:ribosomal protein S11 [Source:HGNC Symbol;Acc:10384]	12	5
ENSG00000206932 RNU6-4P:"RNA, U6 small nuclear 4, pseudogene [Source:HGNC Symbol;Acc:34253]"	7	10
ENSG00000110955 ATP5B:"ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide [Source:HGNC Symbol;Acc:830]"	6	11
ENSG00000127824 TUBA4A:"tubulin, alpha 4a [Source:HGNC Symbol;Acc:12407]"	9	8
ENSG00000156508 EEF1A1:eukaryotic translation elongation factor 1 alpha 1 [Source:HGNC Symbol;Acc:3189]	9	8
ENSG00000196374 HIST1H2BM:"histone cluster 1, H2bm [Source:HGNC Symbol;Acc:4750]"	6	9
ENSG00000100316 RPL3:ribosomal protein L3 [Source:HGNC Symbol;Acc:10332]	9	6
ENSG00000143947 RPS27A:ribosomal protein S27a [Source:HGNC Symbol;Acc:10417]	8	7
ENSG00000123091 RNF11:ring finger protein 11 [Source:HGNC Symbol;Acc:10056]	8	6
ENSG00000207357 RNU6-2:"RNA, U6 small nuclear 2 [Source:HGNC Symbol;Acc:34270]"	7	7
ENSG00000197697 HIST1H2BE:"histone cluster 1, H2be [Source:HGNC Symbol;Acc:4753]"	5	8
ENSG00000206899 RNU6-36P:"RNA, U6 small nuclear 36, pseudogene [Source:HGNC Symbol;Acc:34280]"	5	7
ENSG00000137267 TUBB2A:"tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412]"	5	5

Table S6. Mapping of reads to other chordates. Chordate reads that did not match human sequences (see Fig. 1) were used to search for matches in the nucleotide database. Non *homo sapiens* matches with at least 95% identity and 95% coverage are included. For Bangkok 190 reads mapped to mice/rat genes, for Cairns 79 reads mapped to mice/rat genes. For Bangkok 5 reads mapped to dog genes. For Bangkok 1 read mapped to cow, for Cairns 1 read mapped to cow. The closest *Homo sapiens* genes are included for a random selection of reads and are highlighted in grey.

Bangkok (Mouse/rat)

CTCCAAAGCTATCAAAGTACCGCTGGGTCCAAGGGTAGACAACCAGCAGCCTGCCCAGGGCCTCACCACCA
ACTTCATCGGCGTTCACCTTTCCCCACAGGCCAGAGACAGCAGCCTTCTCAGCATCAGTCAGGTGCACCAT
GATGTCTG

Mus musculus hemoglobin, beta adult t chain (Hbb-bt), mRNA
Sequence ID: NM_008220.5
Identities: 150/150(100%) Gaps: 0/150(0%)

```
Query  1    CTCCAAAGCTATCAAAGTACCGCTGGGTCCAAGGGTAGACAACCAGCAGCCTGCCCAGGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  196  CTCCAAAGCTATCAAAGTACCGCTGGGTCCAAGGGTAGACAACCAGCAGCCTGCCCAGGG  137

Query  61   CCTCACCACCAACTTCATCGGCGTTCACCTTTCCCCACAGGCCAGAGACAGCAGCCTTCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  136  CCTCACCACCAACTTCATCGGCGTTCACCTTTCCCCACAGGCCAGAGACAGCAGCCTTCT  77

Query  121  CAGCATCAGTCAGGTGCACCATGATGTCTG  150
            ||||||||||||||||||||||||||||||
Sbjct  76   CAGCATCAGTCAGGTGCACCATGATGTCTG  47
```

Homo sapiens hemoglobin subunit beta (HBB), mRNA
Sequence ID: NM_000518.4
Identities: 128/148(86%) Gaps0/148(0%)

```
Query  3    CCAAAGCTATCAAAGTACCGCTGGGTCCAAGGGTAGACAACCAGCAGCCTGCCCAGGGCC  62
            ||||||   |||||| ||| |||||||||||||||||| |||||||||||||||||||||
Sbjct  190  CCAAAGGACTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAGCAGCCTGCCCAGGGCC  131

Query  63   TCACCACCAACTTCATCGGCGTTCACCTTTCCCCACAGGCCAGAGACAGCAGCCTTCTCA  122
            |||||||||||||||||  |||||||||| ||||||||| |||  || |||| ||||||
Sbjct  130  TCACCACCAACTTCATCCACGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTCC  71

Query  123  GCATCAGTCAGGTGCACCATGATGTCTG  150
             ||  |||||| ||||||||| ||||||
Sbjct  70   TCAGGAGTCAGATGCACCATGGTGTCTG  43
```

GGGGCCAGCTCCAAGGTGTGCTTCTCATTAGTATACTCCACAGTGCCACCCTTGGCCAGGTCCCTTTGGAA
ATTCCAGGTAAAGCGCAGTGTAATGTCGGCTGTGCCGTTGTACAGCTCCTGCTTCATCTGGGCTCGGCTGG
GTGGGCTG

PREDICTED: Mus musculus piezo-type mechanosensitive ion channel component 1 (Piezo1), transcript variant X6, mRNA
Identities: 150/150(100%) Gaps: 0/150(0%)

```
Query  1     GGGGCCAGCTCCAAGGTGTGCTTCTCATTAGTATACTCCACAGTGCCACCCTTGGCCAGG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5458  GGGGCCAGCTCCAAGGTGTGCTTCTCATTAGTATACTCCACAGTGCCACCCTTGGCCAGG  5399

Query  61    TCCCTTTGGAAATTCCAGGTAAAGCGCAGTGTAATGTCGGCTGTGCCGTTGTACAGCTCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5398  TCCCTTTGGAAATTCCAGGTAAAGCGCAGTGTAATGTCGGCTGTGCCGTTGTACAGCTCC  5339

Query  121   TGCTTCATCTGGGCTCGGCTGGGTGGGCTG  150
             ||||||||||||||||||||||||||||||
Sbjct  5338  TGCTTCATCTGGGCTCGGCTGGGTGGGCTG  5309
```

Homo sapiens piezo type mechanosensitive ion channel component 1 (PIEZO1), mRNA
Sequence ID: NM_001142864.3
Identities: 129/150(86%) Gaps: 0/150(0%)

```
Query  1      GGGGCCAGCTCCAAGGTGTGCTTCTCATTAGTATACTCCACAGTGCCACCCTTGGCCAGG  60
              ||||||||  |||   |||||||||| || | ||||||||||||||| ||||| ||||||
Sbjct  7245   GGGGCCAGGGCCAGCATGTGCTTCTCGTTGGCATACTCCACAGTGCCTCCCTTCGCCAGG  7186

Query  61     TCCCTTTGGAAATTCCAGGTAAAGCGCAGTGTAATGTCGGCTGTGCCGTTGTACAGCTCC  120
              ||||| ||||| |||||||| |||||||| || |||||||| ||||||||||| ||||||
Sbjct  7185   TCCCTCTGGAAGTTCCAGGTGAAGCGCAGGGTGATGTCGGCCGTGCCGTTGTAGAGCTCC  7126

Query  121    TGCTTCATCTGGGCTCGGCTGGGTGGGCTG  150
               ||||||||||||| |||||||| || |||
Sbjct  7125   CGCTTCATCTGGGCACGGCTGGGGGGACTG  7096
```

