

# Entropy Based Analysis of Vertebrate Sperm Protamines Sequences: Evidence of Dityrosine and Cysteine-Tyrosine Cross-Linking in Sperm Protamines

## Supplemental Tables

**Table 1 Highly Conserved Positions in Eutherian P1 Sperm Protamine MSA.**

Rank	Position in Alignment	Relative Entropy (bit)	Represented Residues
1	7	6.157	C: 98.6% R: 1.4%
2	49	6.12	C: 97.9% G: 1.4% S: 0.7%
3	50	5.87	C: 95.1% R: 2.1% Y: 1.4% G: 0.7% S: 0.7%
4	60	5.439	C: 89.5% R: 4.9% S: 4.2% Y: 1.4%
5	38	5.187	C: 86.9% G: 4.1% Y: 2.8% R: 1.4% S: 1.4% V: 1.4% A: 0.7% F: 0.7% H: 0.7%
6	17	4.885	C: 79.3% R: 13.1% G: 5.5% S: 1.4% Y: 0.7%
7	29	4.813	C: 77.2% Y: 13.1% S: 5.5% G: 1.4% R: 1.4% F: 0.7% N: 0.7%
8	6	4.604	C: 95.5% R: 4.5%
9	37	4.33	C: 69.0% S: 19.3% F: 5.5% R: 5.5% T: 0.7%

**Table 2 Highly Conserved Positions in Processed Eutherian P2 Sperm Protamine MSA.**

Rank	Position in Alignment	Relative Entropy (bit)	Represented Residues
1	59	6.381	C: 100.0%
2	75	6.381	C: 100.0%
3	83	6.381	C: 100.0%
4	93	6.381	C: 100.0%
5	107	6.381	C: 100.0%
6	68	5.513	H: 100.0%
7	89	4.721	H: 87.5% N: 6.2% P: 6.2%
8	53	4.635	H: 87.5% G: 6.2% S: 6.2%
9	85	4.543	H: 81.2% Y: 12.5% Q: 6.2%
10	110	4.371	H: 75.0% Y: 18.8% Q: 6.2%
11	54	4.288	Y: 56.2% H: 43.8%

**Table 3 Highly Conserved Positions in Unprocessed Eutherian P2 Sperm Protamine MSA.**

Rank	Position in Alignment	Relative Entropy (bit)	Represented Residues
1	59	6.381	C: 100.0%
2	75	6.381	C: 100.0%
3	83	6.381	C: 100.0%
4	93	6.381	C: 100.0%
5	107	6.381	C: 100.0%
6	14	5.513	H: 100.0%
7	68	5.513	H: 100.0%
8	48	5.126	H: 93.8% Q: 6.2%
9	44	5.093	Y: 100.0%
10	4	4.836	Y: 93.8% C: 6.2%
11	19	4.725	Q: 100.0%
12	26	4.725	Q: 100.0%
13	34	4.725	Q: 100.0%
14	89	4.721	H: 87.5% N: 6.2% P: 6.2%
15	53	4.635	H: 87.5% G: 6.2% S: 6.2%
16	85	4.543	H: 81.2% Y: 12.5% Q: 6.2%
17	110	4.371	H: 75.0% Y: 18.8% Q: 6.2%
18	54	4.288	Y: 56.2% H: 43.8%
19	47	4.171	T: 100.0%

**Table 4 Highly Conserved Positions in Metatherian P1 Sperm Protamine MSA.**

Rank	Position in Alignment	Relative Entropy (bit)	Represented Residues
1	7	4.98	H: 92.6% R: 5.3% N: 2.1%
2	4	4.835	Y: 95.8% C: 3.2% S: 1.1%
3	57	4.733	Y: 93.7% C: 4.2% K: 2.1%
4	16	4.67	Y: 94.7% N: 3.2% F: 2.1%
5	62	4.599	Y: 92.6% C: 3.2% P: 2.1% S: 2.1%
6	75	4.565	Y: 94.5% C: 3.3% N: 2.2%
7	34	4.536	Y: 91.6% S: 4.2% Q: 2.1% M: 1.1% X: 1.1%

**Table 5 Fish Protamines**

Rank	Range	STD
1	K 0.141	K 0.027
2	H 0.185	H 0.035
3	L 0.222	L 0.039
4	T 0.228	T 0.041
5	A 0.256	E 0.045

**Table 6 Eutherian P1 Sperm Protamines**

Rank	Range	STD
1	Q 0.182	Q 0.034
2	K 0.224	P 0.044
3	T 0.224	T 0.046
4	S 0.242	N 0.046
5	N 0.244	A 0.049

**Table 7 Eutherian P2 Sperm Protamines**

Rank	Range	STD
1	Q 0.07	Q 0.017
2	L 0.09	T 0.022
3	T 0.09	L 0.023
4	K 0.09	E 0.024
5	C 0.099	V 0.025

**Table 8 Truncated Eutherian P2 Sperm Protamines**

Rank	Range	STD
1	Q 0.116	K 0.035
2	K 0.117	Q 0.037
3	T 0.127	T 0.04
4	L 0.145	L 0.044
5	C 0.151	G 0.045

**Table 9 Metatherian Sperm Protamines**

Rank	Range	STD
1	K 0.177	N 0.027
2	N 0.179	K 0.03
3	G 0.202	T 0.035
4	A 0.223	A 0.035
5	E 0.235	Q 0.035

