

1 50

H_URE_2 ~GAGAACT AGATTCTTAT TCAAGCATT C TATCGAGCT. CTGCATTTCAT

M_URE_2 ~GAGAACT GGATTCTTAT TCAGGCATT TGTGGAGTT. CTGCATTTCAT

S_URE_2 GCAAAGAACA AAATTATTCT TCAAACCTTC TATCAAGCTT CTGCATTTCAC

T_URE_2 GCAAAGAACA AAATTATTCC TCAAGCTTTC TATCAAGCTT CTGCATTTCAC

Z_URE_2 GCAAAGCACA GAATTATTCT CCCTGCCTTC TATCAAGCTC CTGCATTTCAG

Consensus ~-A-A--AC- --ATT-TT-- -C---C-TTC T-T--AG-T- CTGCATTTC-

51 100

H_URE_2 GGCTGTGTCT AAAGGGCATG TCAG.CCT.T TGATTCTCTC TGAGAGGTAA

M_URE_2 GGCTGTGTCT AAAGGGCATG TCAG.CCT.T TGATTCTCTC TGAGAGGTAA

S_URE_2 GGCCAAGTCT AAAGGGCATG TCAGTCCTCC TG.C.CTCTC ACAGAGGTAA

T_URE_2 GGCCAAGTCT AAAGGGCATG TCAGTCCTCC TG.C.CTCTG AGAGAGGTAA

Z_URE_2 CAGCGGTCT GAAGGGCGCG TCAGTCCGCC TGCCTCTCTC AGAGAGGTAA

Consensus -----GTCT -AAGGGC--G TCAG-CC--- TG---CTCT- --AGAGGTAA

101 150

H_URE_2 TTATCC.TTT TCCTGTCACG GAACAACAAA TGATAGCTAA CTACAGAGGC

M_URE_2 TTATCC.TTT TCCTGTCACG GAACAACAAA TGATAGCTAA CTACAGAGGC

S_URE_2 TTATCC.TTT TCCTGTCAGA GAACAACAAA TGATTGCCGA GTA.TGGGGT

T_URE_2 TTATCC.TTT TCCTGTCAGA GACCAACAAA TGATCGCCAA CTA.T.GGG.

Z_URE_2 TTATCCCTTTT TCCTGTCACA GGGCTCCAAA TGATCTCTAA CCACTGGGGA

Consensus TTATCC-TTT TCCTGTCA-- G--C--CAA TGAT--C--A --A----GG-

151 200

H_URE_2 ACATTTGCAG TAG.TCACAT TCATCAACT. GCAG.AAAAA AAAATTCAA.

M_URE_2 ACATTTGCAG TAG.TCACAT TCATCAACT. GCAGAAAAA AAAATTCAA.