CTCAGACTCAAATATCTTGGCCATATATCTAGGCTCTACTCTGACTANATCATGACTCACANAACCCAATT
ATTTTAACCTACACTCNGCCCCGTGGCGGGTTCCCTGTGCTCATG

Mus musculus targeted non-conditional, lacZ-tagged mutant allele
Siah2:tm1e(EUCOMM)Hmgu; transgenic
Sequence ID: JN948870.1
Identities: 113/116(97%) Gaps: 0/116(0%)

```
Query  1      CTCAGACTCAAATATCTTGGCCATATATCTAGGCTCTACTCTGACTANATCATGACTCAC  60
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  5625   CTCAGACTCAAATATCTTGGCCATATATCTAGGCTCTACTCTGACTAGATCATGACTCAC  5566

Query  61     ANAACCCAATTATTTTAACCTACACTCNGCCCCGTGGCGGGTTCCCTGTGCTCATG  116
              | ||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  5565   ACAACCCAATTATTTTAACCTACACTCTGCCCCGTGGCGGGTTCCCTGTGCTCATG  5510
```

Homo sapiens chromosome 2, alternate assembly CHM1_1.1
Sequence ID: NC_018913.2
Identities: 24/26(92%) Gaps: 0/26(0%)

```
Query  8          TCAAATATCTTGGCCATATATCTAGG  33
                  |||| |||||||||||||||||| ||
Sbjct  84754503   TCAATTATCTTGGCCATATATCTGGG  84754478
```

GGCAATAACTGACAGATGCTCTCTTGGGAACAATTAACCATTGTTCACAGGCAAGAGCAGGAAAGGGGGTT
TAGTGGTACTTGTGAGCCAGGGCAGCGGCCACTCCAGCCACCACCTTCTGGAAGGCAGCCTGTGCAGCGGG
GGTGAAAT

Mus musculus hemoglobin, beta adult s chain (Hbb-bs), mRNA
Sequence ID: NM_001201391.1
Identities: 147/148(99%) Gaps: 0/148(0%)

```
Query  3    CAATAACTGACAGATGCTCTCTTGGGAACAATTAACCATTGTTCACAGGCAAGAGCAGGA  62
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  565  CAACAACTGACAGATGCTCTCTTGGGAACAATTAACCATTGTTCACAGGCAAGAGCAGGA  506

Query  63   AAGGGGGTTTAGTGGTACTTGTGAGCCAGGGCAGCGGCCACTCCAGCCACCACCTTCTGG  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  505  AAGGGGGTTTAGTGGTACTTGTGAGCCAGGGCAGCGGCCACTCCAGCCACCACCTTCTGG  446

Query  123  AAGGCAGCCTGTGCAGCGGGGGTGAAAT  150
            ||||||||||||||||||||||||||||
Sbjct  445  AAGGCAGCCTGTGCAGCGGGGGTGAAAT  418
```

Homo sapiens hemoglobin subunit beta (HBB), mRNA
Sequence ID: NM_000518.4
Identities: 75/93(81%) Gaps: 0/93(0%)

```
Query  56   AGCAGGAAAGGGGGTTTAGTGGTACTTGTGAGCCAGGGCAGCGGCCACTCCAGCCACCAC  115
            |||| ||||| | | |||||| |||||||| |||||||||   ||||| |||||||||||
Sbjct  509  AGCAAGAAAGCGAGCTTAGTGATACTTGTGGGCCAGGGCATTAGCCACACCAGCCACCAC  450

Query  116  CTTCTGGAAGGCAGCCTGTGCAGCGGGGGTGAA  148
             |||||  ||||||||||  | |  ||||||||
Sbjct  449  TTTCTGATAGGCAGCCTGCACTGGTGGGGTGAA  417
```

GCCAGGGCAGCGGCCACTCCAGCCACCACCTTCTGGAAGGCAGCCTGTGCAGCGGGGGTGAAATCCTTGCC
CAGGTGGTGGCCCAGCACAATCACGATCATATTGCCCAGGAGCCTGAAGTTCTCAGGATCCACATGCAGCT
TGTCACAG

TPA_inf: Mus musculus Glna1 gene for globin a1
Sequence ID: LT548150.1

Identities: 150/150(100%) Gaps: 0/150(0%)

```
Query  1    GCCAGGGCAGCGGCCACTCCAGCCACCACCTTCTGGAAGGCAGCCTGTGCAGCGGGGGTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428  GCCAGGGCAGCGGCCACTCCAGCCACCACCTTCTGGAAGGCAGCCTGTGCAGCGGGGGTG  369

Query  61   AAATCCTTGCCCAGGTGGTGGCCCAGCACAATCACGATCATATTGCCCAGGAGCCTGAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368  AAATCCTTGCCCAGGTGGTGGCCCAGCACAATCACGATCATATTGCCCAGGAGCCTGAAG  309

Query  121  TTCTCAGGATCCACATGCAGCTTGTCACAG  150
            ||||||||||||||||||||||||||||||
Sbjct  308  TTCTCAGGATCCACATGCAGCTTGTCACAG  279
```

Homo sapiens hemoglobin subunit delta (HBD), mRNA
Sequence ID: NM_000519.3
Identities: 124/150(83%) Gaps: 0/150(0%)

```
Query  1    GCCAGGGCAGCGGCCACTCCAGCCACCACCTTCTGGAAGGCAGCCTGTGCAGCGGGGGTG  60
            |||||||||   ||||| |||||||||||||||||  ||||||||||       ||||||
Sbjct  623  GCCAGGGCATTAGCCACACCAGCCACCACCTTCTGATAGGCAGCCTGCATTTGTGGGGTG  564

Query  61   AAATCCTTGCCCAGGTGGTGGCCCAGCACAATCACGATCATATTGCCCAGGAGCCTGAAG  120
            || |||||||| | || | || ||||||||  ||| | || |||||||| ||||||||||
Sbjct  563  AATTCCTTGCCAAAGTTGCGGGCCAGCACACACACCAGCACATTGCCCAAGAGCCTGAAG  504

Query  121  TTCTCAGGATCCACATGCAGCTTGTCACAG  150
            |||||||||||||| |||||||||||||||
Sbjct  503  TTCTCAGGATCCACGTGCAGCTTGTCACAG  474
```

GGTTTTTCTTTTTGTTGTTGTTGTTGTAGTGGTGGTGGTGAGAAATCCTTTTTTTGTTGAAAACGTAGTAGTGAAAAATTTAATTCTATGGCTTAAAAATGTATCTGTTACCTAAAAATTTGAAGTTTTACAATTCTGTCTCAACTCCTT

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Bco2:tm1a(KOMP)Wtsi; transgenic
Sequence ID: JN954538.1
Identities: 149/150(99%) Gaps: 0/150(0%)

```
Query  1     GGTTTTTCTTTTTGTTGTTGTTGTTGTAGTGGTGGTGGTGAGAAATCCtttttttGTTGA  60
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  1836  GGTTTTTCTTTTTGTTGTTGTTGTGGTAGTGGTGGTGGTGAGAAATCCTTTTTTTGTTGA  1895

Query  61    AAACGTAGTAGTGAAAAATTTAATTCTATGGCTTAAAAATGTATCTGTTACCTAAAAATT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1896  AAACGTAGTAGTGAAAAATTTAATTCTATGGCTTAAAAATGTATCTGTTACCTAAAAATT  1955

Query  121   TGAAGTTTTACAATTCTGTCTCAACTCCTT  150
             ||||||||||||||||||||||||||||||
Sbjct  1956  TGAAGTTTTACAATTCTGTCTCAACTCCTT  1985
```

