





CLUSTAL multiple sequence alignment by MUSCLE (3.8)

Sapur.15HG074400.1.p			
Sapur.008G005800.1.p	MESSDSRKDLPPPPAIIPADVVKTELGPTYEOTKKAATPKRAPMTRRGF	Sapur.15WG074400.1.p	
Sapur.016G117100.1.p	MHDMDSPDEONGNGSHEALPPPPPDVPPNVVPVKAEPEPFKKKAVRVPIARRGL	Sapur.0086005800.1.p	NGEDFFPRNGRWNFNNKKLVDPVKIEKWAIVNFSARCDIRYLCNNLMKCGDMKGMSISNP
Sapur.0166117100.2.p	MHDMDSPDEQNGNGSHEALPPPPPDVPPNVVPVKAEPEPFKKKAVRVPIARRGL	Sapur.016G117100.1.p	NGEDFFPRNGRWNFNNKKLVEPSRIEKWAVVNFSARCDIRNLVQNLTKCAENKGIPIEDP
Sapur.006G020100.1.p	MESTEDPEAFVPP-PPDALPPPPSEIPPNVVPVQLTTDSVPEETKKISKPKRFPIARRGV	Sapur.016G117100.2.p	NGEDFFPRNGRWNFNNKKLVEPSRIEKWAVVNFSARCDIRNLVQNLTKCAEHKGIPIEDP
Sapur.016G022500.2.p	MESNEEPEAIAPPPDALPPPPPEIPPNVVPVQLTTDTVPEETKKISKPKRSPITRRGV	Sapur.006G020100.1.p	NDEDVIPRNGRWNFNHKKFYEPSKIENWAVVNFSARCDVRGLIRDLIRFGEMKGILISDP
30001101000223001210	PLSHEET LAIM? - FFOMETFFFFEEFFHWWFWQLIIDIWFEEFMALSKEARSFEERAGV	Sapur.0166022500.2.p	NGEDVIPRNGRWNFNHKKFFEPCKIENWAVVNFSARCDVRGLVRDLIRLGEHKGILISDP
Sapur.15NG074400.1.p			
Sapur.008G005800.1.p	GAKGQRIQLLTNHFEVAVPKSNGHFYQYSVALFYEDGRPADGKRIGRKVMDKVQETYDTE	Sapur.15WG074400.1.p	LILVILSHFP
Sapur.016G117100.1.p	GSKGQKMPLLTNHFKVNVTNTEGYFFHYSVSLTYEDGRPVDGKGVGRKVIDRVHETYDTE	Sapur.008G005800.1.p	FEVFEESPQCRREPAPVRVEKHFEVIKSKLP-GPPQFLLCILPERKNSEIYGPHKRKNLS
Sapur.016G117100.2.p	GSKGOKMPLLTNHFKVNVTNTEGYFFHYSVSLTYEDGRPVDGKGVGRKVIDRVHETYDTE	Sapur.0166117100.1.p	FDVFEENPQSRRSPPVLRVEKHFELIQSRLP-GQPKFLLCLLPERKNSDIYGPHKRKNLA
Sapur.006G020100.1.p	GSRGOKIOLLSNHFKVSISNTGGHFFHYSVSLSYEDGRPVEAKGIGRRLIDKVHETYGSD	Sapur.016G117100.2.p	FDVFEENPQSRRSPPVLRVEKHFELIQSRLP-GQPKFLLCLLPERKNSDIYGPHKRKNLA
Sapur.016G022500.2.p	GSRGOKIQLYTNHFKVSISNTSGHFFHYSVSLYYEDGRPVDAKGIGRRLIDKVHETYGSD	Sapur.0066020100.1.p	VDVVDENGQFRRAPPLVRVEKHFEQIQKAFPNSPPRFLVCLLPDKKNSDIYGPWKRKNLA
	GSWGQLIQLVINHFKVSISWISGHFFNTSVSL11EDGKFVDAKGIGKKLIDKVHE11GSD	Sapur.016G022500.2.p	MDVFEENAQFRRAPPLVRVDKMFEQIQTAFPDAPPRFLVCLLPDRKNSDIYGPNKRKNLA :: " .: "
Sapur.15WG074400.1.p		Sapur.15WG074400.1.p	QLGGINSLLSTEHAPSIPLVSKRPTLILGIDV
Sapur.008G005800.1.p	LEGKQLAYDGERTMFTIGSLPHNKLEFTAVLEDVSLTRGGDNDSSRGNGSPGDSDQKRMK		
Sapur.016G117100.1.p	F-GKDFAYDGEKSLFTVGALPRNKLEFTVVLEDVLSNRNNGNASPDGHGSPNEGDRKRLR	Sapur.0086005800.1.p	ELGIVTQCIAPTKLNDQYLTNVLLKINAKLGGMNSLLSTEHAPSIPLVSKRPTLILGHDV
Sapur.016G117100.2.p	F-GKDFAYDGEKSLFTVGALPRNKLEFTVVLEDVLSNRNNGNASPDGHGSPNEGDRKRLR	Sapur.016G117100.1.p	EFGIVTQCIAPQRVNDQYITNVLLKINAKLGGLNSHLAVEHSPSLPLVSNVPTLILGHDV
