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ASIAN2_Ema	GAAGGGCTTT CAATTTTTCA AGGGMATT	TGTAACAGTG ATCGGTTGAC	AACACACAGG AGGCATTTTC	ATCAAGKAAG TTTCCTTATT	CAATTCTGGA TGGAATTAAG
FOR_DS1535	GAAGGGCTTT CAATTTTTCA AGGGAATT	TGTAACAGTG ATCGGTTGAC	AACACACAGG AGGCATTTTC	ATCAAGGAAG TTTCCTTATT	CAATTCTGGA TGGAATTAAG
MAM1_A001_	GAAGGGCTTT CAATTTTTCA AGGGAATT	TGTAACAGTG ATCGGTTGAC	AACACACAGG AGGCATTTTC	ATCAAGGAAG TTTCCTTATT	CAAT-CTGGA TGGAATTAAG
MAST_A001_	GAAGGGCTTT CAATTTTTCA AGGGAATT	TGTAACAGTG ATCGTTTAC	AACACACAAG AGGCATTTTC	ATCAAGGAAG TTTCCTTATT	CAATTCTGGA TGGAATTAAG
SAV1_SE210	GAAGGGCTTT CAATTTTTCA AGGGAATT	TGTAACAGTG ATCGGTTGAC	AACACACAGG AGGCATTTTC	ATCAAGGAAG TTTCCTTATT	CAATTCTGGA TGGAATTAAG

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ASIAN2_Ema	TGGGTTGCCT ATGTCCCTGG TGA	TTAGGGAGAA TTCAC TTGAG	GTCTTGGGAC CGCTCTCTCT	AGGCCCTCC GCCTGAAATA	--TCGAGACA CTCCA ACTCT
FOR_DS1535	TGGGTTGCCT ATGTTCTGG TGA	TTAGGGAGAA TTCAC TTGAG	GTCTTGGGAC CGCTCTCTCT	AGGCCCTCC GCCTGAAATA	--TCGAGACA CTCCA ACTCT
MAM1_SP134	TGGGTTGCCT ATGTCCCTGG TGA	TTAGGGAGAA TTCAC TTGAG	GTCTTGGGAC CGCTCTCTCT	AGGCCCTCC GCCTGAAATA	--TCGAGACA CTCCA ACTCT
MAST_A003_	TGGGTTGCCT ATGTCCCTGG TAA	TTACGGAGAA TTCAC TTGAG	GTCTTGGGAC CGCTCTCTCT	AGGCCCTCT GCCTGAAATA	CCTCGAGACA CTCCA ACTCT
SAV1_SE210	TGGGTTGCCT ATGTCCCTGG TGA	TTAGGGAGAA TTCAC TTGAG	GTCTTGGGAC TGCTCTCTCT	AGGCCCTCC GCCTGAAATA	--TCGAGACA CTCCA ACTCT

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ASIAN2_Ema	AAATAAAGAC AAGATTTTCAT	TTGATGCCTT TTCATTATAA	GACCACTGAT TATTTTATTT	AACTGGAGGC TGCCTCCTTG	CAGGTCTTGG AGTTATC
FOR_DS1535	AAATAAAGAC AAGATTTTCAT	TTGATGCCTT TTCATTCTAA	GACCACTGAT TATTTTATTT	AACTGGAGGC TGCCTCCTTG	CAGGTCTTGG AGCTATC
MAM1_SP134	AAATAAAGAC AAGATTTTCAT	TTGATGCCTT TTCATTATAA	GACCACTGAT TATTTTATTT	AACTGGAGGC TGCCTCCTTG	CAGGTCTTGG AGTTATC
MAST_A007_	AAATAAAGCC AAGA-TTCAT	TTGATGCCTT T--A--AAAA	GACCACTGAT TATTTTATTT	AACTGGAGGC TGCCTCCTTG	CAGGTCTTGG AGCCACC
SAV1_SE210	AAATAAAGAC AAGATTTTCAT	TTGATGCCTT TTCATTATAA	GACCACTGAC TATTTTATTT	AACTGGAGGC TGCCTCCTTG	CAGGTCTTGG AGCTATC

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ASIAN2_Ema	GTAAAAATAT CCTTTCTTAT TG	CACAATGTGT ATTTATTAAT	ATTCCCCTGA CATTTGAGTT	TTACTACTAA TTCTGTGAAT	GATTGTATAT TGCCAGATTA
FOR_DS1535	GTAAAAATAT CCTTTCTTAT TG	CACAATGTGT ATTTATTAAT	ATTCCCCTGA CATTTGAGTT	TTACTA--A TTCTGTGAAT	GATTGTATAT TGCCAGATTA
MAM1_SP134	GTAAAAATAT CCTTTCTTAT TG	CACAATGTGT ATTTATTAAT	ATTCCCCTGA CATTTGAGTT	TTACTACTAA TTCTGTGAAT	GATTGTATAT TGCCAGATTA
MAST_A009_	GTGAAAATAT CCTTTCTTAT TG	CACAATACGT ATTTATTAAT	AGTCCCCCAA CGTTTGAGTT	TTACTACTAA TTCTGTGAAT	GATTGTACAT TGCCAGATTA
SAV1_SE210	GTAAAAATAT CCTTTCTTAT	CACAATGTGT ATTTATTAAT	ATTCCCCTGA CATTTGAGTT	TTACTACTAA TTCTGTGAAT	GATTGTATAT TGCCAGATTA

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ASIAN2_Ema	GGTTTCCATG	AGGCAGGGCT	GACTCSATGG	AAGCTAACAA	CAACAGGAAG
FOR_DS1535	CCAGCTGGCA	GGGGYGCCTG	GGCAGTGTAG	CCTGGAAAGC	CCTGT
MAM1_SP134	GGTTTCCATG	AGGCAGGGCT	GACTCCATGG	AAGCTAACAA	CAACAGGAAG
MAST_A011_	YCACGTGGCA	GGGGCGCCTG	GGCAGTGTAG	CCTGGAAAGC	CCTGT
SAV1_SE210	GGTTTCCATG	AGGCAGGGCT	GACTCGATGG	AAGCTAACAA	CAACAGGAAG
	CCAGCTGGCA	GGGGTGCCTG	GGCAGTGTAG	CCTGGAAAGC	CCTGT
	GGTTTCCATG	AGGCAGGGCT	GACTCGATGG	AAGCTAACAA	CAACAGGAAG
	CCAGCTGGCA	GGGGCGCCTG	GGCAGTGTAG	CCTGGAAAGA	CCTGT
	GGTTTCCATG	AGGCAGGGCT	GACTCCATGG	AAGCTAACAA	CAACAGGAAG
	CCAGCTGGCA	GGGGCGCCTG	GGCAGTGTAG	CCTGGAAAGC	CCTGT

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ASIAN2_Ema	CAATGACAAA	GGCTCTGCC	GTCAGAGGGA	CCCTGCAGCC	CGTGCCAGTG
FOR_DS1535	TGCACGCCCC	GGCCTACTCG	GCAAACCTGCA	CCTCAGCTGC	CGGCCAGGG
MAM1_SP134	CAATGACAAA	GGCTCTGCC	GTCAGAGGGA	CCCTGCAGCC	CGTGCCAGTG
MAST_A012_	TGCACGCCCC	GGCCTACTCG	GCAAACCTGCA	CCTCAGCTGC	CGGCCAGGG
SAV1_SE210	TAATGACAAA	GGCTCTGCC	GTCAGAGGGA	CCCTGCAGCC	CGTGCCAGTG
	TGCACGCCCC	GGCCTACTCG	GCAAACCTGCA	CCTCAGCTGC	CGGCCAGGG
	CAATGACAAA	GGCTCTGCC	GTCAGAGGGA	CCCTGCAGCC	CGTGCCAGTG
	TGCACGCCCC	GGCCTACTCG	GCAAACCTGCA	CCTCAGCTGC	CGGCCAGGG

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ASIAN2_Ema	AGTCCTCCT	CAGTGAAGAC	CACAACCATG	CCCTTGAATG	TCACTGCTTC
FOR_DS1535	CTACAACATC	AAGCGCAAGA	ATG-CCCAGT	CTTAGAACTA	TCAC
MAM1_SP134	AGTCCTCCT	CAGTGAAGAC	CACAACCRTG	TCCTTGAATG	TCACTGCTTC
MAST_A014_	CTACAACATC	AAGCGCAAGA	ATG-CCCAGT	CTTAGAACTA	TCAC
SAV1_SE210	AGTCCTCCT	CAGTGAAGAC	CACAACCATG	CCCTTGAATG	TCACTGCTTC
	CTACAACATC	AAGCGCAAGA	ATG-CCCAGT	CTTAGAACTA	TCAC
	AGTCCTCCT	CAGTGAAGAC	CACAACCRTG	TCCTTGAATG	TCACTGCTTC
	CTACAACATC	AAGCGCAAGA	ATG-CCCAGT	CTTAGAACTA	TCAC
	AGTCCTCCT	CAGTGAAGAC	CACAACCRTG	TCCTTGAATG	TCACTGCTTC
	CTACAACATC	AAGCGCAAGA	ATG-CCCAGT	CTTAGAACTA	TCAC

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ASIAN2_Ema	CAAGGAATGA	CACAGGACCC	TATGAGTGTA	GAACCTGGAA	CCAAGTGAAT
FOR_DS1535	GCCCCCCGTA	GTGACCCATT	CATCCTGAAT	GTTCTCTGTG	AGTAA
MAM1_SP134	CAAGGAATGA	CACAGGACCC	TATGAGTGTA	GAACCTGGAA	CCAAGTGAAT
MAST_A016_	GCCCCCCGTA	GTGACCCATT	CATCCTGAAT	GTTCTCTGTG	AGTAA
SAV1_SE210	CAAGGAATGA	CACAGGACCC	TATGAGTGTA	GAACCTGGAA	CCAAGTGAAT
	GCCCCCCGTA	GTGACCCATT	CATCCTGAAT	GTTCTCTGTG	AGTAA
	CAAGGAATGA	CACAGGACCC	TATGAGTGTA	GAACCTGGAA	CCAAGTGAAT
	GCCCCCCGTA	GTGACCCATT	CATCCTGAAT	GTTCTCTGTG	AGTAA

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ASIAN2_Ema	TTAGAAGTGA	GGCGCTACCC	AGGAAGGAGA	GAGCCCTCTG	TAGCCCAGGA
FOR_DS1535	GAGTTCTGGC	TTCTCAGAG	CCCCTYATCC	TCCTTCAAAC	CTCAGCTTT
MAM1_SP134	TTAGAAGTGA	GGCGCTACCC	AGGAAGGAGA	GAGCCCTCTG	TAGCCCAGGA
MAST_A017_	GAGTTCTGGC	TTCTCAGAG	CCCCTCATCC	TCCTTCAAAC	CTCAGCTTT
SAV1_SE210	TTAGAAGTGA	GGCGCTACCC	AGGAAGGAGA	GAGCCCTCTG	TAGCCCAGGA
	GAGTTCTGGC	TTCTCAGAG	CCCCTCATCC	TCCTTCAAAC	CTCAGCTTT
	TTAGAAGTGA	GGCGCTACCC	AGGAAGGAGA	GAGCCCTCTG	TAGCCCAGGA
	GAGTTCTGGC	TTCTCAGAG	CCCCTCATCC	TCCTTCAAAC	CTCAGCTTT

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ASIAN2_Ema	TGGGTGGAGG	TCCAGGAGAG	CTTTTAAAAG	GCCAAGGTTA	TAGGCTCCAT
	TAGTGCAAAG	TTCTCAACTG	CCTCAGAATA	CAGTCTGAGG	A
FOR_DS1535	TGGGTGGAGG	TCCAGGAGAG	CTTTTAAAAG	GCCAAGGTTA	TAGGCTCCAT
	TAGTGCAAAG	TTCTCAACTG	CCTCAGAATA	CAGTCTGGGG	A
MAM1_SP134	TGGGTGGAGG	TCCAGGAGAG	CTTTTAAAAG	GCCAAGGTTA	TAGGCTCCAT
	TAGTGCAAAG	TTCTCAACTG	CCTCAGAATA	CAGTCTGAGG	A
MAST_A019_	TGGGTGGAGG	CCCAGGAGAG	CTTTTAAAAG	GCCAAGGTTA	TAGGCTCCAT
	TAGTGCAAAG	TTCTCAACTG	CCTCAGAATA	CAGTCTGAGG	A
SAV1_SE210	TGGGTGGAGG	TCCAGGAGAG	CTTTTAAAAG	GCCAAGGTTA	TAGGCTCCAT
	TAGTGCAAAG	TTCTCAACTG	CCTCAGAATA	CAGTCTGAGG	A

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ASIAN2_Ema	GACTAGCATT	TCTCAAAATG	TGAGTTTTGA	CCCATTAGAG	TGTCATGAAA
	TCAACTCAGT	GAGTTGTGAC	CAAAATTTTT	AGAACAAAAT	-GGAATTTAG
	CAGAAA				
FOR_DS1535	GACTAGCATT	TCTCAAAATG	TGAGTTTTGA	CCCATTAGAG	TGTCATGAAA
	TCAACTCAGT	GAGTTGTGAC	CAAAATTTTT	AGAACAAAAT	-GGAATTTAG
	CAGAAA				
MAM1_SP134	GACTAGCMTT	TCTCAAAATG	TGAGTTTTGA	CCCATTAGAG	TGTCATGAAA
	TCAACTCAGT	GAGTTGTGAC	CAAAATTTTT	AGAACAAAAT	-GGAATTTAG
	CAGAAA				
MAST_A021_	GATTAGCATT	TTTCAAAATG	TGAGTTTTGA	CCCATTAGAG	TGTCATGAAA
	TCAACTCAGT	GAGTTGTGAC	CAAAATTTTT	AGAACAAAAA	CGGAATTTAA
	CAAAAA				
SAV1_SE210	GACTAGCATT	TCTCAAAATG	TGAGTTTTGA	CCTATTAGAG	TGTCATGAAA
	TCAACTCAGT	GAGTTGTGAC	CAAAATTTTT	AGAACAAAAT	-GGAATTTAG
	CAGAAA				

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ASIAN2_Ema	TCATTGTCTG	GATTGCTATT	TTATTACCCA	TTAAGTGGTT	AACAGCTTTG
	GTGTTTAAAA	AAGTAATGAG	TGAAGCGTAT	AACCAATCAA	AAA-TGATTG
	TGAGCACCAG	GGA			
FOR_DS1535	TCATTGTCTG	GATTGCTATT	TTATTACCCA	TTAAGTGGTT	AACAGCTTTG
	GTGTTTAAAA	AAGTAATGAG	TGAAGCGTAT	AACCAATCAA	AAA-TGATTG
	TGAGCACCAG	GGA			
MAM1_SP134	TCATTGTCTG	GATTGCTATT	TTATTACCCA	TTAAGTGGTT	AACAGCTTTG
	GTGTTTAAAA	AAGTAATGAG	TGAAGCGTAT	AACCAATCAA	AAA-TGATTG
	TGAGCACCAG	GGA			
MAST_A026_	TCATTGTCTG	GATTGCTATT	TTATTACCCA	TTAAGTGGTT	AACAGCTTTG
	GTGTTTAAAA	AAGTAATGAG	TGAAGTGTAT	AACCAATCAA	AAAATGATTG
	TGAGCACCAG	GGA			
SAV1_SE210	TCATTGTCTG	GATTRCTATT	TTATTACCCA	TTAAGTGGTT	AACAGCTTTG
	GTGTTTAAAA	AAGTAATGAG	TGAAGCRTAT	AACCAATCAA	AAA-TGATTG
	TGAGCACCAG	GGA			

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ASIAN2_Ema	TCATTTTCATT	TATCCGTAAT	CAGTGTCCGC	GGAAGCTGCA	GTCAGGAAAT
	CAAATCTGCT	GCAAAAAGACC	TCTTTAAAAT	GGTAAAAAGC	AAAGATGTCA
	CTTTAAGGA				
FOR_DS1535	TCATTTTCATT	TATCCGTAAT	CAGTGTCCGC	GGAAGCAGCA	GTCAGGAAAT
	CAAATCTGCT	GCAAAAAGACC	TCTTTAAAAT	GGTAAAAWGC	AAAGATGTCA
	CTTTAAGGA				
MAM1_SP134	TCATTTTCATT	TATCCGTAAT	CAGTGTCCGC	GGAAGCAGCA	GTCAGGAAAT
	CAAATCTGCT	GCAAAAAGACC	TCTTTAAAAT	GGTAAAAAGC	AAAGATGTCA
	CTTTAAGGA				
MAST_A033_	TCATTTTCATT	TATCCGTAAT	CAGTGTCCGC	GGAAGCAGCA	GTCAGGAAAT
	CAAATCTGCT	GCAAAAAGACC	TTTTTAAAAT	GGTAAAAAGC	AAAGATGTCA
	CTTTAAGGA				
SAV1_SE210	TCATTTTCATT	TATCCGTAAT	CAGTGTCCGC	GGAAGCAGCA	GTCAGGAAAT
	CAAATCTGCT	GCAAAAAGACC	TCTTTAAAAT	GGTAAAAAGC	AAAGATGTCA
	CTTTAAGGA				

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ASIAN2_Ema	CTCACCTCTC	CCTCCTTAAC	CACTCCTGCC	CCCACAGGCC	TCTCTAGCTA
	AGCCCTGGCA	CTCTCCCCTG	CCCAGGAAGG	CCAGCCCACT	CT
FOR_DS1535	CTCACCTCTC	CCTCCTTAAC	CGCTCCTGCC	CCCACAGGCC	TCTCTAGCTA
	AGCCCTGGCA	CTCTCCCCTG	CCCAGGAAGG	CCAGCCCACT	CT
MAM1_SP134	CTCACCTCTC	CCTCCTTAAC	CACTCCTGCC	CCCACAGGCC	TCTCTAGCTA
	AGCCCTGGCA	CTCTCCCCTG	CCCAGGAAGG	CCAGCCCACT	CT
MAST_A034_	CTCACCTCTC	CCTCCTTAAC	CGCTCCTGTC	CCCACAGGCC	TCTCTAGCTA
	AGCCCTGGTA	CTCTCCCCTG	CCCAGGAAGG	CCAGCCCACT	CT
SAV1_SE210	CTCACCTCTC	CCTCCTTAAC	CGCTCCTGCC	CCCACAGGCC	TCTCTAGCTA
	AGCCCTGGCA	CTCTCCCCTG	CCCAGGAAGG	CCAGCCCACT	CT

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ASIAN2_Ema	TGCTGTTCTG	GGTTCCTAGA	TTGTCATCTG	TGTCTGTTTC	ACATGGTTTC
	TTGGTTCCTT	GTTGTAGGGG	AACAGGGTGG	TGTGTGTGAC	TAAGCCACCA
	TTT				
FOR_DS1535	TGCTGTTCTG	GGTTCCTAGA	TTGTCATCTG	TGTCTGTTTC	ACATGGTTTC
	TTGGTTCCTT	GTTGTAGGGG	AACAGGGTGG	TGTGTGTGAC	TAAGCCACCA
	TTT				
MAM1_SP134	TGCTGTTCTG	GGTTCCTAGA	TTGTCATCTG	TGTCTGTTTC	ACATGGTTTC
	TTGGTTCCTT	GTTGTAGGGG	AACAGGGTGG	TGTGTGTGAC	TAAGCCACCA
	TTT				
MAST_A036_	TGCTGTTCTG	GGTTCCTAGA	TTGTCATCTG	TGTCTGTTTC	ACATAGTTTC
	TTGGTTCCTT	GTTGTAGGGG	AACAGGGTGG	TGTGTGTGAC	TAAGCCACCA
	TTT				
SAV1_SE210	TGCTGTTCTG	GGTTCCTAGA	TTGTCATCTG	TGTCTGTTTC	ACATGGTTTC
	TTGGTTCCTT	GTTGTAGGGG	AACAGGGTGG	TGTGTGTGAC	TAAGCCACCA
	TTT				

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ASIAN2_Ema	TCACATGAGG	ACACTCCTAT	TCTCTGCCCT	TCAAATTCAT	TCTGACCAAG
	AGAGACGCAC	ACAACGCAGC	TCAGAAATGC	TTTAAGATTG	T
FOR_DS1535	TCACATGAGG	ACACTCCTAT	TCTCTGCCCT	TCAAATTCAT	TCTGACCAAG
	AGAGACGCAC	ACAACGCAGC	TCAGAAATGC	TTTAAGATTG	T
MAM1_SP134	TCACATGAGG	ACACTCCTAT	TCTCTGCCCT	TCAAATTCAT	TCTGACCAAG
	AGAGACACAC	ACAACGCAGC	TCAGAAATGC	TTTAAGATTG	T
MAST_A038_	TTATATGAGG	ACACTCCTAT	TCTCTGCTCT	TCAAATTCAT	TCTGACCAAG
	AGAGACGCAC	ACAACGCAGC	TCAGAAATGC	TTTAAGATTG	T
SAV1_SE210	TCACATGAGG	ACACTCCTAT	TCTCTGCCCT	TCAAATTCAT	TCTGACCAAG
	AGAGACGCAC	ACAACGCAGC	TCAGAAATGC	TTTAAGATTG	T

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ASIAN2_Ema	AAAAGACCAT	GGGAACCACT	GAACCAGTAT	AACTTCTGGR	ATGAAGGGAC
	ATCAATAAAT	GCTCCTCACA	GAGCTTCACT	GAGGTCATTC	TGGTCTTT
FOR_DS1535	AAAAGACCAT	GGGAACCACT	GAACCAGTAT	AACTTCTGGA	ATGAAGGGAC
	ATCAATAAAT	GCTCCTCACA	GAGCTTCACT	GAGGTCATTC	TGGTCTTT
MAM1_SP134	AAAAGACCAT	GGGAACCACT	GAACCAGTAT	AACTTCTGGA	ATGAAGGGAC
	ATCAATAAAT	GCTCCTCACA	GAGCTTCACT	GAGGTCATTC	TGGTCTTT
MAST_A042_	AAAAGATCAT	GGGAACCACT	GAACCAGTAT	AACTTCTGGA	ATGAAGGGAC
	ATCAATAAAT	GCTCCTCACA	GAGCTTCACT	GAGGTCATTC	TGGTCTTT
SAV1_SE210	AAAAGACCAT	GGGAACCACT	GAACCAGTAT	AACTTCTGGA	ATGAAGGGAC
	ATCAATAAAT	GCTCCTCACA	GAGCTTCACT	GAGGTCATTC	TGGTCTTT

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ASIAN2_Ema	TACCAAATCT	GGCTTGGCAC	CATTTGCTTA	GTAGAAATCA	ATTCGGAATC
	AGAAGGGCCG	GTTTTGCTAA	TCTTGTACTG	TAAGCCGTAA	GATGAG
FOR_DS1535	TACCAAATCT	GGCTTGGCAC	CATTTGCTTA	GTAGAAATCA	ATTCGGAATC
	AGAAGGGCCG	GTTTTGCTAA	TCTTGTACTG	TAAGCCGTAA	GATGAG
MAM1_SP134	TACCAAATCT	GGCTTGGCAC	CATTTGCTTA	GTAGAAATCA	ATTCGGAATC
	AGAAGGGCCG	GTTTTGCTAA	TCTTGTACTG	TAAGCCGTAA	GATGAG

MAST_A044_	TACTAAATCT	GGCTTGGCAC	CATTTGCTTA	GTAGAAATCA	ATTCAGAACC
SAV1_SE210	AGAAGGGCTG	GTTTTGCTAA	TCTTGTACTG	TAAGCCGTAA	GATGAG
	TACCAAATCT	GGCTTGGCAC	CATTTGCTTA	GTAGAAATCA	ATTCGGAATC
	AGAAGGGCCG	GTTTTGCTAA	TTTTGTACTG	TAAGCCGTAA	GATGAG