Homo sapiens chromosome 1 genomic patch of type NOVEL, GRCh38.p7 PATCHES HSCHR1_4_CTG3
Sequence ID: NW_014040926.1
Identities: 35/41(85%) Gaps: 0/41(0%)

```
Query  3       TTTTTCTTTTTGTTGTTGTTGTTGTAGTGGTGGTGGTGAGA  43
               ||||| || |||||||||||||||| || || || ||||||
Sbjct  294088  TTTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTGAGA  294048
```

ATTGTCCAAGTAGTCCCTTCTATTATTCACTCTAAAGCCAGAGCCACATGGCTGAAACTGCAGAGTTCTACTGCTTGCAGGAACTAGAACATGACCCGCTTGTACTATTACATTATCACCAGCTTTTTGTTCTCCAACTCCTTCACTACC

Mus musculus BAC clone RP24-408G4 from 14, complete sequence
Sequence ID: AC154759.2
Identities: 148/150(99%) Gaps: 0/150(0%)

```
Query  1    ATTGTCCAAGTAGTCCCTTCTATTATTCACTCTAAAGCCAGAGCCACATGGCTGAAACTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252  ATTGTCCAAGTAGTCCCTTCTATTATTCACTCTAAAGCCAGAGCCACATGGCTGAAACTG  193

Query  61   CAGAGTTCTACTGCTTGCAGGAACTAGAACATGACCCGCTTGTACTATTACATTATCACC  120
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  192  CAGAGTTCTGCTGCTTGCAGGAACTAGAACATGACCCGCTTGTACTATTACATTATCACC  133
```

```
Query  121  AGCTTTTTGTTCTCCAACTCCTTCACTACC  150
            |||||| |||||||||||||||||||||||
Sbjct  132  AGCTTTCTGTTCTCCAACTCCTTCACTACC  103
```

Homo sapiens chromosome 1, alternate assembly CHM1_1.1
Sequence ID: NC_018912.2
Identities: 31/36(86%) Gaps: 3/36(8%)

```
Query  14        TCCCTT---CTATTATTCACTCTAAAGCCAGAGCCA  46
                 ||||||   || |||||||||||||||||||| |||
Sbjct  26182260  TCCCTTTACCTCTTATTCACTCTAAAGCCAGATCCA  26182225
```

GGGGCAGCGGCCACTCCAGCCACCACTTCTGGAAGGCAGCCTGTGCAGCGGGGGTGAAATCCTTGCCCAGG
TGGTGGCCCAGCACAATCACGATCATATTGCCCAGGAGCCTGAAGTTCTCAGGATCCACATGCAGCTTGTC
ACAGTGGA

TPA_inf: Mus musculus Glna1 gene for globin a1
Sequence ID: LT548150.1
Identities: 149/150(99%) Gaps: 1/150(0%)

```
Query  2    GGGCAGCGGCCACTCCAGCCACCAC-TTCTGGAAGGCAGCCTGTGCAGCGGGGGTGAAAT  60
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  424  GGGCAGCGGCCACTCCAGCCACCACCTTCTGGAAGGCAGCCTGTGCAGCGGGGGTGAAAT  365

Query  61   CCTTGCCCAGGTGGTGGCCCAGCACAATCACGATCATATTGCCCAGGAGCCTGAAGTTCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  364  CCTTGCCCAGGTGGTGGCCCAGCACAATCACGATCATATTGCCCAGGAGCCTGAAGTTCT  305

Query  121  CAGGATCCACATGCAGCTTGTCACAGTGGA  150
            ||||||||||||||||||||||||||||||
Sbjct  304  CAGGATCCACATGCAGCTTGTCACAGTGGA  275
```

Homo sapiens hemoglobin subunit beta (HBB), mRNA
Sequence ID: NM_000518.4
Identities: 122/148(82%) Gaps: 1/148(0%)

```
Query  2    GGGCAGCGGCCACTCCAGCCACCACTT-CTGGAAGGCAGCCTGTGCAGCGGGGGTGAAAT  60
            |||||   ||||| ||||||||||||| |||  ||||||||||  | |  |||||||| |
Sbjct  474  GGGCATTAGCCACACCAGCCACCACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATT  415

Query  61   CCTTGCCCAGGTGGTGGCCCAGCACAATCACGATCATATTGCCCAGGAGCCTGAAGTTCT  120
            | ||||| | ||| ||| ||||||||   || | ||  ||||||||||||||||||||||
Sbjct  414  CTTTGCCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGCCCAGGAGCCTGAAGTTCT  355

Query  121  CAGGATCCACATGCAGCTTGTCACAGTG  148
            |||||||||| |||||||||||||||||
Sbjct  354  CAGGATCCACGTGCAGCTTGTCACAGTG  327
```

GTTTTCTATATTTCATACAGATATCTCTTTGGGAATGGTATTATTTGGTGAAATTAATGGAGTTAGAATAA
AAATAAATATTTCATAGATTTATATTTTATCACTATATATTTGAAGGCTGAATCTAAATATTGATCTGATA
ATATGAAG

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Bco2:tm1a(KOMP)Wtsi; transgenic
Sequence ID: JN954538.1
Identities: 149/150(99%) Gaps: 0/150(0%)

```
Query  1     GTTTTCTATATTTCATACAGATATCTCTTTGGGAATGGTATTATTTGGTGAAATTAATGG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2100  GTTTTCTATATTTCATACAGATATCTCTTTGGGAATGGTATTATTTGGTGAAATTAATGG  2159

Query  61    AGTTAGAATAAAAATAAATATTTCATAGATTTATATTTTATCACTATATATTTGAAGGCT  120
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  2160  AGTTAGAATAAAAATAAATATTTCATATATTTATATTTTATCACTATATATTTGAAGGCT  2219

Query  121   GAATCTAAATATTGATCTGATAATATGAAG  150
             ||||||||||||||||||||||||||||||
Sbjct  2220  GAATCTAAATATTGATCTGATAATATGAAG  2249
```

Homo sapiens chromosome 1 genomic patch of type NOVEL, GRCh38.p7 PATCHES HSCHR1_5_CTG32_1
Sequence ID: NW_014040927.1
Identities: 33/40(83%) Gaps: 2/40(5%)

```
Query  64    TAGAATAAAAATAAATATTTCATAGATTT--ATATTTTAT  101
             ||||| ||||||| ||||||  || ||||  |||||||||
Sbjct  3095  TAGAAAAAAAATATATATTTTTTATATTTTTATATTTTAT  3056
```

```
GTTTTCTATATTTCATACAGATATCTCTTTGGGAATGGTATTATTTGGTGAAATTAATGGAGTTAGAATAA
AAATAAATATTTCATAGATTTATATTTTATCACTATATATTTGAAGGCTGAATCTAAATATTGATCTGATA
ATATGAAG
```

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Bco2:tm1a(KOMP)Wtsi; transgenic

Identities: 149/150(99%) Gaps: 0/150(0%)

```
Query  1     GTTTTCTATATTTCATACAGATATCTCTTTGGGAATGGTATTATTTGGTGAAATTAATGG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2100  GTTTTCTATATTTCATACAGATATCTCTTTGGGAATGGTATTATTTGGTGAAATTAATGG  2159

Query  61    AGTTAGAATAAAAATAAATATTTCATAGATTTATATTTTATCACTATATATTTGAAGGCT  120
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  2160  AGTTAGAATAAAAATAAATATTTCATATATTTATATTTTATCACTATATATTTGAAGGCT  2219

Query  121   GAATCTAAATATTGATCTGATAATATGAAG  150
             ||||||||||||||||||||||||||||||
Sbjct  2220  GAATCTAAATATTGATCTGATAATATGAAG  2249
```

