

**Figure S6. Protamine 1  
Codeml output file M2**

Arvicola sadipus (ASA)  
 Arvicola terrestris (ATE)  
 Clethrionomys glareolus (CGL)  
 Cricetulus griseus (CGR)  
 Chionomys nivalis (CNI)  
 Microtus agrestis (MAG)  
 Microtus arvalis (MAR)  
 Mesocricetus auratus (MAU)  
 Microtus cabrerai (MCA)  
 Microtus gerbei (MGE)  
 Mus musculus musculus (MMU)  
 Phodopus campbelli (PCM)  
 Pitymys duodecimcostatus (PDU)  
 Pitymys lusitanicus (PLU)  
 Phodopus roborovskii (PRO)  
 Phodopus sugorus (PSU)  
 Sigmodon hispidus (SHI)

17 153

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MAR  ATG  GCC  AGA  TAC  CG-  --C  TAC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  AGC  CGC  GGC  AGG  CGG  AGA  TGT  CGC  AGA  AGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TGC  CGC  CGC  CGC  CGC  CGC  ACA  TAC  ACT  GTG  AGG  TGT  AAA  AGA  TAC
MAG  ATG  GCC  AGA  TAC  CG-  --C  TGC  CGT  AGC  AAA  AGC  AGG  AGC  AGA  TGC  AGC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TGC  CGC  CGC  CGC  CGC  CGC  ACA  TAC  ACC  ATG  AGG  TGT  AAA  AGA  TAC
SHI  ATG  GCC  AGA  TAC  CGA  TGC  TGT  CGA  AGC  AAA  AGC  AGG  AGC  AGA  TGC  CGC  CGC  CGC  AGG  CGA  AGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGA  TGC  TGC  CGC  CGC  CGC  CGC  CGC  ACA  TAC  ACC  CTA  AGG  TGT  AAA  AAA  TAC
MMU  ATG  GCC  AGA  TAC  CGA  TGC  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  CGC  CGT  CGC  AGG  CGA  AGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CGG  CGG  AGG  AGG  CGA  AGA  TGC  TGC  CGT  CGC  CGC  CGC  TCA  TAC  ACC  ATA  AGG  TGT  AAA  AAA  TAC
MAU  ATG  GCC  AGA  TAC  CGA  TGC  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  CGC  CGC  CGC  AGG  CGG  CGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGA  TGC  TGC  CGC  CGC  CGC  CGC  CGC  ACA  TAC  ACC  CTA  AGG  TGT  AAA  AGA  TAC
PSU  ATG  GCC  AGA  TAC  CGA  TGC  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  CGC  CGC  CGC  AGG  CGA  AGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TGC  CGC  CGC  CGC  CGC  CG-  --A  TAC  TCC  CTG  AGG  TGT  AAA  AGA  TAC
PRO  ATG  GCC  AGA  TAC  CGA  TGC  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  CGC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGT  CGG  AGG  AGG  CGA  TGC  TGC  CGG  CGG  AGG  AGG  CGA  AGG  TGC  TGC  CGC  CGC  CGC  AG-  --A  TAC  ACC  CTG  AGG  TGT  AAA  AGA  TAC
CGR  ATG  GCC  AGA  TAC  CGA  TGC  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  CGC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGA  CGG  AGA  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGT  TAC  CGC  CGC  CGC  CGT  ACA  TAC  ACC  CTA  AGG  TGT  AAA  AGG  TAC
CGL  ATG  GCC  AGA  TAC  CG-  --C  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  CGC  CGT  CGC  AGG  CGG  AGA  TGT  CGC  AGA  CGG  AGG  AG-  --A  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TAC  CGC  CGC  CGC  CGC  TCA  TAC  TCC  ATA  ATG  TGT  AAA  AGA  TAC
ASA  ATG  GCC  AGA  TAC  CG-  --C  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  CGC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TAC  CGC  CGC  CGC  CGC  CGC  ACA  TAC  ACC  ATG  AGG  TGT  AAA  AGA  TAC
ATE  ATG  GCC  AGA  TAC  CG-  --C  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  CGC  CRC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TAC  CGC  CGC  CGC  CGC  CGC  ACA  TAC  ACC  ATG  AGG  TGT  AAA  AGA  TAC
CNI  ATG  GCC  AGA  TAC  CG-  --C  TGC  CGC  AGC  CAA  AGC  AGG  AGC  AGA  TGC  CGC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TAC  GGC  CGC  CGC  CGC  ACA  TAC  ACC  CTG  AGG  TGT  AAA  AGA  TAC
PCM  ATG  GCC  AGA  TAC  CG-  --C  TGC  CGC  AGC  CAA  AGC  AGG  AGC  AGA  TGC  CGC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TAC  GGC  CGC  CGC  CGC  ACA  TAC  ACC  CTG  AGG  TGT  AAA  AGA  TAC
MGE  ATG  GCC  AGA  TAC  CG-  --C  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  AGC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGA  AGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGT  TAC  CGC  CGC  CGC  CGC  TCA  TAC  ACC  ATG  AGG  TGT  AAA  AGA  TAC
PDU  ATG  GCC  AGA  TAC  CG-  --C  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  AGC  CGC  CAC  AGG  CGG  AGA  TGT  CGC  AGA  AGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TAC  CGC  CGC  CGC  CGC  TCA  TAC  ACC  ATG  AGG  TGT  AAA  AGA  TAC
PLU  ATG  GCC  AGA  TAC  CG-  --C  TGC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  AGC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGA  AGG  AGG  AGG  CGA  TGC  TGC  CGG  AGG  AGG  AGG  CGA  AGG  TGC  TAC  CGC  CGC  CGC  CGC  TCA  TAC  ACC  ATG  AGG  TGT  AAA  AGA  TAC
MCA  ATG  GCC  AGA  TAC  CG-  --C  TAC  CGC  AGC  AAA  AGC  AGG  AGC  AGA  TGC  AGC  CGC  CGC  AGG  CGG  AGA  TGT  CGC  AGA  CGG  AGG  AGG  CGA  TGC  TGC  CAG  AGC  AGG  AAG  CGA  AGG  TGC  TAC  CGT  CGC  CGC  CGC  TCA  TGC  ACC  ATG  AGG  TGT  AAA  AGA  TAC
  