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ASIAN2_Ema	AAGCTACTTG	GCTGATTGGC	TGGAAGAGAA	CCATATTTGT	GCCAGTTCCA
	AAGAAAGGTG	ATCCAACAGA	GTGAGGAAAT	TATTGAACAA	TATCATTAAAT
	AT				
FOR_DS1535	AAGCTACTTG	GCTGATTGGC	TGGAAGAGAA	CCATATTTGT	GCCAGTTCCA
	AAGAAAGGTG	ATCCAACAGA	GTGAGGAAAT	TATTGAACAA	TATCATTAAAT
	AT				
MAM1_SP134	AAGCTACTTG	GCTGATTGKC	TGGAAGAGAA	CCATATTTGT	GCCAGTTCCA
	AAGAAAGGTG	ATCCAACAGA	GTGAGGAAAT	TATTGAACAA	TATCATTAAAT
	AT				
MAST_A046_	AAGCTACTTG	GCTGATTGGC	TGGAAGAGAA	CCCTATTTGT	GCCAGTTCCA
	AAGAAAGGTG	ATCCAACAGA	GTGAGGAAAT	TATTGAACAA	TATCATTAAAT
	AT				
SAV1_SE210	AAGCTACTTG	GCTGATTGGC	TGGAAGAGAA	CCATATTTGT	GCCAGTTCCA
	AAGAAAGGTG	ATCCAACAGA	GTGAGGAAAT	TATTGAACAA	TATCATTAAAT
	AT				

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ASIAN2_Ema	ACATTCATCA	GCCAGTCTAG	TCCCCCAGTG	GACAATCCTG	CTACGCGTGC
	TAGTGACTGT	TCCAGCGGGG	GG-TTGTAGG	GGCCTACAGG	GG
FOR_DS1535	ACATTCATCA	GCCAGTCTAG	TCCCCCAGTG	GACAATCCTG	CTGCAYGTGC
	TAGTGACTGT	TCCAGSGGGG	GG-TTGTAGG	GGCCTACAGG	GG
MAM1_SP134	ACATTCATCA	GCCAGTCTAG	TCCCCCAGTG	GACAATCCTG	CTACACGTGC
	TAGTGACTGT	TCCAGCGGGG	GG-TTGTAGG	GGCCTACAGG	GG
MAST_A047_	ACATTCATCA	GCCAGTCTAG	TCCCCCAGTG	GACAATCCTG	CTGCATGTGC
	TAGTGACTGT	TCCGGCTGGG	GG-CTGTAGG	GGC-TACAGG	GG
SAV1_SE210	ACATTCATCA	GCCAGTCTAG	TCCCCCAGTG	GACAATCCTG	CTGCACGTGC
	TAGTGACTGT	TCCAGCGGGG	GGTGTAGG	GGCCTACAGG	GG

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ASIAN2_Ema	CACTTAATGT	CCCACAAAGG	AGCTGTTGGC	CTTGCCCTGG	CCCTGGCTCC
	TGTGTTTGTC	CAAACAGCAC	AGACTCTYTT	CTGTTTCTTG	TCCACA
FOR_DS1535	CACTTAATGT	CCCACAAAGG	AGCTGTTGGC	CTTGCCCTGG	CCCTGGCTCC
	TGTGTTTGTC	CAAACAGCAC	AGACTCTCTT	CTGTTTCTTG	TCCACA
MAM1_SP134	CACTTAATGT	CCCACAAAGG	AGCTGTTGGC	CTTGCCCTGG	CCCTGGCTCC
	TGTGTTTGTC	CAAACAGCAC	AGACTCTCTT	CTGTTTCTTG	TCCACA
MAST_A048_	CATTTAATGT	CCTACAAAGG	AGCTGTTGGC	TTTGCCCTGG	CTCTGGCTCC
	TGTGTTTGTC	CAAACAGCAC	AGACTCTCTT	CTGTTTCTTG	TCCACA
SAV1_SE210	CACTTAATGT	CCCACAAAGG	AGCTGTTGGC	CTTGCCCTGG	CCCTGGCTCC
	TGTGTTTGTC	CAAACAGCAC	AGACTCTCTT	CTGTTTCTTG	TCCACA

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ASIAN2_Ema	GGAAGGGCCC	CAAAGGCTG	TCATGGGGCT	TGGGGCACAG	GGCAGTGATT
	CACTCAGTGT	CCTGTCCTGG	GAAGGCTCTG	TGACAGTGCT	CTCAATG
FOR_DS1535	GGAAGGGCCC	CAAAGGCTG	TCATGGGGCT	TGGGGCACAG	GGCAGTGATT
	CACTCAGTGT	CCTGTCCTGG	GAAGGCTCTG	TGACAGTGCT	CTCAACG
MAM1_SP134	GGAAGGGCCC	CAAAGGCTG	TCATGGGGCT	TGGGGCACAG	GGCAGTGATT
	CACTCAGTGT	CCTGTCCTGG	GAAGGCTCTG	TGACRGTGCT	GTCAATG
MAST_A050_	GGAAGGGCCC	CAAAGGCTG	TCATGGGGCT	TGGGGCACAG	GGCAGTGATT
	CACTCAGTGT	CCTGTCCTGG	GAAGGCTCTG	TGACAGTGCT	TTCAATG
SAV1_SE210	GGAAGGGCCC	CAAAGGCTG	TCATGGGGCT	TGGGGCACAG	GGCAGTGATT
	CACTCAGTGT	CCTGTCCTGG	GAAGGCTCTG	TGACAGTGCT	CTCAATG

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ASIAN2_Ema	GGCTGGGCCT	TTCCAGGAGG	GCTCTCCAAG	TATTGCCTTT	CCGAGTATTC
	ACAGCCAACCT	TCCCCACCA	GTCATGAGTT	TTTCCAAGAC	T

FOR_DS1535	GGCTGGGCCT	TTCCAGGAGG	GCTCTCCAAG	TATTGCCTTT	CCGAGTATTC
	ACAGCCAAC	TCCCCACCA	GTCATGAGTT	TTTCCAAGAC	T
MAM1_SP134	GGCTGGGCCT	TTCCAGGAGG	GCTCTCCAAG	TATTGCCTTT	CCGAGTATTC
	CCAGCCAAC	TCCCCACCA	GTCATGAGTT	TTTCCAAGAC	T
MAST_A052_	GGCTGGGCCT	TTCCAGGAGG	GCTCTCCAAG	TATTGCCTTT	CCGAGTATTC
	ACAGCCAAC	TCCCCACCA	GTCATGAGTT	TTTCCAAAAC	T
SAV1_SE210	GGCTGGGCCT	TTCCAGGAGG	GCTCTCCAAG	TATTGCCTTT	CCGAGTATTC
	ACAGCCAAC	TCCCCACCA	GTCATGAGTT	TTTCCAAGAC	T

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ASIAN2_Ema	TTTATTCCAT	TCATATTCTC	CCTGGTCTCA	TCATCAAATC	ATGCGTTGGG
	GGATGTTGAA	TATTTACAGT	TGCTTTTGTA	AAGAGTTTGA	GTTGTTTTGG
	CT				
FOR_DS1535	TTTATTCCAT	TCATATTCTC	CCTGGTCTCA	TCATCAAATC	ATGCGTTGGG
	GGATGTTGAA	TATTTACAGT	TGCTTTTGTA	AAGAGTTTGA	GTTGTTTTGG
	CT				
MAM1_SP134	TTTATTCCAT	TCATATTCTC	CCTGGTCTCA	TCATCAAATC	ATGCGTTGGG
	GGATGTTGAA	TATTTACAGT	TGCTTTTGTA	AAGAGTTTGA	GTTGTTTTGG
	CT				
MAST_A054_	TTTATTCTCT	TCATATTCTC	CCTGGTCTCA	TCATCAAATC	ATGCATTGGG
	GGATGTTGAA	TATTTACAGT	TGCTTTTGTA	AAGAGTTTGA	GTTATTTTTGG
	CT				
SAV1_SE210	TTTATTCCAT	TCATATTCTC	CCTGGTCTCA	TCATCAAATC	ATGCGTTGGG
	GGATGTTGAA	TATTTACAGT	TGCTTTTGTA	AAGAGTTTGA	GTTGTTTTGG
	CT				

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ASIAN2_Ema	TAGTTTTACA	AGGAAATGAG	AAATTTGGTA	GCTGGTGGTA	TTTGAATTTT
	GTTGGAAAGG	AGGCTCTCAC	CACAAAAGGT	TGTGCCTTTG	ATGTGT
FOR_DS1535	TAGTTTTACA	AGGAAATGAG	AAATTTGGTA	GCTGGTGGTA	TTTGAATTTT
	GTTGGAAAGG	AGGCTCTCAC	CACAAAAGGT	TGTGCCTTTG	ATGTGT
MAM1_SP134	TAGTTTTACA	AGGAAATGAG	AAATTTGGTA	GCTGGTGGTA	TTTGAATTTT
	GTTGGAAAGG	AGGCTCTCAC	CACAAAAGGT	TGTGCCTTTG	ATGTGT
MAST_A056_	TAGTTTTACA	AGGAAATGAG	AAATTTGGTA	GCTGGTGGTA	TTTGAATTT-
	GTTGGAAAGG	AGGCTCTCAC	CACAAAAGGT	TGTGCCTTTG	ATGTGT
SAV1_SE210	TAGTTTTACA	AGGAAATGAG	AAATTTGGTA	GCTGGTGGTA	TTTGAATTTT
	GTTGGAAAGG	AGGCTCTCAC	CACAAAAGGT	TGTGCCTTTG	ATGTGT

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ASIAN2_Ema	AGAGTTGATT	CTTTGTACCC	CATCATAAGC	AAACAACAGG	CAGTCCATAT
	GGTGCCTTCT	GGATGGGTTT	GGAGGGGGGA	CAGCCTGGGA	AGGACTGCG
FOR_DS1535	AGAGTTGATT	CTTTGTAYCC	CATCATAAGC	AAACAACAGG	CAGTCCATAT
	GGTGCCTTCT	GGATGGGTTT	GGAGGGGGGA	CAGCCTGGGA	AGGACTGCG
MAM1_SP134	AGAGTTGATT	CTTTGTACCC	CATCATAAGC	AAACAACAGG	CAGTCCATAT
	GGTGCCTTCT	GGATGGGTTT	GGAGGGGGGA	CAGCCTGGGA	AGGACTGCG
MAST_A057_	AGAGTTGATT	CTTTGTACCC	CATCATAAGC	AAACAACAAG	CAGTCCATAT
	GGTGCCTTCT	GGATGGGTTT	AAAGGGGGGA	CAGCCTGGGA	AGGACTGCG
SAV1_SE210	AGAGTTGATT	CTTTGTACCC	CATCATAAGC	AAACAACAGG	CAGTCCATAT
	GGTGCCTTCT	SGATGGGTTT	GGAGGGGGGA	CAGCCTGGGA	AGGACTGCG

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ASIAN2_Ema	TAGTCAGGCT	TTGC-CTAAA	AGTTCAGT-A	AA-CATTT-G	ATATTGGGTT
	CTTTGGCTAG	GAAGGAAAGG	AAATGGAAGG	GAACGGAAGG	CAAGGCAAGG
	GAAGTAAAAC	AAAGAAAATG	GAAGGGA		
FOR_DS1535	TAGTCAGGCT	TTGC-CTAAA	AGTTCAGT-A	AA-CATTT-G	ATATTGGGTT
	CTTTGGCTAG	GAAGGAAAGG	AAATGGAAGG	GAAGGGAAGG	CAAGGCAAGG
	GAAGTAAAAC	AAAGAAAATG	GAAGGGA		
MAM1_SP134	TASTCAGGCT	TTGC-CTAAA	AGTTCAGT-A	AA-CATTT-G	ATATTGGGTT
	CTTTGGCTAG	GAAGGAAAGG	AAATGGAAGG	GAAGGGAAGG	CAAGGCAAGG
	GAAGTAAAAC	AAAGAAAATG	GAAGGGA		
MAST_A069_	TAGTCAGGCT	TTGCATTACA	AGTTCAGTTA	AAACATTTTG	ATATTGGGTT
	CTTTGGCTAG	GAAGGAAAGG	AAATGGAAGG	GAAGGGAAGG	CAAGGCAAGG
	GAAGTAAAAC	AAAGAAAATG	GAAGGGA		

SAV1_SE210	TAGTCAGGCT CTTTGGCTAG GAAGTGAAC	TTGC-CTAAA GAAGGAAAGG AAAGAAAATG	AGTTCAGT-A AAATGGAAGG GAAGGGA	AA-CATTT-G GAAGGGAAGG	ATATTGGGTT CAAGGCAAGG
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ASIAN2_Ema	CCTATTAGCT TGCCCCACT CTAA	AACTAAGAAA CACCCATTGT	CTATTCAAAA AGAGCCTCTA	-GGGTGGAGC TGGGATTTCT	ATTCCTATGA ACTGGCCTTC
FOR_DS1535	CCTATTAGCT TGCCCCACT CTAA	AACTAAGAAA CACCCATTGT	CTACTCAAAA AGAGCCTCTA	-GGGTGGAGC TGGGATTTCT	ATTCCTATGA ACTGGCCTTC
MAM1_SP134	CCTATTAGCT TGCCCCACT CTAA	AACTAAGAAA CACCCATTGT	CTACTCAAAA AGAGCCTCTA	-GGGTGGAGC TGGGATTTCT	ATTCCTATGA ACTGGCCTTC
MAST_A071_	TCTATTAGCT TGCCCCACT CTAA	AACTAAGAAA CACCCATTGT	CTACTCAAAA AGAGCCTCTA	AGGGTGGAGC TGGGATTTCT	ATTCCTATGA ACTGGCCTTC
SAV1_SE210	CCTATTAGCT TGCCCCACT CTAA	AACTAAGAAA CACCCATTGT	CTACTCAAAA AGAGCCTCTA	-GGGTGGAGC TGGGATTTCT	ATTCCTATGA ACTGGCCTTC

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ASIAN2_Ema	TGGGAATCAT ATGTTCTACA AGAGTGGCCA	GGTCCCAGGG TCCAACCTTG	TCAATTGGCA GTGAGTGGCA	AAACAAAATT TCTGGTGTCT	TGTAAAGAAA TAAAATCTTG
FOR_DS1535	TGGGAATCAT ATGTTCTACA AGAGTGGCCA	GGTCCCAGGG TCCAACCTTG	TCAATTGGCA GTGAGTGGCA	AAACAAAATT TCTGGTGTCT	TGTMAAGAAA TAAAATCTTG
MAM1_SP134	TGGGAATCAT ATGTTCTACA AGAGTGGCCA	GGTCCCAGGG TCCAACCTTG	TCAATTGGCA GTGAGTGGCA	AAACAAAATT TCTGGTGTCT	TGTAAAGAAA TAAAATCTTG
MAST_A075_	TGGGAATCAT ATGTTCTACA CAAGGGACCA	GGTCCCAGGG TCCAACCTTG	TCAATTTGCA GTGAGTGGCA	AAACAAAATT TCTAAGGTCT	TGTAAAGAAA TAAATGCTAG
SAV1_SE210	TGGGAATCAT ATGTTCTACA AGAGTGGCCA	GGTCCCAGGG TCCAACCTTG	TCAATTGGCA GTGAGTGGCA	AAACAAAATT TCTGGTGTCT	TGTAAAGAAA TAAAATCTTG

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ASIAN2_Ema	ATGGGAGACT CTGTGATTCT TTTTTTTTT	TGCCACATGC CTGGAAAAC TTTTCTA-CT	ACCCAAATAA GGAAGTCAGA GTTGTCT	CTGCTTCTAA GGAAAGAGAA	CGCACCATCC ATGTTGTTTT
FOR_DS1535	ATGGGAGACT CTGTGATTCT TTTTTTTTT	TGCCACATGC CTGGAAAAC TTTTTTG-CT	ACCCAAATAA GGAAGTCAGA GTTGTCT	CTGCTTCTAA GGAAAGAGAA	CGCACCATCC ATGTTKTKT
MAM1_SP134	ATGGGAGACT CTGTGATTCT TTTTTTT---	TGCCACATGC CTGGAAAAC -----GTCT	ACCCAAATAA GGAAGTCAGA GTTGTCT	CTGCTTCTAA GGAAAAGAA	CGCACCATCC ATGTTGTTTT
MAST_A076_	ATGGGAGACT CTGTGATTCT TTTTTTT---	TGCCACATGC CTGGAAAAC -----T	ACCCAAATAA GGAAGTCAGA TTTGTCT	CTGCTTTTAA GGAAAGAGAA	CGCACCATCC ATGTTTATTT
SAV1_SE210	ATGGGAGACT CTGTGATTCT TTTTTTT-----	TGCCACATGC CTGGAAAAC -----G-CT	ACCCAAATAA GGAAGTCAGA GTTGTCT	CTGCTTCTAA GGAAAGAGAA	CGCACCATCC ATGTTGTTTT

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ASIAN2_Ema	AGGGACCTTG TTTGGAAATC GACGCTT	TAATTTTTGA TTTCCGCTA	GAGGGTGGAA AAGCCAAATT	TGCTTGACTT TCTATATTC	CCAGAATCTG ATAATCTAAA
FOR_DS1535	AGGGACCTTG TTTGGAAATC GATGCTT	TAATTTTTGA TTTCCAGCTA	GAGGGTGGAA AAGCCAAATT	TGCTTGACTT TCTATATTC	CCAGAATCTG ATAATCTAAA
MAM1_SP134	AGGGACCTTG	TAATTTTTGA	GAGGGTGGAA	TGCTTGACTT	CCAGAATCTG

	TTTGGAAATC GACGCTT	TTTCCCGCTA	AAGCCAAATT	TCTATATTTT	ATAATCTAAA
MAST_A077_	AGGGACCTTG TTTGGAAATC GACGCTT	TAATTTTTGA TTTCCAGCTA	GAGGGTGGGA AAGCCAAATT	TGCTTGACTT TCTATATTTT	CCAGAATCTG ATAATCTAAA
SAV1_SE210	AGGGACCTTG TTTGGAAATC GACGCTT	TAATTTTTGA TTTCCAGCTA	GAGGGTGGAA AAGCCAAATT	TGCTTGACTT TCTATATTTT	CCAGAATCTG ATAATCTAAA

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ASIAN2_Ema	CATTTT-GTT AGCTGAGATG	GTTGTTTTT- TCTCGCCTCT	GCTTT-CTTG GCSTGAAGGT	TTGCAAGTCC ATTGTATGTG	ACTGTAGTAC TTGGC
FOR_DS1535	CATTTT-GTT AGCTGAGATG	GTTGTTTTT- TCTCGCCTCT	GCTTT-CTTG GCCTGAAGGT	TTGCAAGTCC ATTGTATGTG	ACTGTAGTAC TTGGC
MAM1_SP134	CATTTT-GTT AGCTGAGATG	GTTGTTTTT- TCTCGCCTCT	GCTTT-CTTG GCCTGAAGGT	TTGCAAGTCC ATTGTATGTG	ACTGTAGTAC TTGGC
MAST_A078_	TATTTTTGTT AGCTGAGATG	GTTGTTTTT TCTCGCCTCT	GCTTTTCTTG ACCTGAAGGT	TTGCAAGTCC ATTGTATGTG	ACTGTAGTAC TTAGC
SAV1_SE210	CATTTT-GTT AGCTGAGATG	GTTGTTTTT- TCTCGCCTCT	GCTTT-CTTG GCCTGAAGGT	TTGCAAGTCC ATTGTATGTG	ACTGTAGTAC TTGGC

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ASIAN2_Ema	GAAAGAGCCC GAGTGTGGCT GGCTAA	CTTTGTTCCA TCCATTGGGC	GAGCTCCTGG CAAAAGGTGG	GTGACAATGG CCTGGCCTTG	CAGGAGAGGG AAGCCCCGAT
FOR_DS1535	GAAAGAGCCC GAGTGTGGCT GGCTAA	CTTTGTTCCA TCCATTGGGC	GAGCTCCTGG CAAAAGGTGG	GCGACAATGG CCTGGCCTTG	CAGGAGAGGG AAGCCCCGAT
MAM1_SP134	GAAAGAGCCC GAGTGTGGCT GGCTAA	CTTTGTTCCA TCCATTGGGC	GAGCTCCTGG CAAAAGGTGG	GCGACAATGG CCTGGCCTTG	CAGGAGAGGG AAGCCCCGAT
MAST_A082_	GAAAGAGCCC GAGTGTGGCT GGCTAA	CTTTGTTCCA TCCATTGGGC	GAGCTCCTGG CAAAAGGTGG	GCGACAATGG CCTGGCCTTG	CAGGAGAGGG AAGCCCCGAT
SAV1_SE210	GAAAGAGCCC GAGTGTGGCT GGCTAA	CTTTGTTCCA TCCATTGGGC	GAGCTCCTGG CAAAAGGTGG	GCGACAATGG CCTGGCCTTG	CAGGAGAGGG AAGCCCCGAT

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ASIAN2_Ema	TGTGACTCTT CCCCACTCGG TCA	GTGTGCTTAA GGGAGCAAAC	CGCTCACAGC CACCTCGGCC	CTGCTAGGTT ACTGGACACG	AGTCGAGCCT GGATCAAGGG
FOR_DS1535	TGTGACTCTT GCCCACTCGG TCA	GTGTGCTTAA GGGAGCAAAC	CGCTCACAGC CACCTCGGCC	CTGCTAGGTT ACTGGACACG	AGTCGAGCCT GGATCAAGGG
MAM1_SP134	TGTGACTCTT CCCCACTCGG TCA	GTGTGCTTAA GGGAGCAAAC	CGCTCACAGC CAYCTCGGCC	CTGCTAGGTT ACTGGACACG	AGTCGAGCCT GGATCAAGGG
MAST_A083_	TGTGATTCTT CCCCACTCGG TCA	GTGTGCTTAA GGGAGCAAAC	CGCTCACAGC CACCTCGGCC	CTGCTAGGTA ACTGGACACG	AGTCGAGCCT GGATCAAGGG
SAV1_SE210	TGTGACTCTT GCCCACTCGG TCA	GTGTGCTTAA GGGAGCAAAC	CGCTCACAGC CACCTCGGCC	CTGCTAGGTT ACTGGACACG	AGTCGAGCCT GGATCAAGGG

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ASIAN2_Ema	GTCTGTCAGG ATCCCCTTAC G	CTTTCTTAGG CTGACCCCCT	AAGGAGAAGA TCCCAGCCTT	GCAGTCTTGT TACTGCGCTG	ACCCCACTGC TTGGCTAAGT
FOR_DS1535	GTCTGTCAGG ATCCCCTTAC G	TTTTCTTAGG CTGACCCCCT	AAGGAGAAGA TCCCAGGCTT	GCAGTCTTGT TACTGCGCTG	ATCCCCTGC TGGGCTAAGT
MAM1_SP134	GTCTGTCAGG	CTTTCTTAGG	AAGGAGAAGA	GCAGYCTTGT	ACCCCACTGC

	ATCCCCTTAC	CTGACCCCCT	TCCCAGCCTT	TACTGCGCTG	TTGGCTAAGT
MAST_A084_	G GTCTGTCAGG	CTTCCTTAGG	AAGGAGAAGA	GCAGTCTTGT	ACCCCACTGC
	ATCCCCTTAC	CTGACCCCCT	TCCCAGCCTT	TACTGTGCTG	TGGGCTAAGT
SAV1_SE210	G GTCTGTCAGG	CTTTCTTAGG	AAGGAGAAGA	GCAGTCTTGT	ACCCCACTGC
	ATCCCCTTAC	CTGACCCCCT	TCCCAGCCTT	TACTGCGCTG	TGGGCTAAGT
	G				

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ASIAN2_Ema	TCCTGCCTCT	CTAGCCCAGT	GGCCTTCCAC	CATCTGTCCA	TGGCCCTGCA
FOR_DS1535	CCTCCTCTCC	TGCCCTGCCA	CCCTGCAGCC	ACCAGGAATT	GTT
	TCCTGCCTCT	CTAGCCCAGT	GGCCTTCCAC	CATCTGTCCA	TGTCCCTGCA
MAM1_SP134	CCTCCTCTCC	TGCCCTGCCA	CCCTGCAGCC	ACCAGGAATT	GTT
	TCCTGCCTCT	CTAGCCCAGT	GGCCTTCCAC	CATCTGTCCA	TGGCCCTGCA
MAST_A085_	CCTCCTCTCC	TGCCCTGCCA	CCCTGCAGCC	ACCAGGAATT	GTT
	TTTTGCCTCT	CTAGCCCAGT	GGCTTTCCAC	CATCTGTCTA	TGGCCCTACC
SAV1_SE210	CCTCCTCTCC	TGCCCTGCCA	CCCTGCAGCC	ACCAGGAATT	GTT
	TCCTGCCTCT	CTAGCCCAGT	GGCCTTCCAC	CATCTGTCCA	TGGCCCTGCA
	CCTCCTCTCC	TGCCCTGCTA	CCCTGCAGCC	ACCAGGAATT	GTT