S_URE_2 GCATTTTCTG GAGCTGAAAT CTGTCAATTG GGAGAAAAAG GGG.TTTAAT

T_URE_2 GCATTTTCTG GAGCTG.AAT TTGTCAATTG GGAGAAAAAG GGGATTTAAT

Z_URE_2 GCTTTGTTAG GGGCTCAGCT TTGGCAATAG GAAGTCGAA GAGCTTTAAT

Consensus -C-TT----G --G-T----T ----CA---- G-AG---AA- ----TT-AA-

201 250

H_URE_2 TTT...A.A. TTGTGCAAC. A....CA.G. .C.T.GC.AC A.TGGGC.TT

M_URE_2 TTT...A.A. TTGTACAAC. A....CA.G. .C.T.GC.AC A.TGGGC.TT

S_URE_2 TTTCT...A. CT.T...TC. A.TGT.AT.T TTTT...CCCC AATGGTCATT

T_URE_2 TTTCTGGCAG CTGTACATCT ACTTTCATGT TTTTCCCCC ACTGGTCATT

Z_URE_2 TTTTCAGACAG CTG..CA.C. A.TGT.ACTT TCATCGCGGC A.TTAT.AAA

Consensus TTT-----A- -T-----C- A-----A--- ---T--C--C A-T-----

251 300

H_URE_2 TT..GAGCAT TTCTGT..T. G.TTC.TCC. CTGTCTCGC. TATTCCTCCC

M_URE_2 TC..GAGC.. TTCTGT..T. G.TTC.TCC. CTGCCTTGC. TAGTCCTCCC

S_URE_2 TC.T.TTCTT T.CTTTTTTT TATT..TCC. C...CCTGCA CAGAGAGTGC

T_URE_2 TCTTGTTTTT TGGGGGGGGG GGTTCCCCCA CTATCCTGCA CAGAGAGCTC

Z_URE_2 NC..CAT.AT AGCGGTCATC NCTACGAGCG C.A..C.GCG C.G.CACTTT

Consensus ----- --T-----C- C-----GC- -----

301 350

H_URE_2 T.CCAGATCT ATTTTTTAAA C...TTTTTT TCTG...GT. TATTT.T.TT

M_URE_2 T.CCAGATCT ATTTTTTAAA CTTTTTTTTT TCTG...GT. TATTT.T.TT

S_URE_2 TGGCGGAGGT .TTTTTCTGC CTGTGAAGCC TTTGAGGGTG TATTTATGAG

T_URE_2 TGCCGGGGCT GTTTGTGCGC CTGTGAAGCC TCTGAGAGTG TATTTATGTG

Z_URE_2 TGTTTGTGAC GTGGGGCCGC GCGCG.CGCG CCTGCCTGTG CA.CGGCCT.

Consensus T----G---- -T----- --T----- --TG---GT- -A-----

351 400

H_URE_2	CCC..C..T.	...T.TTTGT	CTCT..TCTT	.C.CATTT.T	TAC..TC.TC
M_URE_2	CCC..CTTT.	...T.TTTGT	CTCT..TCTT	.C.CATTT.T	TAC..TC.TC
S_URE_2	CCCTACATTA	ACATACCTAT	TTATAGTCCT	ACAC..TTTCT	TACAGTCATC
T_URE_2	CCCTACATTA	ACATACCTAT	TTATAGTCCT	ACAC..TTTCT	TACAGTCATC
Z_URE_2	CCCCGCATTA	GCATATTTAT	TTATAGACTT	ACACTTTTCT	TACAGTCATT
Consensus	CCC--C--T-	---T---T-T	-T-T---C-T	-C-C-TTT-T	TAC--TC-T-

401 450

H_URE_2	TGTACTTT.C	..TTGT....	...TA.A.AG	..TA.AT.TT	.TCC...T..
M_URE_2	TGTACTTT.C	..TTGT....	...TA.A.AG	..TA.AT.TT	.TCC...T..
S_URE_2	TTTTTTTTTCC	TGTTGTGAC.	CATTTACAG	ATTATATATT	GTCCAAGT.A
T_URE_2	TTTTTTTTT.C	TGTTGTGAC.	CATTTACAG	ATTATATATT	GTCCAAGT.A
Z_URE_2	TTTGCGCAAC	AAATTTTACA	CTCGACATTG	TCTGTGTAAT	TTCCCTTTCA
Consensus	T-T-----C	--TT-T----	-----A--G	--T---T--T	-TCC---T--

451 500

H_URE_2	.T.TGTGGC.	.TC.TCAT.T	CT..TTT.TCC	CCCATT..GA	.AG.GCTATG
M_URE_2	.T.TGTGGC.	.TC.TCGT.T	CT..TTT.TTC	CCCATT..GA	.AG.GCTATG
S_URE_2	AT.T.TCCCT	TTCCCTCATCT	GTGTTT.TTT	ACCTTTTACA	GAAAGGAGTG
T_URE_2	AT.T.TCCCT	TTCAGCATCT	GTGTTT.TTT	ACCTTTTACA	GAAAGGAGTG
Z_URE_2	GTGTCTCTCT	GTTTTCTCCT	CTCTTTTCTT	CCCTTTTACA	AAGAGCCATG
Consensus	-T-T-T--C-	-T---C---T	-T-TTT----	-CC-TT--G-	-A--G---TG

501 550

H_URE_2	AATGTA..GA	AAATTATCAC	AATTACTCAT	ATAATTGAGC	C.TCTTTGTA
M_URE_2	AATGTA..GA	AAATTATCAC	AATTACTCAT	ATAATTGAGC	C.TCTTTGTA
S_URE_2	AATGGAGGGA	AAATTATCAC	AATTACTCAT	ATAATTGAGC	CGTCTTTGTA
T_URE_2	AATGGAGGGA	AAATTATCAC	AATTACTCAT	ATAATTGAGC	CGTCTTTGTA
Z_URE_2	AATGGATGGA	AAATTATCAC	AATTACTCAC	ATAATTGAGC	CGTCTTTGTG
Consensus	AATG-A--GA	AAATTATCAC	AATTACTCA-	ATAATTGAGC	C-TCTTTGT-