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Printing out site pattern counts

17 120 P

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MAR  --C  AAA  AAA  ACA  ACT  AGA  AGA  AGA  AGA  AGC  AGC  AGG  AGG  AGG  AGG  AGG  AGG  AGG  AGG  ATG  CG-  CGA  CGA  CGC  CGC  CGC  CGC  CGC  CGG  CGG  GCC  GGC  GTG  TAC  TAC  TAC  TGC  TGC  TGC  TGT
MAG  --C  AAA  AAA  ACA  ACC  AGA  AGA  AGA  AGA  AGC  AGC  AGG  AGG  AGG  AGG  AGG  AGG  AGG  AGG  ATG  CG-  CGA  CGA  CGC  CGC  CGC  CGC  CGT  CGG  CGG  GCC  CGC  ATG  TAC  TAC  TGC  TGC  TGC  TGT
SHI  TGC  AAA  AAA  ACA  ACC  AAA  AGA  AGA  AGA  AGC  CGC  AGA  AGG  AGG  AGG  AGG  AGG  AGG  ATG  CGA  CGA  CGA  CGC  CGC  CGC  CGC  CGA  CGA  CGG  GCC  CGC  CTA  TAC  TAC  TGT  TGC  TGC  TGT
MMU  TGC  AAA  AAA  TCA  ACC  AAA  AGA  AGA  AGA  AGC  CGC  AGA  AGG  AGG  AGG  AGG  AGG  AGG  ATG  CGA  CGA  CGA  CGC  CGC  CGT  CGT  CGC  CGA  CGG  GCC  CGC  ATA  TAC  TAC  TGC  TGC  TGC  TGT
  
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MAU TGC AAA AAA ACA ACC AGA AGA AGA CGA AGC CGC AGA AGG AGG AGG AGG AGG AGG AGG CGG ATG CGA CGA CGA CGC CGC CGC CGC CGG CGG GCC CGC CTA TAC TAC TGC TGC TGC TGC TGT  
 PSU TGC AAA AAA --A TCC AGA AGA AGA AGA AGC CGC AGG AGG AGG AGG AGG AGG AGG CGG ATG CGA CGA CGA CG- CGC CGC CGC CGC CGA CGG GCC CGC CTG TAC TAC TGC TGC TGC TGC TGT  
 PRO TGC AAA AAA --A ACC AGA AGA AGT AGA AGC CGC AGG AGG AGG AGG AGG AGG AGG CGG CGG ATG CGA CGA CGA AG- CGC CGC CGC CGC CGG CGG GCC CGC CTG TAC TAC TGC TGC TGC TGC TGT  
 CGR TGC AAA AAA ACA ACC AGG AGA AGA AGA AGC CGC AGG AGA AGG AGG AGG AGG AGG AGG CGG ATG CGA CGA CGA CGT CGC CGC CGC CGC CGA CGG GCC CGC CTA TAC TAC TGC TAC TGC TGT TGT  
 CGL --C AAA AAA TCA TCC AGA AGA AGA AGA AGC CGC AGG AGG AGG AGG AGG AGG AGG CGG ATG CG- --A CGA CGC CGC CGC CGT CGC CGG CGG GCC CGC ATA TAC TAC TGC TAC TGC TGC TGT  
 ASA --C AAA AAA ACA ACC AGA AGA AGA AGA AGC CGC AGG AGG AGG AGG AGG AGG AGG CGG ATG CG- CGA CGA CGC CGC CGC CGC CGG CGG GCC CGC ATG TAC TAC TGC TAC TGC TGC TGT  
 ATE --C AAA AAA ACA ACC AGA AGA AGA AGA AGC CGC AGG AGG AGG AGG AGG AGG AGG CGG ATG CG- CGA CGA CGC CGC CGC CGC CGG CGG GCC CGC ATG TAC TAC TGC TAC TGC TGC TGT  
 CNI --C AAA CAA ACA ACC AGA AGA AGA AGA AGC CGC AGG AGG AGG AGG AGG AGG AGG CGG ATG CG- CGA CGA CGC CGC GGC CGC CGC CGG CGG GCC CGC CTG TAC TAC TGC TAC TGC TGC TGT  
 PCM --C AAA CAA ACA ACC AGA AGA AGA AGA AGC CGC AGG AGG AGG AGG AGG AGG AGG CGG ATG CG- CGA CGA CGC CGC GGC CGC CGC CGG CGG GCC CGC CTG TAC TAC TGC TAC TGC TGC TGT  
 MGE --C AAA AAA TCA ACC AGA AGA AGA AGA AGC AGC AGG AGG AGG AGG AGG AGG AGG AGG ATG CG- CGA CGA CGC CGC CGC CGC CGG CGG GCC CGC ATG TAC TAC TGC TAC TGC TGC TGT  
 PDU --C AAA AAA TCA ACC AGA AGA AGA AGA AGC AGC AGG AGG AGG AGG AGG AGG AGG ATG CG- CGA CGA CGC CGC CGC CGC CGG CGG GCC CGC ATG TAC TAC TGC TAC TGC TGC TGT  
 PLU --C AAA AAA TCA ACC AGA AGA AGA AGA AGC AGC AGG AGG AGG AGG AGG AGG AGG ATG CG- CGA CGA CGC CGC CGC CGC CGG CGG GCC CGC ATG TAC TAC TGC TAC TGC TGC TGT  
 MCA --C AAA AAA TCA ACC AGA AGA AGA AGA AGC AGC AGG AGG AGG AAG AGG AGG AGC CGG ATG CG- CGA CGA CGC CGC CGT CGC CGC CGG CAG GCC CGC ATG TAC TGC TAC TAC TGC TGC TGT