PREDICTED: Homo sapiens ST6 beta-galactoside alpha-2,6-sialyltransferase 1 (ST6GAL1), transcript variant X9, mRNA

Sequence ID: NC_018912.2

Identities: 54/69(78%) Gaps:2/69(2%)

```
Query  68         ATAAAAATAAATATTTCATAGATTTATATTTTATCACTATATATTTGAAGGCTGAATCTA  127
                  ||||| |||||||||| ||| |||||   | ||| | ||||||||| |    ||||| ||
Sbjct  216475256  ATAAATATAAATATTTGATATATTTAA--TATATTAATATATATTTAATATATGAATATA  216475313

Query  128        AATATTGAT  136
                  |||||||||
Sbjct  216475314  AATATTGAT  216475322
```

```
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TGGCTATT
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GAGATGATGGAT
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```

Cairns (Mouse/rat)

```
TTTCCTCCCCAAGCTACTCTTGGTTATAGTGCTTCATCATAGCAATAGTAACCCCATCTAAGATAACACCT
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ATGGCTGTGAGACACCATGCGGTTGCTGGGAATTGAACTTTGGACCTCTGG
```

Mouse DNA sequence from clone RP23-134I10 on chromosome 17, complete sequence
Sequence ID: CT009607.7
Identities: 192/193(99%) Gaps: 0/193(0%)

```
Query  1      TTTCCTCCCCAAGCTACTCTTGGTTATAGTGCTTCATCATAGCAATAGTAACCCCATCTA  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  51815  TTTCCTCCCCAAGCTACTCTTGGTTATAGTGCTTCATCATAGCAATAGTAACCCCATCTA  51756

Query  61     AGATAACACCTCTAATACTTTCAACAGAGTTTCTGTTTCTGTCCTCAGACACACCAGAAG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  51755  AGATAACACCTCTAATACTTTCAACAGAGTTTCTGTTTCTGTCCTCAGACACACCAGAAG  51696

Query  121    AGGGCATAAGATCCCATTACAGATGGCTGTGAGACACCATGCGGTTGCTGGGAATTGAAC  180
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  51695  AGGGCATAAGGTCCCATTACAGATGGCTGTGAGACACCATGCGGTTGCTGGGAATTGAAC  51636

Query  181    TTTGGACCTCTGG  193
              |||||||||||||
Sbjct  51635  TTTGGACCTCTGG  51623
```

Homo sapiens chromosome 20, alternate assembly CHM1_1.1
Sequence ID: NC_018931.2
Identities: 24/24(100%) Gaps: 0/24(0%)

```
Query  83        AACAGAGTTTCTGTTTCTGTCCTC  106
                 ||||||||||||||||||||||||
Sbjct  56417389  AACAGAGTTTCTGTTTCTGTCCTC  56417412
```

```
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TTTTATTTT
```

Mus musculus BAC clone RP23-106G24 from chromosome 3, complete sequence
Sequence ID: AC163297.4
Identities: 151/151(100%) Gaps: 0/151(0%)

```
Query  1      TCTGTAGACCAGGCTGGCTTCAAAGATCTGCCTTCCTCTGTCTCCTAAGTGCTGGGATTA  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30148  TCTGTAGACCAGGCTGGCTTCAAAGATCTGCCTTCCTCTGTCTCCTAAGTGCTGGGATTA  30089

Query  61     AAGGTTTACACTACCACCACTAGCAATTAAGATACAAATTATAAGACTTAAGATTTTAGG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30088  AAGGTTTACACTACCACCACTAGCAATTAAGATACAAATTATAAGACTTAAGATTTTAGG  30029

Query  121    TAGATGTAATTATACTTATAATTTTTATTTT  151
              |||||||||||||||||||||||||||||||
Sbjct  30028  TAGATGTAATTATACTTATAATTTTTATTTT  29998
```

PREDICTED: Homo sapiens centrosomal protein 63 (CEP63), transcript variant X31, mRNA
Sequence ID: XM_017007267.1
Identities: 39/49(80%) Gaps: 0/49(0%)

```
Query  44    cctaagtgctgggattaaaggTTTACACTACCACCACTAGCAATTAAGA  92
             || ||||||||| |||| | || |   ||||||||||| ||| ||||||
Sbjct  1741  CCAAAGTGCTGGAATTACAAGTGTGAGCTACCACCACTGGCAGTTAAGA  1789
```

```
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GACGGTGTAGTTCCAGAGCTTGACAGAGTTGGTAAAGAATTCCT
```

Mouse DNA sequence from clone RP23-240F13 on chromosome X, complete sequence
Sequence ID: AL844583.6
Identities: 185/186(99%) Gaps: 0/186(0%)

```
Query  1     CTAGAAAGACATTTTACCTTGTTTCAATATGAAAGCAATGGAATAAACCATGTACAAACT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2178  CTAGAAAGACATTTTACCTTGTTTCAATATGAAAGCAATGGAATAAACCATGTACAAACT  2119

Query  61    AAAAAAGAACTGAGCCAGAACATACACAAGGTCCCAGGTTCTATCCCCAGCACCACAAAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2118  AAAAAAGAACTGAGCCAGAACATACACAAGGTCCCAGGTTCTATCCCCAGCACCACAAAA  2059

Query  121   ATCAGTAAGTACAGATTTGAAAGACGGTGTAGTTCCAGAGCTTGACAGAGTTGGTAAAGA  180
             ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  2058  ATCAGTAAGTACAGATTTGAAAGACAGTGTAGTTCCAGAGCTTGACAGAGTTGGTAAAGA  1999

Query  181   ATTCCT  186
             ||||||
Sbjct  1998  ATTCCT  1993
```

Homo sapiens chromosome 2, alternate assembly CHM1_1.1
Sequence ID: NC_018913.2
Identities: 25/26(96%) Gaps: 0/26(0%)

```
Query  61        AAAAAAGAACTGAGCCAGAACATACA  86
                 ||||||||||||||||||| ||||||
Sbjct  32235984  AAAAAAGAACTGAGCCAGACCATACA  32235959
```

```
AAGAGAAAGACCTTGGTCTTATGACGATCATATGCCCCAGTACAGGGGAATGCCAGGGCCAGGAAGCAGGA
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AAG
```

Mus musculus 6 BAC RP24-194N1 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence
Sequence ID: AC155727.6
Identities: 145/145(100%) Gaps: 0/145(0%)

```
Query  1       AAGAGAAAGACCTTGGTCTTATGACGATCATATGCCCCAGTAcaggggaatgccagggcc  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164283  AAGAGAAAGACCTTGGTCTTATGACGATCATATGCCCCAGTACAGGGGAATGCCAGGGCC  164342

Query  61      aggaagcaggagtgggtgggttggggagcagggcggggggagggTATAGGGAGCTTTGGG  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164343  AGGAAGCAGGAGTGGGTGGGTTGGGGAGCAGGGCGGGGGGAGGGTATAGGGAGCTTTGGG  164402

Query  121     CATAGCATTTGAAATGTAAATGAAG  145
               |||||||||||||||||||||||||
Sbjct  164403  CATAGCATTTGAAATGTAAATGAAG  164427
```

Homo sapiens chromosome 7, alternate assembly CHM1_1.1
Sequence ID: NC_018918.2
Identities: 25/28(89%) Gaps: 0/28(0%)

```
Query  116        TTGGGCATAGCATTTGAAATGTAAATGA  143
                  |||||||||  ||||||||||||| |||
Sbjct  133050342  TTGGGCATATTATTTGAAATGTAACTGA  133050369
```