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ASIAN2_Ema	GAGACGTTGC	TCTAGGAGGG	TCTTGTCTGC	CTTCCTGCCC	CAAACACACA
FOR_DS1535	GTAAGGATTG	GCCCCCAGC	ACCTCCTAAA	GGAGATGGAC	CAGT
	GAGACGTTGC	TCTAGGAGGG	TCTTGTCTGC	CTTCCTGCCC	CAAACACACA
MAM1_SP134	GTAAGGATTG	SCCCCCAGC	ACCTCCTAAA	GGAGATGGAC	CAGT
	GAGACATTGC	TCTAGGAGGG	TCTTGTCTAC	CTTCCTGCCC	CAAACACACA
MAST_A086_	ATAAGGATTG	GCCCCCAGC	ACCTCCTAAA	GGAGATGGAC	CAGT
	GAGATGTTGC	TCTAGGAGGG	TCTTGTCTGC	CTTCCTGCCC	CAAACACACA
SAV1_SE210	GTAAGGATTG	GCCCCCAGC	ACCTTCTAAA	GGAGATGGAC	CAGT
	GAGACGTTGC	TCTAGGAGGG	TCTTGTCTGC	CTTCCTGCCC	CAAACACACA
	GTAAGGATTG	GCCCCCAGC	ACCTCCTAAA	GGAGATGGAC	CAGT

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ASIAN2_Ema	AAAACCTCAGG	GCCCCTTGTT	TAAAATCATG	AATTTCAAGA	AGGAGATGTA
FOR_DS1535	TTAAACCAAG	CGTGGGGTCC	CTCTAAGCGT	GAAACCCCGT	CCAACTGC
	AAAACCTCAGG	GCCCCTTGTT	TAAAATCATG	AATTTCAAGA	AGGAGATGTA
MAM1_SP134	TTAAACCAAG	CGTGGGGTCC	CTCTAAGCGT	GAAACCCCGT	CCAACTGC
	AAAACCTCAGG	GCCCCTTGTT	TAAAATCATG	AATTTCAAGA	AGGAGATGTA
MAST_A087_	TTAAACCAAG	CGTGGGGTCC	CTCTAAGCGT	GAAACCCCGT	CCAACTGC
	AAAACCTCAGG	GCCCCTTGTT	TAAAATCACG	AATTTCAAGA	AGGAGATGTA
SAV1_SE210	TGAAACCAAG	CGTGGGATCC	CCCTAAGCGT	GAAACCCTGT	CCAACTGC
	AAAACCTCAGG	GCCCCTTGTT	TAAAATCATG	AATTTCAAGA	AGGAGATGTA
	TTAAACCAAG	CGTGGGGTCC	CTCTAAGCGT	GAAACCCCGT	CCAACTGC

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ASIAN2_Ema	AGAAAATCTT	AAATCTTTGT	GCTTGAAGGG	GCTTTGAGAG	ATACCTATGT
FOR_DS1535	CCGTTTCCTGG	TCTTAGTGTG	AGTAAGAGCT	GATGGGACAA	CATGGCCAGA
	GCG				
	AGAAAATCTT	AAATCTTTGT	GCTTGAAGGG	GCTTTGAGAG	ATACCTATGT
MAM1_SP134	CCGTTTCCTGG	TCTTAGTGTG	AGTAAGAGCT	GATGGGACAA	CATGGCCAGA
	GCG				
	AGAAAATCTT	AAATCTTTGT	GCTTGAAGGG	GCTTTGAGAG	ATACCTATGT
MAST_A088_	CCGTTTCCTGG	TCTTAGTGTG	AGTAAGAGCT	GATGGGACAA	CATGGCCAGA
	GCG				
SAV1_SE210	AGAAAATCTT	AAATCTTTGT	GCTTGAAGGG	GCTTTGAGAG	ATACCTATGT
	CCGTTTCCTGG	TCTTAGTGTG	AGTAAGAGCT	GATGGGACAA	CATGGCCAGA
	GCG				

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ASIAN2_Ema	TGACATAGTT	TCCAGCATCA	TAGTAATACA	CAAGGCA-CC	AGAGAATGAC
	AGACAGGTGG	TGGCATTTC	AGTAAGATGT	GTCCATTTC-	ACAA
FOR_DS1535	TGACATAGTT	TCCAGCATCA	TAGTAATACA	CAAGGCA-CC	AAAGAATGAC
	AGACAGGTGG	TGACATTTC	AGTAAGATGT	GTCCATTTC-	ACAA
MAM1_SP134	TGACATAGTT	TCCAGCATCA	TAGTAATACA	CAAGGCA-CC	ACAGAATGAC
	AGACAGGTGG	TGGCATTTC	AGTAAGATGT	GTCCATTTC-	ACAA
MAST_A091_	TGACATAGTT	TCCAGCATCA	TAGTAATACA	CAAGGCACCC	ACAGAATGAC
	AGACAGGTGG	TGGCATTTC	AGTAAGGTGT	GTCCATTTC	ACAA
SAV1_SE210	TGACATAGTT	TCCAGCATCA	TAGTAATACA	CAAGGCA-CC	ACAGAATGAC
	AGACAGGTGG	TGGCATTTC	AGTAAGATGT	GTCCACTTC-	ACAA

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ASIAN2_Ema	ATTTAAGCTT	TGGAATTCTG	CTAATCCAAG	GCGACAGGAG	ACCTGCCCTT
	CAGTCCAACA	TGGTGTGTGT	GTGTTTGAGT	ATATGTGTGG	ATATCAAC
FOR_DS1535	ATTTAAGCTT	TGGAATTCTG	CTAATCCAAG	GCGACAKGAG	ACCTGCCCTT
	CAGTCCAACA	TGGTGTGTGT	GTGTTTGAGT	ATATGTGTGG	RTATCAAC
MAM1_SP134	ATTTAAGCTT	TGGAATTCTG	CTAATCCAAG	GCGACAGGAG	ACCTGCCCTT
	CAGTCCAACA	TGGTGTGTGT	GTGTTTGAGT	ATATGTGTGG	ATATCAAC
MAST_A094_	ATTTAAGCTT	TGGAATTCTG	CTAATCCAAG	GCGACAGGAG	ACCTGCCCTT
	CAGTCCAACA	TGGTGTGTGT	GTGTTTGAGT	ATATGTGTGG	GTATCAAC
SAV1_SE210	ATTTAAGCTT	TGGAATTCTG	CTAATCCAAG	GCGACAGGAG	ACCTGCCCTT
	CAGTCCAACA	TGGTGTGTGT	GTGTTTGAGT	ATATGTGTGG	ATATCAAC

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ASIAN2_Ema	ACAACAACAT	GGACAAAATA	CTGAACAACA	CGGGAAGCAT	CAAAAAGAAGA
	TGGAAAGAAT	ACACAGAACC	ATTGTACCAA	AAAGAACTGG	TCAATGTACA
FOR_DS1535	ACAACAACAT	GGACAAAATM	CTGAACAACA	CGGGAAGCAT	CAAAAAGAAGA
	TGGAAAGAAT	ACACAGAATC	ATTGTACCAA	AAAGAACTGG	TCAATGTACA
MAM1_SP134	ACAACAACAT	GGACAAAATA	CTGAACAACA	CGGGAAGCAT	CAAAAAGAAGA
	TGGAAAGAAT	ACACAGAATC	ATTGTACCAA	AAAGAACTGG	TCAATGTACA
MAST_A097_	ATAATAATAT	GGACAAAATA	CTGAACAACA	CGGGAAGCAT	CAAAAAGAAGA
	TGGAAAGAAT	ACACAGAATC	ATTGTACCAA	AAAGAATTGG	TCAATGTACA
SAV1_SE210	ACAACAACAT	GGACAAAATA	CTGAACAACA	CGGGAAGCAT	CAAAAAGAAGA
	TGGAAAGAAT	ACACAGAATC	ATTGTACCAA	AAAGAACTGG	TCAATGTACA

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ASIAN2_Ema	TGAGCATCTT	CCTTAGGCCA	CATTTTCATGA	GAAGGCTGTG	GTCTGGAGCC
	CTGGGTTGGG	GGAAGTCAGT	TGTTTCATCT	TCCAATTACC	CACAGTGAGC
FOR_DS1535	TGAGCATCTT	CCTTAGGCCA	CATTTTCATGA	GAAGGCTGTG	GTCTGGAGCC
	CTGGGTTGGG	GGAAGTCAGT	TGTTTCATCT	TCCAATTACC	CACAGTGAGC
MAM1_SP134	TGAGCATCTT	CCTTAGGCCA	CATTTTCATGA	GAAGGCTGTG	GTCTGGAGCC
	CTAGGTTGGG	GGAAGTCAGT	YGTTTCATCT	TCCAATTACC	CACAGTGAGC
MAST_A099_	TGAGCATCTT	CCTTAGGCCA	CATTTTCATGA	GAAGGCTGTG	GTCTGGAGCC
	CTGGGTTGGG	GGAAGTCAGT	CATTTTCATCT	TCCAATTACC	CACAATGAAC
SAV1_SE210	TGAGCATCTT	CCTYAGGCCA	CATTTTCATGA	GAAGGCTGTG	GTCTGGAGCC
	CTGGGTTGGG	GGAAGTCAGT	TGTTTCATCT	TCCAATTACC	CACAGTGAGC

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ASIAN2_Ema	AGAGCAAATG	GGCCAGAGGA	CGCCCCATCA	TCCACTGCCA	TCCAGTCGAT
	CCTGCCAGAG	TCGCTGAGAA	GACAAACCTC	CATCCTATTC	CGTTTG
FOR_DS1535	AGAGCAAATG	GGCCAGAGGA	CGCCCCATCA	TCCACTGCCA	TCCAGTCGAT
	CCTGCCAGAG	TCGCTGAGAA	GACAAACTTC	CATCCTATTC	CGTTTG
MAM1_SP134	AGAGCAAATG	GGCCAGAGGA	CGCCCCATCA	TCCACTGCCA	TCCAGTCGAT
	CCTGCCAGAG	TCGCTGAGAA	GACAAACTTC	CATCCTATTC	CGTTTG
MAST_A101_	AGAGCAAATG	GGCCAGAGAA	TGCCCCATTA	TCCATTGCCA	TCCAGTCGAT
	CCTGCCAGAG	TCGCTGAGAA	GACAAACTTC	CATCCTATTC	CGTTTG

SAV1_SE210 AGAGCAAATG GGCCAGAGGA CGCCCCATCA TCCACTGCCA TCCAGTCGAT
CCTGCCAGAG TCGCTGAGAA GACAAACATC CATCCTATTC CGTTTG

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ASIAN2_Ema ACATTCTAGA TCCTCCTGCC CAGCATTCTG GCCTCTGCTA GACACACCCC
CAGCAGCATT CCTGGCATTG TAGGCTCCAA ACAGGTTCTA GAGCTT
FOR_DS1535 ACATTCTAGA TCCTCCTGCC CAGCATTCTG GCCTCTGCTA GACACACCCC
CAGCAGCATT CCTGGCATTG TAGGCTCCAA ACAGGTTCTA GAGCTT
MAM1_SP134 ACATTCTAGA TCCTCCTGCC CAGCATTCTG GCCTCTGCTA GACACACCCC
CAGCAGCATT CCTGGCATTG TAGGCTCCAA ACAGGTTCTA GAGCTT
MAST_A105_ ACATTCTAGA CCCTCCTGCC CCGCATTCTG GCCTCTGCTA GACACACCCC
CAGCAGCATT CCTGGCATTG TAGGCTCCAA ACAGGTTCTA GAGCTT
SAV1_SE210 ACATTCTAGA TCCTCCTGCC CAGCATTCTG GCCTCTGCTA GACACACCCC
CAGCAGCATT CCTGGCATTG TAGCCTCCAA ACAGGTTCTA GAGCTT

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ASIAN2_Ema CCTATCATTC ACCTTCACTA AGAATATTGC TTGACTTGCA GAGGTCATGA
AGAACTGGAA TCTTGCAGGC TTTAACGAGG AAAAAGAAAA TTTAAAAGTC
TCTATA
FOR_DS1535 CCTATCATTC ACCTTCACTA AGAATATTGC TTGACTTGCA GAGGTCATGA
AGAACTGGAA TCTTGCAGGC TTTAACGAGG AAAAAGAAAA TTTAAAAGTC
TCTATA
MAM1_SP134 CCTATCATTC ACCTTCACTA AGAATATTGC TTGACTTGCA GAGGTCATGA
AGAACTGGAA TCTTGCAGGC TTTAACGAGG AAAAAGAAAA TTTAAAAGTC
TCTATA
MAST_A107_ CCTATCATTC ACCTTCACTA AGAATATTGC TTGACTTGCA GAGGTCATGA
AGAACTGGAA TCTTGCAGGC TTTAACGAAG AAAAAGAAAA TTTAAAAGTC
TCTGTA
SAV1_SE210 CCTATCATTC ACCTTCACTA AGAATATTGC TTGACTTGCA GAGGTCATGA
AGAACTGGAA TCTTGCAGGC TTTAACGAGG AAAAAGAAAA TTTAAAAGTC
TCTATA

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ASIAN2_Ema TAGTGGAAGC CCCTGGTGGC GGCGAGGCTG CGAAGCACCG GGCCCTGGAT
GGCGGAGGCT CCTCCTCCTT CGTCTGCCGC CGAGGAGACG CCGA
FOR_DS1535 TAGTGGAAGC CCCTGGTGGC GGCGAGGCTG CGAAGCACCG GGCCCTGGAT
GGCGGAGGCT CCTCCTCCTT CGTCTGCCGC CGAGGAGACG CCGA
MAM1_SP134 TAGTGGAAGC CCCTGGTGGC GGCGAGGCTG CGAAGCACCG GGCCCTGGAT
GGCGGAGGCT CCTCCTCCTT CGTCTGCCGC CGAGGAGACG CCGA
MAST_A109_ TGGTGGAAGC CTTTGGTGGC GGCGAGGTTG CGAAGCACCG GGCCCTGGAT
GGCGGAGGCT CCTCCTCCTT CGTCTGCTGC CGAGGAGAGG CCGC
SAV1_SE210 TAGTGGAAGC CCCTGGTGGC GGCGAGGCTG CGAAGCACCG GGCCCTGGAT
GGCGGAGGCT CCTCCTCCTT CGTCTGCCGC CGAGGAGACG CCGA

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ASIAN2_Ema CTGGTGGATT TGAAGTCTG ACCTTTT-GA TTAGCAGCCA AGCTCTTAAC
CACTGTGCCA CCAACTTCCA GATGCCTGCT ACCCAGGCAT AAAA-GATTT
TA
FOR_DS1535 CTGGTGGATT TGAAGTCTG ACCTTTT-GA TTAGCAGCCA AGCTCTTAAC
CACTGTGCCA CCAACTTCCA GATGCCTGCT ACCCAGGCAT AAAA-GATTT
TA
MAM1_SP134 CTGGTGGATT TGAAGTCTG ACCTTTT-GA TTAGCAGCCA AGCTCTTAAC
CACTGTGCCA CCAACTTCCA GATGCCTGCT ACCCAGGCAT AAAA-GATTT
TA
MAST_A112_ CTGGTGGATT TGAAGTCTG ACCTTTTTGA TTAGCAGCCA AGCTCTTAAC
CACTGTGCCA CCAACTTCCA GATGCCTGCT ACCCAGGCAT AAAAAGATTT
TA
SAV1_SE210 CTGGTGGATT TGAAGTCTG ACCTTTT-GA TTAGCAGCCA AGCTCTTAAC
CACTGTGCCA CCAACTTCCA GATGCCTGCT ACCCAGGCAT AAAA-GATTT
TA

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ASIAN2_Ema	TCCTGATGGG ATCAGCGTTG CT	GTGGGGCCGG CTCATCTCGA	CAGAGCAGAG GTGGCCAGTG	GGGATTTTTT AACAAGAGAA	AGCCTGAATT GTCAAATCTC
FOR_DS1535	TCCTGATGGG ATCAGCGTTG CT	GTGGGGCCGG CTCATCTCGA	CAGAGCAGAG GTGGTCAGTG	GGGATTTTTT AACAAGAGAA	AGCCTGAATT GTCAAATCTC
MAM1_SP134	TCCTGATGGG ATCAGCGTTG CT	GTGGGGCCGG CTCATCTCGA	CAGAGCAGAG GTGGCCAGTG	GGGATTTTTT AACAAGAGAA	AGCCTGAATT GTCAAATCTC
MAST_A113_	TTCTGATGGG ATCAGCGTTG CT	GTGGGGCCGG CTCATTTCTGA	CAGAGCAGAG GTGGCCAGTG	GGGATTTTTT AACAAGAGAA	AGCCTGAATT GTCAAATCTC
SAV1_SE210	TCCTGATGGG ATCAGCGTTG CT	GTGGGGCCGG CTCATCTCGA	CAGAGCAGAG GTGGTCAGTG	GGGATTTTTT AACAAGAGAA	AGCCTGAATT GTCAAATCTC

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ASIAN2_Ema	TTCTATCTTC AAATGAGTCT	CCAGCCACTC CTGAGAAGCT	TGAGGAACTG GGGTGTGTGG	GTATGGGTCA CTGGGCCCAA	GTAGGTGGGA GAGGTAAT
FOR_DS1535	TTCTATCTTC AAATGAGTCT	CCAGCCACTC CTGAGAAGCT	TGAGGAACTG GGGTGTGTGG	GTATGGGTCA CTGGGCCCAA	GTAGGTGGGA GAGGTAAT
MAM1_SP134	TTCTATCTTC AAATGAGTCT	CCAGCCACTC CTGAGAAGCT	TGAGGAACTG GGGTGTGTGG	GTATGGGTCA CTGGGCCCAA	GTAGGTGGGA GAGGTAAT
MAST_A117_	TTCTATCTTC AAATGAGTCT	CCAGCCACTC CTGAGAAGCT	TGAGGAACTG GGGTGTGTGG	GTATGGGTCA CTGGGCCCAA	GTAGGTGGGA GAAGTAAT
SAV1_SE210	TTCTATCTTC AAATGAGTCT	CCAGCCACTC CTGAGAAGCT	TGAGGAACTG GGGTGTGTGG	GTATGGGTCA CTGGGCCCAA	GTAGGTGGGA GAGGTAAT

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ASIAN2_Ema	AACTGTGCTC AGCGGGCCTT TTCAG	CATAAGGCTT TCTTCTGAGG	TCAATGGCTG TGCCTCTGGG	TGATCTTCAG TGGACTCGAA	GAGGTAAGTC CTGCCAACCT
FOR_DS1535	AACTGTGCTC AGCGGGCCTT TTCAG	CATAAGGCTT TCTTCTGAGG	TCAATGGCTG TGCCTCTGGG	TGATCTTCAG TGGAYTCGAA	GAAGT----C CTGCCAACCT
MAM1_SP134	AACTGTGCTC AGCGGGCCTT TTCAG	CATAAGGCTT TCTTCTGAGG	TCAATGGCTG TGCCTCTGGG	TGATCTTCAG TGGACTCGAA	GAAGTAAGTC CTGCCAACCT
MAST_A122_	AACTGTGCTC ACGGGGCCTT TTCAG	CATAAGGCTT TCTTCTGAGG	TCAATGGCTG TGCCTCTGGG	TGATCTTCAG TGGACTCGAA	GAAGTAAGTC CTGCCAACCT
SAV1_SE210	AACTGTGCTC AGCGGGCCTT TTCAG	CATAAGGCTT TCTTCTGAGG	TCAATGGCTG TGCCTCTGGG	TGATCTTCAG TGGACTCGAA	GAAGTAAGTC CTGCCAACCT

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ASIAN2_Ema	GGTAAATAAG TGCAGCAAAG CA	AACTTTAACT GCCTAATACA	CTTGAAGCCG TAATTTAGTC	GAAGGATCTG ATGAAAGGCC	GGGAATCGAA AAAA-TAGAT
FOR_DS1535	GGTAAATAAG TGCAGCAAAG CA	AACTTTAACT GCCTAATACA	CTTGAAGCCA TAATTTAGTC	GAAGGATCTG ATGAAAGGCC	GGGAATCGAA AAAA-TAGAT
MAM1_SP134	GGTAAATAAG TGCAGCAAAG CA	AACTTTAACT GCCTAATACA	CTTGAAGCCA TAATTTAGTC	GAAGGATCTG ATGAAAGGCC	GGGAATCGAA AAAA-TAGAT
MAST_A123_	GGTAAATAAG TGCAGCAAAG CA	AACTTTAACT GCCTAATACA	CTTGAAGCCA TAATTTAGTC	GAAGGATCTG ATGAAAGGCC	GGGAATCGAA AAAAATAGAT
SAV1_SE210	GGTAAATAAG TGCAGCAAAG CA	AACTTTAACT GCCTAATACA	CTTGAAGCCA TAATTTAGTC	GAAGGATCTG ATGAAAGGCC	GGGAATCGAA AAAA-TAGAT

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ASIAN2_Ema	AAAGGCCTGG	CAATTT--GC	TTCTGAAAAA	TTATCCATCG	AAAACCCAAT
	GGGCACAGCT	TTACTCTGAC	ACACATGGGG	TCGCCATGAG	TCG
FOR_DS1535	AAAGGCCTGG	CAATTT--AC	TTCTGAAAAA	TTATCCATCG	AAAACCCAAT
	GAGCACAGCT	TTACTCTGAC	ACACATGGGG	TCGCCATGAG	TCG
MAM1_SP134	AAAGGCCTGG	CAATTT--AC	TTCTGAAAAA	TTATCCATCG	AAAACCCAAT
	GAGCACAGCT	TTACTCTGAC	ACACATGGGG	TCGCCATGAG	TCG
MAST_A128_	AAAGGCCTGG	CGATTTGTA-	TTC--AAAAA	TTATCCATCG	AAAACCCAAA
	GAGCACAGCT	TTACTCTGAC	ACACATGGGG	TCGCCATGAG	TCG
SAV1_SE210	AAAGGCCTGG	CAATTT--AC	TTCTGAAAAA	TTATCCATCG	AAAACCCAAT
	GAGCACAGCT	TTACTCTGAC	ACACATGGGG	TCGCCATGAG	TCG

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ASIAN2_Ema	TCCTGGAAGC	ACACAGACCT	GTGCCAACAG	AACCTCTCCT	GGCATGCTGG
	AATTGGCCCT	GTTGTCATCC	CCACATTTTT	CT-CTGGAAC	AAGGAGATAA
	A				
FOR_DS1535	TCCTGGAAGC	ACACAGACCT	GTGCCAACAG	AACCTCTCCT	GGCATGCTGG
	AATTGGCCCT	GTTGTCATCC	CCACATTTTT	CT-CTGGAAC	AAGGAGATAA
	A				
MAM1_SP134	TCCTGGAAGC	ACACAGACCT	GTGCCAACAG	AACCTCTCCT	GGCATGCTGG
	AATTGGCCCT	GTTGTCATCC	CCACATTTTT	CT-CTGGAAC	AAGGAGATAA
	A				
MAST_A140_	TCCTGGAAGC	ACATAGACCT	GTGCCAACAG	AACCTCTCCT	GGCATGCTGG
	AATTGGCCCT	GTTGTCATCC	CTACATTTTT	CTTCTGGAAC	AAGGAGATAA
	A				
SAV1_SE210	TCCTGGAAGC	ACACAGACCT	GTGCCAACAG	AACCTCTCCT	GGCATGCTGG
	AATTGGCCCT	GTTGTCATCC	CCACATTTTT	CT-CTGGAAC	AAGGAGATAA
	A				