1 1 1 1 1 1 2 1 1 3 1 1 1 1 1  
 3 1 1 1 1 1 1 1 1 3 1 1 1 1 1  
 1 1 1 2 1 1 1 3 1 2

CODONML (in paml version 4.4d, March 2011) 1.phy  
 Model: One dN/dS ratio for branches  
 Codon frequency model: Fcodon  
 Site-class models: PositiveSelection  
 ns = 17 ls = 51

Codon usage in sequences

Phe	TTT	0	0	0	0	0	0	0	0	Ser	TCT	0	0	0	0	0	0	0	0	0	Tyr	TAT	0	0	0	0	0	0	Cys	TGT	2	2	3	2	2	2
	TTC	0	0	0	0	0	0	0	0		TCC	0	0	0	0	0	1	1	1	1		TAC	4	3	3	3	3		TGC	5	6	6	7	7	7	
Leu	TTA	0	0	0	0	0	0	0	0		TCA	0	0	0	1	0	0	0	0	0	***	TAA	0	0	0	0	0	***	TGA	0	0	0	0	0	0	
	TTG	0	0	0	0	0	0	0	0		TCG	0	0	0	0	0	0	0	0	0		TAG	0	0	0	0	0		Trp	TGG	0	0	0	0	0	0
Leu	CTT	0	0	0	0	0	0	0	0	Pro	CCT	0	0	0	0	0	0	0	0	0	His	CAT	0	0	0	0	0	Arg	CGT	0	1	0	2	0	0	
	CTC	0	0	0	0	0	0	0	0		CCC	0	0	0	0	0	0	0	0	0		CAC	0	0	0	0	0		CGC	7	7	8	7	9	8	
	CTA	0	0	1	0	1	0	0	0		CCA	0	0	0	0	0	0	0	0	0	Gln	CAA	0	0	0	0	0		CGA	2	2	5	4	4	4	
	CTG	0	0	0	0	0	0	1	0		CCG	0	0	0	0	0	0	0	0	0		CAG	0	0	0	0	0		CGG	2	3	2	3	3	2	
Ile	ATT	0	0	0	0	0	0	0	0	Thr	ACT	1	0	0	0	0	0	0	0	0	Asn	AAT	0	0	0	0	0	Ser	AGT	0	0	0	0	0	0	
	ATC	0	0	0	0	0	0	0	0		ACC	0	1	1	1	1	0	0	0	0		AAC	0	0	0	0	0		AGC	4	4	3	3	3	3	
	ATA	0	0	0	1	0	0	0	0		ACA	1	1	1	0	1	0	0	0	0	Lys	AAA	2	2	3	3	2	2	Arg	AGA	5	5	5	5	5	5
Met	ATG	1	2	1	1	1	1	0	0		ACG	0	0	0	0	0	0	0	0	0		AAG	0	0	0	0	0		AGG	10	9	8	7	8	9	
Val	GTT	0	0	0	0	0	0	0	0	Ala	GCT	0	0	0	0	0	0	0	0	0	Asp	GAT	0	0	0	0	0	Gly	GGT	0	0	0	0	0	0	
	GTC	0	0	0	0	0	0	0	0		GCC	1	1	1	1	1	1	1	1	1		GAC	0	0	0	0	0		GGC	1	0	0	0	0	0	
	GTA	0	0	0	0	0	0	0	0		GCA	0	0	0	0	0	0	0	0	0	Glu	GAA	0	0	0	0	0		GGA	0	0	0	0	0	0	
	GTG	1	0	0	0	0	0	0	0		GCG	0	0	0	0	0	0	0	0	0		GAG	0	0	0	0	0		GGG	0	0	0	0	0	0	