Sapur.006G020100.1.p	LAGKDFAYDGEKSLFTIGAMPRNKHEFTVLLDSFTSNRNSGNGSPVGNGSPKETDKKRMR	Sapur.016G117100.2.p	EFGIVTQCIAPQRVNDQYITNVLLKINAKLGGLNSMLAVEHSPSLPLVSNVPTLILGHDV
Sapur.016G022500.2.p	LAGKDFAYDGEKSLFTIGALPRNKHEFTVLLDSFSSNRNSGNGSPVGNGSPNETDKKRIR	Sapur.006G020100.1.p	EYGIFNQCLAPTRVNEQYILNVLLKINAKLGGLNSLLAMEQSRNIPFVSKVPTIIFGMDV
3apur.0100022500.2.p	LAGADEATOGERSEF11GALERNA/IEF1VLLUSESSARRISGRASSEVGRASSERETURARIK	Sapur.016G022500.2.p	EYGIFNQCLAPTRVNDQYILNVLLKINAKLGGLNSLLAMEQSRNIPFVSKVPTIIFGMDV '***;**: ': .:*:*: "*::::*:*:
Sapur.15HG074400.1.p		Sapur.15WG074400.1.p	SHGSPGHSDVPSIAAVIN
Sapur.008G005800.1.p	RPYHSKTIKVQISYATKIPVQAIAAVLQGQESEHFQEAVRVLDIILRQNAARQGCLLVRQ	Sapur.008G005800.1.p	SHGSPGHSDVPSIAAVVSSRQWPLISRYRAYVRTQSQKVEMIANLFKPVAGTAEDQGIIR
Sapur.0166117100.1.p	RPYHSKTFKVEISFAAKIPMQAIANALRGQESENSQEAFRVLDIILRQHAAKQGCLLVRQ	Sapur.016G117100.1.p	SHGSPGQSDVPSIAAVVSSRQWPLISRYRACVRTQSPKLEMIDSLFKQVSET-EDEGIIR
Sapur.016G117100.2.p	RPYHSKTFKVEISFAAKIPMQAIANALRGQESENSQEAFRVLDIILROHAAKOGCLLVRO	Sapur.016G117100.2.p	SHGSPGQSDVPSIAAVVSSRQWPLISRYRACVRTQSPKLEMIDSLFKQVSET-EDEGIIR
Sapur.006G020100.1.p	RAFQSKTFKVEMSFAAKIPMQAIAAALRGQESENSQEALRVLDIILRQHAAKQGCLLVRQ	Sapur.006G020100.1.p	SHGSPGQSDMPSIAAVVSSRNWPLLSRYRASVRSQSPKVEMVDSLFTLTPDKKDDSGIVR
Sapur.016G022500.2.p	WALQSKTFKVEMSFAAKIPMQAIAAALRGQESENSQEALRVLDIILRQHAAKQGCLLVRQ	Sapur.016G022500.2.p	SHGSPGQSDIPSIAAVVSSRNMPLLSRYRASVRSQSPKVEHVDSLFKQTADKKDDSGIVR
Sapur.15WG074400.1.p		Sapur.15WG074400.1.p	FLSVV
Sapur.008G005800.1.p	SFFHNNPRNFIELGGGVMGCRGFHSSFRAAONGLSLNIDVSTTMIVKPGPVVDFLIMNON	Sapur.008G005800.1.p	ESLVDFYSSSGKRKPDQIIIFRDGVSESQFSQVLNIELEQIIEACKFLDENWCPKFMVII
Sapur.016G117100.1.p	SFFHNDPKNFVDLGGGVLGCRGFHSSFRTSOGGLSLNIDVSTTMIIOPGPVVDFLIANON	Sapur.016G117100.1.p	ELLLDFYVTSGKRKPDQIIIFRDGVSESQFNQVLNIELDQINEACKFLDEKWSPKFVVIV
Sapur.016G117100.2.p	SFFHNDPKNFVDLGGGVLGCRGFHSSFRTSQGGLSLNIDVSTTMIIQPGPVVDFLIANQN	Sapur.016G117100.2.p	ELLLDFYVTSGKRKPDQIIIFRDGVSESQFNQVLNIELDQINEACKFLDEKHSPKFVVIV
Sapur.006G020100.1.p	SFFHNDPKNYVDLGGGVLGCRGFHSSFRASQGGLSLNMDGSTTTIIQPGPLIDFLIANQN	Sapur.006G020100.1.p	ELLLDYYKSSGQTKPAQIIIFRDGVSESQFNQVLNIELDQIIEACKFLDESWSPKFTVIV
Sapur.016G022500.2.p	SFFHNNPKNYVDLGGGVLGCRGFHSSFRALQGGLSLNMDGSTTTIIQPGPLIDFLIANON	Sapur.016G022500.2.p	ELLLDYYKSSGQTKPAQIIIFRDGVSESQFNQVLNIELDQIIEACKFLDESWSPKFTVIV
			***
		Sapur.15NG074400.1.p	PCA
Sapur.15HG074400.1.p	HPY	Sapur.008G005800.1.p	AQKNHHTKFFQSGSPDNVPPGTVIDNKVCHPRNNDFYNCAQAGNIGTTRPTHYHVLHDEL