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ASIAN2_Ema	ACCCCTGAGA	TTCAGGCCAA	GCCCTACTTC	TCTGCAGAGG	TGATGGAGCC
	TGGGAGCTGG	GCCAAGTAAA	GCCTTTT-CC	AGCCTTTCAA	AGACTTTTCA
	T				
FOR_DS1535	ACCCCTGAGA	TTCAGGCCAA	GCCCTACTTC	TCTGCAGAGG	TGATGGAGCC
	TGGGAGCTGG	GCCAAGTAAA	GCCTTTT-CC	AGCCTTTCAA	AGACTKTTCA
	T				
MAM1_SP134	ACCCCTGCTA	TTCAGGCCAA	GCCCTACTTC	TCTGCAGAGG	TGATGGAGCC
	TGGGAGCTGG	GCCAAGTAAA	GCCTTTT-CC	AGCCTTTCAA	AGACTTTTCA
	T				
MAST_A141_	ACTCTTGAGA	TTCAGGCCAA	GCCCTACTTC	TCTGCAGAGG	TGATGGAGCC
	TGGGAGCTGG	GCCAAGTAAA	GCCTTTTCC	AGCCTTTCAA	AGACTTTTCA
	T				
SAV1_SE210	ACCCCTGAGA	TTCAGGCCAA	GCCCTACTTC	TCTGCAGAGG	TGATGGAGCC
	TGGGAGCTGG	GCCAAGTAAA	GCCTTTT-CC	AGCCTTTCAA	AGACTGTTCA
	T				

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ASIAN2_Ema	TTTAGTGATG	ATAGTCCAGG	TGGAGGCACA	CACCAAGGGC	AAAGAAACAT
	GGAGAGCAGC	GTTCTCAACC	CCGACGCATG	TTAGGATCAC	CTGGAAAATG
	GC				
FOR_DS1535	TTTAGTGATG	ATAGTCCAGG	TGGAGGCACA	CACCAAGGGC	AAAGAAACAT
	GGAGAGCAGC	RTTCTCAACC	CCGACGCATG	TTAGGATCAC	CTGGAAAATG
	GC				
MAM1_SP134	TTTAGTGATG	ATAGTCCAGG	TGGAGGCACA	CACCAAGGGC	AAAGAAACAT
	GGAGAGCAGC	GTTCTCAACC	CCGACGCATG	TTAGGATCAC	CTGGAAAATG
	GC				
MAST_A144_	TTTAGTGATG	ATAGTCCAGG	TGGAGGCACA	CACCAAGGGC	AAAGAAACAT
	GGAGAGCAGC	GTTCTCAACC	CCGACGCATG	TTAGGATCAC	CTGGAAAATA
	AC				
SAV1_SE210	TTTAGTGATG	ATAGTCCAGG	TGGAGGCACA	CACCAAGGGC	AAAGAAACAT
	GGAGAGCAGC	GTTCTCAACC	CCGACGCATG	TTAGGATCAC	CTGGAAAATG
	GC				

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ASIAN2_Ema	TACGTTGAAC GGCCCTCTCT G	ACAGAGCAAC TCCCCTCTAG	TCCTTCTGTC GAATTTTACA	TGCCTCAGAC GGTTACAGCT	TCCATCCTCA TCTTCATGGG
FOR_DS1535	TACGTTGAAC GGCCCTCTCT G	ACAGAGCAAC TCCCCTCTAG	TCCTTCTGTC GAATTTTCA	TGCCTCAGAC GGTTACAGCT	TCCATCCTCA TCTTCATGGG
MAM1_SP134	TACGTTGAAC GGCCCTCTCT G	ACAGAGCAAC TCCCCTCTAG	TCCTTCTGTC GAATTTTACA	TGCCTCAGAC GGTTACAGCT	TCCATCCTCA TCTTCATGGG
MAST_A145_	TATTTTGAAC GGCCCTCTCT A	ACAGAGCAAC TCCCCTCTAG	TCCTTCTGTC GAATTTTACA	TGCCTTAGAC GGTTACAGCT	TCCATCCTCA TCTTCGTGGG
SAV1_SE210	TACGTTGAAC GGCCCTCTCT G	ACAGAGCAAC TCCCCTCTAG	TCCTTCTGTC GAATTTTACA	TGCCTCAGAC GGTTACAGCT	TCCATCCTCA TCTTCATGGG

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ASIAN2_Ema	CAAAGTTCAA TTCCTGGTCC	CGCTGCAGCC CCACTGTGTA	CCTTCTGCTG CTCGTTCATT	CTAA-GAAAC TCCTGAAAGT	AGACTGTTAC TG
FOR_DS1535	CAAAGTTCAA TTCCTGGTCC	CGCTGCAGCC CCACTGTGTA	CCTTCTGCTG CTCGTTCATT	CTAA-GAAAC TCCTGAAAGT	AGACTGTTAC TG
MAM1_SP134	CAAAGTTCAA TTCCTGGTCC	CGCTGCAGCC CCACTGTGTA	CCTTCTGCTG CTCGTTCATT	CTAA-GAAAC TCCTGAAAGT	AGACTGTTAC TG
MAST_A146_	AAAAGTTCAA TTCCTGGTCC	CGCTGCAGCC CCACTATGTA	CCTTCTGCTG CTCGTTCATT	CTAAAGAAAC TCCTGAAAGT	AGACTGTTAC TG
SAV1_SE210	CAAAGTTCAA TTCCTGGTCT	CGCTGCAGCC CCACTGTGTA	CCTTCTGCTG CTCGTTCATT	CTAA-GAAAC TCCTGAAAGT	AGACTGTTAC TG

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ASIAN2_Ema	TACATTAGTC CAGGC-ATGG CCAG	CCTAACTAGA ACTCCTCTGC	GAGTCAGCCT AGCTCTGGAA	GTCCCTTGAA GTCCAGGATG	GCTCTGAAGC GCGTTTCCCT
FOR_DS1535	TACATTAGTC CAGGC-ATGG CCAG	CCTAACTAGA ACTCCTCTGC	GAGTCAGCCT AGCTCTGGAA	GTCCCTTGAA GTCCAGGATG	GCTCTGAAGC GCGTTTCCCT
MAM1_SP134	TACATTAGTC CAGGC-ATGG CCAG	CCTAACTAGA ACTCCTCTGC	GAGTCAGCCT AGCTCTGGAA	GTCCCTTGAA GTCCAGGATG	GCTCTGAAGC GCGTTTCCCT
MAST_A148_	TACATTAGTC CAGGCGATGG CCAG	CCTAACTAGA ACTCCCCTGC	GAGTCAGCCT AGCTCTGAAA	GTCCCTTGAA GTCCCGGATG	GCTCTGAAGC GCGTTTCCCT
SAV1_SE210	TACATTAGTC CAGGC-ATGG CCAG	CCTAACTAGA ACTCCTCTGC	GAGTCAGCCT AGCTCTGGAA	GTCCCTTGAA GTCCAGGATG	GCTCTGAAGC GCGTTTCCCT

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ASIAN2_Ema	AGCCCTTCCC CACGAGCAGC	AGCGTCCCTA ACAAGCGTCT	CCTGGGCCTC GCATGGTGAT	CCTCACCTGG CACATCGATG	GGTGGATGTC CGTTTGCA
FOR_DS1535	AGCCCTTCCC CACGAGCAGC	AGCGTCCCTA ACAAGCGTCT	CCTGGGCCTC GCATGGTGAT	CCTCACCTGG CACATCGATG	GGTGGATGTC CGTCTGCA
MAM1_SP134	AGCCCTTCCC CACGAGCAGC	AGCGTCCCTA ACAAGCGTCT	CCTGGGCCTC GCATGGTGAT	CCTCACCTGG CACATCGATG	GGTGGATGTC CGTTTGCA
MAST_A155_	AGCCCTTCCC CACGAGCAAC	CGAGTCCCTG ACAAGCGTCT	CCTGGGCCCC GCATGGTGAT	CCTCACCTGG CACATCGATG	GGCGGATGTC CGTTTGCA
SAV1_SE210	AGCCCTTCCC CACGAGCAGC	AGCGTCCCTA ACAAGCGTCT	CCTGGGCCTC GCATGGTGAT	CCTCACCTGG CACATCGATG	GGTGGATGTC CGTCTGCA

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ASIAN2_Ema	TGCACTTGAG TGCCAAGTGC TGGACCC	AGG-CACTGG TGTGGCCCC-	TGCAGACCTC AAGCAACACC	CAGGCCCCCA AGTGTGGAGC	GCCCCACCC- CCTGGACCTC
FOR_DS1535	TGCACTTGAG	AGG-CACTGG	TGCAGACCTC	CAGGCCCCCA	GCCCCACCC-

	TGCCACGTGC	TGTGGCCCC-	AAGCAACACC	AGTGTGGAGC	CCTGGACCTC
	TGGACCC				
MAM1_SP134	TGCACTTGAG	AGG-CACTGG	TGCAGATGTC	CAGGCCCCCA	GCCCCACCC-
	TGCCAAGTGC	TGTGGCCCC-	AAGCAACACC	AGTGTGGAGC	CCTGGACCTC
	TGGACCC				
MAST_A156_	TGCACTTGAG	AGG-CACTGG	TGCAGACCTC	CAGGCCCCCA	GCCCCACCCC
	TGCCAAGAGC	TGTGGCCCC	AAGCAACACC	AGTGTGGACC	CCTGGACCTC
	TGGACCC				
SAV1_SE210	TGCACTTGAG	AGG-CACTGG	TGCAGACCTC	CAGGCCCCCA	GCCCCACCC-
	TGCCAAGTGC	TGTGGCCCC-	AAGCAACATC	AGTGTGGAGC	CCTGGACCTC
	TGGACCC				

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ASIAN2_Ema	TTCTTCAGAA	TCAGAGCTGC	CCTAGGCATA	AAATTCTTAA	CCCTCTAGCT
	TAATCCAAAT	GCAATGAGTC	AGTCAGAAAAG	TAAA-TGGGA	ACCACTGG
FOR_DS1535	TTCTTCAGAA	TCAGAGCTGC	CCTAGGCATA	AAATTCTTAA	CCCTCTAGCT
	TAATCCAAAT	GCAATGAGTC	AGTCAGAAAAG	TAAA-TGGGA	ACCACTGG
MAM1_SP134	TTCTTCAGAA	TCAGAGCTGC	CCTAGGCATA	AAATTCTTAA	CCCTCTAGCT
	TAATCCAAAT	GCAATGAGTC	AGTCAGAAAAG	TAAA-TGGGA	ACCACTGG
MAST_A165_	TTCTTCAGAA	TCAGAGCTGC	CCTAGGCATA	AAATTCTTAA	CCCTCTAGCT
	TAATCCAAAT	GCAATGAGTC	AGTCAGAAAAG	TAAAATGGGA	ATCACTGG
SAV1_SE210	TTCTTCAGAA	TCAGAGCTGC	CCTAGGCATA	AAATTCTTAA	CCCTCTAGCT
	TAATCCAAAT	GCAATGAGTC	AGTCAGAAAAG	TAAA-TGGGA	ACCACTGG

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ASIAN2_Ema	ATTCATTCTT	TCACCTTCTCT	TCCCCAACTT	GTGCTCAGGG	CCCTCATGCT
	GCCTATCTGT	CCAGGAATGG	CGGAAAATTA	GATATCACAT	AAAAGTAA
FOR_DS1535	ATTCATTCTT	TCACCTTCTCT	TCCCCAACTT	GTGCTCAGGG	CCCTCATGCT
	GCCTATCTGT	CCAGGAATGG	CGGAAAATTA	GATATCACAT	AAAAGTAA
MAM1_SP134	ATTCATTCTT	TCACCTTCTCT	TCCCCAACTT	GTGCTCAGGG	CCCTCATGCT
	GCCTATCTGT	CCAGGAATGG	CGGAAAATTA	GATATCACAT	AAAAGTAA
MAST_A173_	ATTTATTCTT	TCACCTTCTCT	TCTCCAACCT	GTGCTCAGGG	CCCTCATGCT
	GCCTATCTGT	CCAGGAATGG	CAGAAAATTA	GATATCACAT	AAAAGTAA
SAV1_SE210	ATTCATTCTT	TCACCTTCTCT	TCCCCAACTT	GTGCTCAGGG	CCCTCATGCT
	GCCTATCTGT	CCAGGAATGG	CGGAAAATTA	GATATCACAT	AAAAGTAA

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ASIAN2_Ema	GAATGATATC	ATACTGCCCC	TTCAGAGATM	TGCCGCCATC	AGGTTATTAG
	GTGGTTTCTG	TGCCCCCGTG	CATTTAAAAT	GGCCTAAAA-	TTAA
FOR_DS1535	GAATGATATC	ATACTGCCCC	TTCTGAGATC	TGCCRCCATC	AGGTTATTAG
	GTGGTTTCTG	TGCCCCCGTG	CATTTAAAAT	GGCCTAAAA-	TTAA
MAM1_SP134	GAATGATATC	ATACTGCCCC	TTCAGAGATC	TGCCGCCATC	AGGTTATTAG
	GTGGTTTCTG	TGCCCCCGTG	CATTTAAAAT	GGCCTAAAA-	TTAA
MAST_A178_	GAATGATATC	ATACTGTTCC	TTCTGAGATC	TGCCGCCATC	AGGTTATTAG
	GTGGTTTCTG	TGCCCCCGTG	CATTTAAAAT	GGCCTAAAA	TTAA
SAV1_SE210	GAATGATATC	ATACTGCCCC	TTCTGAGATC	TGCCACCATC	AGGTTATTAG
	GTGGTTTCTG	TGCCCCCGTG	CATTTAAAAT	GGCCTAAAA-	TTAA

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ASIAN2_Ema	CCGTGATGTC	CTTTTTTGGC	TTTCGGTCTT	TCCTGATGAT	GTGTCCAGAG
	TAAGTAAGCT	AAGTCTTGCC	ATCCTTGCTG	CCAAGGAACC	TTCAGGA
FOR_DS1535	CCGTGATGTC	CTTTTTTGGC	TTTCGGTCTT	TCCTGATGAT	GTGTCCAGAG
	TAAGTAAGCT	AAGTCTTGCC	ATCCTTGCTG	CCAAGGAACC	TTCAGGA
MAM1_SP134	CCGTGATGTC	CTTTTTTGGC	TTTCGGTCTT	TCCTGATGAT	GTGTCCAGAG
	TAAGTAAGCT	AAGTCTTGCC	ATCCTTGCTG	CCAAGGAACC	TTCAGGA
MAST_A179_	TTGTGATGTC	CTTTTTTGGC	TTTTGGTCTT	TCCTGATGAT	GTGTCCAGAG
	TAAGTAAGCT	AAGTCTTGCC	ATCCTTGCTG	CCAAGGAACC	TTCAGGA
SAV1_SE210	CCGTGATGTC	CTTTTTTGGC	TTTCGGTCTT	TCCTGATGAT	GTGTCCAGAG
	TAAGTAAGCT	AAGTCTTGCC	ATCCTTGCTG	CCAAGGAACC	TTCAGGA

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ASIAN2_Ema	AGGAATTCTT	TCTAGGGAG-	---ACATTTA	GAGACAAGTA	AATAGCAGAG
FOR_DS1535	GGCTGCAGAC	ACAGCCTCCC	AGCACAGAAG	AAAGGAGGGC	TGGCAACAG
MAM1_SP134	AGGAATTCTT	TCTAGGGAG-	---ACATTTA	GAGACAAGTA	AATAGCAGAG
MAST_A180_	GGCTGCAGAC	ACAGCCTCCC	AGCACAGAAG	AAAGGAGGGC	TGGCAACAG
SAV1_SE210	AGGAATTCTT	TCTAGGGAGG	GAGACATTTA	GAGACAAGTA	AATAGCAGAG
	GGCTGCAGAC	ACAGCCTCCC	AGCATAGAAG	AAAGGAGGGC	TGGCAACAG
	AGGAATTCTT	TCTAGGGAG-	---ACATTTA	GAGACAAGTA	AATAGCAGAG
	GGCTGCAGAC	ACAGCCTCCC	AGCACAGAAG	AAAGGAGGGC	TGGCAACAG

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ASIAN2_Ema	GAGAAATAAC	CAGCACAGCC	TCTCGCTGCC	CCTTGGCTGA	CTTCCTTGGA
FOR_DS1535	GTCCGTTTCA	CCGAGGAACT	GGCTCGGTGA	CTTGAGCCTA	AGCTCTGGCT
MAM1_SP134	CACAT				
MAST_A186_	GAGAAATAAC	CAGCACAGCC	TCTCGCTGCC	CCYTGGCTGA	CTTCCTTGGA
SAV1_SE210	GTCCGTTTCA	CCGAGGAACT	GGCTCCGTGA	CTTGAGCCTA	AGCTCCGGCT
	CACAT				
	GAGAAATAAC	CAGCACAGCC	TCTCGCTGCC	CCTTGGCTGA	CTTCCTTGGA
	GTCCGTTTCA	CCGAGGAACT	GGCTCGGTGA	CTTGAGCCTA	AGCTCTGGCT
	CACAT				
	GAGAAATAAC	TAGCACAGCC	CCTCGCTGCC	TCCTGGCTGA	CTTCCTTGGA
	GTCCGTTTCA	CCGAGGGACT	GGCTCCGTGA	CTTGAGCCTA	AGCTCCGGCT
	TACAT				
	GAGAAATAAC	CAGCACAGCC	TCTCGCTGCC	CCCTGGCTGA	CTTCCTTGGA
	GTCCGTTTCA	CCGAGGAACT	GGCTCCGTGA	CTTGAGCCTA	AGCTCCGGCT
	CACAT				

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ASIAN2_Ema	AAATGAAGTC	GAGGGCTGGG	GGTCCCCAC	CTCCTGAAGG	GAAGGCAGCT
FOR_DS1535	AAYGTTAACT	GAATGCTTGC	TCTGTTGTTG	GAGCCTTCGT	GTC
MAM1_SP134	AAATGAAGTC	GAGGGCTGGG	GGTCCCCAC	CTCCTGAAGG	GAAGGCAGCT
MAST_A190_	AAYGTTAACT	GAATGCTTGC	TCTGTTGTTG	GAGCCTTCGT	GTC
SAV1_SE210	AAATGAAGTC	GAGGGCTGGG	GGTCCCC-AC	CTCCTAAAGG	GAAGGCAGCT
	AACGTTAACT	GAATGCTTGC	TCTATTGTTG	GAGCCTTCGC	GTC
	AAATGAAGTC	GAGGGCTGGG	GGTCCCCAC	CTCCTGAAGG	GAAGGCAGCT
	AACGTTAACT	GAATGCTTGC	TCTGTTGTTG	GAGCCTTCGT	GTC

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ASIAN2_Ema	ACTTGGCCCT	TTCTGTGTCT	TACGCTGTTG	CCAGCAGTAA	GGGGTTTCTC
FOR_DS1535	AAAAATTTCC	CACTGCAGCT	CATTTTAATG	TGGGAAGTTG	CCAGGGAAGC
MAM1_SP134	TTC				
MAST_A191_	ACTTGGCCCT	TTCTGTGTCT	TCCGCTGTTG	CCAGCAGTAA	GGGGTTTCTC
SAV1_SE210	AAAAATTTCC	CACTGCAGCT	CATTTTAATG	TGGGAAGTTG	CCAGGGAAGC
	TTC				
	ACTTGGCCCT	TTCTGTGTCT	TACGCTGTTG	CCAGCAGTAA	GGGGTTTCTC
	AAAAATTTCC	CACTGCAGCT	CATTTTAATG	TGGGAAGTTG	CCAGGGAAGC
	TTC				
	ACTTGGCCCT	TTCTGTGTCT	TACGCTGTTG	CCAGCAGTAA	GGGGTTTCTC
	AAAAATTTCC	CACTGCAGCT	CATTTTAATG	TGGGAAGTTG	CCAGGGAAGC
	TTC				

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ASIAN2_Ema	GAGGGCTGTT	GGTGGGGGAA	ACGAAGGGGG	AGAGGGCACC	ACTTTTCCTA
FOR_DS1535	GCCTTTGGGC	CCAGATCTCG	GGGTGGTGGT	GGTGGAGTGG	GCTGAGGTAA
	GACATCCCGG	ATTCCCG			
	TAGGGCTGTT	GGTGGGGGAA	ACGAAGGGGG	AGAGGGCACC	ACTTTTCCTA
	GCCTTTGGGC	CCAGATCTCG	GGGCGGTGGT	GGTGGAGTGG	GCTGAGGTAA

MAM1_SP134	GACATCCCGG GAGGGCTGTT GCCTTTGGGC	ATTCCCG GGTGGGGGAA CCAGATCTCG	ACGAAGGGGG GGGTGGTGGT	AGAGGGCACC GGTGGAGTGG	ACTTTTCCTA GCTGAGGTAA
MAST_A195_	GACATCCCGG GAGGGCTGTT GTCTTTGGGC	ATTCCCG GGCGGGG-AA CCAGATCTCG	ACGAAGGGG- GGGTGGTCAT	AGAGGGCACC AATGAAGTGG	ACTTCTCCTA ACTGAGGTAA
SAV1_SE210	GACATCCCGG GAGGGCTGTT GCCTTTGGGC	ATTCCCG GGTGGGGGAA CCAGATCTCG	ACGAAGGGGG GGGTGGTGGT	AGAGGGCACC GGTGGAGTGG	ACTTTTCCTA GCTGAGGTAA

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ASIAN2_Ema	ATTTTCATAT CTTCTCCTGG	GGATCCCCAG AGGTTGACCA	GCTCAGGGAA ACCAATAGCC	GGGACCTTTC CACTGGCTAT	TTAAGTCTTG A
FOR_DS1535	ATTTTCATAT CTTCTCCTGG	GGATCCCCAG AGGTTGACCA	GCTCAGGGAA ACCAATGGCC	GGGACCTTTC CACTGGCTAT	TTAAGTCTTG A
MAM1_SP134	ATTTTCATAT CTTCTCCTGG	GGATCCCCAG AGGTTGACCA	GCTCAGGGAA ACCAATAGCC	GGGACCTTTC CACTGGCTAT	TTAAGTCTTG A
MAST_A196_	GTTTTTATAT CTTCTCCTGG	GGATCCCCAG AGGTTGACCA	GCTCAGGGAA ACCAATAGCC	GGGACCTTTC CGCTGGCTAT	TTAAGTCTTG A
SAV1_SE210	ATTTTCATAT CTTCTCCTGG	GGATCCCCAG AGGTTGACCA	GCTCAGAGAA ACCAATGGCC	GGGACCTTTC CACTGGCTAT	TTAAGTCTTG A

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ASIAN2_Ema	AAGTACCCCA AGAGCTTTCT GTATGGAT	TTAATTCTAA AAGAGGGGCC	ACACAGCTGT GCAGTGTCTC	CAGAGGGTCT TACTAGGCAG	TCAACAACCT TACCCACCTG
FOR_DS1535	AAGTACCCCA AGAGCTTTCT GTATGGAT	TTAATTCTAA AAGAGGGGCC	ACACAGCTGT GCAGTGTCTC	CAGAGGGTCT TACTAGGCAG	TCAACAACCT TACCCACCTG
MAM1_SP134	AAGTACCCCA AGAGCTTTCT GTATGGAT	TTAATTCTAA AAGAGGGGCT	ACACAGCTGT GCAGTGTCTC	CAGAGGGTCT TACTAGGCAG	TCAACAACCT TACCCACCTG
MAST_A199_	AAGTACCCCA AGAGCTTTCT GTATGGAT	TTAATTCTAA AAGAGGGGCC	ACACAGCTGT TCAGTGTCTC	CAGAGGGTCT TACTAGGCAG	TCAACAACCT TACCCACCTG
SAV1_SE210	AAGTACCCCA AGAGCTTTCT GTATGGAT	TTAATTCTAA AAGAGGGGCT	ACACAGCTGT GCAGTGTCTC	CAGAGGGTCT TACTAGGCAG	TCAACAACCT TACCCACCTG

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ASIAN2_Ema	GAGGCTTCCT AGACACAATT TTCTGAAAAA	CTGGGAGGCC CCGTCCTTAG A	AGCCCCCTTC CATGGCCCCA	C-AGGTGGGT CAAGACACAC	GTCCCCCAGG GGCCTGCTGC
FOR_DS1535	GAGGCTTCCT AGACACAATT TTCTGAAAAA	CTGGGAGGCC CCGTCCTTAG A	AGCCCCCTTC CATGGCCCCA	C-AGGTGGGT CAAGACACAC	GTCCCCCAGG GGCCTGCTGC
MAM1_SP134	GAGGCTTCCT AGACACAATT TTCTGAAAAA	CTGGGAGGCC CCGTCCTTAG A	AGCCCCCTTC CATGGCCCCA	C-AGGTGGGT CAAGACACAC	GTCCCCCAGG GGCCTGCTGC
MAST_A200_	GAGGCTTCCT AGACACAATT TTCTGAAAAA	CTAGGAGGCC CCGTCCTTAG A	AGCCCCCTTC CATGGCCCCA	CCAGGTGGGT CAAGACACAC	GTCCCCCAGG GGCCTGCTGT
SAV1_SE210	GAGGCTTCCT AGACACAATT TTCTGAAAAA	CTGGGAGGCC CCGTCCTTAG A	AGCCCCCTTC CATGGCCCCA	C-AGGTGGGT CAAGACACAC	GTCCCCCAGG GGCCTGCTGC