	10	20	30	40
PRTA_ACIST	-ARRRRRHAS	TKLKR---	----RRRRH	GKSKHK
PRT_ORYLA	----MRRQAS	LPARRRRVR	RTRVRRRRR	VGRRRH
PRT_PERFV	--PRRRRHAA	RPVRRRRTR	RSSRVHRRR	AVRRRR
PRTB_MUGCE	--PRRRRETS	RPIRRRRAR	RAPI-RRRR	VVRRRR
PRT1_SCOSC	-MPRRRRRAS	RPVRRRRAR	RSTAVRRRR	VVRRRR
PRT2_SCOSC	-MPRRRRRAS	RPIRRRRAR	RSTAVRRRR	VVRRRR
PRT_DICLA	--PRRRRQAS	RPVRRRRTR	RSTAERRRR	VVRRRR
PRTY_THUTH	--PRRRRQAS	RPVRRRRYR	RSTAARRRR	VVRRRR
PRTZ_THUTH	--PRRRRRSS	RPVRRRRYR	RSTVARRRR	VVRRRR
PRTZ1_SAROR	--PRRRRRSS	RPVRRRRYR	RSTAARRRR	VVRRRR
PRTB_ACIGU	--ARRRRRSS	RPQRRRR--	----RRHGR	RRRGRR
PRTB_ACIST	--ARRRRRSS	RPQRRRR--	----RRHGR	RRRGRR
PRTY1_CLUHA	--ARRRRSSS	RPIRRRRPR	RT---TRRR	AGRRRR
PRTY1_CLUPA	--ARRRRSSS	RPIRRRRPR	RT---TRRR	AGRRRR
PRT1_ESOLU	-PRRRRASSG	RPVRRRRP-	KMS--RRRR	GGRRRR
PRTZ_CLUPA	ARRRSRRAS	RPVRRRRP-	RVS--RRRR-	-ARRRR
PRTZ_CLUHA	ARRRSRRAS	RPVRRRRP-	RVS--RRRR-	-ARRRR
PRT4_ONCMY	-MPRRRR-AS	RRIRRRRP-	RVS--RRRRG	GRRRRR
PRTY2_CLUPA	-PRRTRRAS	RPVRRRRP-	RVS--RRRR-	-ARRRR
PRTY2_CLUHA	-PRRTRRAS	RPVRRRRP-	RVS--RRRR-	-ARRRR
PRT3A_ONCMY	-PRRRRRSSS	RPIRRRRP-	RVS--RRRR-	GGRRRR
PRTIB_ONCMY	PRRRRRSSS	RPIRRRRP-	RVS--RRRR	GGRRRR
PRT1B_ONCMY	-MPRRRR-AS	RRIRRRRP-	RVS--RRRR	GGRRRR
PRT1A_ONCMY	-MPRRRR-AS	RRVRRRRP-	RVS--RRRR	GGRRRR
PRTC3_ONCMY	-MPRRRR-AS	RPVRRRRP-	RVS--RRRR	GGRRRR
PRT2C_ONCMY	-MPRRRRSSR	RPVRRRRP-	RVSR-RRRR	GGRRRR
PRT14_ONCMY	-MPRRRRSSR	PPVRRRRP-	RVSR-RRRR	GGRRRR
PRT2_ONCMY	--PRRRRSSS	RPVRRRAR-	RVSR-RRRR	GGRRRR
PRT2A_ONCMY	--PRRRRSSS	RPVRRRRA-	RVSR-RRRR	GGRRRR
PRTIA_ONCMY	--PRRRRSSS	RPVRRRRPR	RVSR-RRRR	GGRRRR
PRT1_ONCKE	-MPRRRRSSS	RPVRRRRP-	RVSR-RRRR	GGRRRR
PRT2B_ONCMY	-MPRRRRSSS	RPVRRRRP-	RVSR-RRRR	GGRRRR
PRT16_ONCMY	-MPRRRRSSS	RPVRRRRA-	RVSR-RRRR	GRRRRR
PRT17_ONCMY	-MPRRRRSSS	RPVRRRRP-	RVSR-RRRR	GRRRRR

Supplemental Figure 1. Alignment of fish protamines.