Sapur.008G005800.1.p	VRDPYHIDWTKAKRTLKNLRIKTNHSNTEYKITGLSEKSCREQTFSLNQRSGRVGDGEVQ	Sapur.016G117100.1.p	AQKNHHTKFFQPGSPDNVPPGTVIDNKVCHPRNNDFYLCAHAGNIGTTRPTHYHVLLDEV
Sapur.016G117100.1.p	VRDPFSLDWAKAKRTLKNLRVKTSPSNQEYKITGLSEKTCKEQLFQLKQKNGGDGGAE	Sapur.016G117100.2.p	AQKNHHTKFFQPGSPDNVPPGTVIDNKVCHPRNNDFYLCAHAGNIGTTRPTHYHVLLDEV
Sapur.016G117100.2.p	VRDPFSLDWAKAKRTLKNLRVKTSPSNQEYKITGLSEKTCKEQLFQLKQKNGGDGGAE	Sapur.0066020100.1.p	AQKNHHTKFFQDGSPDNVPPGTVIDSAVCHPQNYDFYNCAHAGNIGTTRPTHYHVLLDEI
Sapur.006G020100.1.p	VSNPFQIDWAKAKRTLKNLRIRVSPTNQEYRITGLSENTCKEQMF5LKSRATDGNDVE	Sapur.016G022500.2.p	AQKNHHTKFFQDGSPDNVPPGTVIDNAVCHPQSYDFYNCAHAGNIGTTRPTHYHVLLDEI
Sapur.016G022500.2.p	VSNPFQIDWAKAKRTMKNLRIKVSPTNQEYRITGISENSCKEQLFSLKSRAAGGNDVE *:		
Canin 15UG074400 * -	*	Sapur.15WG074400.1.p	
Sapur.15NG074400.1.p		Sapur.008G005800.1.p	GFSADDLQELVHSLSYVYQRSTTAVSLVAPVCYAHLAASQMAQFIKFDDLSDTSSSHGEV
Sapur.008G005800.1.p	TIEVTVYDYFVNHRNMQLKYSADFPCINVGKPKRPSYFPLELCNLVSLQRYTKALSNLQR	Sapur.016G117100.1.p	GFSADDLQELVHSLSYVYQRSTTAISVVAPICYAHLAASQMGQFIKFEDMSETSSSHGGV
Sapur.016G117100.1.p	AVEITVYDYFVNHRNIDLRYSGDLPCINVGKPKRPTYIPLELCSLVSLQRYTKALSTLQR	Sapur.016G117100.2.p	GFSADDLQELVHSLSYVYQRSTTAISVVAPICYAHLAASQMGQFIKFEDMSETSSSHGGV
Sapur.016G117100.2.p	AVEITVYDYFVNHRNIDLRYSGDLPCINVGKPKRPTYIPLELCSLVSLQRYTKALSTLQR	Sapur.006G020100.1.p	GFSADDLQELIHSLSYVYQRSTTAISVVAPVRYAHLAASQISQFLKCDDMSETSSSHGGL
Sapur.006G020100.1.p	SLDVTVYHYFVNHRNIDLRYSGDLPCINVGKPKRPTYIPVELCSLLPLQRYIKALTVLQR	Sapur.0166022500.2.p	GFSADDLQELIHSLSYVYQRCTTAISLVAPVRYAHLAATQISQFLKFDDMSETSSSH
Sapur.016G022500.2.p	SFDITVYDYFVNHRSIDLRYSGDLPCINVGKPKRPTYIPVELCSLLSLQRYTKALTVLQR	STREET, STREET	34-4-1-4-1-4-1-4-1-4-1-4-1-4-1-4-1-4-1-4
F 151/5074400 *		Sapur.15WG074400.1.p	
Sapur.15WG074400.1.p		Sapur.008G005800.1.p	TIPGAVPVPELPRLHDNVSSSMFFC
Sapur.008G005800.1.p	ASLVEKSRQKPQERHRSLTDALRSSNYDADPMLRSSGISISPQFTQVEGRVLSAPRLKVG	Sapur.016G117100.1.p	TSAGAVPVPQLPKLQEKVCNSHFFC
Sapur.0166117100.1.p	SSLVEKSRQKPQERMTVLSNALKSSKYDAEPMLRSCGISISPSFTQVEGRVLSAPKLKVG	Sapur.016G117100.2.p	TSAGAVPVPQLPKLQEKVCNSHFFC
Sapur.016G117100.2.p	SSLVEKSRQKPQERHTVLSNALKSSKYDAEPHLRSCGISISPSFTQVEGRVLSAPKLKVG	Sapur.006G020100.1.p	TSAGQIPVPELPELHRNVCSSHFFC
Sapur.006G020100.1.p	SQLVEKSRQKPQEKIRILTDVPKSNNYAAEPMLRSCGITISSQFTHVQGRVLTAPKLKAG	Sapur.016G022500.2.p	
Sapur.016G022500.2.p	SQLVEKSRQKPQEKIRILADVMKSNNYAAEPMLSSCGITISSQFTEVQGRVLPAPKLKAG		