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ASIAN2_Ema	TGTGGGCCCA ACCTACCAGA	GGGGATGGGC TCAAGGATGG	CTCTGCTGGA AGCCCCCTCGT	GCCCATCATG GGCATAAGTGG	GATCATGGAT
FOR_DS1535	TGTGGGCCCA ACCTACCAGA	GGGGATGGGC TCAAGGATGG	CTCTGCTGGA AGCCCCCTCGT	GCCCATCATG GGCATAAGTGG	GATCATGGAT
MAM1_SP134	TGTGGGCCCC ACCTACCAGA	GGGGATGGGC TCAAGGATGG	CTCTGCTGGA AGCCCCCTCGT	GCCCATCATG GGCATAAGTGG	GATCATGGAT

MAST_A201_	ACCTACCAGA TGTGGGCCCA ACCTACCAGA	TCAAGGATGG GGGGATGGGC TCAAGGATGG	AGCCCCTCGT CTCTGCTGGA AGCCCCTCGT	GGCATAGTGG GCCCATCATG GGCACAGTGG	GATCATTGAT GATCATGGAT
SAV1_SE210	TGTGGGCCCA ACCTACCAGA	GGGGATGGGC TCAAGGATGG	CTCTGCTGGA AGCCCCTCGT	GCCCATCATG GGCACAGTGG	GATCATTGAT

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ASIAN2_Ema	CCAAGAATGC TCAGCAAAAT	CTTAATAGTC ATACTAAAAA	ATTAATTTCA TATCCTCCTG	CAAAGCTTCT TGATAATGAA	TCTATATATG TGATGTCTTG
FOR_DS1535	CCAAGAATGC TCAGCAAAAT	CTTAATAGTC ATACTAAAAA	ATTAATTTCA TATCCTCCTG	CAAAGCTTCT TGATAATGAA	TCTATATATG TRATGTATTG
MAM1_SP134	CCAAGAATGC TCAGCAAAAT	CTTAATAGTC ATACTAAAAA	ATTAATTTCA TATCCTCCTG	CAAAGCTTCT TGATAATGAA	TCTATATATG TGATGTATTG
MAST_A205_	CCAAGAATGC TCAGCAAAAT	CTTAATAGTC ATACTAAAAA	ATTAATTTCA TATCCTCCTG	CAAAGCTTCT CGATAATGAA	---ATATATG TGATGTATTG
SAV1_SE210	CCAAGAATGC TCAGCAAAAT	CTTAATAGTC ATACTAAAAA	ATTAATTTCA TATCCTCCTG	CAAAGCTTCT TGATAATGAA	TCTATATATG TGATGTATTG

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ASIAN2_Ema	CCCCACACC GGAATCAGCT ACCG	ATCCCTGCTG CCTGTGCAGA	GCACCTCCTC AAGGGTTAAT	TGCAGGAAAG TCCCTCTT-G	GGAGTGAGCT GAGGGATTAT
FOR_DS1535	CCCCACACC GGAATCAGCT ACTG	ATCCCTGCTG CCTGTGCAGA	GCACCTCCTC AAGGGTTAAT	TGCAGGAAAG TCCCTCTT-G	GGAGTGAGCT GAGGGATTAT
MAM1_SP134	CCCCACACC GGAATCAGCT ACCG	ATCCCTGCTG CCTGTGCAGA	GCACCTCCTC AAGGGTTAAT	TGCAGGAAAG TCCCTCTT-G	GGAGTGAGCT GAGGGATTAT
MAST_A208_	CCTCCACACC GGAATCAGCT ACCA	ATCCCTGCTG CCTGTGCAGA	GCACCTCCTC AAGGGTTAAT	GGCAGGAAAG TCCCTCTTAA	GGAGTGAGCT AAAAGATTAT
SAV1_SE210	CCCCACACC GGAATCAGCT ACCC	ATCCCTGCTG CCTGTGCAGA	GCACCTCCTC AAGGGTTAAT	TGCAGGAAAG TCCCTCTT-G	GGAGTGAGCT GAGGGATTAT

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ASIAN2_Ema	CAGTTATACT TATTTATCAG	TCTTTTTCAA ATTTCCACCT	ACCCAGAGAC ATTACACATT	TTCCAGCATT CCCTGTCATC	TGGACCCTTC AGTTTCTT
FOR_DS1535	CAGTTATACT TATTTATCAG	TCTTTTTCAA ATTTCCACCT	ACCCAGAGAC ATTACACATT	TTCCAGCATT CCCTGTCATC	TGGACCCTTC AGTTTCTT
MAM1_SP134	CAGTTATACT TATTTATCAG	TCTTTTTCAA ATTTCCACCT	ACCCAGAGAC ATTACACATT	TTCCAGCATT CCCTGTCATC	TGGACCCTTC AGTTTCTT
MAST_A212_	TAGTTATATT TATTTATCAG	TTTTTTTTCAA ATTTCCACCT	ACCCAGAGAC ATTACACATT	TTCCAGCATT CCCTGTCATC	TGGACCCTTC AGTTTCTT
SAV1_SE210	CAGTTATACT TATTTATCAG	TCTTTTTCAA ATTTCCACCT	ACCCAGAGAC ATTACACATT	TTCCAGCATT CCCTGTCATC	TGGACCCTTC AGTTTCTT

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ASIAN2_Ema	TGGCCTGTCT TCCACGCTCC GGCTC	GCCACCCTCC CTGGCTGGTC	ATTT-CTCCC AATACCCACC	CTTCAATCCA CACTTTCAAG	CCAGCCATCT TTCTAACAGT
FOR_DS1535	TGGCCTGTCT TCCACGCTCC GGCTC	GCCACCCTCC CTGGCTGGTC	ATTT-CTTCC AATACCCACC	CTTCAATCCA CACTTTCAAG	CCAGCCATCT TTCTAACAGT
MAM1_SP134	TGGCCTGTCT TCCACGCTCC GGCTC	GCCACCCTCC CTGGCTGGTC	ATTT-CTCCC AATACCCACC	CTTCAATCCA CACTTTCAAG	CCAGCCATCT TTCTAACAGT
MAST_A415_	TGGCCTCTCT GCCACGCTCC GGCTC	GCCACCCTCC -TGGCTGGTC	ATTTTCTTCC ACTACCCACC	CTTCAATCCA CACTTTCAAG	CCAGCCATCT TTCTAACAGT
SAV1_SE210	TGGCCTGTCT TCCACGCTCC GGCTC	GCCACCCTCC CTGGCTGGTC	ATTT-CTCCC AATACCCACC	CTTCAATCCA CACTTTCAAG	CCAGCCATCT TTCTAACAGT

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ASIAN2_Ema	CCCAAGGAGC	TGGATCCCTC	TGCTGTGCTC	CCCTTGGATT	GTCTTCTTGC
	ATTTGTGTTT	TTTGATGCTA	ACTGGTGTGG	CTACTTGCAC	CGGAGAG
FOR_DS1535	CCCAAGGAGC	TGGATCCCTC	TGCTGTGCTC	CCCTTGGATT	GTCTTCTTGC
	ATTTGTGTTT	TTTGATGCTA	ACTGGTGTGG	CTACTTGCAC	CGGAGAG
MAM1_SP134	CCCAAGGAGC	TGGATCCCTC	TGCCGTGCTC	CCCTTGGATT	GTCTTCTTGC
	ATTTGTGTTT	TTCGATGCTA	ACTGGTGTGG	CTACTTGCAC	CGGAGAG
MAST_A355_	TCCAAGGAGC	TGGATCCCTC	TGCTGTGCTC	CCCTTGGATT	GTCTTCTTGC
	ATTTGTGTTT	TTTGATGCTA	ACTGGTGTGG	CTACTTGCAC	CGGAGAG
SAV1_SE210	CCCAAGGAGC	TGGATCCCTC	TGCTGTGCTC	CCCTTGGATT	GTCTTCTTGC
	ATTTGTGTTT	TTTGATGCTA	ACTGGTGTGG	CTACTTGCAC	CGGAGAG

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ASIAN2_Ema	TAAGAACCTC	TGTAACAGTG	GGAGGAGAGT	ATCATGGCCA	AGAAAGCTCT
	GCTCAAGAGA	AGGCACAGAG	CCTGGGCACA	GACGCTGGGC	CAGAG
FOR_DS1535	TAAGAACCTC	TGTAACAGTG	GGAGGAGAGT	ATCATGGCCA	AGAAAGCTCT
	GGTCAAGAGA	AGGCACAGAG	CCTGGGCACA	GACGCTGGGC	CAGAG
MAM1_SP134	TAAGAACCTC	TGTAACAGTG	GGAGGAGAGT	ATCATGGCCA	AGAAAGCTCT
	GCTCAAGAGA	AGGCACAGAG	CCTGGGCACA	GACGCTGGGC	CAGAG
MAST_A214_	TAAGAACCTC	TGTAACAGTG	GGAGGAGAGT	ATCATGGCCA	AGAAAGCTCT
	GATCAAGAGA	AGGCACAGAG	CCTGGGCACA	GACGCCGGGC	CAGAA
SAV1_SE210	TAAGAACCTC	TGTAACAGTG	GGAGGAGAGT	ATCATGGCCA	AGAAAGCTCT
	GCTCAAGAGA	AGGCACAGAG	CCTGGGCACA	GACGCTGGGC	CAGAG

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ASIAN2_Ema	CAGTAAAACA	CGTGTAAAG	ATTACAAATT	GTTTAACAAG	TTTTGGCAAA
	CAAGTCCCCT	GGTGGTCTTG	AAATTTCTGA	GAAGCAGATG	GAAGAGGTAC
	AGTTTTATAG	AT			
FOR_DS1535	CAGTAAAACA	CGTGTAAAG	ATTACAAATT	GTTTAACAAG	TTTTGGCAAA
	CAAGTCCCCT	GGTGGTCTTG	AAATTTCTGA	GAAGCAGATG	GAAGAGGTAC
	AGTTTTATAG	AT			
MAM1_SP134	CAGTAAAACA	CGTGTAAAG	ATTACAAATT	GTTTAACAAG	TTTTGGCAAA
	CAAGTCCCCT	GGTGGTCTTG	AAATTTCTGA	GAAGCAGATG	GAAGAGGTAC
	AGTTTTATAG	AT			
MAST_A215_	TAGTAAAACA	CGTGTAAAG	ATTACAAATT	GTTTAACAAG	TTTTGGCAAA
	CAAGTCCCCT	GGTGGTCTTG	AAATTTCTGA	GAAGCAGATG	GAAGAGGTAC
	AGTTTTATAG	AT			
SAV1_SE210	CAGTAAAACA	CGTGTAAAG	ATTACAAATT	GTTTAACAAG	TTTTGGCAAA
	CAAGTCCCCT	GGTGGTCTTG	AAATTTCTGA	GAAGCAGATG	GAAGAGGTAC
	AGTTTTATAG	AT			

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ASIAN2_Ema	CTCAGAGTGG	GGGCCTAACG	CCAGATGTAG	TGCTCTGGTG	AGTCCAGGGT
	GGGGTGTTAC	TCAGCCTACA	ATCCCCCACC	CACACTTCGC	CAG
FOR_DS1535	CTCAGAGTGG	GGGCCTAATG	CCAGATGTAG	TGCTCTGGTG	AGTCCAGGGT
	GGGGTGTTAC	TCAGCCTACA	ATCCCCCACC	CACACTTCGC	CAG
MAM1_SP134	CTCAGAGTGG	GGGCCTAACA	CCAGATGTAG	TGCTCTGGTG	AGTCCAGGGT
	GGGGTGTTAC	TCAGCCTACA	ATCCCCCACC	CACACTTCGC	CAG
MAST_A216_	CTCAGAGTGG	GG-CCTAACA	CCAGATGTAG	TGCTCTGGTG	AGTCCAGGGT
	GGGGTGTTAC	TCAGCCCACA	GTCCCCCACC	CACACTTCCC	CAA
SAV1_SE210	CTCAGAGTGG	GGGCCTAATG	CCAGATGTAG	TGCTCTGGTG	AGTCCAGGGT
	GGGGTGTTAC	TCAGCCTACA	ATCCCCCACC	CACACTTCGC	CAG

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ASIAN2_Ema	GATATGTCCT	GGAGAGGGCT	CTGGAAGATG	CCCTTTCTCA	GGGATGTTGG
	AGAAAGGCAG	CCACCTGCTA	TGGGGCCTGG	CATTCTTGCC	AGGGGCTGGG
FOR_DS1535	GATATGTCCT	GGAGAGGGCT	CTGGAAGATG	CCCTTTCTCA	GGGATGTTGG
	AGAAAGGCAG	CCACCTGCTA	TGGGGCCTGG	CATTCTTGCC	AGGGGCTGGG
MAM1_SP134	GATATGTCCT	GGAGAGGGCT	CTGGAAGATG	CCCTTTCTCA	GGGATGTTGG
	AGAAAGGCAG	CCACCYGCTA	TGGGGCCTGG	CATTCTTGCC	AGGGGCTGGG

MAST_A217_	GATATGTCCT	GGAGAGGGCT	CTGGAAGATG	CCCTTTCTCA	GGGATGTTGG
SAV1_SE210	AGAAAAGCAG	CCACCTGCTA	TGGGGCCTGG	CATTCTTGCC	AGGGGCTGGG
	GATATGTCCT	GGAGAGGGCT	CTGGAAGATG	CCCTTTCTCA	GGGATGTTGG
	AGAAAAGCAG	CCACCTGCTA	TGGGGCCTGG	CATTCTTGCC	AGGGGCTGGG
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	5 99				
ASIAN2_Ema	CTGGTCCTCC	CTCGTTTCTG	GACCTTTGCT	CATCCTGCCC	TCCCTATAAT
FOR_DS1535	GGCCGCCTTT	TCCCCACTCC	TCCTATCCCA	ATCTCAGTGC	TTTCTGTCT
	CTGGTCCTCC	CTCGTTTCTG	GACCTTTGCT	CATCCTGCCC	TCCCTATAAT
	GGCCGCCTGT	TCCCCACTCC	TCCTATCCCA	ATCTCAGTGC	TTTCTGTCT
MAM1_SP134	CTGGTCCTCC	CTCGTTTCTG	GACCTTTGCT	CATCCTGCCC	TCCCTATAAT
	GGCCGCCTTT	TCCCCACTCC	TCCTATCCCA	ATCTCAGTGC	TTTCTGTCT
MAST_A219_	CTGGTCCTCC	CTCGTTTCTG	GACCTTTGCT	CATCCTGCCC	TCCCTATAAT
	GGCCGCCTGT	TCCCCACTCC	TCCTATCCCA	ATCTCAGTGC	TTTCTGTCT
SAV1_SE210	CTGGTCCTCC	CTCGTTTCTG	GACCTTTGCT	CATCCTGCCC	TCCCTATAAT
	GGCMGCCTGT	TCCCCACTCC	TCCTATCCCA	ATCTCAGTGC	TTTCTGTCT
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	5 103				
ASIAN2_Ema	GGGCGACCTT	--CTCGCTCT	CTGGCTAAGC	CCATGGACCT	CTTACAACCT
	GTTCACGTGA	CGTGGGTTGT	ACAAATACTC	AGGCCACCC	AATGTTCTCC
	TTC				
FOR_DS1535	GGGCGACCTT	--CTCGCTCT	CTGGCTAAGC	CCATGGACCT	CTCACAACCT
	GTTCACGTGA	CGTGGGTTGT	ACAAATACTC	AGGCCACCC	AATGTTCTCC
	TTC				
MAM1_SP134	GGGCGACCTT	--CTCGCTCT	CTGGCTAAGC	CCATGGACCT	CTTACAACCT
	GTTCACGTGA	CGTGGGTTGT	ACAAATACTC	AGGCCACCC	AATGTTCTCC
	TTC				
MAST_A220_	CGTCGACCTC	GCCTCGCTCT	CTGGCTAAGC	CCATGGACCT	CTCGCAACCT
	GTTACATAAA	TGTGGGTTAT	ACAAATACTC	AGGCCACCC	AATGTTCTCC
	TTC				
SAV1_SE210	GGGCGACCTT	--CTCGCTCT	CTGGCTAAGC	CCATGGACCT	CTTACAACCT
	GTTCACGTGA	CGTGGGTTGT	ACAAATACTC	AGGCCACCC	AATGTTCTCC
	TTC				
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ASIAN2_Ema	AGTTTTCTCT	TCCAAGGCC	CTGAGTTCTT	CTGGCTTTTA	GACATCAAAG
	CGTTATGTG	CCTGTTCTTT	TCAGAAGCTG	CTCTCTCTCC	CGAGAGACTT
	TTCTT				
FOR_DS1535	AGTTTTCTCT	TCCAAGGCC	CTGAGTTCTT	CTGGCTTTTA	GACATCAAAG
	CGTTATGTG	CCTGTTCTTT	TCAGAAGCTG	CTCTCTCTCC	CGAGAGACTT
	TTCTT				
MAM1_SP134	AGTTTTCTCT	TCCAAGGCC	CTGAGTTCTT	CTGGCTTTTA	GACATCAAAG
	CGTTATGTG	CCTGTTCTTT	TCAGAAGCTG	CTCTCTCTCC	CGAGAGACTT
	TTCTT				
MAST_A294_	AGTTTTCTCT	TCTAAGGCC	CTGAGTTCTT	CTGGCTTTTA	GACATCAAAG
	CGTTATGTG	CCTGTTCTTT	TCAGAAGCTG	CTCTCTCTCC	CAAGAGACTT
	TTCTT				
SAV1_SE210	AGTTTTCTCT	TCCAAGGCC	CTGAGTTCTT	CTGGCTTTTA	GACATCAAAG
	CGTTATGTG	CCTGTTCTTT	TCAGAAGCTG	CTCTCTCTCC	CGAGAGACTT
	TTCTT				
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ASIAN2_Ema	TGAGCTTCAG	GTGCTGCTGG	GAGGGGCCAT	CAAGGCAATC	CCTCCCAGGG
	AGGAGGGCTG	GTTCTGTGGG	CAACGCGGCC	AGAGTGAGTA	ACCAG
FOR_DS1535	TGAGCTTCAG	GTGCTGCTGG	GAGGGGCCAT	CAAGGCAATC	CCTCCCAGGG
	AGGAGGGCTG	GTTCTGTGGG	CAACKCGGCC	AGAGTGAGTA	ACCAG
MAM1_SP134	TGAGCTTCAG	GTGCTGCTGG	GAGGGGCCAT	CAAGGCAATC	CCTCCCAGGG
	AGGAGGGCTG	GTTCTGTGGG	CAACGCGGCC	AGAGTGAGTA	ACCAG
MAST_A222_	TGAGCTTCAG	GTGCTGCTGG	GAGGGGCCAT	CAAGGCAATC	CCTCCCAGGG
	AGGAGGGCTG	GTTCTGTGGG	CAAAGCTGCC	AGAGTGAGTA	ACCAG
SAV1_SE210	TGAGCTTCAG	GTGCTGCTGG	GAGGGGCCAT	CAAGGCAATC	CCTCCCAGGG
	AGGAGAGCTG	GTTCTGTGGG	CAACGTGGCC	AGAGTGAGTA	ACCAG

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ASIAN2_Ema	TCAATATCTC	CTCACCTGGA	CCTCAGACCC	TTGTTTTCCA	TTCCACAAAG
	CCACAGGGAC	AAGATTGAGC	CTCTCCCACC	CCAGTGCACA	R
FOR_DS1535	TCAATATCTC	CYCACCTGGA	CMTCAGACCC	TTGTTTTCCA	TTCCACAAAS
	CCACAGGGAC	AAGATTGAGC	CTCTCCCACC	CCAGTGCACA	G
MAM1_SP134	TCAATATCTC	CTCACCTGGA	CCTCAGACCC	TTGTTTTCCA	TTCCACAAAG
	CCACAGGGAC	AAGATTGAGC	CTCTCCCACC	CCAGTGCACA	G
MAST_A223_	TCAATATCTC	CTCACCTGGA	CCTCAGACCC	TTGTTTTCCA	TTCCACAAAG
	CCACAGGGCC	AAGATTGAGC	CACTCCCACC	CCAGTGCACA	G
SAV1_SE210	TCAATATCTC	CTCACCTGGA	CCTCAGACCC	TTGTTTTCCA	TTCCACAAAG
	CCACAGGGAC	AAGATTGAGC	CTCTCCCACC	CCAGTGCACA	G

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ASIAN2_Ema	CACCTGTTCT	ATATTTTGTGTA	TTACCTGTAG	TGGATAAAAA	ATAGCAGAGC
	AAAAACTAGG	CTTTCATCAG	-CTTTTTTGT	TTTGTTTTGT	TTT-----CA
	GGGACAAAAC	ATTTAAACAA	ACATGTTTTT	CTTT	
FOR_DS1535	CACCTGTTCT	ATATTTTGTGTA	TTACCTGTAG	TGGATAAAAA	ATAGCAGAGC
	AAAAACTAGG	CTTTCATCAG	-CTTTTTTGT	TTTGTTTTGT	TTTGTTTTCA
	GGGACAAAAC	ATTTAAACAA	ACATATTTTT	CTTT	
MAM1_SP134	CACCTGTTCT	ATATTTTGTGTA	TTACCTGTAG	TGGATAAAAA	ATAGCAGAGC
	AAAAACTAGG	CTTTCATCAG	-CTTTTTTGT	TTTGTTTTGT	TTTGTTTTCA
	GGGACAAAAC	ATTTAAACAA	ACATGTTTTT	CTTT	
MAST_A224_	CACCTGTTCT	ATATTTTGTGTA	TTACCTGTAG	TGGATA----	---GCAGAGC
	AAAAACTAGG	CTTTCATCAG	TCTTTTTTGT	TTTGTTTTGT	TTTGTTTTCA
	GGGACAAAAC	ATTTAAACAA	ACATGTTTTT	CTTT	
SAV1_SE210	CACCTGTTCT	ATATTTTGTGTA	TTACCTGTAG	TGGATAAAAA	ATAGCAGAGC
	AAAAACTAGG	CTTTCATCAG	-CTTTTTTGT	TTTGTTTTGT	TTT-----CA
	GGGACAAAAC	ATTTAAACAA	ACATGTTTTT	CTTT	

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ASIAN2_Ema	GAACTAAGCT	GAGTTCATC	AATACACCAG	GCTATTTTCAG	GCCTCCCTAA
	CTTTGCTCAA	GCTGCTCCCC	AGGGCTGCAA	TCCCCTTCTT	ATCTCA
FOR_DS1535	GAACTAAGCT	GAGTTCATC	AATACACCAG	GCTATTTTCAG	GCCTCCCTAA
	CTTTGCTCAA	GCTGCTCCCC	AGGGCTGCAA	TCCCCTTCTT	ATCTCA
MAM1_SP134	GAACTAAGCT	GAGTTCATC	AATACACCAG	GCTATTTTCAG	GCCTCCCTAA
	CTTTGCTCAA	GCTGCTCCCC	AGGGCTGCAA	TCCCCTTCTT	ATCTCA
MAST_A357_	GAACTAAGCT	GAGTTCATC	AATACACCAG	GTTATTTTCAG	GCTTCACTAA
	CTTTGCTCAA	GCTGCTCCCC	AGGGCTGCAA	TCCCCTTCTT	ATCTCA
SAV1_SE210	GAACTAAGCT	GAGTTCATC	AATACACCAG	GCTATTTTCAG	GCCTCCCTAA
	CTTTGCTCAA	GCTGCTCCCC	AGGGCTGCAA	TCCCCTTCTT	ATCTCA

