

3L:6790158..6794941	1	TTGGCGGCCC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGCATCCC	TCAATAGTCT	AAGCCAGCAG	CAACAGCAGC
NM_001300028.1		TTGGCGGCCC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGCATCCC	TCAATAGTCT	AAGCCAGCAG	CAACAGCAGC
XM_032718652.1		TTGGCGGCCC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGCATCCC	TCAATAGTCT	AAGC-----	-----C
XM_002093923.3		TTGGCGGCCC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGCATCCC	TCAATAGTCT	AAGCCAGCAG	CAACAGCAGC
XM_001971497.3		TTGGCGGCCC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGCATCCC	TCAATAGTCT	AAGCCAGCAG	CAACAGCAGC
XM_016170968.3		TTGGCGGCCC	ACTAGCAATC	AGAAAT-----	-----	-----	-----	-----	-----	-----	-----
XM_014909173.3		TTGGCGGCCC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGCATCCC	TCAATAGTCT	AAGCCAGCAA	CAGCAGCAGC
XM_001352804.4		TTGGCGGCTC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGCATCCC	TCAATAGTCT	TAGCCAACAG	CAACAACAAC
XM_026991802.1		TTGGCGGCTC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGCATCCC	TCAATAGTCT	AAGCCAACAG	CAACAACAAC
XM_002046808.4		TTGGCGGCTC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGC-----	-----CAACAGTCT	GCACCAGCAA	CAACAGCAAC
XM_002067683.4		TTAACGGCCC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	CGGATCAACT	CCTGCATCCA	ATAATAGTCT	GAGTCAACAG	CAACAGCAGC
XM_002007431.4		TTGGCGGCTC	ACTAGCAATC	AGAAATCCAG	GAGTCGAACT	CAGCTGCAGC	TGCGTCCACT	CCTGCA-----	-----AACAGTCT	GCACCAACAG	CAACAGCAAC
XM_040319882.1		CTGGCGGCCC	ACTAGCAATC	AGAGCACCAG	GAGTCCA---	-----C	GGCGTCGGCC	CAGGCGGCC	-----	-----	-----
XM_061644256.1		CTGGCGGCCC	ACTAGCAATC	AGAGCACCAG	GAGTCCA---	CGGCGTCGGC	CAGGCGGCC	CAGGCAGCCC	-----	AGGCGGCGG	CCCAGGCGGC
XM_040367106.2		CTGGCGGCCC	ACTAGCAATC	AGAGCACCAG	GAGTCCA---	-----C	GGCGTCGGCC	CAGGCGGCC	-----	-----	-----
XM_053810540.1		CTAGCGGCCC	ACTAG-----	-----	-----	-----	-----	-----	-----	-----	-----

3L:6790158..6794941	101	AG--CAG--	-----	CAACAG	-----CA	G-----	-----CAGCAGC	AACACCAGCA	ACAG-----	-----CAGCAAC	AT-----
NM_001300028.1		AG--CAG--	-----	CAACAG	-----CA	G-----	-----CAGCAGC	AACACCAGCA	ACAG-----	-----CAGCAAC	AT-----
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XM_001971497.3		AGCAACAG--	-----	CAGCAG	-----CA	G-----	-----CAGCAGC	AACACCAGCA	ACAG-----	-----CAGCAGC	AT-----CA
XM_016170968.3		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
XM_014909173.3		AGCAACAA--	-----	CAACAG	-----CA	G-----	-----CAGCAGC	AACACCAGCA	ACAG-----	-----CAGCAGC	AA-----CA
XM_001352804.4		AGCAACAGCA	GCAACAGCAG	CAGCAACAG	-----CA	G-----	-----CAGCAGC	AACAACAGCA	GCAG-----	-----CAGCAGC	AAGTGTTGCA
XM_026991802.1		AGCAACAGCA	GCAACAGCAG	CAGCAACAG	-----CA	G-----	-----CAGCAGC	AACAACAGCA	GCAGCAGCAG	CAACAGCAGC	AAGTGTTGCA
XM_002046808.4		AGCAGCAACA	CCAACAGCAA	CAACAACAGC	AACACCAACA	A-----	-----CAACAGC	AACAGCAGCA	GCAGCAGCAG	-----CAGCAAC	AACAGCAGCA
XM_002067683.4		AGCAGCAG--	-----	-----	-----	-----	-----CAGCAAC	AACAGCAGCA	ACAG-----	-----CAGCAGC	AG-----
XM_002007431.4		AACAACAGCA	GCAACACCAA	CAGCAACAGC	AACACCAACA	GCAGCAACAG	CAACAGCAGC	AACAGCAGCA	GCAGCAGCAG	CAACAACAAC	AGCAGCAGCA
XM_040319882.1		-----	-----	-----	-----CA	G-----	-----	-----	-----	-----	-----
XM_061644256.1		CCAGGCGGCG	GCC-----	-----	-----CA	GGCCGCC TTC	TTACGCCGA	TCCACCACCC	GCAC-----	GCCCAGCTCC	AC-----
XM_040367106.2		-----	-----	-----	-----CA	G-----	-----	-----	-----	-----	-----
XM_053810540.1		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

3L:6790158..6794941	201	-CAGCAGCAG
NM_001300028.1		-CAGCAGCAG
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XM_002093923.3		----CAGCAG
XM_001971497.3		GCAGCAGCAG
XM_016170968.3		-----
XM_014909173.3		CCAGCAGCAG
XM_001352804.4		ACATCAGCAG
XM_026991802.1		ACATCAGCAG
XM_002046808.4		GCAGCAGCAG
XM_002067683.4		----CAGCAA
XM_002007431.4		GCAGCAGCAG
XM_040319882.1		-----GCAG
XM_061644256.1		-CATCACCAC
XM_040367106.2		-----
XM_053810540.1		-----