Phe	TTT	0	0	0	0	0	0	0	0	Ser	TCT	0	0	0	0	0	0	0	0	0	Tyr	TAT	0	0	0	0	0	Cys	TGT	2	3	2	2	2	2	
	TTC	0	0	0	0	0	0	0	0		TCC	0	0	0	1	0	0	0	0	0		TAC	3	4	4	4	4		TGC	7	5	5	5	5	5	
Leu	TTA	0	0	0	0	0	0	0	0		TCA	0	0	1	0	0	0	0	0	0	***	TAA	0	0	0	0	0	***	TGA	0	0	0	0	0	0	
	TTG	0	0	0	0	0	0	0	0		TCG	0	0	0	0	0	0	0	0	0		TAG	0	0	0	0	0		Trp	TGG	0	0	0	0	0	0
Leu	CTT	0	0	0	0	0	0	0	0	Pro	CCT	0	0	0	0	0	0	0	0	0	His	CAT	0	0	0	0	0	Arg	CGT	0	1	1	0	0	0	
	CTC	0	0	0	0	0	0	0	0		CCC	0	0	0	0	0	0	0	0	0		CAC	0	0	0	0	0		CGC	8	8	8	9	8	8	
	CTA	0	1	0	0	0	0	0	0		CCA	0	0	0	0	0	0	0	0	0	Gln	CAA	0	0	0	0	0	1		CGA	3	4	1	2	2	2

	CTG	1	0	0	0	0	1		CCG	0	0	0	0	0	0		CAG	0	0	0	0	0	0		CGG	4	2	3	3	3	3
Ile	ATT	0	0	0	0	0	0		Thr	ACT	0	0	0	0	0		Asn	AAT	0	0	0	0	0		Ser	AGT	1	0	0	0	0
	ATC	0	0	0	0	0	0			ACC	1	1	0	1	1			AAC	0	0	0	0	0			AGC	3	3	3	3	3
	ATA	0	0	1	0	0	0			ACA	0	1	0	1	1		Lys	AAA	2	2	2	2	2		Arg	AGA	4	5	5	5	5
Met	ATG	1	1	2	2	2	1			ACG	0	0	0	0	0			AAG	0	0	0	0	0			AGG	8	9	7	9	9
Val	GTT	0	0	0	0	0	0		Ala	GCT	0	0	0	0	0		Asp	GAT	0	0	0	0	0		Gly	GGT	0	0	0	0	0
	GTC	0	0	0	0	0	0			GCC	1	1	1	1	1			GAC	0	0	0	0	0			GGC	0	0	0	0	0
	GTA	0	0	0	0	0	0			GCA	0	0	0	0	0		Glu	GAA	0	0	0	0	0			GGA	0	0	0	0	0
	GTG	0	0	0	0	0	0			GCG	0	0	0	0	0			GAG	0	0	0	0	0			GGG	0	0	0	0	0

Phe	TTT	0	0	0	0	0	0		Ser	TCT	0	0	0	0	0		Tyr	TAT	0	0	0	0	0		Cys	TGT	2	2	2	2	2
	TTC	0	0	0	0	0	0			TCC	0	0	0	0	0			TAC	4	4	4	4	4			TGC	5	5	5	5	5
Leu	TTA	0	0	0	0	0	0			TCA	0	1	1	1	1		***	TAA	0	0	0	0	0		***	TGA	0	0	0	0	0
	TTG	0	0	0	0	0	0			TCG	0	0	0	0	0			TAG	0	0	0	0	0		Trp	TGG	0	0	0	0	0
Leu	CTT	0	0	0	0	0	0		Pro	CCT	0	0	0	0	0		His	CAT	0	0	0	0	0		Arg	CGT	0	0	0	0	1
	CTC	0	0	0	0	0	0			CCC	0	0	0	0	0			CAC	0	0	1	0	0			CGC	8	8	7	8	7
	CTA	0	0	0	0	0	0			CCA	0	0	0	0	0		Gln	CAA	1	0	0	0	0			CGA	2	2	2	2	2
	CTG	1	0	0	0	0	0			CCG	0	0	0	0	0			CAG	0	0	0	0	1			CGG	3	2	2	2	2
Ile	ATT	0	0	0	0	0	0		Thr	ACT	0	0	0	0	0		Asn	AAT	0	0	0	0	0		Ser	AGT	0	0	0	0	0
	ATC	0	0	0	0	0	0			ACC	1	1	1	1	1			AAC	0	0	0	0	0			AGC	3	4	4	4	5
	ATA	0	0	0	0	0	0			ACA	1	0	0	0	0		Lys	AAA	1	2	2	2	2		Arg	AGA	5	5	5	5	5
Met	ATG	1	2	2	2	2	2			ACG	0	0	0	0	0			AAG	0	0	0	0	1			AGG	9	10	10	10	7
Val	GTT	0	0	0	0	0	0		Ala	GCT	0	0	0	0	0		Asp	GAT	0	0	0	0	0		Gly	GGT	0	0	0	0	0
	GTC	0	0	0	0	0	0			GCC	1	1	1	1	1			GAC	0	0	0	0	0			GGC	1	0	0	0	0
	GTA	0	0	0	0	0	0			GCA	0	0	0	0	0		Glu	GAA	0	0	0	0	0			GGA	0	0	0	0	0
	GTG	0	0	0	0	0	0			GCG	0	0	0	0	0			GAG	0	0	0	0	0			GGG	0	0	0	0	0

Codon position x base (3x4) table for each sequence.