## **Supplementary Figure S4B**

4 4 4 Sapur.15WG074400.1.p 0.17169 Sapur.008G005800.1.p 0.07189 Sapur.016G117100.1.p 0 Sapur.016G117100.2.p 0 Sapur.006G020100.1.p 0.03899 Sapur.016G022500.2.p 0.03156

Cluster 187938 Original Location: Chr15Z:5200310-5200523 Displayed Location: Chr15Z:5200405-5200526 Strand: + GGAGGCACUGAUGAUGUUGUUGACAGAAGAUAGAGAGCACAGAUGAUGGUAUGCAAUGGGCUCUGCAUCCCACUCCUUUUGUGCUCUCUAAGCUUCUGUCAUCACUUUCAGCCCCCGACCCCC .cucuaagcuucugucaucc. 1=19 a=1 UCUCUAAGCUUCUGUCAUC 1=19 a=2
UCUCUAAGCUUCUGUCAUCU 1=22 a=5 GCUCUCUAAGCUUCUGUCAU 1=20 a=4
GCUCUCUAAGCUUCUGUCAUCA 1=22 a=19
GCUCUCUAAGCUUCUGUCAUCACCCCCCGACu 1=38 a=1 GCUCUCUAAGCUUCUGUCAUCC 1=22 a=3 GCUCUCHAAGCUUCUGUCAUCU 1=22 a=98
GCUCUCHAAGCUUCUGUCAUCU 1=23 a=1 GCUCUCUAAGCUUCUGUCAUa 121 a=4
GCUCUCUAAGCUUCUGUCAUu 121 a=36
GCUCUCUAAGCUUCUGUCAUU 121 a=36
GCUCUCUAAGCUUCUGUAAUC 121 a=4 GCUCUCUAAGCUUCUJUCAUC 1=21 a=1 GCUCUCUAAGCUUCaGUCAUC. 1=21 a=3 GCUCUAAGCUUAUGUCAUCA. 1=22 a=1 GCUCUCUAUGCUUCUGUCAUC 1=21 a=77
GCUCUCUAUGCUUCUGUCAUCA 1=22 a=3 GCUCUUUAAGCUUCUGUCAUC 1=21 a=1 GCUGACUANGCUUCUGUCAUC 1=21 a=2 GgUCUCUAAGCUUCUGUCAUC 1=21 a=2 .cCUCUCUAAGCUUCUGUCAUC 1=21 a=1 .ncucucuaagcuucugucauc ...CUCUCUCAAGCUUCUGUCAUC 1=21 a=5 
 CCACUCCUUUGUGCUCUAAGCU.
 1=24 a=1

 CCACUCCUUUGUGCUCUAAGCUU
 1=25 a=2

 UUGACAGAAGAUAGAGAGCA
 1=20 a=8

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 1=21 a=611
 .....UUGACAGAAGAUAGAGAGCACAc UUGACAGAAGAUAGAGAGCACc. 1=22 a=6 UUGACAGAAGAUAGAGAGCACu 1=22 a=247 UUGACAGAAGAUAGAGAGCAu 1=21 a=1 
 UUGACAGAAGAUAGAGAGCAUA
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 1=22 a=1
 UUGAgAGAGAUAGAGCACA 1=22 a=1
UUGgCAGAAGAUAGAGAGCACA 1=21 a=2
UUUACAGAAGAUAGAGAGCACA 1=22 a=1 
 UBGACAGAAGAUAGAGACAC
 1=21 a=1

 UBGACAGAAGAUAGAGACAC
 1=22 a=3

 UCGACAGAAGAUAGAGAGCAC
 1=21 a=1

 aUGACAGAAGAUAGAGAGCAC
 1=21 a=1
 < 