551 600

H_URE_2	GCAAGTGCAA	CTCCAGTAG.	..CCTTTCTC	CATCA.TGAA	AATGGTTTCA
M_URE_2	GCAAGTACGA	CTCCAGTAG.	..CCTTTCTC	CATCA.TGAA	AATGGTTTCA
S_URE_2	GCAAGTGCA	CTTCAGTAGC	CCCCTTTTTT	CATCAGACAA	AATGGTTTCA
T_URE_2	GCAAGTGCA	CTTCAGTAGC	CCCCTTTTTT	CATCAGCCAA	AATGGTTTCA
Z_URE_2	GCAAGTGCA	CTCGAGGAG.	..CCTTTTTT	CATCAGCCAA	AATGGTTTCA
Consensus	GCAAGT-C--	CT--AG-AG-	--CCTTT-T	CATCA---AA	AATGGTTTCA

601 650

H_URE_2	TTATA.GGGT	TTTTTCATATT	CTCTGACAC.	CATCTACACA	GAGGAACAGG
M_URE_2	TTATA.GGGT	TTTTTCATATT	CCCTGACAC.	CATCTACACA	GAGGAGCAAG
S_URE_2	TTATATGGGT	TTTTTCATATT	CCCTGACACA	GGGCTCTGCT	GAGGGCCTGG
T_URE_2	TTATATGGGT	TTTTTCATATT	CCCTGACACA	GGGCTCTGCT	GAGGGCCTGG
Z_URE_2	TTATA.GGGG	TTTTTCATATT	CCCTGACACG	GGGCGCAGGG	GGGGCCGCGG
Consensus	TTATA-GGG-	TTTTTCATATT	C-CTGACAC-	----C-----	G-GG-----G

651 700

H_URE_2	CGTGCGAGATG	AGATGTGCTA	GGAACAGGCT	AGATCAGTAA	GGTCACAGTA
M_URE_2	CGTGCGAGATG	AGATGTGCTG	GGAACAGGCT	AGATCAGTAA	GGTCACAGTA
S_URE_2	CGCGTGAGATG	AGATGCCGGA	TGAACAAAGT	GAATCATTAA	GGTCACAGTA
T_URE_2	CGCGTGAGATG	AGATGCAGGA	TGAACAGAGT	GAATCATTAA	GGTCACAGTA
Z_URE_2	TGTGCGCAGG	AGTCGCTGGG	GGAGAAGGGT	GGATCATTAA	GGTCACAGTG
Consensus	-G-G---A-G	AG--G-----	-GA--A---T	--ATCA-TAA	GGTCACAGT-

701 750

H_URE_2	GGAAATAATTA	GCTCTGCTAT	GGAAAGAGCA	TCTAG.GCCT	TT.TACT...
M_URE_2	GGAAATAATTA	GCTCTGCTAT	GGAAAGAGCA	TCCAG.GCCT	TT.TACT...
S_URE_2	GGAAATAATTA	TCCCAGCTAT	GGAAAGAGCA	T.CAG..CCT	TTATTCTC..
T_URE_2	GGAAATAATTA	TCCCAGCTAT	GGAAAGAGCA	T.CAG..CCT	TTATTCTC..
Z_URE_2	GGGATAATTA	TCTTGA	GGAAAGAGCA	TCCAGCACCT	TTTTTCTCTT
Consensus	GG-AATAATTA	-C-----CTAT	GGAAAGAGCA	T--AG--CCT	TT-T-CT---