#1: MAR  
position 1: T:0.22449 C:0.22449 A:0.48980 G:0.06122  
position 2: T:0.04082 C:0.06122 A:0.12245 G:0.77551  
position 3: T:0.06122 C:0.44898 A:0.20408 G:0.28571  
Average T:0.10884 C:0.24490 A:0.27211 G:0.37415

#2: MAG  
position 1: T:0.22449 C:0.26531 A:0.48980 G:0.02041  
position 2: T:0.04082 C:0.06122 A:0.10204 G:0.79592  
position 3: T:0.06122 C:0.44898 A:0.20408 G:0.28571  
Average T:0.10884 C:0.25850 A:0.26531 G:0.36735

#3: SHI  
position 1: T:0.23529 C:0.31373 A:0.43137 G:0.01961  
position 2: T:0.03922 C:0.05882 A:0.11765 G:0.78431  
position 3: T:0.05882 C:0.43137 A:0.29412 G:0.21569  
Average T:0.11111 C:0.26797 A:0.28105 G:0.33987

#4: MMU  
position 1: T:0.25490 C:0.31373 A:0.41176 G:0.01961  
position 2: T:0.03922 C:0.05882 A:0.11765 G:0.78431

position	3:	T:0.07843	C:0.43137	A:0.27451	G:0.21569
Average		T:0.12418	C:0.26797	A:0.26797	G:0.33987

#5: MAU

position	1:	T:0.23529	C:0.33333	A:0.41176	G:0.01961
position	2:	T:0.03922	C:0.05882	A:0.09804	G:0.80392
position	3:	T:0.03922	C:0.47059	A:0.25490	G:0.23529
Average		T:0.10458	C:0.28758	A:0.25490	G:0.35294

#6: PSU

position	1:	T:0.26531	C:0.30612	A:0.40816	G:0.02041
position	2:	T:0.04082	C:0.04082	A:0.10204	G:0.81633
position	3:	T:0.04082	C:0.46939	A:0.22449	G:0.26531
Average		T:0.11565	C:0.27211	A:0.24490	G:0.36735

#7: PRO

position	1:	T:0.24490	C:0.32653	A:0.40816	G:0.02041
position	2:	T:0.04082	C:0.04082	A:0.10204	G:0.81633
position	3:	T:0.06122	C:0.46939	A:0.18367	G:0.28571
Average		T:0.11565	C:0.27891	A:0.23129	G:0.37415

#8: CGR

position	1:	T:0.23529	C:0.31373	A:0.43137	G:0.01961
position	2:	T:0.03922	C:0.05882	A:0.11765	G:0.78431
position	3:	T:0.07843	C:0.43137	A:0.25490	G:0.23529
Average		T:0.11765	C:0.26797	A:0.26797	G:0.34641

#9: CGL

position	1:	T:0.27660	C:0.27660	A:0.42553	G:0.02128
position	2:	T:0.06383	C:0.06383	A:0.12766	G:0.74468
position	3:	T:0.06383	C:0.46809	A:0.21277	G:0.25532
Average		T:0.13475	C:0.26950	A:0.25532	G:0.34043

#10: ASA

position	1:	T:0.22449	C:0.28571	A:0.46939	G:0.02041
position	2:	T:0.04082	C:0.06122	A:0.12245	G:0.77551
position	3:	T:0.04082	C:0.46939	A:0.20408	G:0.28571
Average		T:0.10204	C:0.27211	A:0.26531	G:0.36054

#11: ATE

position	1:	T:0.22917	C:0.27083	A:0.47917	G:0.02083
position	2:	T:0.04167	C:0.06250	A:0.12500	G:0.77083
position	3:	T:0.04167	C:0.45833	A:0.20833	G:0.29167
Average		T:0.10417	C:0.26389	A:0.27083	G:0.36111

#12: CNI

position	1:	T:0.22449	C:0.30612	A:0.42857	G:0.04082
position	2:	T:0.04082	C:0.06122	A:0.12245	G:0.77551
position	3:	T:0.04082	C:0.46939	A:0.20408	G:0.28571
Average		T:0.10204	C:0.27891	A:0.25170	G:0.36735

#13: PCM

position	1:	T:0.22449	C:0.30612	A:0.42857	G:0.04082
position	2:	T:0.04082	C:0.06122	A:0.12245	G:0.77551
position	3:	T:0.04082	C:0.46939	A:0.20408	G:0.28571
Average		T:0.10204	C:0.27891	A:0.25170	G:0.36735

#14: MGE

```

position 1:  T:0.24490  C:0.24490  A:0.48980  G:0.02041
position 2:  T:0.04082  C:0.06122  A:0.12245  G:0.77551
position 3:  T:0.04082  C:0.46939  A:0.20408  G:0.28571
Average     T:0.10884  C:0.25850  A:0.27211  G:0.36054

```

```

#15: PDU
position 1:  T:0.24490  C:0.24490  A:0.48980  G:0.02041
position 2:  T:0.04082  C:0.06122  A:0.14286  G:0.75510
position 3:  T:0.04082  C:0.46939  A:0.20408  G:0.28571
Average     T:0.10884  C:0.25850  A:0.27891  G:0.35374

```

```

#16: PLU
position 1:  T:0.24490  C:0.24490  A:0.48980  G:0.02041
position 2:  T:0.04082  C:0.06122  A:0.12245  G:0.77551
position 3:  T:0.04082  C:0.46939  A:0.20408  G:0.28571
Average     T:0.10884  C:0.25850  A:0.27211  G:0.36054

```

```

#17: MCA
position 1:  T:0.24490  C:0.26531  A:0.46939  G:0.02041
position 2:  T:0.04082  C:0.06122  A:0.16327  G:0.73469
position 3:  T:0.06122  C:0.46939  A:0.20408  G:0.26531
Average     T:0.11565  C:0.26531  A:0.27891  G:0.34014