	10	20	30	40	50	60
AOA2K5CXY9_AOTNA	MARHRCCSR	--SQRSR-R	--DRQRRR	-TPRRRSCRR	--RTA-RRCG	RRR--YKPRC RRN-
HSP1_RHIFE	MARYSCSRH	--SRSRSR-R	---R-RQR	-RRRRRSCGR	--RR--RACY	RRYTVRYRRR RRRR
HSP1_HIPCO	MARYRCCSRH	--SRSRCR-R	---R-RRRSR	-RRRRRSCGR	--RR--RAGY	RRY---TVRY RRRR
A8IYA4_ANTAM	MARYRCCLTH	--SRSRCRPR	---RRRRRRCR	-KLRRRRCRR	-PRR--RVCC	RRY--TAIRC TR--
A8IYA7_9CETA	MARYRCCLTH	--SRSGCR-R	---RRRRRCR	-RRRRRRCRR	--RRR-RVCC	RRY--TVVRC TRQ-
HSP1_CAPHI	MARYRCCLTH	--SRSRCR-R	---RRRRRCR	-RRRRRRCRR	--RRR-RVCC	RRY--TVVRC TRQ-
HSP1_SHEEP	MARYRCCLTH	--SRSRCR-R	---RRRRRCR	-RRRRRRCRR	--RRR-RVCC	RRY--TVVRC TRQ-
A8IYA2_OVIDA	MARYRCCLTH	--SRSRCR-R	---RRRRRCR	-RRRRRRCRR	--RRR-RVCC	RRY--TVVRC TRQ-
HSP1_BOVIN	MARYRCCLTH	--SGSRCR-R	---RRRRRCR	-RRRRRRCRR	--RRR-RVCC	RRY--TVIRC TRQ-
AOA068B2A1_BOSIN	MARYRCCLTH	--SGSRCR-R	---RRRRRCR	-RRRRRRCRR	--RRR-RVCC	RRY--TVIRC TRQ-
AOA193KZWO_9CETA	MARYRCCLTH	--SGSRCR-R	---RRRRRCR	-RRRRRRCRR	--RR-----	--RR-----
C8C436_PLAMN	MARNRCCSRQ	--SRSRCR-R	---P-KRGR	-SRRRRRCYQR	--RR--RVCC	RRY--TTIRC ARQ-
A8IYB4_PHYMC	MARNRCCSRQ	--SRSRCR-R	---P-RRRCR	-SPRRRRYQR	--RR--RVCC	RRY--TVTRC ARQ-
C8C437_KOGSI	MARNRCCSRQ	--SRGRCR-R	---P-RRRCR	-SPKRRRYQR	--RR--RVCC	RRS--ATMRC ASQ-
C8C438_KOGBR	MARNRCCSRQ	--SRGRCR-R	---P-RRRYR	-SPRRRRYQR	--RR--RVCC	RRS--TTMRC ASQ-
HSP1_PIG	MARYRCCSRH	--SRSRCR-P	---R-RRRCR	-RRRRRRCPR	--RRR-AVCC	RRY--TVIRC RRC-
A8IYC1_POTPR	MARYRCCSRH	--SRSRCR-P	---R-RRRCR	-RRRRRRCPR	--RRR-AVCC	RRY--TVIRC RRC-
F7VJK3_FELCA	MARYRCCSRH	--SRSRCR-R	---R-RRRCR	-RRRRRRCRR	-PRK--RVCS	RRY--RVGRC RRR-
HSP1_OTOHE	MARYRCCSR	--SRSRCR-R	---R-RRKY	-RRRRRRCR	--RRR-RVCC	RRY--TMVRC RRR-
C8C444_HEXLI	MARYRCCSRP	--SRSRCR-R	---Q-RRRCR	-RRRRRRCRQ	--RRR-RVCC	RRY--TMVRC TRQ-
A8IYB9_HIPAM	MARYRCCSRP	--SRSRCR-R	---Q-RRRCR	-RRRRRRCRQ	--RRR-RVCC	RRY--TMVRC TRQ-
HSP1_EQUAS	MARYRCCSRQ	--SGSRCR-R	---RRRRRCR	-RRRRRRCRR	--RR--VCC	RRY--TVLRC RRRR
HSP1_HORSE	MARYRCCSRQ	--SGSRCR-R	---RRRRRCR	-RRRRRRCRR	--RR--VCC	RRY--TVLRC RRRR
HSP1_HYPSA	MARYRRCR--	--SRSRCR-R	---R-RRRCH	-RRRRRRCRR	--RRRRRACC	RRY-----RC RRR-
HSP1_NEOBU	MARYRRCR--	--SRSRCR-R	---R-RRRCH	-RRRRRRCRR	--RRRRRACC	RRY-----RC RRR-
HSP1_RHIHA	MARYRCCSR	--SRSRCRPR	----RRRCR	-RRRRRRCRR	--RR--RVCC	RRY--SARC RRRR
HSP1_MURCY	MARYRCCR--	--SRSRCR-R	---R-RRRCH	-RRRRRRCRR	--RRR-RVCC	RRY--TVIRC RRR-
HSP1_PTEPA	MARYRCCSRP	--SRSRCR-R	---R-RRRCR	-RRRRRRCRR	--RR--RVCC	RRY--TVRC RRR-
HSP1_DESRO	MARYRCCSRP	--SRSRCR-R	---R-RRRCR	-RRRRRRCRR	--RR--RVCC	RRY--TVRC RRR-
HSP1_MONRE	MARYRCCSRP	--SRSRCR-R	---R-RRRCR	-RRRRRRCRR	--RR--RVCC	RRY--TVRC RRR-
HSP1_MORME	MARYRCCSRP	--SRSRCR-R	---R-RRRCR	-RRRRRRCRR	--RR--RVCC	RRY--TVRC RRR-
HSP1_MYODA	MARYRCCR--	--SRSRCR-R	---R-RRRCY	-RRRRRRCRR	--RRRRRVCC	RRY----SRC RRR-
F7VJK7_MYOLU	MARYRCCR--	--SRSRCR-R	---R-RRRCY	-RRRRRRCRR	--RRRRRVCC	RRY----SRC RRR-
HSP1_GLABE	MARYRCCR--	--SRSRCR-R	---R-RRRY	-RRRRRRCRR	--RRR-RVCC	RRY----VRC RRR-
HSP1_NATST	MARYRCCSRQ	--SRSRCR-P	---R-RRRCR	-TRRRRRCRR	--RR--RVCC	RRY--TVVRC RRR-
HSP1_CHIMC	MARYRCCSRQ	--SRSRCR-R	---R-RRRCR	-TRRRRRCRR	--RR--RVCC	RRY--TVVRC RRR-
HSP1_EPTFU	MARYRCCR--	--SRSRCR-R	---R-RRRCY	-RRRRRRCRR	--RR--RVCC	RRY--TVIRC RRR-
HSP1_EPTBR	MARYRCCR--	--SRSRCR-R	---R-RRRCY	-RRRRRRCRR	--RR--RVCC	RRY--TVIRC RRR-
HSP1_CORTO	MARYRCCSRQ	--SRSRCR-R	---R-RRRCY	-RRRRRRCRR	--RRR-RVCC	RRY----TRY RRR-
HSP1_PLEAU	MARYRCCSRQ	--SRSRCR-R	---R-RRRCY	-RRRRRRCRR	--RR--RVCC	RRY--TVVRC RRR-
HSP1_PTEHP	MARYRCCSRQ	--SRSRCR-R	---R-RRRCR	-RRRRRRCRR	--RR--RVCC	RRY--TVRC RRRR
F7VJK4_CANLF	MARYRCCSRQ	--SRSRCR-R	---R-RRRCR	-RRRRRRCRR	RRR--RVCC	RRY--TVVRC RRR-
C8C440_EUBGL	MARNRCCSRQ	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARR-
C8C439_EUBAS	MARNRCCSRQ	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARR-
B1ACJ7_BALMY	MARNRCCSRQ	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARR-
B1ACJ8_EUBJA	MARNRCCSRQ	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARR-