```
ACCATGAGGTGCTGAGAAGAAGGTATATCCTTTTGTTTTAGGATAAAATGTTCTGTAGATATCTGTCAGAT
CCATTTGTTTCATCACTTCTGTTAGTTTCACTGTGTCCCTGTTTAGTTTCTGTTTCAATGATCTGTCCATT
GGTGAAAGTGGTGTG
```

Mus musculus immunoglobulin kappa chain complex (Igk) on chromosome 6
Sequence ID: NG_005612.1
Identities: 156/157(99%) Gaps: 0/157(0%)

```
Query  1      ACCATGAGGTGCTGAGAAGAAGGTATATCCTTTTGTTTTAGGATAAAATGTTCTGTAGAT  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  34862  ACCATGAGGTGCTGAGAAGAAGGTATATCCTTTTGTTTTAGGATAAAATGTTCTGTAGAT  34921

Query  61     ATCTGTCAGATCCATTTGTTTCATCACTTCTGTTAGTTTCACTGTGTCCCTGTTTAGTTT  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  34922  ATCTGTCAGATCCATTTGTTTCATCACTTCTGTTAGTTTCACTGTGTCCCTGTTTAGTTT  34981

Query  121    CTGTTTCAATGATCTGTCCATTGGTGAAAGTGGTGTG  157
```

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                |||||||| ||||||||||||||||||||||||||||
Sbjct  34982  CTGTTTCCATGATCTGTCCATTGGTGAAAGTGGTGTG  35018
```

No match for *Homo Sapiens*

CCTGAACTTTGAATGCCAAGAAAAGTAATTTCTTTCCAATGAATAAGTCAGTATCAATGTCAAAATCACTGGTCCCATCAGGTTCACTGCCCATTCTGCAATTTGAAGCCATTCTCATAGAGGAATACACTGAGGATGTTTG

Mus musculus, clone RP23-367H12, complete sequence

Sequence ID: AC117668.9

Identities: 142/142(100%) Gaps:0/142(0%)

```
Query  1       CCTGAACTTTGAATGCCAAGAAAAGTAATTTCTTTCCAATGAATAAGTCAGTATCAATGT  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173441  CCTGAACTTTGAATGCCAAGAAAAGTAATTTCTTTCCAATGAATAAGTCAGTATCAATGT  173382

Query  61      CAAAATCACTGGTCCCATCAGGTTCACTGCCCATTCTGCAATTTGAAGCCATTCTCATAG  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173381  CAAAATCACTGGTCCCATCAGGTTCACTGCCCATTCTGCAATTTGAAGCCATTCTCATAG  173322

Query  121     AGGAATACACTGAGGATGTTTG  142
               ||||||||||||||||||||||
Sbjct  173321  AGGAATACACTGAGGATGTTTG  173300
```

Homo sapiens chromosome 13, alternate assembly CHM1_1.1

Sequence ID: NC_018924.2

Identities: 52/64(81%) Gaps: 0/64(0%)

```
Query  3         TGAACTTTGAATGCCAAGAAAAGTAATTTCTTTCCAATGAATAAGTCAGTATCAATGTCA  62
                 ||| | ||| ||| |||| ||||| |||| ||||||||||| ||||||||  |||  |||
Sbjct  59369862  TGATCCTTGCATGACAAGGAAAGTCATTTATTTCCAATGAACAAGTCAGTCACAAAATCA  59369803

Query  63        AAAT  66
                 ||||
Sbjct  59369802  AAAT  59369799
```

AGAGAGACAAGAAAGTGATATGGGCAAAGAATCCAAAGATAGTTCTGAACAATCCCCTGGAGCTCTGGACTGTACATACTTCAGCAGTAGTCTACTTTCTCATCTGCATAAAGACTGCTTGCTCTGCCCTGGATCAAGACTACTACAAAGATCAGAGGGCTGGAGAGATGGTTCAGCAG

Mus musculus BAC clone RP24-107H20 from chromosome 17, complete sequence

Sequence ID: AC183093.2

Identities: 179/179(100%) Gaps: 0/179(0%)

```
Query  1       AGAGAGACAAGAAAGTGATATGGGCAAAGAATCCAAAGATAGTTCTGAACAATCCCCTGG  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134954  AGAGAGACAAGAAAGTGATATGGGCAAAGAATCCAAAGATAGTTCTGAACAATCCCCTGG  135013

Query  61      AGCTCTGGACTGTACATACTTCAGCAGTAGTCTACTTTCTCATCTGCATAAAGACTGCTT  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  135014  AGCTCTGGACTGTACATACTTCAGCAGTAGTCTACTTTCTCATCTGCATAAAGACTGCTT  135073

Query  121     GCTCTGCCCTGGATCAAGACTACTACAAAGATCAGAGGGCTGGAGAGATGGTTCAGCAG  179
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  135074  GCTCTGCCCTGGATCAAGACTACTACAAAGATCAGAGGGCTGGAGAGATGGTTCAGCAG  135132
```

Homo sapiens chromosome 1 genomic patch of type NOVEL, GRCh38.p7 PATCHES HSCHR1_4_CTG3

Sequence ID: NW_014040926.1

Identities: 29/33(88%) Gaps: 1/33(3%)

```
Query  80      TTCAGCAGTAGTCTACTTTCTCATCTGCATAAA  112
               |||| || ||||||||||| || ||||||||||
Sbjct  181480  TTCACCA-TAGTCTACTTTTTCTTCTGCATAAA  181449
```

CTGTGTTCATTAAGAGATGATGTAACTCTTTAGCAGTGTTCTCCTGTATTTCTTTAAGTGATTTATTAAAGTCCTTCTTGATGTCCTCTACCATCATCATGAGATATGCTTTTAAATCTAGGTCTAGGTTCTCAGGTGTGTTGGGGTTCCCTGGACTGGGCGAAGTGGGTG

Mus musculus BAC clone RP23-241M6 from 16, complete sequence

Sequence ID: AC122817.3

Identities: 171/171(100%) Gaps: 0/171(0%)

```
Query  1       CTGTGTTCATTAAGAGATGATGTAACTCTTTAGCAGTGTTCTCCTGTATTTCTTTAAGTG  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct  118365  CTGTGTTCATTAAGAGATGATGTAACTCTTTAGCAGTGTTCTCCTGTATTTCTTTAAGTG  118306

Query  61      ATTTATTAAAGTCCTTCTTGATGTCCTCTACCATCATCATGAGATATGCTTTTAAATCTA  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  118305  ATTTATTAAAGTCCTTCTTGATGTCCTCTACCATCATCATGAGATATGCTTTTAAATCTA  118246

Query  121     GGTCTAGGTTCTCAGGTGTGTTGGGGTTCCCTGGACTGGGCGAAGTGGGTG  171
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  118245  GGTCTAGGTTCTCAGGTGTGTTGGGGTTCCCTGGACTGGGCGAAGTGGGTG  118195
```

Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 3, mRNA

Identities: 30/35(86%) Gaps: 0/35(0%)

```
Query  60    GATTTATTAAAGTCCTTCTTGATGTCCTCTACCAT  94
             ||||||||||||||| | | || ||| ||||||||
Sbjct  1397  GATTTATTAAAGTCCCTTTGGAAGTCTTCTACCAT  1431
```

CTTTCATAGTCTCTGGTGAAAAGTCTGGTATAATTCTGATAGGCCTGCCTTTATATGTTACTTGACCCTTT
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ACTTCTTTTCTGGTCCAGTATATTTGGATTTCTGTA