```

Sums of codon usage counts

```

-----
Phe F TTT    0 | Ser S TCT    0 | Tyr Y TAT    0 | Cys C TGT    36
      TTC    0 |       TCC    2 |       TAC   62 |       TGC    95
Leu L TTA    0 |       TCA    6 | *** * TAA    0 | *** * TGA    0
      TTG    0 |       TCG    0 |       TAG    0 | Trp W TGG    0
-----
Leu L CTT    0 | Pro P CCT    0 | His H CAT    0 | Arg R CGT    6
      CTC    0 |       CCC    0 |       CAC    1 |       CGC   133
      CTA    3 |       CCA    0 | Gln Q CAA    2 |       CGA    45
      CTG    4 |       CCG    0 |       CAG    1 |       CGG    44
-----
Ile I ATT    0 | Thr T ACT    1 | Asn N AAT    0 | Ser S AGT    1
      ATC    0 |       ACC   14 |       AAC    0 |       AGC    58
      ATA    2 |       ACA    9 | Lys K AAA   34 | Arg R AGA    84
Met M ATG   25 |       ACG    0 |       AAG    1 |       AGG   148
-----
Val V GTT    0 | Ala A GCT    0 | Asp D GAT    0 | Gly G GGT    0
      GTC    0 |       GCC   17 |       GAC    0 |       GGC    3
      GTA    0 |       GCA    0 | Glu E GAA    0 |       GGA    0
      GTG    1 |       GCG    0 |       GAG    0 |       GGG    0
-----

```

(Ambiguity data are not used in the counts.)

Codon position x base (3x4) table, overall

```

position 1:  T:0.23986  C:0.28520  A:0.44988  G:0.02506
position 2:  T:0.04177  C:0.05847  A:0.12053  G:0.77924
position 3:  T:0.05251  C:0.45943  A:0.22076  G:0.26730
Average     T:0.11138  C:0.26770  A:0.26372  G:0.35720

```

Codon frequencies under model, for use in evolver (TTT TTC TTA TTG ... GGG):  
0.00000000 0.00000000 0.00000000 0.00000000

```

0.00000000 0.00237129 0.00703089 0.00000000
0.00000000 0.07351005 0.00000000 0.00000000
0.04152249 0.11263637 0.00000000 0.00000000
0.00000000 0.00000000 0.00351544 0.00461361
0.00000000 0.00000000 0.00000000 0.00000000
0.00000000 0.00119405 0.00234363 0.00115340
0.00727578 0.16726607 0.05548489 0.05335568
0.00000000 0.00000000 0.00234363 0.02883506
0.00115340 0.01659904 0.01054633 0.00000000
0.00000000 0.00000000 0.03984170 0.00115340
0.00116125 0.06924847 0.09911285 0.17186489
0.00000000 0.00000000 0.00000000 0.00115340
0.00000000 0.02015598 0.00000000 0.00000000
0.00000000 0.00000000 0.00000000 0.00000000
0.00000000 0.00355694 0.00000000 0.00000000