B1ACJ6_CAPMR	MARNRCCSRQ	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARQ-
B1ACI8_MEGNO	MARNRCCSRP	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARQ-
B1ACI9_BALPH	MARNRCCSRP	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARQ-
B1ACJ3_BALBN	MARNRCCSRP	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC AGQ-
B1ACJ4_BALAC	MARNRCCSRP	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC AGQ-
B1ACJ1_BALBO	MARNRCCSRP	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARQ-
B1ACJ5_ESCRO	MARNRCCSRP	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARQ-
B1ACJ2_BALED	MARNRCCSRP	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARQ-
B1ACJ0_BALMU	MARNRCCSRP	--SRSRRCR-R	---P-RQR	-SQRRCRR	--RR--RVCC	RRY--TTVRC ARQ-
C8C435_BERBI	MARNRCCSRQ	--SQRRCR-R	---P-RRRN	-SRRRCRR	--RR--RVCC	RRY--TAIRC ARQ-
A8IYB7_ZIPCA	MARNRCCSRQ	--SQRRCR-R	---P-RRRY	-SRRRCRR	--RR--RVCC	RRY--TAIRC ARQ-
C8C432_MESGR	MARNRCCSRQ	--SQRRCR-R	---P-RRRY	-SRRRCRR	--RR--RVCC	RRY--TAIRC ARQ-
C8C434_TASSH	MARNRCCSRQ	--SQRRCR-R	---P-RRRY	-SRRRCRR	--RR--RVCC	RRY--TAIRC ARQ-
C8C433_MESBI	MARNRCCSRQ	--SQRRCR-R	---P-RRRY	-SRRRCRR	--RR--RVCC	RRY--TAIRC ARQ-
C8C431_MESPE	MARNRCCSRQ	--SQRRCR-R	---P-RRRY	-SRRRCRR	--RR--RVCC	RRY--TAIRC ARQ-
HSP1_ORCOR	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--QR--RVCC	RRY--TTTRC ARQ-
C8C425_GLOMA	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
C8C426_GRAGR	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
B4VYM8_PSECS	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
C8C424_FERAT	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
F5CBD0_PENEL	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
C8C423_LAGAC	MARNR-CRSP	--SQRRCR-R	---P-RRRCL	-RRRCRR	--RR--RVCC	RRY--TTTRC AR--
F5CBC9_CPCPM	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--ATTRC ARQ-
F5CBC8_LAGAL	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC ASQ-
C8C421_TURTR	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
F5CBC0_TURAD	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
B4VYN1_STECO	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
F5CBC1_STELO	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC AR--
F5CBC5_LAGHO	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC AR--
F5CBB9_DELCA	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC AR--
F5CBC3_STEAT	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC AR--
F5CBC4_SOUC	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
F5CBD1_9CETA	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
F5CBC7_LAGOL	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC AR--
B4VYM9_STEBR	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
F5CBC2_STEFR	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC AR--
C8C62_SOTFL	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC AR--
F5CBC42_LISBO	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
B4VYN0_DELDE	MARNR-CRSP	--SQRRCR-R	---P-RRRCR	-RRRCRR	--RR--RVCC	RRY--TTTRC AR--
C8C428_NEOPH	MARNR-CRSP	--SQRRCR-C	---P-RRRY	-SKRRRCRR	--RR--RVCC	RRY--TRRC ARQ-
C8C427_9CETA	MARNR-CRSP	--SQRRCR-C	---P-RRRY	-SKRRRCRR	--RR--RVCC	RRY--TRRC ARQ-
B4VYM6_PHOPH	MARNR-CRSP	--SQRRCR-C	---P-RRRY	-SKRRRCRR	--RR--RVCC	RRY--TRRC ARQ-
F5CIP3_LIPVE	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-SKRRRCRR	--RR--RVCC	RRY--TTMRC AKQ-
C8C430_DELLE	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-SKRRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
C8C429_MONMO	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-SKRRRCRR	--RR--RVCC	RRY--TTTRC ARQ-
A8IYB2_PONBL	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-SKRRRCRR	--RR--RVCC	RRY--TSVRC ARQ-
A8IYA9_INIGE	MARNR-CRSP	--SQRRCR-R	---P-RRRY	-SKRRRCRR	--RR--RVCC	RRY--TTVRC ARQ-