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ASIAN2_Ema	ACTGTTGCCG	GCACCTGGGG	AGGGGGCTCA	GCTGGAGGAG	TCAGTTCTTG
	CAGCCTGCTT	CCCCTCCACC	CTACTACGCC	TTCCACAGGA	ATTGGGGTCG
	CCTGCTG				
FOR_DS1535	ACTGTTGCCG	GCACCTGGGG	AGGGGGCTCA	GCTGGAGGAG	TCAGTTCTTG
	CAGCCTGCTT	CCCCTCCGCC	CTACTACGCC	TTCCACAGGA	ATTGGGGTCG
	CCTGCTG				
MAM1_SP134	ACTGTTGCCG	GCACCTGGGG	AGGGGGCTCA	GCTGGAGGAG	TCAGTTCTTG
	CAGCCTGCTT	CCCCTCCGCC	CTACTACGCC	TTCCACAGGA	ATTGGGGTCG
	CCTGCTG				
MAST_A225_	ACTGTTGCCG	GCACCTGGGG	AGGGGGCTCA	GCTGGAGGAG	TCAGTTCTTC
	CAGCCTGCTT	CCCCTCCGCC	CTACTACGCC	TTCCACAAGA	ATTGGGATCG
	CCTACTA				
SAV1_SE210	ACTGTTGCCG	GCACCTGGGG	AGGGGGCTCA	GCTGGAGGAG	TCAGTTCTTG
	CAGCCTGCTT	CCCCTCCGCC	CTACTACGCC	TTCCACAGGA	ATTGGGGTCG
	CCTGCTG				

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ASIAN2_Ema	CACTCAGAAC	ACGACTGYGG	AAGAGCTGCC	TCCTTAATGA	CGCCCTTACT
	GAGGCAGACG	GATTAAAGCC	TTCGGGACCT	TCATTTGCTG	ATGTGCCACG
	A				

FOR_DS1535	CACTCAGAAC GAGGCAGACG A	ACGACTGCRG GATTAAGCC	AAGAGCTGCC TTCGGGACCT	TCCTTAATGA TCATTTGCTG	CGCCCTTACT ATGTGCCACG
MAM1_SP134	CACTCAGAAC GAGGCAGACG A	ATGACTGCGG GATTAAGCC	AAGAGCTGCC TTCGGGACCT	TCCTTAATGA TCATTTAATG	CGCCCTTACT ATGTGCCACG
MAST_A418_	TACTCAGAAC GAGGCAGACG A	ACGACTGGGG GATTAAGCC	AAGAGCTGCC TTCGGGACCT	TCCTTAATGA TCATTTGCTG	CGCCCTTACT ATGTGCCATG
SAV1_SE210	CACTCAGAAC GAGGCAGACG A	ACGACTGCGG GATTAAGCC	AAGAGCTGCC TTCGGGACCT	TCCTTAATGA TCATTTGCTG	CGCCCTTACT ATGTGCCACG

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ASIAN2_Ema	AGTAGAGAGA AAGGTACAAG	AACAGGGAAA GGATGAGGCT	GACTTTCCAG GAATGCAACA	GTGACAGGAA TACCAGCTCT	CCGGAGAAGC ATCCAG
FOR_DS1535	AGTAGAGAGA AAGGTACAAG	AACAGGGAAA GGATGAGGCT	GACTTTCCAG GAATGCAACA	GTGACAGGAA TACCGGCTCT	CCGGAGAAGC ATCCAG
MAM1_SP134	AGTAGAGAGA AAGGTACAAG	AACAGGGAAA GGATGAGGCT	GACTTTCCAG GAATGCAACA	GTGACAGGAA TACCAGCTCT	CCGGAGAAGC ATCCAG
MAST_A227_	AGCAGAGAGA AAGGTACAAG	AACAGGGAAA GGATGAGGCT	GACTTTCCAG GAATGCAACA	GTGACAGGAA TACCGGCTCT	CCGGAGAAGC ATCCAG
SAV1_SE210	AGTAGAGAGA AAGGTACAAG	AACAGGGAAA GGATGAGGCT	GACTTTCCAG GAATGCAACA	GTGACAGGAA TACCGGCTCT	CCGGAGAAGC ATCCAG

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ASIAN2_Ema	TGTGGTACTG ATCCATATTT	TGCCAAGCCT GACAGATGGG	TCCACATATT CAGTCTGAGG	ACTACGTAGC CCTTCAGGAT	TACTCCAATT TTAAAAACT
FOR_DS1535	TGTGGTACTG ATCCATATTT	TGCCAAGCCT GACAGATGGG	TCCACATATT CAGTCTGAGG	ACTACGTAGC CCTTCAGRAT	TACTCCAATT TTAAAAACT
MAM1_SP134	TGTGGTACTG ATCCATATTT	TGCCAAGCCT GACAGATGGG	TCCACATATT CAGTCTGAGG	ACTACGTAGC CCTTCAGRAT	TACTCCAATT TTAAAAACT
MAST_A229_	TGTGGTACTG ATCCATATTT	TGCCAAGCCT GACAGATGGG	TCCACATATT CAGTCTGAGG	ACTACATAGC CCTTCAGAAG	TACTCCAATT TTAAAAACT
SAV1_SE210	TGTGGTACTG ATCCATATTT	TGCCAAGCCT GACAGATGGG	TCCACATATT CAGTCTGAGG	ACTACGTAGC CCTTCAGAAT	TACTCCAATT TTAAAAACT

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ASIAN2_Ema	CCCCGACCCC CCCTTGGCGT GCTT	TCCGTTGAAA CCTCAACTCT	TTCACCTGTC ACTGTCTGAC	-AGG-CTGCT CGACTGCCTG	GAAGCCCTTG AGCAGCAGGT
FOR_DS1535	CCCCGACCCC CCCTTGGCGT GCTT	TCCGTTGAAA CCTCAACTCT	TTCACCTGTC ACTGTCTGAC	-AGG-CTGCT CGACTGCCTG	GAAGCCCTTG AGCAGCAGGT
MAM1_SP134	CCCCGACCCC CCCTTGGCGT GCTT	TCCGTTGAAA CCTCAACTCT	TTCACCTGTC ACTGTCTGAC	-AGG-CTGCT CGACTGCCTG	GAAGCCCTTG AGCAGCAGGT
MAST_A299_	CCCCGACCCC CCCTTGGCGT GCTT	TCCGTTGAAA CCTCAACTCT	TTCACCTGTT ACTGTCTGAC	-AGG-CTGCT CGACTGCCTG	GAAGCCCTTG AGCAGCAGGT
SAV1_SE210	CCCCGACCCC CCCTTGGCGT GCTT	TCCGTTGAAA CCTCAACTCT	TTCACCTGTC ACTGTCTGAC	-AGG-CTGCT CGACTGCCTG	GAAGCCCTTG AGCAGCAGGT

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ASIAN2_Ema	GTCACCTTGCC CCCCTGACAG GT	TCAGAAACAC CAGAGTGATC	AGGCGAAGAT ACCCATGGGC	TGAACTGGGA AGCCCTCTTA	CCTTGCCCTG ACCTCCCTGA
FOR_DS1535	GTCACCTTGCC CCCCTGACAG GT	TCAGAAACAC CAGAGTGATC	AGGCGAAGAY ACCCATGGGC	TGAACTGGGA AGCCCTCTTA	CCTTGCCCTG ACCTCCCTGA
MAM1_SP134	GTCACCTTGCC CCCCTGACAG	TCAGAAACAC CAGAGTGATC	AGGCGAAGAT ACCCATGGGC	TGAACTGGGA AGCCCTCTTA	CCTTGCCCTG ACCTCCCTGA

MAST_A300_	GT GTCACCTTGCC CCCCTGACAA	TTAGAAACAC CAGAGTGATC	AGGCGAAGAT ACCCATAGGC	TGAAGTGGGA AGCCCTCTTA	CCTTGCCCTG ACCTCCCTGA
SAV1_SE210	GT GTCACCTTGCC CCCCTGACAG	TCAGAAACAC CAGAGTGATC	AGGCGAAGAT ACCCATGGGC	TGAACTGGGA AGCCCTCTTA	CCTTGCCCTG ACCTCCCTGA

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ASIAN2_Ema	TAACTAGGAA TATTCGTGGA	ACCTAGAAGA TGACAGAGCC	ATAGTTTCTG TATTTTGCAG	CTTGTATGAC TTTCTATTCA	AGGGATCTTT CA
FOR_DS1535	TAACTAGGAA TATTCGTGGA	ACCTAGAAGA TGACAGAGCC	ATAGTTTCTG TATTTTGCAG	CTTGTATGAC TTTCTATTCA	AGGGATCTTT CA
MAM1_SP134	TAACTAGGAA TATTCGTGGA	ACCTAGAAGA TGACAGAGCC	ATAGTTTCTG TATTTTGCAG	CTTGTATGAC TTTCTATTCA	AGGGATCTTT CA
MAST_A301_	TAATTAGGAA TATTCATGAA	ATCTAGAAGA TGACAGAGCC	ATAGTTTCTG TATTTTGCAG	CTTGTATGAC TTTCTATTCA	AGGGATCTTT CA
SAV1_SE210	TAACTAGGAA TATTCGTGGA	ACCTAGAAGA TGACAGAGCC	ATAGTTTCTG TATTTTGCAG	CTTGTATGAC TTTCTATTCA	AGGGATCTTT CA

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ASIAN2_Ema	TATATGCACA GTTTCCTACA	TACCGTAGTC GAGTAGAACT	TAACCC-AAA GCCCCATAGA	AAACCCAGGG GTTTCCAAGG	CCGCCGAGTT AGTGCC
FOR_DS1535	TATATGCACA GTTTCCTACA	TACCGTAGTC GAGTAGAACT	TAACCC-AAA GCCCCATAGA	AA-CCCAGGG GTTTCCAAGG	CCGCCGAGTT AGTGCC
MAM1_SP134	TATATGCACA GTTTCCTACA	TACCGTAGTC GAGTAGAACT	TAACCC-AAA GCCCCATAGA	AAACCCAGGG GTTTCCAAGG	CCGCCGAGTT AGTGCC
MAST_A302_	TATATGCACA GTTTCCTACA	TACCGTAGTC GAGTAGAACT	TAACCC-AAA GCCCCATAGA	AAACCCAGTG ATTTCCAAGG	CCGCCGAGTT AGTGCC
SAV1_SE210	TATATGCACA GTTTCCTACA	TACCGTAGTC GAGTAGAACT	TAACCCAAA GCCCCATAGA	AA-CCCAGGG GTTTCCAAGG	CCGCCGAGTT AGTGCC

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ASIAN2_Ema	CRTATCGGTG CATGTACTION	CAACTTCCTG CCTCAGGTAC	GGGCTCAGCC GTGTGGTCTT	CACAGGTGCA GGTCTGGCCT	GATCCCCTCC GAT
FOR_DS1535	CGTATCGGTG CATGTACTION	CAACTTCCTG CCTCAGGTAC	GGGCTCAGCC GTGTGGTCTT	CACAGGTGCA GGTMTGGCCT	GATCCCCTCC GAT
MAM1_SP134	CGTATCGGTG CATGTACTION	CAACTTCCTG CCTCAGGTAC	GGGCTCAGCC GTGTGGTCTT	CACAGGTGCA GGTCTGGCCT	GATCCCCTCC GAT
MAST_A232_	TGTATCGGTG CATGTACTION	CAACTTCCTG CCTCAGGTAC	GGGCTCAGCC GTGTGGTCTT	CACAGGTGCA AGTCTGGCCT	GATCCCCTCC GGT
SAV1_SE210	CGTATCGGTG CATGTACTION	CAACTTCCTG CCTCAGGTAC	GGGCTCAGCC GTGTGGTCTT	CACAGGTGCA GGTCTGGCCT	GATCCCCTCC GAT

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ASIAN2_Ema	GAGTGGTGGG CTGGAGGGGG	GTTACAGGT -CAGGACTGC	CCCTCTGGCA AGTCCGGGAG	GCCCAGGTGT ACCTGTGCTG	GGGGATTGGA
FOR_DS1535	GAGTGGTGGG CTGGAGGGGG	GTTACAGGT -CAGGACTGC	CCCTCTGGCA AGTCTGGGAG	GCCCAGGTGT ACCTGTGCTG	GGGGATTGGA
MAM1_SP134	GAGTGGTGGG CTGGAGGGGG	GTTACAGGT -CAGGACTGC	CCCTCTGGCA AGTCCGGGAG	GCCCAGGTGT ACCTGTGCTG	GGGGATTGGA
MAST_A358_	GAGTGGTGGG CTGGAGGGGG	GTTACAGGT GCAGGACTGC	CCCTCTGGCA AGTCTGGGAG	GCCCAGGTG- ACCTGTACTA	--GGATTGGA
SAV1_SE210	GAGTGGTGGG CTGGAGGAGG	GTTACAGGT -CAGGACTGC	CCCTCTGGCA AGTCTGGGAG	GCCCAGGTGT ACCTGTGCTG	GGGGATTGGA

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ASIAN2_Ema	GCAGCATCCC A-TCGCCACG	TGCCGGGCCA AGCTGCTGTG	AGGGCAGCTC GTTTAGCACR	TGCCGAC-AC CTGCAGACAT	CACCAAGTTC G
FOR_DS1535	GCAGCATCCC A-TCGCCACG	TGCCGGGCCA AGCTGCTGTG	AGGGCAGCTC GTTTAGCACR	TGCCGAC-AC CTGCAGACAT	CACCAAGTTC G

MAM1_SP134	GCAGCATCCC A-TCGCCACG	TGCCAGGCCA AGCTGCTGTG	AGGGCAGCTC GTTTAGCACG	TGCCGAC-AC CTGCAGACAT	CACCAAGTTC G
MAST_A304_	ACAGCATCCC AGTCGCCACG	TGCCAGGCCA AGCTGCTGTG	AGGGCAGCTC GTTTAGCACG	TGCCGACCAC CTGCAAACAC	CACCAAGTTC A
SAV1_SE210	GCAGCATCCC A-TCGCCACG	TGCCAGGCCA AGCTGCTGTG	AGGGCAGCTC GTTTAGCACG	TGCCGAC-AC CTGCAGACAT	CACCAAGTTC G

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ASIAN2_Ema	TGATTTTTTA CCCATCCCAA	TTTCTCCACC CACTCCGGCA	CAAAAACCAA ACCCATTCTT	ACTCGTATAC CGGCGTTCCA	AGGCTCCCCA AGT
FOR_DS1535	TGATTTTTTA CCCATCCCAA	TTTCTCCACC CACTCCGGCA	CAAAAACCAA ACCCATTCTT	ACTCGTATAC CGGCGTTCCA	AGGCTCCCCA AGT
MAM1_SP134	TGATTTTTTA CCCATCCCAA	TTTCTCCACC CACTCCGGCA	CAAAAACCAA ACCCATTCTT	ACTCGTATAC CGGCGTTCCA	AGGCTCCCCA AGT
MAST_A305_	TGATTTTTTA CCCATCCCAA	TTTCTCCACC CACTCCGGCA	CAAAAATCAA ACCCATTCTT	ACTCGTATAT CGGCGTTCCA	AGGCTCCCCA AGT
SAV1_SE210	TGATTTTTTA CCCATCCCAA	TTTCTCCACC CACTCCGGCA	CAAAAACCAA ACCCATTCTT	ACTCGTATAC CGGCGTTCCA	AGGCTCCCCA CGT

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ASIAN2_Ema	GTTAAACACC CACATGTGGA AGG	GGACCAGACC TTGCATAGGG	ACAAGTGGG- CTCGCTGGTG	TGGGAGCCAG GTGAGCAACA	ACTGGAACTA GAAACTGATT
FOR_DS1535	GTTAAACACC CACGTGTGGA AGG	GGACCAGACC TTGCATAGGG	ACAAGTGGGG CTCGCTGGTG	TGGGAGCCGG GTGAGCAACA	ACTGGAACTA GAAACTGATT
MAM1_SP134	GTTAAACACC CATGTGTGGA AGG	GGACCAGACC TTGCATAGGG	ACAAGTGGG- CTCGCTGGTG	TGGGAGCCAG GTGAGCAACA	ACTGGAACTA GAAACTGATT
MAST_A306_	GTTAAACACC CACGTGTGGA AAA	GGACCAGACC TTGCATAGGG	ATAAGTGGGG CTCACTGGTG	TGGGAGCCGG GTGAGCAACA	ACTGGAACTA GAAACTGATT
SAV1_SE210	GTTAAACACC CACGTGTGGA AGG	GGACCAGACC TTGCATAGGG	ACAAGTGGGG CTCGCTGGTG	TGGGAGCCAG GTGAGCAACA	ACTGGAACTA GAAACTGATT

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ASIAN2_Ema	CAAATTTGGA ATGAGGGATC AGCTTCAGT	TGCCTCTCCA GGCCAGCAGA	CGGGGATCCT GAAGGGTCCT	AACTTTTCTT TGTTGAAACC	CTATTCGACA AAGGAAGAAG
FOR_DS1535	CAAATTTGGA GTGAGGGATC AGCTTCAGT	TGCCTCTCCA GGCCAGCAGA	CGGGGATCCT GAAGGGTCCT	AACTTTTCTT TGTTGAAACC	GTATTTGACA AAGGAAGAAG
MAM1_SP134	CAAATTTGGA RTGAGGGATC AGCTTCAGT	TGCCTCTCCA GGCCAGCAGA	CGGGGATCCT GAAGGGTCCT	AACTTTTCTT TGTTGAAACC	STATTYGACA AAGGAAGAAG
MAST_A233_	CAAATTTGGA GTGAGGGATC AGCTTCAGT	TGCCTCTCCA GGCCAGCAGA	CGGGGATCCT GAAGGGTCCT	AACTTTTCTT TGTTGAAACC	GTATTCGATG AAGGAAGAAG
SAV1_SE210	CAAATTTGGA GTGAGGGATC AGCTTCAGT	TGCCTCTCCA GGCCAGCAGA	TGGGGATCCT GAAGGGTCCT	AACTTTTCTT TGTTGAAACC	GTATTTGACA AAGGAAGAAG

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ASIAN2_Ema	CTGGCAAGTG TGGTGGTGTT	CTGGTGGGTG CATCCGGCTC	TGGGTGTGCC CTGCAGTCCC	CATCATCCTC ACTGCCCACG	CTGCTGATCC TGTC
FOR_DS1535	CTGGCAAGTG TGGTGGTGTT	CTGGTGGGTG CATCCGGCTC	TGGGTGTGCC CTGCAGTCCC	CATCATCCTC ACTGCCCACG	CTRCTGATCC TGTC
MAM1_SP134	CTGGCAAGTG TGGTGGTGTT	CTGGTGGGTG CATCCGGCTC	TGGGTGTGCC CTGCAGTCCC	CATCATCCTC ACTGCCCACG	CTGCTGATCC TGTC
MAST_A234_	CTGGCAAGTG TGGTGGTGTT	CTGGTGGGTG CATCCGACTC	TGGGTGTGCC CTGCAGTCCC	CATCATCCTC ACTGCCCACG	CTGCTGATCC TATC
SAV1_SE210	CTGGCAAGTG	CTGGTGGGTG	TGGGTGTGCC	CATCATCCTC	CTGCTGATCC

TGGTGGTGTT CATCCGGCTC CTGCAGTCCC ACTGCCACG TGTC

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ASIAN2_Ema	AAGACAGCTA	CCTGGTCAAC	CAACTGGAAG	AGATCTGTAT	TTATGCCTAT
	TCCAAATAAA	GGTGATCCAA	CAGAATGCAG	AAATTATCTA	ACAATAT
FOR_DS1535	AAGACAGCTA	CCTGGTCAAC	CAACTGGAAG	AGATCTGTAT	TTATGCCTAT
	TCCAAATAAA	GGTGATCCAA	CAGAATGCAG	AAATTATCTA	ACAATAT
MAM1_SP134	AAGACAGCTA	CCTGGTCAAC	CAACTGGAAG	AGATCTGTAT	TTATGCCTAT
	TCCAAATAAA	GGTGATCCAA	CAGAATGCAG	AAATTATCTA	ACAATAT
MAST_A421_	AAGACAGCTA	CCTGGTCAAC	CAACTGGAAG	AGATCTGTAG	TTATACCTAT
	TTCAAAGAAA	GGTGATCCAG	CAGAATGTGG	AAATTATCAA	ACAATAT
SAV1_SE210	AAGACAGCTA	CCTGGTCAAC	CAACTGGAAG	AGATCTGTAT	TTATGCCTAT
	TCCAAATAAA	GGTGATCCAA	CAGAATGCAG	AAATTATCTA	ACAATAT

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ASIAN2_Ema	TGTCTTTGTG	CCACTCTGAA	TCCATCTTGA	GATCCCCTCT	TCTCTCCCTT
	TTAAAGAGAG	CTGGCAAAC	CACCTCCTGG	TAACTCCCTG	CTGATTCCAA
	GAATC				
FOR_DS1535	TGTCTTTGTG	TCACTCTGAA	TCCATCTTGA	GATCCCCTCT	TCTCTCCCTT
	TTAAAAAGAG	CTGGCAAAC	CACCTCCTGG	TAACTCCCTG	CTGATTCCAA
	GAATC				
MAM1_SP134	TGTCTTTGTG	CCACTCTGAA	TCCATCTTGA	GATCCCCTCT	TCTCTCCCTT
	TTAAAGAGAG	CTGGCAAAC	CACCTCCTGG	TAACTCCCTG	CTGATTCCAA
	GAATC				
MAST_A360_	TGTCTTTGTG	CCACTCTGAA	TCCATCTTGA	GATCCCCTCT	TTTCTCCCTT
	TTAAAGAGAG	CTGGCAAAC	CACCTCCTGG	TAACTCCCTG	CTGATTCCAA
	GAATC				
SAV1_SE210	TGTCTTTGTG	CCACTCTGAA	TCCATCTTGA	GATCCCCTCT	TCTCACCTT
	TTAAAGAGAG	CTGGCAAAC	CACCTCCTGG	TAACTCCCTG	CTGATTCCAA
	GAATC				

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ASIAN2_Ema	TCTTGCCCAG	CCCTGCTGGG	GACCTGGCTG	GGCACAGGGT	CCCTGTCGCT
	CAGACCGAGG	CTCTCAGCTG	ACTTCCTGAA	GGCCCAGAAA	CTC
FOR_DS1535	TCTTGCCCAG	CCCTGCTGGG	GACCTGGCTG	GGCACAGGGT	CCCTGTCGCT
	CAGACCGAGG	CTCTCAGCTG	ACTTCCTGAA	GGCCCAGAAA	CTC
MAM1_SP134	TCTTGCCCAG	CCCTGCTGGG	GACCTGGCTG	GGCACAGGGT	CCCTGTCGCT
	CAGACCGAGG	CTCTCAGCTG	ACTTCCTGAA	GGCCCAGAAA	CTC
MAST_A235_	TCTTGCCCCA	CCCTACTGGG	ACTTGTTG	AGCACAGGGT	CCCTGTCGCT
	CAGACCAAGG	CTCTCAGCTG	ACTTCCTGAA	GGCCCAGAAA	CTC
SAV1_SE210	TCTTGCCCAG	CCCTGCTGGG	GACCTGGCTG	GGCACAGGGT	CCCTGTCGCT
	CAGACCGAGG	CTCTCAGCTG	ACTTCCTGAA	GGCCCAGAAA	CTC

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ASIAN2_Ema	TTAGTTGTGT	GCCAATTGTA	GAACAACTT	TGGAAGCATA	ATAGTGGTAT
	TCATAAGACT	TTCTGTGCTA	TATGTGGGAC	CCTCCTGGAA	CTGTT
FOR_DS1535	TTAGTTGTGT	GCCAATTGTA	GAACAACTT	TGGAAGCATA	ATAGTGGTAT
	TCATAAGACT	TTCTGTGCTA	TATGTGGGAC	CCTCCTGGAA	CTGTT
MAM1_SP134	TTAGTTGTGT	GCCAATTGTA	GAACAACTT	TGGAAGCATA	ATAGTGGTAT
	TCATAAGACT	TTCTGTGCTA	TATGTGGGAC	CCTCCTGGAA	CTGTT
MAST_A423_	TTAGTTGTGT	GCCAATTTTA	GAACAACTT	TGGAAGTGTG	ATAGTGGTAT
	TCATAAGACT	TTCTGTGCTA	TATGTGGGAC	CCTCCTGGAA	CTGTT
SAV1_SE210	TTAGTTGTGT	GCCAATTGTA	GAACAACTT	TGGAAGCATA	ATAGTGGTAT
	TCATAAGACT	TTCTGTGCTA	TATGTGGGAC	CCTCCTGGAA	CTGTT