```

Nei & Gojobori 1986. dN/dS (dN, dS)  
(Pairwise deletion)  
(Note: This matrix is not used in later ML analysis.  
Use runmode = -2 for ML pairwise comparison.)

```

MAR
MAG 0.2959 (0.0272 0.0919)
SHI 0.2052 (0.0464 0.2261) 0.2323 (0.0321 0.1382)
MMU 0.2470 (0.0608 0.2462) 0.1921 (0.0368 0.1914) 0.1242 (0.0177 0.1424)
MAU 0.2417 (0.0370 0.1530) 0.2189 (0.0228 0.1044) 0.0799 (0.0088 0.1104) 0.1893 (0.0267 0.1413)
PSU 0.5987 (0.0481 0.0948) 0.4577 (0.0284 0.0622) 0.1551 (0.0183 0.1182) 0.2389 (0.0323 0.1353) 0.0779 (0.0091 0.1173)
PRO 0.5106 (0.0482 0.0943) 0.4594 (0.0285 0.0620) 0.0994 (0.0183 0.1846) 0.2397 (0.0323 0.1349) 0.0781 (0.0091 0.1170) 0.3229 (0.0183 0.0568)
CGR 0.1749 (0.0464 0.2651) 0.1534 (0.0321 0.2092) 0.0854 (0.0177 0.2073) 0.1471 (0.0358 0.2432) 0.0429 (0.0088 0.2057) 0.1548 (0.0183 0.1184) 0.0992 (0.0183 0.1849)
PDU 0.7284 (0.0632 0.1142) 0.0907 (0.0576 0.0635) 0.3562 (0.0583 0.1636) 0.2981 (0.0383 0.1285) 0.5199 (0.0484 0.0931) 0.4180 (0.0347 0.0830) 0.6685 (0.0553 0.0828) 0.1903 (0.0383 0.2014)
ASA 0.7767 (0.0461 0.0593) 0.6171 (0.0180 0.0293) 0.2360 (0.0322 0.1366) 0.2396 (0.0369 0.1540) 0.3175 (0.0229 0.0722) 0.9495 (0.0286 0.0301) 0.9530 (0.0286 0.0300) 0.0798 (0.0136 0.1708) 1.2388 (0.0381 0.0307)
ATE 0.7673 (0.0469 0.0611) 0.6096 (0.0184 0.0301) 0.2329 (0.0328 0.1409) 0.3021 (0.0376 0.1244) 0.3139 (0.0234 0.0744) 0.9382 (0.0291 0.0310) 0.9417 (0.0291 0.0309) 0.0787 (0.0139 0.1764) -1.0000 (0.0388 0.0000) -1.0000 (0.0000 0.0000)
CNI 1.1317 (0.0657 0.0581) 1.6143 (0.0463 0.0287) 0.2477 (0.0372 0.1501) 0.3659 (0.0613 0.1676) 0.3239 (0.0278 0.0858) 1.3102 (0.0386 0.0294) 1.3148 (0.0386 0.0294) 0.0996 (0.0184 0.1844) 1.3891 (0.0633 0.0456) -1.0000 (0.0275 0.0000) -1.0000 (0.0280 0.0000)
PCM 1.1317 (0.0657 0.0581) 1.6143 (0.0463 0.0287) 0.2477 (0.0372 0.1501) 0.3659 (0.0613 0.1676) 0.3239 (0.0278 0.0858) 1.3102 (0.0386 0.0294) 1.3148 (0.0386 0.0294) 0.0996 (0.0184 0.1844) 1.3891 (0.0633 0.0456) -1.0000 (0.0275 0.0000) -1.0000 (0.0280 0.0000)
MGE 1.5471 (0.0458 0.0296) 0.2951 (0.0179 0.0608) 0.2931 (0.0510 0.1740) 0.1903 (0.0367 0.1928) 0.3954 (0.0416 0.1051) 0.6064 (0.0381 0.0628) 0.6088 (0.0381 0.0626) 0.1520 (0.0320 0.2107) 0.5910 (0.0378 0.0640) 0.6117 (0.0180 0.0294) 0.6041 (0.0183 0.0304) 1.6005 (0.0462 0.0288) 1.6005 (0.0462 0.0288)
PDU 1.8426 (0.0551 0.0299) 0.4392 (0.0270 0.0615) 0.3435 (0.0604 0.1760) 0.2358 (0.0460 0.1951) 0.4796 (0.0509 0.1062) 0.7520 (0.0477 0.0635) 0.7549 (0.0478 0.0633) 0.1937 (0.0413 0.2132) 0.7326 (0.0474 0.0648) 0.9106 (0.0271 0.0298) 0.8991 (0.0276 0.0307) 1.9068 (0.0556 0.0291) 1.9068 (0.0556 0.0291) -1.0000 (0.0089 0.0000)
PLU 1.5471 (0.0458 0.0296) 0.2951 (0.0179 0.0608) 0.2931 (0.0510 0.1740) 0.1903 (0.0367 0.1928) 0.3954 (0.0416 0.1051) 0.6064 (0.0381 0.0628) 0.6088 (0.0381 0.0626) 0.1520 (0.0320 0.2107) 0.5910 (0.0378 0.0640) 0.6117 (0.0180 0.0294) 0.6041 (0.0183 0.0304) 1.6005 (0.0462 0.0288) 1.6005 (0.0462 0.0288) -1.0000 (0.0000 0.0000) -1.0000 (0.0089 0.0000)
MCA 0.7923 (0.0744 0.0939) 1.0465 (0.0645 0.0617) 0.5673 (0.1001 0.1765) 0.6810 (0.0849 0.1246) 0.8470 (0.0902 0.1065) 1.3846 (0.0881 0.0637) 1.3900 (0.0882 0.0635) 0.3739 (0.0800 0.2139) 1.3486 (0.0876 0.0650) 2.1703 (0.0648 0.0298) 2.1436 (0.0660 0.0308) 3.2496 (0.0950 0.0292) 3.2496 (0.0950 0.0292) 0.7314 (0.0454 0.0621) 0.8705 (0.0547 0.0628) 0.7314
(0.0454 0.0621)

```

TREE # 1: (4, (3, (((((6, 13), 7), (5, 8)), ((10, 11), (9, (12, (17, ((2, 1), (14, (15, 16)))))))))); MP score: -1

This is a rooted tree. Please check!

lnL(ntime: 32 np: 37): -474.830556 +0.000000

```

18..4 18..19 19..3 19..20 20..21 21..22 22..23 23..6 23..13 22..7 21..24 24..5 24..8 20..25 25..26 26..10 26..11 25..27 27..9 27..28 28..12 28..29 29..17 29..30 30..31
31..2 31..1 30..32 32..14 32..33 33..15 33..16
0.059598 0.057709 0.093223 0.129838 0.027068 0.000004 0.000004 0.081958 0.057421 0.116827 0.031363 0.074864 0.150471 0.000004 0.000004 0.000004 0.000004 0.145277 0.000004 0.084345 0.027080 0.204942 0.000004 0.000004
0.048501 0.172945 0.055220 0.000004 0.000004 0.027589 0.000004 2.155747 0.397201 0.489333 0.000001 9.962781

```

Note: Branch length is defined as number of nucleotide substitutions per codon (not per nucleotide site).

tree length = 1.64629

(4: 0.059598, (3: 0.093223, (((((6: 0.081958, 13: 0.057421): 0.000004, 7: 0.116827): 0.000004, (5: 0.074864, 8: 0.150471): 0.031363): 0.027068, ((10: 0.000004, 11: 0.000004): 0.000004, (9: 0.145277, (12: 0.084345, (17: 0.204942, ((2: 0.048501, 1: 0.172945): 0.000004, (14: 0.000004, (15: 0.027589, 16: 0.000004): 0.000004): 0.055220): 0.000004): 0.027080): 0.000004): 0.000004): 0.129838): 0.057709);