Mus musculus BAC clone RP24-238D1 from chromosome 13, complete sequence

Sequence ID: AC155297.2

Identities: 175/176(99%) Gaps:0/176(0%)

```
Query  1      CTTTCATAGTCTCTGGTGAAAAGTCTGGTATAATTCTGATAGGCCTGCCTTTATATGTTA  60
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  36942  CTTTCAAAGTCTCTGGTGAAAAGTCTGGTATAATTCTGATAGGCCTGCCTTTATATGTTA  36883

Query  61     CTTGACCCTTTTCCCTTACTACTTTTAATATTCTATCTTTATTTAGTGCATTAGCTGCTC  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  36882  CTTGACCCTTTTCCCTTACTACTTTTAATATTCTATCTTTATTTAGTGCATTAGCTGCTC  36823

Query  121    TGATTATTATGTGTTGGGAGGAACTTCTTTTCTGGTCCAGTATATTTGGATTTCTG  176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  36822  TGATTATTATGTGTTGGGAGGAACTTCTTTTCTGGTCCAGTATATTTGGATTTCTG  36767
```

Homo sapiens chromosome 6, alternate assembly CHM1_1.1

Sequence ID: NC_018917.2

Identities: 28/31(90%) Gaps: 0/31(0%)

```
Query  2          TTTCATAGTCTCTGGtgaaaagtctggtata  32
                  |||||||||||||||||| ||||| | ||||
Sbjct  128154102  TTTCATAGTCTCTGGTGAGAAGTCAGCTATA  128154072
```

AGCTTGCAAGGAGAAGGAGAAGAGCCCTTAGGGAGCTGCTTTCATCTCAGAGCAACCCAGTTTCTGTTTTA
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TGCTGTGTGGCGAGCTGCTCAGGAGTGTCT

Mus musculus BAC clone RP23-205D14 from chromosome 12, complete sequence

Sequence ID: AC153147.7

Identities: 172/172(100%) Gaps: 0/172(0%)

```
Query  1      AGCTTGCAAGGAGAAGGAGAAGAGCCCTTAGGGAGCTGCTTTCATCTCAGAGCAACCCAG  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13381  AGCTTGCAAGGAGAAGGAGAAGAGCCCTTAGGGAGCTGCTTTCATCTCAGAGCAACCCAG  13440

Query  61     TTTCTGTTTTaaaaaaaaaaCAGTGAGCTCACTGTGTGCTCCAGAGCAATAATCAACTTA  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13441  TTTCTGTTTTAAAAAAAAAACAGTGAGCTCACTGTGTGCTCCAGAGCAATAATCAACTTA  13500

Query  121    GCCTGGCTGGCTTGAAGCAGAGTGCTGTGTGGCGAGCTGCTCAGGAGTGTCT  172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13501  GCCTGGCTGGCTTGAAGCAGAGTGCTGTGTGGCGAGCTGCTCAGGAGTGTCT  13552
```

Homo sapiens chromosome 14, alternate assembly CHM1_1.1

Sequence ID: NC_018925.2

Identities: 93/119(78%) Gaps: 8/119(6%)

```
Query  11        GAGAAGGAGAAGAGCCCTTAGGGAGCTGCT--TTCATCTCAGAGCAACCCAGTTTCTGTT  68
                 ||| |||||  ||||||| |||||||  ||  ||||||||| |||| ||   ||||||||
Sbjct  77436498  GAGGAGGAG--GAGCCCT-AGGGAGCCCCTCTTTCATCTCAAAGCAGCCAGATTTCTGTT  77436554

Query  69        TTaaaaaaaaaaCAGTGAGCTCACTGTGTGCTCCAGAGCAATAATCAACTTAGCCTGGC  127
                 ||   ||||   ||||||||||||||||  ||| ||||||||||| |||||   |||||
```

```
Sbjct  77436555  TTTGCAAAA---CAGTGAGCTCACTGTGCACTCTAGAGCAATAATAAACTTTCTCTGGC  77436610
```

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```

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```

Bangkok (Dog)

TTTTGCAGGCCATCACTAAAGGAGTTCAGCACCTTCTTGCCATGGGCCTTCACTTTAGCATTGCTCATAAC
AACATCAGGAGTGGACAGGTCCCCAAAGGAGTCAAAGAACCTCTGAGTCCAGGGGTAGACAATCAGCAGCC
TGCCCAGG

Canis lupus familiaris GLNA2 gene for globin A2
Sequence ID: LT548211.1
Identities 148/150(99%) Gaps 0/150(0%)

```
Query  1    TTTTGCAGGCCATCACTAAAGGAGTTCAGCACCTTCTTGCCATGGGCCTTCACTTTAGCA  60
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  233  TTTTTCAGGCCATCACTAAAGGAGTTCAGCACCTTCTTGCCATGGGCCTTCACTTTAGCA  174

Query  61   TTGCTCATAACAACATCAGGAGTGGACAGGTCCCCAAAGGAGTCAAAGAACCTCTGAGTC  120
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173  TTGCTCATAACAGCATCAGGAGTGGACAGGTCCCCAAAGGAGTCAAAGAACCTCTGAGTC  114

Query  121  CAGGGGTAGACAATCAGCAGCCTGCCCAGG  150
            ||||||||||||||||||||||||||||||
Sbjct  113  CAGGGGTAGACAATCAGCAGCCTGCCCAGG  84
```

Homo sapiens hemoglobin subunit beta (HBB), mRNA
Sequence ID: NM_000518.4
Identities 127/145(88%) Gaps 0/145(0%)

```
Query  6    CAGGCCATCACTAAAGGAGTTCAGCACCTTCTTGCCATGGGCCTTCACTTTAGCATTGCT  65
            |||||||||||||||||     ||||| ||||||||||| |||||||| ||||  ||||
Sbjct  278  CAGGCCATCACTAAAGGCACCGAGCACTTTCTTGCCATGAGCCTTCACCTTAGGGTTGCC  219

Query  66   CATAACAACATCAGGAGTGGACAGGTCCCCAAAGGAGTCAAAGAACCTCTGAGTCCAGGG  125
            ||||||| |||||||||||||||| ||||||||||| |||||||||||||| ||||| ||
Sbjct  218  CATAACAGCATCAGGAGTGGACAGATCCCCAAAGGACTCAAAGAACCTCTGGGTCCAAGG  159

Query  126  GTAGACAATCAGCAGCCTGCCCAGG  150
            |||||| | ||||||||||||||||
Sbjct  158  GTAGACCACCAGCAGCCTGCCCAGG  134
```

CATACTGTTGCATTCATGCCAACCCTACTTACAGACATCTCAAAACTAGCAGTAATTAAGTTAAACGGTCC
CCCCAAATCCCACAATTCAAGCTAAACTCGAAGTTAACAGCTACAGGAGTGGCACCTACACGTTAATGCTA
GCTGAAGCACAGGCAGCGGGGGGACGTTTCATCCCGCTCTCCCAAGCACAGGACACTGG