F7VJK6_LOXAF	MARYRCCSR	--SRSRCSR	---R-RRSH	-RRRRRCRR	--RRTRCC	RRR--YSLRR RRY-
HSP1_PONPY	MARYRCCSR	--SQRRCR-R	---R-RRCH	-RRRRRCRR	--RRRAMCC	RRR--YLRRC RRY-
H2NQ55_PONAB	MARYRCCSR	--SQRRCR-R	---R-RQR	-RRRRRCRR	--RRRAMCC	RRR--YLRRC RRR-
HSP1_GALVR	MARYRCCR--	--SRSRCR-R	---R-RRSCR	-RRRRRCRR	--RA--RRSC	RRR--YSLRC CRRY-
HSP1_SAGIM	MARYRCCSRQ	--SRSRCY-R	---Q-RRRGR	-RRRRRCRR	--RA--SRCC	RRR--YKLT CRRY-
AOA2R8PK40_CALJA	MARYRCCSRQ	--SRSRCY-R	---Q-RRRGR	-RRRRRCRR	--RA--SRCC	RRR--YKLP CRRY-
HSP1_ALOSE	MARYRCCSR	--SRSRCSR	---Q-RPCR	-RRRRRCRR	--RA--SRCC	RRR--YLRRC RRY-
HSP1_SAISS	MARYRCCSR	--SRSRCSR	---R-RRRCR	-TRRRRCRR	--RA--RRCC	RRR--YKLR CRRY-
AOA2K6TB39_SAISS	MARYRCCSR	--SRSRCSR	---R-RRRCR	-TRRRRCRR	--RA--RRCC	RRR--YKLR CRRY-
AOA2K5R6E5_CEBCA	MARYRCCSR	--SRSRCSR	---Q-RRRGR	-RRRRRCRR	--RA--RRCC	RRR--YLRRC RRY-
HSP1_RABIT	MARYRCCSRQ	--SRSRCR-R	---R-RRRCR	-RRRRRCRR	--RRV-RKCC	RRR--YLRRC RRY-
HSP1_CAVPO	MARYRCCSRP	--SRSRCR-R	---R-RRRFY	-RRRRRCRR	--RR--RCC	RRR--YLRRC RRY-
HSP1_COLGU	MARYRCCSRQ	--SRSRCC-R	---Q-RRRGR	-RRRRRCRR	--RR--RCC	RRR--YLRRC RRY-
F7VJK5_ERIEU	MARYRCCSRQ	--SRSRCC-R	RRYR-RRRCR	-RRRRRCRR	--RRR-ACC	RRR--Y---- RRY-
C3U1R1_9MURI	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
HSP1_MOUSE	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1R5_MUSSP	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1Q6_MUSMB	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1Q9_MOUSE	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1R0_MOUSE	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1Q8_MUSMC	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1R4_MUSSI	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1Q7_MUSCO	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1R3_MUSMA	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1R2_MUSPA	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
HSP1_RAT	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
C3U1S7_APOSY	MARYRCCSRK	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
HSP1_NASLA	MAKSRCCGSQ	--SRSRCC-R	---P-RQR	-RRRRRCRR	--RRRAMCC	RRR--YLRRC RRY-
HSP1_TRAJO	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
HSP1_TRAPH	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
LOC34_TRAPH	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
HSP1_TRACR	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
HSP1_TRAOB	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
LOC39_9PRIM	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
LOCNC1_TRAPH	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
HSP1_SEMEN	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
HSP1_TRAVT	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
HSP1_TRAPL	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
HSP1_TRAGE	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
HSP1_TRAFR	MARYRCCSRQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
S4SNK2_9PRIM	-----RSQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
S4SLN4_9PRIM	-----RSQ	--SRSRCC-R	---P-RRRCR	-RRRRRCRR	--RRRATCC	RRR--YLRRC RRY-
F7VJK8_OTOGA	MARYRCCSRQ	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
HSP1_PILBA	MARYRCCSRQ	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
HSP1_MACMU	MARYRCCSRQ	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
HSP1_PAPCY	MARYRCCSRQ	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RR--RRCC	RRR--YLRRC RRY-
AOA096MLL5_PAPAN	MARYRCCSRQ	--SRSRCC-R	---Q-RRRGR	-RRRRRCRR	--RRRAMCC	RRR--YLRRC RRY-
HSP1_HYLLA	MARYRCCSRQ	--SRSRCC-R	---R-RRRCR	-RRRRRCRR	--RRRAMCC	RRR--YLRRC RRY-
HSP1_HUMAN	MARYRCCSRQ	--SRSRCC-R	---Q-RQR	-RRRRRCRR	--RRRAMCC	RRR--YLRRC RRY-
HSP1_GORG	MARYRCCSRQ	--SRSRCC-R	---Q-RQR	-RRRRRCRR	--RRRAMCC	RRR--YLRRC RRY-
HSP1_PANTR	MARYRCCSRQ	--SRSRCC-R	---Q-RQR	-RRRRRCRR	--RRRAMCC	RRR--YLRRC RRY-
HSP1_PANPA	MARYRCCSRQ	--SRSRCC-R	---Q-RQR	-RRRRRCRR	--RRRAMCC	RRR--YLRRC RRY-