(MMU: 0.059598, (SHI: 0.093223, (((PSU: 0.081958, PCM: 0.057421): 0.000004, PRO: 0.116827): 0.000004, (MAU: 0.074864, CGR: 0.150471): 0.031363): 0.027068, ((ASA: 0.000004, ATE: 0.000004): 0.000004, (CGL: 0.145277, (CNI: 0.084345, (MCA: 0.204942, ((MAG: 0.048501, MAR: 0.172945): 0.000004, (MGE: 0.000004, (PDU: 0.027589, PLU: 0.000004): 0.000004): 0.055220): 0.000004): 0.027080): 0.000004): 0.000004): 0.129838): 0.057709);

Detailed output identifying parameters

kappa (ts/tv) = 2.15575

dN/dS (w) for site classes (K=3)

p: 0.39720 0.48933 0.11347  
w: 0.00000 1.00000 9.96278

dN & dS for each branch

branch	t	N	S	dN/dS	dN	dS	N*dN	S*dS
18..4	0.060	87.2	65.8	1.6198	0.0238	0.0147	2.1	1.0
18..19	0.058	87.2	65.8	1.6198	0.0230	0.0142	2.0	0.9
19..3	0.093	87.2	65.8	1.6198	0.0372	0.0230	3.2	1.5
19..20	0.130	87.2	65.8	1.6198	0.0518	0.0320	4.5	2.1
20..21	0.027	87.2	65.8	1.6198	0.0108	0.0067	0.9	0.4
21..22	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
22..23	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
23..6	0.082	87.2	65.8	1.6198	0.0327	0.0202	2.9	1.3
23..13	0.057	87.2	65.8	1.6198	0.0229	0.0141	2.0	0.9
22..7	0.117	87.2	65.8	1.6198	0.0466	0.0288	4.1	1.9
21..24	0.031	87.2	65.8	1.6198	0.0125	0.0077	1.1	0.5
24..5	0.075	87.2	65.8	1.6198	0.0299	0.0184	2.6	1.2
24..8	0.150	87.2	65.8	1.6198	0.0600	0.0371	5.2	2.4
20..25	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
25..26	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
26..10	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
26..11	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
25..27	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
27..9	0.145	87.2	65.8	1.6198	0.0580	0.0358	5.1	2.4
27..28	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
28..12	0.084	87.2	65.8	1.6198	0.0336	0.0208	2.9	1.4
28..29	0.027	87.2	65.8	1.6198	0.0108	0.0067	0.9	0.4
29..17	0.205	87.2	65.8	1.6198	0.0818	0.0505	7.1	3.3
29..30	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
30..31	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
31..2	0.049	87.2	65.8	1.6198	0.0193	0.0119	1.7	0.8
31..1	0.173	87.2	65.8	1.6198	0.0690	0.0426	6.0	2.8
30..32	0.055	87.2	65.8	1.6198	0.0220	0.0136	1.9	0.9
32..14	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
32..33	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0
33..15	0.028	87.2	65.8	1.6198	0.0110	0.0068	1.0	0.4
33..16	0.000	87.2	65.8	1.6198	0.0000	0.0000	0.0	0.0

Naive Empirical Bayes (NEB) analysis  
Positively selected sites (\*: P>95%; \*\*: P>99%)  
(amino acids refer to 1st sequence: MAR)

	Pr(w>1)	post mean +- SE for w
31 R	0.619	6.549
38 C	0.995**	9.914
43 T	0.993**	9.902
45 T	0.567	6.081
46 V	1.000**	9.961

Bayes Empirical Bayes (BEB) analysis (Yang, Wong & Nielsen 2005. Mol. Biol. Evol. 22:1107-1118)  
 Positively selected sites (\*: P>95%; \*\*: P>99%)  
 (amino acids refer to 1st sequence: MAR)

	Pr(w>1)	post mean +- SE for w
31 R	0.634	5.453 +- 3.799
38 C	0.996**	8.158 +- 1.837
43 T	0.993**	8.140 +- 1.874
45 T	0.677	5.713 +- 3.630
46 V	1.000**	8.189 +- 1.782

The grid (see ternary graph for p0-p1)

w0: 0.050 0.150 0.250 0.350 0.450 0.550 0.650 0.750 0.850 0.950  
 w2: 1.500 2.500 3.500 4.500 5.500 6.500 7.500 8.500 9.500 10.500

Posterior on the grid

w0: 0.308 0.225 0.168 0.123 0.083 0.049 0.025 0.012 0.005 0.002  
 w2: 0.000 0.001 0.011 0.038 0.081 0.129 0.168 0.191 0.196 0.186

Posterior for p0-p1 (see the ternary graph)

0.000  
 0.001 0.001 0.001  
 0.000 0.001 0.005 0.006 0.003  
 0.000 0.000 0.001 0.007 0.019 0.017 0.007  
 0.000 0.000 0.000 0.001 0.007 0.023 0.046 0.031 0.009  
 0.000 0.000 0.000 0.000 0.001 0.006 0.018 0.047 0.069 0.038 0.008  
 0.000 0.000 0.000 0.000 0.000 0.001 0.003 0.014 0.029 0.062 0.067 0.033 0.006  
 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.002 0.006 0.019 0.029 0.053 0.047 0.022 0.004  
 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.001 0.004 0.006 0.017 0.021 0.036 0.031 0.014 0.002  
 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.001 0.001 0.003 0.005 0.012 0.014 0.024 0.022 0.010 0.002

sum of density on p0-p1 = 1.000000

Time used: 2:00