PREDICTED: Canis lupus familiaris ornithine decarboxylase 1 (ODC1), mRNA
Sequence ID:XM_851618.5
Identities 201/201(100%) Gaps 0/201(0%)

```
Query  1     CATACTGTTGCATTCATGCCAACCCTACTTACAGACATCTCAAAACTAGCAGTAATTAAG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1850  CATACTGTTGCATTCATGCCAACCCTACTTACAGACATCTCAAAACTAGCAGTAATTAAG  1791

Query  61    TTAAACGGTCCCCCCAAATCCCACAATTCAAGCTAAACTCGAAGTTAACAGCTACAGGAG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1790  TTAAACGGTCCCCCCAAATCCCACAATTCAAGCTAAACTCGAAGTTAACAGCTACAGGAG  1731

Query  121   TGGCACCTACACGTTAATGCTAGCTGAAGCACAGGCAGCGGGGGGACGTTTCATCCCGCT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1730  TGGCACCTACACGTTAATGCTAGCTGAAGCACAGGCAGCGGGGGGACGTTTCATCCCGCT  1671

Query  181   CTCCCAAGCACAGGACACTGG  201
             |||||||||||||||||||||
Sbjct  1670  CTCCCAAGCACAGGACACTGG  1650
```

Homo sapiens ornithine decarboxylase 1 (ODC1), transcript variant 4, mRNA
Sequence ID: NM_001287190.1
Identities: 170/205(83%) Gaps 5/205(2%)

```
Query  1     CATACTGTTGCATTCATGCCAACCCTACT--TACA--GACATCTCAAAACTAGCAGTAAT  56
             ||||  | ||||| |||| | ||||||||  ||||  ||||| |||||||||||||||||
Sbjct  1814  CATATGGCTGCAT-CATGGCGACCCTACTCTTACAAAGACATTTCAAAACTAGCAGTAAT  1756

Query  57    TAAGTTAAACGGTCCCCCCAAATCCCACAATTCAAGCTAAACTCGAAGTTAACAGCTACA  116
             ||||||| | ||||||||||||||||  ||||||||||||||| | |||||||||||||
Sbjct  1755  TAAGTTACATGGTCCCCCCAAATCCCTTAATTCAAGCTAAACTTGCAGTTAACAGCTACC  1696

Query  117   GGAGTGGCACCTACACGTTAATGCTAGCTGAAGCACAGGCAGCGGGGGGACGTTTCATCC  176
              |||||  | |||||| ||||| ||||| ||||||||||| ||   | | ||||||||||
Sbjct  1695  AGAGTGCTATCTACACATTAATACTAGCCGAAGCACAGGCTGCTCTGTGGCGTTTCATCC  1636
```

```
Query  177   CGCTCTCCCAAGCACAGGACACTGG  201
             | |||||||| ||||| ||||| ||
Sbjct  1635  CACTCTCCCAGGCACAAGACACAGG  1611
```

```
ATATCACTGAGCTGAACAAATAAGTCACCTCTGAGTACATAAGGAAAAATAAACACATGCTAAATGGATAA
AACATTACAAACTACATCTTTACTAAACCATCTATACCTCTAACACCTCTAACACTTCAGAAGCTTAGAGA
TTCA
```

PREDICTED: Canis lupus familiaris ring finger protein 11 (RNF11), transcript variant X4, mRNA
Sequence ID: XM_005629010.3
Identities: 146/146 (100%) Gaps 0/146(0%)

```
Query  1     ATATCACTGAGCTGAACAAATAAGTCACCTCTGAGTACATAAGGAAAAATAAACACATGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1774  ATATCACTGAGCTGAACAAATAAGTCACCTCTGAGTACATAAGGAAAAATAAACACATGC  1715

Query  61    TAAATGGATAAAACATTACAAACTACATCTTTACTAAACCATCTATACCTCTAACACCTC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1714  TAAATGGATAAAACATTACAAACTACATCTTTACTAAACCATCTATACCTCTAACACCTC  1655

Query  121   TAACACTTCAGAAGCTTAGAGATTCA  146
             ||||||||||||||||||||||||||
Sbjct  1654  TAACACTTCAGAAGCTTAGAGATTCA  1629
```

Homo sapiens ring finger protein 11 (RNF11), mRNA
Sequence ID: NM_014372.4
Identitites : 126/144(88%) Gaps: 10/144(6%)

```
Query  1     ATATCACTGAGCTGAACAAATAAGTCACCTCTGAGTACATAAGGAAAAATAAACACATGC  60
             ||||||||||| ||||| |||||||||||| |||||||||| | ||||||||||||||||
Sbjct  2339  ATATCACTGAGGTGAACCAATAAGTCACCTTTGAGTACATATGAAAAAATAAACACATGC  2280

Query  61    TAAATGGATAAAACATTACAAACTACATCTTTACTAAACCATCTATACCTCTAACACCTC  120
             |||||||||||||||||||  ||||||||||||||| ||||||| |         |||||
Sbjct  2279  TAAATGGATAAAACATTAC-TACTACATCTTTACTAGACCATCTCT---------ACCTC  2230

Query  121   TAACACTTCAGAAGCTTAGAGATT  144
             ||||||||||||||||||||||||
Sbjct  2229  TAACACTTCAGAAGCTTAGAGATT  2206
```

```
CTCAATGGTACTTGTGAGCCAGGGCATTGGCCACACCAGCCACCACCTTCTGATAGGCAGCCTGCACCTGA
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GGGATCCACGTGCAGCTTGTCACAGTGAAGCTCACTGAGCTTAGCAAAGGTGCCCTTGAGG
```

Canis lupus familiaris hemoglobin subunit beta-like (LOC480784), mRNA
Sequence ID: NM_001270884.1
Identities: 202/203(99%) Gaps:0/203(0%)

```
Query  1    CTCAATGGTACTTGTGAGCCAGGGCATTGGCCACACCAGCCACCACCTTCTGATAGGCAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  513  CTCAATGGTACTTGTGAGCCAGGGCATTGGCCACACCAGCCACCACCTTCTGATAGGCAG  454

Query  61   CCTGCACCTGAGGGGTGAATTCTTTGCCAAAGTGGTGAGCCAGCACACACACAAGCACGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  453  CCTGCACCTGAGGGGTGAATTCTTTGCCAAAGTGGTGAGCCAGCACACACACAAGCACGT  394

Query  121  TGCCCAGGAGCTTGAAATTCTCGGGATCCACGTGCAGCTTGTCACAGTGAAGCTCACTGA  180
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  393  TGCCCAGGAGCTTGAAGTTCTCGGGATCCACGTGCAGCTTGTCACAGTGAAGCTCACTGA  334

Query  181  GCTTAGCAAAGGTGCCCTTGAGG  203
            |||||||||||||||||||||||
Sbjct  333  GCTTAGCAAAGGTGCCCTTGAGG  311
```

Homo sapiens hemoglobin subunit delta (HBD), mRNA
Sequence ID: NM_000519.3
Identities:184/203 (91%) Gaps: 0/203(0%)

```
Query  1    CTCAATGGTACTTGTGAGCCAGGGCATTGGCCACACCAGCCACCACCTTCTGATAGGCAG  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  640  CTCAATGGTACTTGTGAGCCAGGGCATTAGCCACACCAGCCACCACCTTCTGATAGGCAG  581

Query  61   CCTGCACCTGAGGGGTGAATTCTTTGCCAAAGTGGTGAGCCAGCACACACACAAGCACGT  120
```

```
             ||||||  || ||||||||||| |||||||||| | | |||||||||||||| ||||| |
Sbjct  580   CCTGCATTTGTGGGGTGAATTCCTTGCCAAAGTTGCGGGCCAGCACACACACCAGCACAT  521

Query  121   TGCCCAGGAGCTTGAAATTCTCGGGATCCACGTGCAGCTTGTCACAGTGAAGCTCACTGA  180
             |||||| |||| |||| ||||| |||||||||||||||||||||||||| |||||||| |
Sbjct  520   TGCCCAAGAGCCTGAAGTTCTCAGGATCCACGTGCAGCTTGTCACAGTGCAGCTCACTCA  461

Query  181   GCTTAGCAAAGGTGCCCTTGAGG  203
             ||| || ||| ||||||||||||
Sbjct  460   GCTGAGAAAAAGTGCCCTTGAGG  438
```