Supplemental Figure 2. Alignment of Eutherian P1 type sperm protamines.

	10	20	30	40	50	60
PRM2_RATTU	MVRYRMRSPS	ESP HQGPGQD	HESEEQG---	-QGQELNPER	VEDYGRTHRG	--HHRHRRCS
PRM2_MOUSE	MVRYRMRSPS	EGPHQGPGQD	HEREEQG---	-QGQGLSPER	VEDYGRTHRG	HHHHRHRRCS
PRM2_RATFU	MVRYRMRSPS	EGPHQGPGQD	HEREEQG---	-QGQELSPER	VEDYGRTHRG	--HHRHRRCS
PRM2_ALOSE	MVRYHVRSPS	ERPHEEYRQL	VNGQEQGRHG	QEEQGMSAEG	VEGYGRTHQG	CYGYRRRLCS
PRM2_CALJA	MVRYRVRSPS	ERPHEEYRQL	VNWQEQGRNG	QEEQGLSAEG	GEVYGRTHQG	YSSYRRRRCS
PRM2_SEMEN	MVRYRMRSLs	ERPHEVHGQQ	VYGQEQGHNG	QEEQGLSPEH	VEVYERTHQG	YSHHRRRRCS
PRM2_ERYPA	MVRYRTRSLs	ERPHEVHGQQ	VHGQDQGHNG	QEEQGLSPEH	VEVYERTHQG	HSHHRRRRCS
PRM2_MACNE	MVRYRMRSLs	ERPHEVHGQQ	VHGQDQGHNG	QEEQGLNPEH	VEVYERTHRG	HSHHRRRRCS
PRM2_MACFU	MVRYRMRSLs	ERPHEVHGQQ	VHGQDQGHNG	QEEQGLNPEH	VEVYERTHRG	HSHHRRRRCS
PRM2_MACMU	MVRYRMRSLs	ERPHEVHGQQ	VHGQDQGHNG	QEEQGLNPEH	VEVYERTH-G	HSHYRRRHCS
PRM2_GORGO	MVRCRVRSPS	ERSHEVYRQQ	LHGQEQGHHG	QEEQGLSPEH	VEVYERTH-G	HSHYRRRHCS
PRM2_PANPA	MVRYRVRSPS	EPSHEVYRQQ	LHGQEQGHHG	QEEQGLSPEH	VEVYERTH-G	HSHYRRRHCS
PRM2_PANTR	MVRYRVRSPS	EPSHEVYRQQ	LHGQEQGHHG	QEEQGLSPEH	VEVYERTH-G	HSHYRRRHCS
PRM2_HUMAN	MVRYRVRSLs	ERSHEVYRQQ	LHGQEQGHHG	QEEQGLSPEH	VEVYERTH-G	QSHYRRRHCS
PRM2_PONPY	MVRYCVRSLs	ERSHEVYGQQ	LHGQEQGHHD	QEEQGLSPEQ	VEVYERTQ-G	HSHYRRRHCS
PRM2_HYLLA	MVRYCVRSLs	ERSHEVYGQQ	LRGQEQGHHG	QEEQGLSPED	VEVYERTH-G	HSHYRRRHCS
	70	80	90	100	110	120
PRM2_RATTU	RKRLHRIHKR	R-RSCRRRRR	HSCCHRRRRH	RGCRRSRRRR	RCRCRKCRRH	CH
PRM2_MOUSE	RKRLHRIHKR	R-RSCRRRRR	HSCCHRRRRH	RGCRRSRRRR	RCRCRKCRRH	HH
PRM2_RATFU	RKRLHRIHKR	R-RSCRRRRR	HSCCHRRRRH	RGCRRSRRRR	RCKCRKCRRH	CH
PRM2_ALOSE	RRRLYRVHRR	RRSFCRRRC-	--CRYRRRR	RGCRTRRRRT	-----CRRH	--
PRM2_CALJA	RRRLYRVHRR	RRSFCRRRRR	RSCRYRRRPR	RGCRSRRRRR	-----CRRY	--
PRM2_SEMEN	RRRLYRIVHRR	RHRSCRRRRR	RSCRHRRRRH	RGCRTRRRR	-----CRRY	--
PRM2_ERYPA	QRRLHRIHRR	RHRSCRRRRR	RSCRHRRRRH	RGCRTRRRR	-----CRRY	--
PRM2_MACNE	RRRLHRIHRR	RHRSCRRRRR	RSCRHRRRRH	RGCRTRRRR	-----CRRH	--
PRM2_MACFU	RRRLHRIHRR	RHRSCRRRRR	RSCRHRRRRH	RGCRTRRRR	-----CRRH	--
PRM2_MACMU	RRRLHRIHRR	RHRSCRRRRR	RSCRHRRRRH	RGCRTRRRR	-----CRRH	--
PRM2_GORGO	RRRLRRIHRQ	QHRSCRRRKR	RSCRHRRRRH	KGCRTRRRRT	-----CRRH	--
PRM2_PANPA	RRRLRRIHRQ	QHRSCRRRKR	RSCRHRRRRH	RGCRTRRRRT	-----CRKH	--
PRM2_PANTR	RRRLRRIHRQ	QHRSCRRRKR	RSCRHRRKHR	RGCRTRRRRT	-----CRRH	--
PRM2_HUMAN	RRRLHRIHRR	QHRSCRRRKR	RSCRHRRRRH	RGCRTRRRRT	-----CRRH	--
PRM2_PONPY	RRRLHRIHRQ	QHRSCKRRRR	HSCRHRRKHR	RGCRTRRRRT	-----CRRH	--
PRM2_HYLLA	RRRLHRIHRQ	QHRSCGRRRR	RSCRQRRRHR	RGCRTRRRR	-----CRRH	--