751 800

H_URE_2	.GCTA.CATA	AATGTACTGT	CCATGGCCTTT	TAGTCACAAA	AAAAACTTTAC
M_URE_2	.GCTA.CATA	AATGTACTGT	CCGTGGCCTTT	TAGCCAC.AA	AAAAACTTTAC
S_URE_2	CCCCGGCACA	AATGCAATGT	CCATGG.C.T	T.....	.AGAACTTTG
T_URE_2	CCCCAGCACA	AATGCAATGT	CCATGG.C.T	T.....	.AGAACTTTG
Z_URE_2	CCCCGCCACA	AAAGCACCGT	CCATGGCCTT	TCGGCAC..A	AAGAACTTTGG
Consensus	--C---CA-A	AA-G-A--GT	CC-TGG---T	T-----	-A-AACTT--

801 850

H_URE_2	TAACAAATGG	AGCTCCCGCC	TACTACTT.T	GA..A	.A.....A.A
M_URE_2	TAACAAATGG	AGCTCCCGCC	TACTACTT.T	GA..A	.A.....A.A
S_URE_2	TTGCAAATGG	AGTTTCCACC	TTCCACTTAT	ACAAAGACGA	GAGGGGGAGA
T_URE_2	TTACAAATGG	AGTTTCCACC	TTCCACTTAT	ACAAAGACGA	GAGGGGGAGA
Z_URE_2	AAATAAATGG	AGCTTCCACC	TACAACTTAT	TCACA.A..A	GA....GAGA
Consensus	----AAATGG	AG-T-CC-CC	T-C-ACTT-T	-----A--A	-A-----A-A

851 900

H_URE_2	..AAGATTTG	TATCAACACT	ACAATTTTCC	ATCATTAAGA	CTAATAACA.
M_URE_2	..AAGATTTG	TATCAACACT	ACAATTTTCC	ATCATTAAGA	CTAATAACA.
S_URE_2	GCAAGACTTG	TATCAACATG	ACAATTTTCC	ATCATTAAGA	CTAATGACAG
T_URE_2	GCAAGACTTG	TATCAACATG	ACAATTTTCC	ATCATTAAGA	CTAATGACAG
Z_URE_2	G..AGACTTG	TATCAACATG	ACAATTTTCC	ATTATTAGGA	CTAATGGC.G
Consensus	---AGA-TTG	TATCAACA--	ACAATTTTCC	AT-ATTA-GA	CTAAT--C--

901 950

H_URE_2	.CAGAGCCTA	GTATACATCA	AGGGGAATA.	AAAAGAAAAA	TCTCACATTTC
M_URE_2	.CAGAGCCTA	GTATACATCA	AGGGGAATA.	AAAAGAAAAA	TCTCACATTTC
S_URE_2	GCACAGACT.	GTGGGGATCA	AGGGGAGCAC	AAAAAAGAG	AGGCGCATTC
T_URE_2	GCACAGACT.	GTGGGGATCA	AGGGGAGCAC	AAAAAAGAG	AGGCGCATTC
Z_URE_2	G.GCTGCCT.	TAGGAGATCA	AGGGGAG...	AGGG	GGACGCGTTC
Consensus	-----G-CT-	-----ATCA	AGGGGA----	-----A----	---C-C-TTC

951 1000

H_URE_2	AAGTGGCGGC	TGGGTGCTGA	CCTTTGTTCC	CTTTTTTTTGT	GTACGACTTA
M_URE_2	AAGTGGTGGC	TGGGCGCTGA	CCTTTGTTCC	CCCTTTTTTGT	ATACGACTTA
S_URE_2	AGGTGTTGGC	TGAGTGCTGA	CCTCC.TT.C	CTGTCTTTGT	GTGCGACTTA
T_URE_2	AGGTGTTGGC	TGAGTGCTGA	CCTCC.TT.C	CTGTCTTTGT	TGGAGACTTA
Z_URE_2	AGGTG.TGCT	GGAGTACTGA	CCTCT.CC.C	CCGTCTTTGT	TTGGGACTTA
Consensus	A-GTG--G--	-G-G--CTGA	CCT-----C	C--T-TTTGT	----GACTTA

1001 1024

H_URE_2	ACTCTTTACA	AAAAAGAGCC	ACAC
M_URE_2	ACTCTTTACA	AAAAAGAGCC	ACAC
S_URE_2	ACTCTTTACA	AAAA.TCTAG	AG~~
T_URE_2	ACTCTTAACA	AAAACATAAA	AG~~
Z_URE_2	ACTCCGAACA	AAAACCTTAA	AG~~
Consensus	ACTC---ACA	AAAA-----	A---