CCGCATGATCTCTGCAGCTTCTCTTTCGGTGAAAGCCAGGTCACCACGCTCCTGAATCCGGCTGAATAGCT
CACCACCTTCCATGCATTCCATGACGATGAGGAGACAGCGCTTGCTGTGATGCATGTTCTCATACACGTCC
AGGATGCGCACAATGTGAGGGCCACCCGAGGCCTGCCAGTGGTGGTCCACCTCCTGCCGGGCCTTGGGGCT
GTCGTACAGGAGCTTCAGGGCACATTTCTG

PREDICTED: Canis lupus familiaris mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3), mRNA
Sequence ID: XM_541872.5
Identities: 243/243(100%) Gaps: 0/243(0%)

```
Query  1     CCGCATGATCTCTGCAGCTTCTCTTTCGGTGAAAGCCAGGTCACCACGCTCCTGAATCCG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  693   CCGCATGATCTCTGCAGCTTCTCTTTCGGTGAAAGCCAGGTCACCACGCTCCTGAATCCG  634

Query  61    GCTGAATAGCTCACCACCTTCCATGCATTCCATGACGATGAGGAGACAGCGCTTGCTGTG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  633   GCTGAATAGCTCACCACCTTCCATGCATTCCATGACGATGAGGAGACAGCGCTTGCTGTG  574

Query  121   ATGCATGTTCTCATACACGTCCAGGATGCGCACAATGTGAGGGCCACCCGAGGCCTGCCA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  573   ATGCATGTTCTCATACACGTCCAGGATGCGCACAATGTGAGGGCCACCCGAGGCCTGCCA  514

Query  181   GTGGTGGTCCACCTCCTGCCGGGCCTTGGGGCTGTCGTACAGGAGCTTCAGGGCACATTT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  513   GTGGTGGTCCACCTCCTGCCGGGCCTTGGGGCTGTCGTACAGGAGCTTCAGGGCACATTT  454

Query  241   CTG  243
             |||
Sbjct  453   CTG  451
```

PREDICTED: Homo sapiens mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3), transcript variant X1, misc_RNA
Sequence ID: XR_940501.1
Identities: 219/243(90%) Gaps: 0/243(0%)

```
Query  1     CCGCATGATCTCTGCAGCTTCTCTTTCGGTGAAAGCCAGGTCACCACGCTCCTGAATCCG  60
             |||||| ||||||||||||||||| || ||||||||| |||| ||||||||||||||||
Sbjct  566   CCGCATTATCTCTGCAGCTTCTCTCTCAGTGAAAGCCTGGTCGCCACGCTCCTGAATCCT  507

Query  61    GCTGAATAGCTCACCACCTTCCATGCATTCCATGACGATGAGGAGACAGCGCTTGCTGTG  120
             |||||| | |||||||||||||||||||||||||| ||||||||||||||||||||  ||
Sbjct  506   GCTGAACAACTCACCACCTTCCATGCATTCCATGATGATGAGGAGACAGCGCTTGCCATG  447

Query  121   ATGCATGTTCTCATACACGTCCAGGATGCGCACAATGTGAGGGCCACCCGAGGCCTGCCA  180
              ||||||||||||||||| ||||||||||  ||||| || ||||| || || ||||||||
Sbjct  446   GTGCATGTTCTCATACACATCCAGGATGCAGACAATATGGGGGCCGCCAGAAGCCTGCCA  387

Query  181   GTGGTGGTCCACCTCCTGCCGGGCCTTGGGGCTGTCGTACAGGAGCTTCAGGGCACATTT  240
             ||| ||||| |||||||||||||||||||||||||| |||||||||||||||||||| ||
Sbjct  386   GTGATGGTCTACCTCCTGCCGGGCCTTGGGGCTGTCATACAGGAGCTTCAGGGCACACTT  327

Query  241   CTG  243
             |||
Sbjct  326   CTG  324
```

Cairns (Cow)

CCCTCCCAGCATCAGGGTCTTTTCCAATGAGTCAACTCTTCGCATGAGATGGCCAAAGTATTGGAGTTTCA
GCTTCAGCATCAGTCCTTCCAATGAACACCCAGGATTGGTCTCCTTTAGGATGGACTGCTTGGATCTCCTT
GCAGTCCAAGGG

PREDICTED: Bos indicus angiotensin II receptor type 1 (AGTR1), mRNA
Sequence ID: XM_019961143

Identities 149/154(97%) Gaps 0/154(0%)

```
Query  1     CCCTCCCAGCATCAGGGTCTTTTCCAATGAGTCAACTCTTCGCATGAGATGGCCAAAGTA  60
             ||||| |||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  2063  CCCTCTCAGCATCAGGGTCTTTTCCAATGAGTCAACTCTTCGCATGAGGTGGCCAAAGTA  2122

Query  61    TTGGAGTTTCAGCTTCAGCATCAGTCCTTCCAATGAACACCCAGGATTGGTCTCCTTTAG  120
             |||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||
Sbjct  2123  TTGGAGTTTCAGCTTCAGCATCAGTCCTTCCAATGAACACCCAGGACTGATCTCCTTTAG  2182

Query  121   GATGGACTGCTTGGATCTCCTTGCAGTCCAAGGG  154
             ||||||||| ||||||||||||||||||||||||
Sbjct  2183  GATGGACTGGTTGGATCTCCTTGCAGTCCAAGGG  2216
```

Homo sapiens angiotensinogen (AGT), mRNA

Sequence ID: NM_000029.3

Identities 25/26(96%) Gaps 0/26(0%)

```
Query  84    GTCCTTCCAATGAACACCCAGGATTG  109
             |||||||||| |||||||||||||||
Sbjct  1012  GTCCTTCCAAGGAACACCCAGGATTG  987
```

Bangkok (Cow)

GGCTGGATGGCATCACTGACTCAATGGACATGAGTCTGAGTGAACTCCGGGAGTTGGTGATGGACAGGGAG
GCCTGTCGTGCTGCGATTCATGGGGTTGCAAAGAGTCGG

Bos taurus Y Chr BAC CH240-49F14 (Children's Hospital Oakland Research Institute Bovine BAC Library (male)) complete sequence

Sequence ID: AC226423.5

Identities 107/110 (97%) Gaps 0/110 (0%)

```
Query  1     GGCTGGATGGCATCACTGACTCAATGGACATGAGTCTGAGTGAACTCCGGGAGTTGGTGA  60
             ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  5350  GGCTGGATGGCATCACTGACTCAATGGACGTGAGTCTGAGTGAACTCCGGGAGTTGGTGA  5409

Query  61    TGGACAGGGAGGCCTGTCGTGCTGCGATTCATGGGGTTGCAAAGAGTCGG  110
             |||||||||||||||| ||||||| |||||||||||||||||||||||||
Sbjct  5410  TGGACAGGGAGGCCTGGCGTGCTGTGATTCATGGGGTTGCAAAGAGTCGG  5459
```

Homo sapiens chromosome 15, alternate assembly CHM1_1.1

Sequence ID: NC_018926.2

Identitites 27/30(90%) Gaps 1/30(3%)

```
Query  42        GAACTCCGGGAGTTGGTGATGGACAGGGAG  71
                 |||||| || |||| |||||||||||||||
Sbjct  78558460  GAACTCAGG-AGTTTGTGATGGACAGGGAG  78558488
```