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ASIAN2_Ema	CTGGGTACAC	TTGTGTGGAA	ATTGCTAATG	TTAAGTCTTT	AATATTCTGT
	TTCATGTTTT	GTTGTTGTTG	TTAGGTGCCA	TCAAATCAAT	TCA
FOR_DS1535	CTGGGTACAC	TTGTGTGGAA	ATTGCTAATG	TTAAGTCTTT	AATATTCTGT
	TTCATGTTTT	GTTGTTGTTG	TTAGGTGCCA	TCAAATCAAT	TCA
MAM1_SP134	CTGGGTACAC	TTGTGTGGAA	ATTGCTAATG	TTAAGTCTTT	AATATTCTGT

MAST_A236_	TTCATGTTTT TTGGGTATAC TTCATGTTTT	GTTGTTGTTG TTGTGTGGAA GTTGTTTTTG	TTAGGTGCCA ATTGCTAATG TTAGGTGCCA	TCAAATCAAT TTAAGTCTTT TCAAATCAGT	TCA AATATTCTGT TCA AATATTCTGT TCA
SAV1_SE210	CTGGGTACAC TTCATGTTTT	TTGTGTGGAA GTTGTTGTTG	ATTGCTAATG TTAGGTGCCA	TTAAGTCTTT TCAAATCAAT	AATATTCTGT TCA

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ASIAN2_Ema	ACACACAACC GGGTGCCAGT TGCGGGTG	TTAATGATCA GAGGGTCACT	CAGAGGACGT GGGAAGAGAT	CTCACCCCTT ACCCAGAAA	TCCTTCACAT -GGTGTCTTT
FOR_DS1535	ACACACAACC GGGTGCCAGT TGCGGGTG	TTAATGATCA GAGGGTCACT	CAGAGGACGT GGGAAGAGAT	CTCACCCCTT ACCCAGAAA	TCCTTCACAT -GGTGTCTTT
MAM1_SP134	ACACACAACC GGGTGCCAGT TGCGGGTG	TTAATGATCA GAGGGTCACT	CAGAGGACGT GGGAAGAGAT	YTCACCCCTT ACCCAGAAA	TCCTTCACAT -GGTGTCTTT
MAST_A237_	ACACACAACC GGGTGCCAGT TGCGGGTA	TTAATGATCA GAGGGTCACT	CAGAGGACGT GGGAAGAGAT	CTCACCCCTT ATCCAGAAA	TCCTTCACAT AGGTGTCTTT
SAV1_SE210	ACACACAACC GGGTGCCAGT GGCGGGTG	TTAATGATCA GAGGGTCACT	CAGAGGACGT GGGAAGAGAT	CTCACCCCTT ACCCAGAAA	TCCTTCACAT -GGTGTCTTT

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ASIAN2_Ema	AATTACTAAT AAATATTTCC	TACAGTTAGG ACATGCTTGC	AATGCTAGAA AGTTTGTTTT	TTAAAAAATT AATGTGGAGG	ATGCTACCAA GTG
FOR_DS1535	AATTACTAAT AAATATTTCC	TACAGTTAGG ACATGCTTGC	AATGCTAGAA AGTTTGTTTT	TTAAAAAATT AATGTGGAGG	ATGCTACCAA GTG
MAM1_SP134	AATTACTAAT AAATATTTCC	TACAGTTAGG ACATGCTTGC	AATGCTAGAA AGTTTGTTTT	TTAAAAAATT AATGTGGAGG	ATGCTACCAA GTG
MAST_A238_	AATTACTAAT AAATATTTCC	TACAGTTAGG ACATGCTTGC	AATGCTAGAA AGTTTGTTTT	TTAAAAAATT AATGTGGAAG	ATGCTACCAA GTA
SAV1_SE210	AATTACTAAT AAATATTTCC	TACAGTTAGG ACATGCTTGC	AATGCTAGAA AGTTTGTTTT	TTAAAAAATT AATGTGGAGG	ATGCTACCAA GTG

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ASIAN2_Ema	TTGAATTGCC TGCCACATCT TTAGGTTATC	CCATAGGGTT TTCTCCCTTG A	TCCAAGGCTG GAGTGGTTGG	TAATCTTTAT TGGGTTTGAA	GGAAGCAGAC CTGCCAECTT
FOR_DS1535	TTGAATTGCC TGCCACATCT TTAGGTTATC	CCATAGGGTT TTCTCCCTTG A	TCCAAGGCTG GAGTGGTTGG	TAATCTTTAT TGGGTTTGAA	GGAAGCAGAC CTGCCAECTT
MAM1_SP134	TTGAATTGCC TGCCACATCT TTAGGTTATC	CCATAGGATT TTCTCCCTTG A	TCCAAGGCTG GAGTGGTTGG	TAATCTTTAT TGGGTTTGAA	GGAAGCAGAC CTGCCAECTT
MAST_A309_	TAGAATTGCC TGCCACATCT TTTGTTAGC	CCCTAGGGTT TTCTCCCTTG A	TCCAAGGCTG GAGTGGTTGG	TAATCTTTAT TGGATTTGAA	GAAAGCAGAT CTACCAACCT
SAV1_SE210	TTGAATTGCC TGCCACATCT TTAGGTTATC	CCATAGGGTT TTCTCCCTTG A	TCCAAGGCTG GAGTGGTTGG	TAATCTTTAT TGGGTTTGAA	GGAAGCAGAC CTGCCAECTT

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ASIAN2_Ema	CTACAAAGAT AATTTGATGG CACT	CTCTTTGTAT ATGCAAGCAA	GAGACTCCAA ACTGTCCCTT	CTGGCTGGAA TGTGGGGAGG	GTTTTTTGGG AAAGCTTCGG
FOR_DS1535	CTACAAAGAT AATTTGATGG CACT	CTCTTTGTAT ATGCAAGCAA	GAGACTCCAA ACTGTCCCTT	CTGGCTGGAA TGTGGGGAGG	GTTTTTTGGG AAAGCTTCGG
MAM1_SP134	CTACAAAGAT AATTTGATGG CACT	CTCTTTGTAT ATGCAAGCAA	GAGACTCCAA ACTGTCCCTT	CTGGCTGGAA TGTGGGGAGG	GTTTTTTGGG AAAGCTTCGG
MAST_A311_	TTACAAAGAT	TTCTTTGTAT	GAGACTCCAA	CTGGCTGGAA	GTTTTTTGGG

	AATTTGATGG CACT	ATGCAAGCAA	ACTGTCCCTT	TGTGGGGAGG	AAAGCTTCGG
SAV1_SE210	CTACAAAGAT AATTTGATGG CACT	CTCTTTGTAT	GAGACTCCAA ACTGTCCCTT	CTGGCTGGAA TGTGGGGAGG	GTTTTTTGGG AAAGCTTCGG

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ASIAN2_Ema	CCATTAAGAG GGTGAAAGTG TG	AGACTGAGAA GTGTACAGA	GGAGCAGCCA AGCCAAAGAA	GTTGGGCAAA ATAAAGGAAA	ATGAAAACCA GGTGGTCAAC
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FOR_DS1535	CCACTACGAG GGTGAAAGTG TG	AGATTGAGAA GTGTACAGA	GGAGCAGCCA AGCCAAAGAA	GTTGGGCAAA ATAAAGGAAA	ATGAAAACCA GGTGGTCAAC
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MAM1_SP134	CCATTAAGAG GGTGAAAGTG TG	AGACTGAGAA GTGTACAGA	GGAGCAGCCA AGCCAAAGAA	GTTGGGCAAA ATAAAGGAAA	ATGAAAACCA GGTGGTCAAC
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MAST_A239_	CCATTAAGTG GGTGAAAGTT TA	AGACTGAGAA GTGTACAGA	GGAGCAGCCT AGCCAAAGAA	GTTGGGCAAA ATAAAGGAAA	ATGAAAACCA GGTGATCAAC
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SAV1_SE210	CCATTAAGAG GGTGAAAGTG TG	AGACTGAGAA GTGTACAGA	GGAGCAGCCA AGCCAAAGAA	GTTGGGCAAA ATAAAGGAAA	ATGAAAACCA GGTGGTCAAC
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ASIAN2_Ema	ACCGGGGCTG CGGCCGAGGG CTGAACAAAC	ACGAGGTCGC GACCTGGGTT CAG	GGGTTGACAG GAGGGTCACG	GCCACTGGCT TCCCGAGAAG	GAGGGGTTCGC ATGTCCCAGA
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FOR_DS1535	ACCGGGGCTG CGGCCGAGGG CTGAGCAAAC	ACGAGGTCGY GACCTGGGTT CAG	GGGTTGACAG GAGGGTCACG	GCCACTGGCT TCCCGAGAAG	GAGGGGTTCGC ATGTCCCAGA
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MAM1_SP134	ACCGGGGCTG CGGCCGAGGG CTGAGCAAAC	ACGAGGTCGC GACCTGGGTT CAG	GGGTTGACAG GAGGGTCACG	GCCACTGGCT TCCCGAGAAG	GAGGGGTTCGC ATGTCCCAGA
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MAST_A312_	ACCGGGGCTG CGGCCGAGGG CTGAGCAAAC	ACGAGGTCGC GACCTGGGTT CAG	GGGTTGACAG GAGGGTCACG	GCCACTGGCT TCCCGAGAAG	GAGGGGTTCGC ATGTCCCAGA
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SAV1_SE210	GCCGGGGCTG CGGCCGAGGG CTGAGCAAAC	ACGAGGTCGC GACCTGGGTT CAG	GGGTTGACAG GAGGGTCACG	GCCACTGGCT TCCCGAGAAG	GAGGGGTTCGC ATGTCCCAGA
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ASIAN2_Ema	AAAAGTTCTT CTATTAATAA TTTGTA	CTTAACAGTC AAAA-G-CAA	AGATCACACA TATCTAAAAT	CTATCAGAGC GCTGTGCTGG	ATTCGTATTT CTAGACATAT
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FOR_DS1535	AAAAGTTCTT CTATTAATAA TTTGTA	---AACAGTC AAAAAG-CAA	AGATCACACA TATCTAAAAT	CTATCAGAGC GCTGTGCTGG	ATTCGTATTT CTAGACATAT
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MAM1_SP134	AAAAGTTCTT CTATTAATAA TTTGTA	CTTAACAGTC AAAAAG-CAA	AGATCACACA TATCTAAAAT	CTATCAGAGC GCTGTGCTGG	ATTCGTATTT CTAGACATAT
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MAST_A241_	AAAAGTTCTT CTATTAATAA TTTGTA	CTTAACAGTC AAAAAGACAA	AGATCACACA CATCTAAAAT	CTATCAGAGC GCTGGGCTGG	ATTCGTATTT CTAGACTTAT
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SAV1_SE210	AAAAGTTCTT CTATTAATAA TTTGTA	CTTAACAGTC AAA--G-CAA	AGATCACACA TATCTAAAAT	CTATCAGAGC GCTGTGCTGG	ATTCGTATTT CTAGACATAT
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ASIAN2_Ema	CCAAATA-TA GCCATCAGCT AA	AATGCATTTT TCTCAAGGAG	CCATTGGATT CTGAGGGTGA	GGCCAAGTAG ATCTCATTAA	AACTGGATTA CCAACCTTAGA
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FOR_DS1535	CCAAATA-TA GCCATCAGCT	AATGCATTTT TCTCAAGGAG	CCATTGGATT CTGAGGGTGA	GGCCAAGTAG ATCTCATTAA	AACTGGATTA CCAACCTTAGA
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MAM1_SP134	AA CCAAATAATA GCCATCAGCT	AATGCATTTT TCTCAAGGAG	CCATTGGATT CTGAGGGTGA	GGCCAAGTAG ATCTCATTAA	AACTGGATTA CCAACCTTAGA
MAST_A313_	AA CCAAATA-TA GCCATCAGCT	AATGCATTTT TCTCAAGGAG	CCATTGGATT CTGAGGGTGA	GGCCAAGTAG ATCTCATTAA	AATTGGATTA CCAACCTTAGA
SAV1_SE210	AA CCAAATA-TA GCCATCAGCT	AATGCATTTT TCTCAAGGAG	CCATTGGATT CTGAGGGTGA	GGCCAAGTAG ATCTCATTAA	AGCTGGATTA CCAACCTTAGA

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ASIAN2_Ema	GCCTGGACAC TTAGAGCATA	CTAACAGGGC CTGCTCCTTC	CCTCAATGCA CTTCTAACTA	AGTGCCCCAA CTGCTCCAGA	CACTCTTGTC CCTGCTTTCC
FOR_DS1535	AG GCCTGGACAC TTAGAGCATA	CTAACAGGGC CTGCTCCTTC	CCTCAATGCA CTTCTAACTA	AGTGCCCCAA GTGCTCCAGA	CACTCTTGTC CCTGCTTTCC
MAM1_SP134	AG GCCTGGACAC TTAGAGCATA	CTAACAGGGC CTGCTCCTTC	CCTCAATGCA CTTCTAACTA	AGTGCCCCAA CTGCTCCAGA	CACTCTTGTC CCTGCTTTCC
MAST_A314_	AG GTCTGGACAC TTAGAGCATA	CTAACAGGGC CTGCTCCTTC	CCTCAATGCA CTTCTAACTA	AGTGCCCCAA CTGCTCCAGA	CACTCTTGTC CCTGCTTTCC
SAV1_SE210	AG GCCTGGACAC TTAGAGCATA	CTAACAGGGC CTGCTCCTTC	CCTCAATGCA CTTCTAACTA	AGTGCCCCAA CTGCTCCAGA	CACTCTTGTC CCTGCTTTCC

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ASIAN2_Ema	TGTTGACTGG AGAGGGGCGG GTGCTTC	TGTGTAAATT CTGAATGTTC	TGGGGTCAAA TCCTCTACCA	GCTGAATCAC CCTCGCCCCA	CTGGGTCAAG CTTTTCAGCT
FOR_DS1535	TGTTGACTGG AGAGGGGAGG GTGCTTC	TGTGTAAATT CTGAATGTTC	TGGGGTCAAA TCCTCTACCA	GCTGAATCAC CCTCGCCCCA	CTGGGTCAAG CTTTTCAGCT
MAM1_SP134	TGTTGACTGG AGAGGGGCGG GTGCTTC	TGTGTAAATT CTGAATGTTC	TGGGGTCAAA TCCTCTACCA	GCTGAATCAC CCTCGCCCCA	CTGGGTCAAG CTTTTCAGCT
MAST_A243_	TGTTGACTGG AGAGGGGAGG GTGCTTC	TGTGTAAATT CTGAATGTTC	TGGGGTCAAA TCCTCTACCA	GCTGAATCAC CCTCGCCCCA	CTGGGTCAAG CTTTTCAGCT
SAV1_SE210	TGTTGACTGG AGAGGGGAGG GTGCTTC	TGTGTAAATT CTGAATGTTC	TGGGGTCAAA TCCTCTACCA	GCTGAATCAC CCTCGCCCCA	CTGGGTCAAG CTTTTCAGCT

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ASIAN2_Ema	CAACAGAAAA GGCTGTGGAT AAC	TAATTATTTA AGGAAACCAG	AACTGTGCAA CCTTGGTAAA	AGAAGTAATT GGGAGAGAAG	TGAATTTGAA TCAAGAAAAG
FOR_DS1535	AAC CAACAGAAAA GGCTGTGGAT	TAATTATTTA AGGAAACCAG	AACTGTGCAA CCTTGGTAAA	AGAAGTAATT GGGAGAGAAG	TGAATTTGAA TCAAGAAAAG
MAM1_SP134	AAC CAACAGAAAA GGCTGTGGAT	TAATTATTTA AGGAAACCAG	AACTGTGCAA CCTTGGTAAA	AGAAGTAATT GGGAGAGAAG	TGAATTTGAA TCAAGAAAAG
MAST_A244_	AAC TAACAGAAAA GGCTGTGGAT	TAATTATTTA AGGAAACCAG	AACTGTGCAA CCTTGGTAAA	AGAAGTAATT GGGAGAAAAG	TGAATTTGAA TCAAGAAAAG
SAV1_SE210	AAC CAACAGAAAA GGCTGTGGAT	TAATTATTTA AGGAAACCAG	AACTGTGCAA CCTTGGTAAA	AGAAGTAATT GGGAGAGAAG	TGAATTTGAA TCAAGAAAAG

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ASIAN2_Ema	GTGAGAAGAG AGCACGGGAG TGAGCTTTCT	ACCCTGGCCC AGGGAGGTGA TCTTCCTC	GGTGGGAGGC GAGGAGAGGG GAGGAGAGGG	GGAGAAGGGA AGTTAGTGGA AGTTAGTGGA	GGGAGAAAGG CCAACCTACA CCAACCTACA
FOR_DS1535	GTGAGAAGAG AGCATGGGAG TGAGCTTTCT	ACCCTGGCCC AGGGAGGTGA TCTTCCTC	GGTGGGAGGC GAGGAGAGGG GAGGAGAGGG	GGAGAAGGGA AGTTAGTGGA AGTTAGTGGA	GGGAGAAAGG CCAACCTACA CCAACCTACA
MAM1_SP134	GTGAGAAGAG AGCATGGGAG TGAGCTTTCT	ACCCTGGCCT AGGGAGGTGA TCTTCCTC	GGTGGGAGGC GAGGAGAGGG GAGGAGAGGG	GGAGAAGGGA AGTTAGTGGA AGTTAGTGGA	GGGAGAAAGG CCAACCTACA CCAACCTACA
MAST_A315_	GTGAGAAGAG AGCATGGGAG TAAGCTTTCT	ACCCTGGCCC AGGGAGGTGA TCTTCCTC	GGTGGGAGGC GAGGAGAGGG GAGGAGAGGG	GGAGGAGGGA AGTTAGTGGA AGTTAGTGGA	GGGAGAAAGG CCAACCTACA CCAACCTACA
SAV1_SE210	GTGAGAAGAG AGCATGGGAG TGAGCTTTCT	ACCCTGGCCC AGGGAGGTGA TCTTCCTC	GGTGGGAGGC GAGGAGAGGG GAGGAGAGGG	GGAGAAGGGA AGTTAGTGGA AGTTAGTGGA	GGGAGAAAGG CCAACCTACA CCAACCTACA

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ASIAN2_Ema	TTGGAAAACA TTACCTCTTC	GAGAAGCCAG TCTGCTAACA	ATTCGCTCAG TCCATGTTCC	CCTCGCCCTG ACACAGCAAT	CTCTGTCCTC CTCTGTCCTC
FOR_DS1535	TTGGAAAACA TTACCTCTTC	GAGAAGCCAG TCTGCTAACA	ATTCGCTCAG TCCATGTTCC	CCTCGCCCTG ACACAGCAAT	CTCTGTCCTC CTCTGTCCTC
MAM1_SP134	TTGGAAAACA TTACCTCTTC	GAGAAGCCAG TCTGCTAACA	ATTCGCTCAG TCCATGTTCC	CCTCGCCCTG ACACAGCAAT	CTCTGTCCTC CTCTGTCCTC
MAST_A317_	TTGGAAAACA TTAC-TCTTC	GAGGAGCCAG TCTGCTAACA	ATTCGCTCAG TCCATGTTCC	CCTCGCCCTG ACACAGCAAT	CTGTGTGCTC CTGTGTGCTC
SAV1_SE210	TTGGAAAACA TTACCTCTTC	GAGAAGCCAG TCTGCTAACA	ATTCGCTCAG TCCATGTTCC	CCTCGCCCTG ACACAGCAAT	CTCTGTCCTC CTCTGTCCTC

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ASIAN2_Ema	TACTAGGTGC GCATCCTGAA TCCAAA	CAAACACCCT AGGCTGGGGA	CAGAATTGGG GTCTGTGGAC	GCCTGTGGAA TTACACAACC	CTCAACAGAA TCAGAGGGCT
FOR_DS1535	TACTAGGTGC GCATCCTGAA TCCAAA	CAAACACCCT AGGCTGGGGA	CAGAATTGGG GTCTGTGGAC	GCCTGTGGAA TTACACAACC	CTCAACAGAA TCAGAGGGCT
MAM1_SP134	TACTAGGTGC GCATCCTGAA TCCAAA	CAAACACCCT AGGCTGGGGA	CAGAATTGGG GTCTGTGGAC	GCCTGTGGAA TTACACAACC	CTCAACAGAA TCAGAGGGCT
MAST_A364_	TACTAGGTGC GCATCCTGAA TCCAAA	CAAACACCCT AGGCTGGGGA	TAGAACTGGG GTCTGTGGAC	GGCTGTGGAA TTACACAACC	CTCAACAAAA TCAGAGGGTT
SAV1_SE210	TACTAGGTGC GCATCCTGAA TCCAAA	CAAACACCCT AGGCTGGGGA	CAGAATTGGG GTCTGTGGAC	GCCTGTGGAA TTACACAACC	CTCAACAGAA TCAGAGGGCT

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ASIAN2_Ema	CAGAAGGTGA GGCCCCTGCC CCAGGC	CAGGGGGTTC CTGGGGGGCC	AAGTCCCCT GCCTCTGAGG	TCAAAGCTGC TGACCAACCT	TCACGGGAGG TCCTGGTTTG
FOR_DS1535	CAGAAGGTGA GGCCCCTGCC CCAGGC	CAGTGGGTTC CTGGGGGACC	AAGTCCCCT GCCTCTGAGG	TCAAAGCTGC TGACCAACCT	TCACGGGAGG TCCTGGTTTG
MAM1_SP134	CAGAAGGTGA GGCCCCTGCC CCAGGC	CAGGGGGTTC CTGGGGGGCC	AAGTCCCCT GCCTCTGAGG	TCAAAGCTGC TGACCAACCT	TCACGGGAGG TCCTGGTTTG
MAST_A245_	CAGAAGATGA GGCCCCTGCC CCAGGA	CAGGAGGTTC CTGGGGTACC	AAGTCCCCT GCCTCTGAGA	TCAAAGCTGC TGACCAACCT	TCACGGGAGG TCCTGGTTTG
SAV1_SE210	CAGAAGGTGA GGCCCCTGCC CCAGGC	CAGTGGGTTC CTGGGGGACC	AAGTCCCCT GCCTCTGAGG	TCAAAGCTGC TGACCAACCT	TCACGGGAGG TCCTGGTTTG

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ASIAN2_Ema	CATGTGTGTC T-GGAAGTAG AAACTTCCAA	AGAGTAAAAC ATTACAARAC ACTTTTGGT	TGTCATAGGG GTTTCTTTCA	TTTT-CAATG AAACGTCTCT	GCTAATTTTT AGGTGGACTC
FOR_DS1535	CATGTGTGTC T-GGAAGTAG AAACTTCCAA	AGAGTAAAAC ATTACAAGAC ACTTTTGGT	TGTCATAGGG GTTTCTTTCA	TTTT-CAATG AAACGTCTCT	GCTAATTTTT AGGTGGACTC
MAM1_SP134	CATGTGTGTC T-GGAAGTAG AAACTTCCAA	AGAGTAAAAC ATTACAAGAC ACTTTTGGT	TGTCATAGGG GTTTCTTTCA	TTTT-CAATG AAACGTCTCT	GCTAATTTTT AGGTGGACTC
MAST_A246_	CATGTGTGTC TTGGAAGTAG AAACTTCCAA	AGAGTAAAAC ATCACAAGAC ACTTTTGGT	TGTCATAGGG CTTTCTTTCA	TTTTTCAACG AAACGTCTCT	GCTAATTTTT AGGTGGACTC
SAV1_SE210	CATGTGTGTC T-GGAAGTAG AAACTTCCAA	AGAGTAAAAC ATTACAAGAC ACTTTTGGT	TGTCATAGGG GTTTCTTTCA	TTTT-CAATG AAACGTCTCT	GCTAATTTTT AGGTGGACTC

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ASIAN2_Ema	GTCTGGCAGA AAACCGACCG	ACTGTGCATT CTGTCCCCTG	CCATGCCTGG AACGCGTTCC	GTGACCTGGT AAAACAAGCA	TCAATGGGGG TTC
FOR_DS1535	GTCTGGCAGA AAACCGACCG	ACTGTGCATT CTGTCCCCTG	CCATGCCTGG AACGCGTTCC	GTGACCTGGT AAAACAAGCA	TCAATGGGGG TTC
MAM1_SP134	GTCTGGCAGA AAACCGACCG	ACTGTGCATT CTGTCCCCTG	CCATGCCTGG AACGCGTTCC	GTGACCTGGT AAAACAAGCA	TCAATGGGGG TTC
MAST_A247_	-TCTGGCAGA AAACCGACCG	ACTGTGCATT CTGTCCCCTG	CCATGCCTGG AACGCGTTCC	GTGACCTAGT AAAACAAGCA	TCAATGGGGG- TTC
SAV1_SE210	GTCTGGCAGA AAACCGACCG	ACTGTGCATT CTGTCCCCTG	CCATGCCTGG AACGCGTTCC	GTGACCTGGT AAAACAAGCA	TCAATGGGGG TTC