Supplemental Figure 3. Alignment of Eutherian P2 type sperm protamines.

	10	20	30	40	50	60
HSP1_PERGU	MASYR-NSRS	RSRSRF-RRR	RRGRSRVRGR	DARQGRSSR-	RRRRGKGR--	--AHSGKKGKGR
HSP1_ISOMA	MASYR-NSRS	RSRSRF-RRR	RGRRSRVRGR	DARQGRSSR-	RRRRGKGR--	--AHSGKKGKGR
HSP1_MONDO	MARYRRRSRS	RSRSRYGRRR	RRSRS----R	RRRSRRRRR-	---RRGRR--	---GRGYHRR
HSP1_DIDVI	MARYRRRSRS	RSRSRYGRRR	RRSRS----R	RRRSRRRRR-	---RRGRR--	---GRGYHRR
HSP1_DROGL	MVRYRRHSRS	RSRSRY-RRR	RRRR--LRNR	RRYRRSRRG	RRRRRRGS--	---RRGYSTR
HSP1_NOTTY	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSQ	RRYRRHRRS	GRRRRRGR--	---RRGY-RR
HSP1_PHACI	MARYR-HSRS	RSRSRY-QRR	RRRRSRYRSQ	RRYRRRRGS	RRRRRRGR--	---RRGY-RR
HSP1_HYPMS	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRGR	RRYRRSRR-	RRRRRRGR--	---RRGYRRR
HSP1_LAGHI	MARYR-HSRS	RSRSRY-RRQ	RRRRSRYRSR	RRYRRR-Q-	-RRSRGR--	---RRGYSTR
HSP1_DENDO	MARYR-HSRS	RXRSRY-RRR	RRXRSRYRSX	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_AEPRU	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_PSECU	MARYR-HSRS	RSRSRYRRRR	RRRRSRYRGR	RRYRRSRR-	RRRRRRGR--	CLGRRGYRRR
HSP1_TRIVU	MARYR-HSRS	RSRSRYRRRR	RRRRSRYRSR	RRYRRSRR-	-RRRRGR--	---RRGYSTR
HSP1_CAEFU	MARYR-HSRS	RSRSRYRRRR	RRRRSRYRSR	RRYRRSRR-	-RRRRGR--	---RRGYSTR
HSP1_POTLO	MARYR-HSRS	RSRXRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_LAGFA	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_BETPE	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_ONCFR	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_MACRU	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSQ	RRYRGRRR-	-RRSRGR--	---RRGYSTR
HSP1_PETCN	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_MACPA	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	-RRSRGR--	---RRGYSTR
HSP1_MACEU	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_MACAG	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	-RRSRGR--	---RRGYSTR
HSP1_DORVA	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_PETXA	MARYR-HSXS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_THYST	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_MACGI	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_DORMU	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_WALBI	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_MACRG	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	RRSRGR--	---RRGYSTR
HSP1_ONYUN	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	-RRSRGR--	---RRGYSTR
HSP1_DENGO	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	-RRSRGR--	---RRGYSTR
HSP1_SETBR	MARYR-HSRS	RSRSRY-RRR	RRRRSRYRSR	RRYRGRRR-	-RRSRGR--	---RRGYSTR
HSP1_DASHA	MARYRRRSRS	RSRSRY-RRR	RRRRSRGR-R	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SARHA	MARYRRRSRS	RSRSRY-RRR	RRRRSRGR-R	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_DASMA	MARYRRRSRS	RSRSRY-RRR	RRRRSRGR-R	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_DASSP	MARYRRHSRS	RSRSRY-RRR	RRRRSRGR-R	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_NEOLO	MARYRRHSRS	RSRSRY-RRR	RRRRSRGR-R	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_DASVI	MARYRRHSRS	RSRSRY-RRR	RRRRSRGR-R	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PHADO	MARYRRHSRS	RSRSRY-RRR	RRRRSRGR-R	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_DASAL	MARYRRHSRS	RSRSRY-RRR	RRRRSRGR-R	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_DASGE	MARYRRHSRS	RSRSRY-RRR	RRRRSRGR-R	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_DASRO	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PSEBA	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PARAP	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PSENI	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_DASBY	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_MYOME	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_MYOWA	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PSEMD	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PSEWO	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIGR	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIBI	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMILO	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_ANTFL	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_NINTI	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_NINYV	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PARRT	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMILE	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PHATA	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIPS	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_ANTBE	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_MICHA	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_ANTGO	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_ANTMI	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_ANTNA	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_ANTSW	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_MURME	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIDO	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIHI	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIMA	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIOO	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIYO	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PLAMM	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIAR	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_DASCR	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_ANTLE	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_ANTST	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_MURLO	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_MYRFA	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_NINRI	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIGA	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMIGI	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PHACL	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMI MU	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMI VI	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_THYCY	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMI AI	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMI CR	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_SMI DL	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_ANTLA	MARYRRHSRS	RSRSRY-RRR	RRRRSRHNR	RRYRRSRR-	HSRRRRGR--	---RRGYSTR
HSP1_PLAMS	MARCRHRSRS	RSRSRN-QCQ	RRRRRY-NR	RRYRRSRR-	HSRRRRGR--	---RRGCSRR
HSP1_PLAIN	MARSRRHSRS	RSRSR--NQC	QRRRRTYNR	RRYRRSRR-	HSRRRRGR--	---RRGCSRR
HSP1_PLAGI	MARCRHRSRS	RSRSRN-QCQ	RRRR-RHYNR	RRYRRSRR-	HSRRRRGR--	---RRGCSRR
HSP1_PLATE	MARCRHRSRS	RSRSRN-QCQ	RRRRSHYNR	RRYRRSRR-	HSRRRRGR--	---RRGCSRR
	70	80	90			
HSP1_PERGU	RSG-----SR	RRKRNNNTEN	K			
HSP1_ISOMA	RSG-----SR	RRKRNNENK-	-			
HSP1_MONDO	SPHRR---RR	RRRR-----	-			
HSP1_DIDVI	SPHRR---RR	RRRR-----	-			
HSP1_DROGL	RYQSR---RR	RRRRY-----	-			
HSP1_NOTTY	RYH-----S	HRRRY-----	-			
HSP1_PHACI	RYS-----RR	--RRY-----	-			
HSP1_HYPMS	RYS-----RR	RRRRYY-----	-			
HSP1_LAGHI	RYSRRRYSRR	RRRRY-----	-			
HSP1_DENDO	RYS-----RR	RRRRY-----	-			
HSP1_AEPRU	RYS-----R	RRRRY-----	-			
HSP1_PSECU	RYS-----RR	RRRRY-----	-			
HSP1_TRIVU	RYS-----RR	GRRRY-----	-			
HSP1_CAEFU	RYS-----RR	RRRRY-----	-			
HSP1_POTLO	RYS-----R	RRRRY-----	-			
HSP1_LAGFA	RYS-----RR	RRRRY-----	-			
HSP1_BETPE	RYS-----RR	RRRRY-----	-			
HSP1_ONCFR	RYS-----RR	RRRRY-----	-			
HSP1_MACRU	RYS-----R	RRRRY-----	-			
HSP1_PETCN	RYS-----RR	RRRRY-----	-			
HSP1_MACPA	RYS-----RR	RRRRY-----	-			
HSP1_MACEU	RYS-----RR	RRRRY-----	-			
HSP1_MACAG	RYS-----RR	RRRRY-----	-			
HSP1_DORVA	RYS-----RR	RRRRY-----	-			
HSP1_PETXA	RYS-----RR	RRRRY-----	-			
HSP1_THYST	RYS-----RR	RRRRY-----	-			
HSP1_MACGI	RYS-----R	RRRRY-----	-			
HSP1_DORMU	RYS-----RR	RRRRY-----	-			
HSP1_WALBI	RYS-----RR	RRRRY-----	-			
HSP1_MACRG	RYS-----RR	RRRRY-----	-			
HSP1_ONYUN	RYS-----RR	RRRRY-----	-			
HSP1_DENGO	RYS-----RR	RRRRY-----	-			
HSP1_SETBR	RYS-----RR	RRRRY-----	-			
HSP1_DASHA	RYS-----RR	GRRRY-----	-			
HSP1_SARHA	RYS-----RR	GRRRY-----	-			
HSP1_DASMA	RYS-----RR	GRRRY-----	-			
HSP1_DASSP	RYS-----RR	GRRRY-----	-			
HSP1_NEOLO	RYS-----RR	GRRRY-----	-			
HSP1_DASVI	RYS-----RR	GRRRY-----	-			
HSP1_PHADO	RYS-----RR	GRRRY-----	-			
HSP1_DASAL	RYS-----RR	GRRRY-----	-			
HSP1_DASGE	RYS-----RR	GRRRY-----	-			
HSP1_DASRO	RYS-----RR	GRRRY-----	-			
HSP1_PSEBA	RYS-----RR	GRRRY-----	-			
HSP1_PARAP	RYS-----RR	GRRRY-----	-			
HSP1_PSENI	RYS-----RR	GRRRY-----	-			
HSP1_DASBY	RYS-----RR	GRRRY-----	-			
HSP1_MYOME	RYS-----RR	GRRRY-----	-			
HSP1_MYOWA	RYS-----RR	GRRRY-----	-			
HSP1_PSEMD	RYS-----RR	GRRRY-----	-			
HSP1_PSEWO	RYS-----RR	GRRRY-----	-			
HSP1_SMIGR	RYS-----RR	GRRRY-----	-			
HSP1_SMIBI	RYS-----RR	GRRRY-----	-			
HSP1_SMILO	RYS-----RR	-RRRY-----	-			
HSP1_ANTFL	RYS-----RR	GRRRY-----	-			
HSP1_NINTI	RYS-----RR	GRRRY-----	-			
HSP1_NINYV	RYS-----RR	GRRRY-----	-			
HSP1_PARRT	RYS-----RR	GRRRY-----	-			
HSP1_SMILE	RYS-----RR	GRRRY-----	-			
HSP1_PHATA	RYS-----RR	GRRRY-----	-			
HSP1_SMIPS	RYS-----RR	GRRRY-----	-			
HSP1_ANTBE	RYS-----RR	GRRRY-----	-			
HSP1_MICHA	RYS-----RR	GRRRY-----	-			
HSP1_ANTGO	RYS-----RR	GRRRY-----	-			
HSP1_ANTMI	RYS-----RR	GRRRY-----	-			
HSP1_ANTNA	RYS-----RR	GRRRY-----	-			
HSP1_ANTSW	RYS-----RR	GRRRY-----	-			
HSP1_MURME	RYS-----RR	GRRRY-----	-			
HSP1_SMIDO	RYS-----RR	GRRRY-----	-			
HSP1_SMIHI	RYS-----RR	GRRRY-----	-			
HSP1_SMIMA	RYS-----RR	GRRRY-----	-			
HSP1_SMIOO	RYS-----RR	GRRRY-----	-			
HSP1_SMIYO	RYS-----RR	GRRRY-----	-			
HSP1_PLAMM	RYS-----RR	GRRRY-----	-			
HSP1_SMIAR	RYS-----RR	GRRRY-----	-			
HSP1_DASCR	RYS-----RR	GRRRY-----	-			
HSP1_ANTLE	RYS-----RR	GRRRY-----	-			
HSP1_ANTST	RYS-----RR	GRRRY-----	-			
HSP1_MURLO	RYS-----RR	GRRRY-----	-			
HSP1_MYRFA	RYS-----RR	GRRRY-----	-			
HSP1_NINRI	RYS-----RR	GRRRY-----	-			
HSP1_SMIGA	RYS-----RR	GRRRY-----	-			
HSP1_SMIGI	RYS-----RR	GRRRY-----	-			
HSP1_PHACL	RYS-----RR	GRRRY-----	-			
HSP1_SMI MU	RYS-----RR	GRRRY-----	-			
HSP1_SMI VI	RYS-----RR	GRRRY-----	-			
HSP1_THYCY	RYS-----RR	GRRRY-----	-			
HSP1_SMI AI	RYS-----RR	GRRRY-----	-			
HSP1_SMI CR	RYS-----RR	GRRRY-----	-			
HSP1_SMI DL	RYS-----RR	GRRRY-----	-			
HSP1_ANTLA	RYS-----RR	GRRRY-----	-			
HSP1_PLAMS	RCS-----RR	RRRRRC-----	-			
HSP1_PLAIN	RCS-----RR	RRRRRC-----	-			
HSP1_PLAGI	RCS-----RR	RRRRRC-----	-			
HSP1_PLATE	RCS-----RR	RRRRRC-----	-			

Supplemental Figure 4. Alignment of Metatherian P1 type sperm protamines.