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ASIAN2_Ema	AAAGAACACA TT-CGTAGTA GTCCTGAGAC	AAAGCTTGTT CTTGGAGATG ATCAGGT	GGGTGTCGTG TTGGGAAAA-	AAAAGCAAGA GATGCTTTCT	AGCCCATTTT TTTAAAGGCC
FOR_DS1535	AAAGAACACA TT-CGTAGTA GTCCTGAGAC	AAAGCTTGTT CTTGGAGATG ATCAGGT	GGGTGTCGTG TTGGGAAAA-	AAAAGCAASA GATGCTTTCT	AGCCCATTTT TTTAAAGGCC
MAM1_SP134	AAAGAACACA TT-CGTAGTA GTCCTGAGAC	AAAGCTTGTT CTTGGAGATG ATCAGGT	GGGTGTCGTG TTGGGAAAA-	AAAAGCAAGA GATGCTTTCT	AGCCCATTTT TTTAAAGGCC
MAST_A366_	AAACAACA-A TTTCGTAGTA GTCCTGAGAC	AAAGCTTGTT CTTGGAGACG ATCAGGT	GGGTGTCGTG CTGGGAAAA	AAAAGCAAGA GATGCGTTGT	AGCCCATTTT TTTCAAGGCC
SAV1_SE210	AAAGAACACA TT-CGTAGTA GTCCTGAGAC	AAAGCTTGTT CTTGGAGACG ATCAGGT	GGGTGTCGTG TTGGGAAAA-	AAAAGCAAGA GATGCTTTCT	AGCCCATTTT TTTAAAGGCC

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ASIAN2_Ema	TCGCTTACAT GGGAAAGAAT	CTGGGGGAGA TGGGGCTGGG	AATGTTACC GGTGGTAGCT	TTCACTCGAG GAGCCACAGA	CCTTGCACCA GTGTG
FOR_DS1535	TCGCTTACAT GGGAAAGAAT	CTGGGGGAGA TGGAGCTGGG	AATGTTACC GGTGGTAGCT	TTCACTCGAG GAGCCACAGA	CCTTGCACCA GTGTG
MAM1_SP134	TCGCTTACAT GGGAAAGAAT	CTGGGGGAGA TGGGGCTGGG	AATGTTACC GGTGGTAGCT	TTCACTCGAG GAGCCACAGA	CCTTGCACCA GTGTG
MAST_A320_	TTGCTTACAT GGGAAAGAAT	CTGGGGGAGA TGGGGCTGGG	AATGTTACC GGTGGTAGCT	TTCACTCGAG GAGCCACAGA	CCTTGCACCA GTATG
SAV1_SE210	TCGCTTACAT GGGAAAGAAT	CTGGGGGAGA TGGGGCTGGG	AATGTTACC GGTGGTAGCT	TTCACTCGAG GAGCCACAGA	CCTTGCACCA GTGTG

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ASIAN2_Ema	GGCCTGAAGG GAGTTGGCAG	CAAGGAGGCG AGGTCAAGCC	CAGCTGGGAG CACTGCTGCC	CGGTACGGA CGCCTCCCAG	GCTGCTCAGA GAT-GGG
FOR_DS1535	GGCCTGAAGG GAGTTGGCAG	CAAGGAGGCG AGGTCAAGCC	CAGCTGGGAG CACTGCTGCC	CGGTACGGA CGCCTCCCAG	GCTGCTCAGA SAT-GGG
MAM1_SP134	GGCCTGAAGG	CAAGGAGGCG	CAGCTGGGAG	CGGTACGGA	GCTGCTCAGA

MAST_A321_	GAGTTGGCAG	AGGTCAGGCC	CACTGCTGCC	CGCCTCCCAG	GAT-GGG
SAV1_SE210	GGTCTGAAGG	CAAGGAGGCC	CAGCTGGGAG	CGGTACACGA	GCTGCTCAGA
	GAGTTGGCAG	AGGTCAGGCC	CACTGCTGCC	CGCCTCCCAG	GAT-GGG
	GGCCTGAAGG	CAAGGAGGCC	CAGCTGGGAG	CGGTACACGA	GCTGCTCAGA
	GAGTTGGCAG	AGGTCAGGCC	CACTGCTGCC	CGCCTCCCAG	GAT-GGG

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ASIAN2_Ema	AAGAGTAAAG	CTAGAGAATT	AATTCTAATA	AATACTTGTG	TCTCAAAGTA
FOR_DS1535	AAA-GCCTGA	AATGGGCGTC	AGGAAACGTT	CATGTGCAAG	GTGAAGATCA
MAM1_SP134	ATAACTG				
MAST_A249_	AAGAGTAAAG	CTAGAGAATT	AATTCTAATA	AATACTTGTG	TCTCAAAGTA
SAV1_SE210	AAA-GCCTGA	AATGGGCGTC	AGGAAACGTT	CATGTGCAAG	GTGAAGATCA
	ATAACTG				
	AAGAGTAAAG	CTAGAGAATT	AATTCTAATA	AATACTTGTG	TCTCAAAGTA
	AAA-GCCTGA	AATGGGCGTC	AGGAAACGTT	CATGTGCAAG	GTGAAGATCA
	ATAACTG				
	AAGAGTAAAG	CTAGAGAATT	AATTCTAATA	AATACTTGTG	YCTCAAAGTA
	AAA-GCCTGA	AATGGGCGTC	AGGAAACGTT	CATGTGCAAG	GTGAAGATCA
	ATAACTG				

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ASIAN2_Ema	TTCACTATTC	TTTTGGTTTT	CCTTTTCTTC	TCTCCTGTGT	CTCTTCCACA
FOR_DS1535	GATATTGCTG	CCTCTCTTTG	GCATCAGTTC	GGGTCTTGAA	AATGTGGCCA
MAM1_SP134	CCTGTGAAT				
MAST_A368_	TTCACTATTC	TTTTGGTTTT	CCTTTTCTTC	TCTCCTGTGT	CTCTTCCACA
SAV1_SE210	GATATTGCTG	CCTCTCTTTG	GCATCAGTTC	GGGTCTTGAA	AATGTGGCCA
	CCTGTGAAT				
	TTCACTATTC	TTTTGGTTTT	CCTTTTCTTC	TCTCCTGTGT	CTCTTCCACA
	GATATTGCTG	CCTCTCTTTG	GCATCAGTTC	GGGTCTTGAA	AATGTGGCCA
	CCTGTGAAT				
	TTCACTATTC	TTTTGGTTTT	CCTTTTCTTC	TCTCCTGTGT	CTCTTCCACA
	GATATTGCTG	CCTCTCTTTG	GCATCAGTTC	GGGTCTTGAA	AATGTGGCCA
	CCTGTGAAT				

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ASIAN2_Ema	CTCAGAGTGG	GGTGAGGAAT	TCCATTTTGA	ATGCTTCCAT	TTATCTAGCT
FOR_DS1535	GTGATTTTCA	GCTCTCTGAG	TGTGAGGGGA	CCCTTGAGAC	TACCACA
MAM1_SP134	CTCAGAGTGG	GGTGAGGAAT	TCCATTTTGA	ATGCTTCCAT	TTATCTAGCT
MAST_A324_	GTGATTTTCA	GCTCTCTGAG	TGTGAGGGGA	CCCTTGAGAC	TACCACA
SAV1_SE210	CTCAGAGTGG	GGTGAGGAAT	TCCATTTTGA	ATGCTTCCAT	TTATCTAGCT
	GTGATTTTCA	GCTCTCTGAG	TGTGAGGGGA	CCCTTGAGAC	TACCACA
	CTCAGAGTGG	GGTGAGGAAT	TCCATTTTGA	ATGCTTCCAT	TTATCTAGCT
	GTGATTTTCA	GCTCTCTGAG	TGTGAGGGGA	CCCTTGAGAC	TACCACA

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ASIAN2_Ema	TTTCAATTCT	ATTTTAAAAT	ACACATGTGG	AAGAGGCTCC	WTTACTGGGAT
FOR_DS1535	TCATGGAAGT	TGCATGAGTG	CGGTGATTTG	GGAACCTAGA	GGTGATAGGT
MAM1_SP134	GCA				
MAST_A326_	TTTCAATTCT	ATTTTAAAAT	ACACATGTGG	AAGAGGCTCC	TTACTGGGAT
	TCATGGAAGT	TGCATGAGTG	CGGTGATTTG	GGAACCTAGA	GGTGATAGGT
	GCA				
	TTTCAATTCT	ATTTTAAAAT	ACACATGTGG	AAGAGGCTCC	TTACTGGGAT
	TCATGGAAGT	TGCATGAGTG	CGGTGATTTG	GGAACCTAGA	GGTGATAGGT
	GCA				
	TTTCAATTCT	ATTTTAAAAT	ACACATGTGG	AAGAGGCTCC	TTACTGGGAT

	TCATGGAAT GCA	TGCATGAGTG	TGGTGATTTG	GGAGCCTAGA	GGTGATAGGT
SAV1_SE210	TTTTCAATTCT TCATGGAAGT GCA	ATTTTAAAAAT TGCATGAGTG	ACACATGTGG CGGTGATTTG	AAGAGGCTCC GGAACCTAGA	TACTGGGAT GGTGATAGGT

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ASIAN2_Ema	CAAATTGTGT TTCAGGCCTT TTAGGTGAGC	TTCATCGGGT TCTTCTGAGG GG	TTCCAATGAC CATCTCTGGG	TGATTTTTCA TGGACTCGAA	GAAGTGGGT CCACCAGCCT
FOR_DS1535	CAAATTGTGT TTCAGGCCTT TTAGGTGAGC	TTCATCGGGT TCTTCTGAGG GG	TTTCAATGAC CATCTCTGGG	TGATTTTTCA TGGACTCGAA	GAAGTGGGT CCACCAGCCT
MAM1_SP134	CAAATTGTGT TTCAGGCCTT TTAGGTGAGC	TTCATCGGGT TCTTCTGAGG GG	TTTCAATGAC CATCTCTGGG	TGATTTTTCA TGGACTCGAA	GAAGTGGGT CCACCAGCCT
MAST_A251_	CAAATTGTGT TTCAGGCCTT TTAGGTGAGT	TTCATCGGGT TCTTCTGAGG GG	TTTCAATGAC CATCTCTGGG	TGATTTTTCA TGGACTCGAA	GAAGTGGGT CCACCAGCCT
SAV1_SE210	CAAATTGTGT TTCAGGCCTT TTAGGTGAGC	TTCATCGGGT TCTTCTGAGG GG	TTTCAATGAC CATCTCTGGG	TGATTTTTCA TGKACTCGAA	GAAGTGGGT CCACCAGCCT

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ASIAN2_Ema	CCGCCAAGAC TGCCCCTGCC AGGCC	CTGGATT-AA TCTCTGCACC	AAACTCAATC CAGAGCTGGC	CCTCAGTCAC GGCTGGGCAT	TATCACCAC- TGGCGGCCCC
FOR_DS1535	CCGCCAAGAC TGCCCCTGCC AGGCC	CTGGATT-AA TCTCTGCACC	AAACTCAATC CAGAGCTGGC	CCTCAGTCAC GGCTGGGCAT	TATCACCAC- TGGCGGCCCC
MAM1_SP134	CCGCCAAGAC TGCCCCTGCC AGGCC	CTGGATT-AA TCTCTGCACC	AAACTCAATC CAGAGCTGGC	CCTCAGTCAC AGCTGGGCAT	TAGCACCAC- TGGCGGCCCC
MAST_A252_	CCGCCAAGAC TGCCCCTGCC AGACC	CTGGATTTAA TCTCTGCACC	AAACTCAATC CAGAGCTGGC	CCTCAGTCAC GGCTGGGCAT	TACCACCACC TGGTGGCCCC
SAV1_SE210	CCGCCAAGAC TGCCCCTGCC AGGCC	CTGGATT-AA TCTCTGCACC	AAACTCAATC CAGAGCTGGC	CCTCAGTCAC GGCTGGGCAT	TATCACCAC- TGGCGGCCCC

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ASIAN2_Ema	AAAACGGAGG GCCTAGTGGG AA	TTCGGCAGCC GTAGAATTGT	CAGGGTCAAC GTAAGAGCGT	TGTCTCTAGA TAGACGGGGC	GCAGGGATGG CTGGGAGAGG
FOR_DS1535	AAAACGGAGG GCCTAGTGGG AA	TTCGGCAGCC GTAGAATTGT	CAGGGTCAAC GTAAGAGCGT	TGTCTCTAGA TAGACGGGGC	GCAGGGATGG CTGGGAGAGG
MAM1_SP134	AAAACGGAGG GCCTAGTGGG AA	TTCGGCAGCC GTAGAATTGT	CAGGGTCAAC GTAAGAGCGT	TGTCTCTAGA TAGACGGGGC	GCAGGGATGG CTGGGAGAGG
MAST_A328_	AAAACGGAGG GCCTAGTGGG AA	TTCGGCAGCC GTAGAATTGC	CAGGGTCAAC ATAAGAGCAT	CGTCTCTAGA TAGGCGGGGC	GCAGGGATGG CTGGGAGAGG
SAV1_SE210	AAAACGGAGG GCCTAGTGGG AA	TTCGGCAGCC GTAGAATTGT	CAGGGTCAAC GTAAGAGCGT	TGTCTCTAGA TAGACGGGGC	GCAGGGATGG CTGGGAGAGG

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ASIAN2_Ema	TGTT-ATTT- CTGCAGGAAT TCCCTCTA	ATGCTGAGCA GAAAGCAAGA	TTTCTGGGGG ATCCTGCAGG	CCAGACAATT CGGCTCCTTC	AACTTTTT-A CTTGAGGGGA
FOR_DS1535	TGTT-ATTT- CTGCAGGAAT	ATGCTGAGCA GAAAGCAAGA	TTTCTGGGGG ATCCTGCAGG	CCAGACAATT CGGCTCCTTC	AACTTTTT-A CTTGAGGGGA

MAM1_SP134	TCCCTCCTA TGTT-ATTT- CTGCAGGAAT TCCCTCCTA	ATGCTGAGCA GAAAGCAAGA	TTTCTGGGGG ATCCTGCAGG	CCAGACAATT CGGCTCCTTC	AACTTTTT-A CTTGAGGGGA
MAST_A254_	TGTTTTATTTT CTGCAGGAAT TCCCTCCTA	ATGCTGAGCA GAAAGCAAGA	TTTCTGGGGG ATCCTGCAGG	CCAGACAATT CGGCTCCTTC	AACTTTTTTA CTTAAAGTAA
SAV1_SE210	TGTT-ATTT- CTGCAGGAAT TCCCTCCTA	ATGCTGAGCA GAAAGCAAGA	TTTCTGGGGG ATCCTGCAGG	CCAGACAATT CGGCTCCTTC	AACTTTTT-A CTTGAGGGGA

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ASIAN2_Ema	GAAACACACC GTTCTTGTGT	AAAAGACATC CTTCAGAAAA	TGAAACACAG TCCAGAAGGG	ACCAAGTGGTG CCCCAAAAA-	CAAGGCCATA G
FOR_DS1535	GAAACACACC GTTCTTGTGT	AAAAGACGTC CTTCAGAAAA	TGAATCACAG TCCAGAAGGG	ACCAATGGTG CCCCAAAAA-	CAAGGCCATA G
MAM1_SP134	GAAACACACC GTTCTTGTGT	AAAAGACGTC CTTCAGAAAA	TGAATCACAG TCCAGAAGGG	ACCAAGTGGTG CCCCAAAAA-	CAAGGCCATA G
MAST_A330_	GAAATACACC GTTCTTGTGT	AAAAGACGTC CTTCAGAAAA	TGAATCACAG TCCAGAAGGG	ACCAAGTGGTG CCCCAAAAA	CAAGGCCATA G
SAV1_SE210	GAAACACACC GTTCTTGTGT	AAAAGACGTC CTTCAGAAAA	TGAATCACAG TCCAGAAGGG	ACCAAGTGGTG CCCCAAAAA--	CAAGGCCATA G

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ASIAN2_Ema	ACAAAGAGGT CTGGCGATTT GTTGTA	GGGCAGTTTG GCTCCCGTAA	AACCCATCCA AGATTACAGC	GTGGGTCCAT CTAGAAAACC	GGAGAAAGAC CTATGGAATA
FOR_DS1535	ACAAAGAGGT CTGGCGATTT GTTGTA	GGGCAGTTTG GCTCCCGTAA	AACCCATCCA AGATTACAGC	GTGGGTCCAT CTAGAAAACC	GGAGAAAGAC CTATGGAACA
MAM1_SP134	ACAAAGAGGT CTGGCGATTT GTTGTA	GGGCAGTTTG GCTCCCGTAA	AACCCATCCA AGATTACAGC	GTGGGTCCAT CTAGAAAACC	GGAGAAAGAC CTATGGAACA
MAST_A331_	ACAAAGAGGT CTGGCGATTT GTTGTA	GGGCAGTTTG GCTCCCGTAA	AACCCATCCA AGATTACAGC	GTGGGTCCAT CTAGAAAACC	GGAGAAAGAC TTATGGAACA
SAV1_SE210	ACAAAGAGGT CTGGCGATTT GTTGTA	GGGCAGTTTG GCTCCCGTAA	AACCCATCCA AGATTACAGC	GTGGGTCCAT CTAGAAAACC	GGAGAAAGAC CTATGGAACA

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ASIAN2_Ema	CTCCTGAGTC CCTTGTCATT AT	TCCCTTT-GC CAGTCTGTGC	TCAAGACTTG TGTCACTCAA	TGTCTGTCAC GCCCTCCCCA	ACCAGACAGA CCATAAGTAA
FOR_DS1535	CTCCTGAGTC CCTTGTCATT AT	TCCCTTT-GC CAGTCTGTGC	TCAAGACTTG TGTCACTCAA	TGTCTGTCAC GCCCTCCCCA	ACCAGATAGA CCATAAGTAA
MAM1_SP134	CTCCTGAGTC CCTTGTCATT AT	TCCCTTT-GC CAGTCTGTGC	TCAAGACTTG TGTCACTCAA	TGTCTGTCAC GCCCTCCCCA	ACCAGACAGA CCATAAGTAA
MAST_A373_	CTCCTGAGTC CCTTGTCATT AT	TTCCTTTTGT CAGTCTGTGC	TTAAGACTTG TGTCACTCAA	TGTCTGTCAC GCCCTCCCCA	ACCAGACAGA CCATAAGTAA
SAV1_SE210	CTCCTGAGTC CCTTGTCATT AT	TCTCTTT-GC CAGTCTGTGC	TCAAGACTTG TGTCACTCAA	TGTCTGTCAC GCCCTCCCCA	ACCAGATAGA CCATAAGTAA

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ASIAN2_Ema	TCCAAGTCAT TCCAAATCCT GTG	CAGTGAGTGC CTTTGAGGCC	CACAGGCGTC TCCATTTCTC	ACCCCTAAAC CGCCATAAAA	TACTGCATAT TGCTGGGTCT
FOR_DS1535	TCCAAGTCAT TCCAAATCCT	CAGTGAGTGC CTTTGAGGCC	CACGGGCGTC TCCATTTCTC	ACCCCTAAAC CGCCATAAAA	TACTGCATAT TGCTGGGTCT

MAM1_SP134	GTG TCCAAGTCAT TCCAATCCT	CAGTGAGTGC CTTTGAGGCC	CACAGGCGTC TCCATTTCTC	ACCCCTAAAC CGCCATAAAA	TACTGCATAT TGCTGGGTCT
MAST_A255_	GTG TCCAAGTCAT TCTAAATCCT	CAGTGAGTGC CTTTGAGGCC	CACGGGCGTC TCCATTTCTC	ACCCCTAAAC CGCCATAAAA	TACTGCATAT TGCTGGGTCT
SAV1_SE210	GTA TCCAAGTCAT TCCAATCCT	CAGTGAGTGC CTTTGAGGCC	CACGGGCGTC TCCATTTCTC	ACCCCTAAAC CGCCATAAAA	TACTGCATAT TGCTGGGTCT

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ASIAN2_Ema	AAATCTGAGC CTTTGTTTTC	TGGCAAAACT CATTAGTGTG	CTTCCTGGCT TGTTGTCGTC	TGCCCTGATG ACAGTAACTG	AGCAGACCAT
FOR_DS1535	AAATCTGAGC CTTTGTTTTC	TGGCAAAACT CATTAGTGTG	CTTCCTGGCT TGTTGTCGTC	TGCCCTGATG ACAGTAACTG	AGCAGACCAT
MAM1_SP134	AAATCTGAGC CTTTGTTTTC	TGGCAAAACT CATTAGTGTG	CTTCCTGGCT TGTTGTCGTC	TGCCCTGATG ACAGTAACTG	AGCAGACCAT
MAST_A332_	AAATTTGAGC CTTTGTTTTC	TGGCAAAACT CATTAGTGTG	CTTCCTGGCT TGTTGTCGTC	TGCCCTGATG ACAGTAACTG	AGCAGACCAT
SAV1_SE210	AAATCTGAGC CTTTGTTTTC	TGGCAAAACT CATTAGTGTG	CTTCCTGGCT TGTTGTCGTC	TGCCCTGATG ACAGTAACTG	AGCAGACCAT

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ASIAN2_Ema	AGCTCCCCTC TGTCACAGGG CTT	CTGCTATAACC AGGTTCTCAC	CCACAGAGTT TCAAAAGCCC	GCTGAGGAAT TTTCTGGGAA	CCCTCCTCCC TGCCACAGCC
FOR_DS1535	AGCTCCCCTC TGTCACAGGG CTT	CTGCTATAACC AGGTTCTCAC	CCACAGAGTT TCAAAAGCCC	GCTGAGGAAT TTTCTGGGAA	CCCTCCTCCC TGCCACAGCC
MAM1_SP134	AGCTCCCCTC TGTCACAGGG CTT	CTGCTATAACC AGGTTCTCAC	CCACAGAGTT TCAAAAGCCC	GCTGAGGAAT TTTCTGGGAA	CCCTCCTCCC TGCCACAGCC
MAST_A257_	AGCTCCCCTC TGTCACAGGG CTT	CTGCTATATC AGGTTCTCAC	CCACAGAGTT TCAAAAGCCC	GCTGAGGAAT TTTCTGGGAA	CCCTCCTCCC TGCCACAGCC
SAV1_SE210	AGCTCCCCTC TGTCACAGGG CTT	CTGCTATAACC AGGTTCTCAC	CCACAGAGTT TCAAAAGTCC	GCTGAGGAAT TTTCTGGGAA	CCCTCCTCCC TGCCACAGCC

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ASIAN2_Ema	ATTTTAACTC TGAGGAATTT A	TATCTGGTGC GGGAAGGGTG	TATGAAAACA AGTGAGAAGG	GGCAGAAAGC GGTTTGAAC	TATTAGGACA ACAATCTGAA
FOR_DS1535	ATTTTAACTC TGAGGAATTT A	TATCTGGTGC GGGAAGGGTG	TATGAAAACA AGTGAGAAGG	GGCAGAAAGC GGTTTGAAC	TATTAGGACA ACAATCTGAA
MAM1_SP134	ATTTCAACTC TGAGGAATTT A	TATCTGGTGC GGGAAGGGTG	TATGAAAACA AGTGAGAAGG	GGCAGAAAGC GGTTTGAAC	TATTAGGACA ACAATCTGAA
MAST_A333_	ATTTTAACTC TGAGGAATTT A	TATCTGGTGC GGGAAGGGTG	TATGAAAACA AATGAGAAGG	GGCAGAAAGC GGTTTGAAC	TATTAGGACA ACAGTCTGAA
SAV1_SE210	ATTTTAACTC TGAGGAATTC A	TATCTGGTGC GGGAAGGGTG	TATGAAAACA AGTGAGAAGG	GGCAGAAAGC GGTTTGAAC	TATTAGGACA ACAATCTGAA

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ASIAN2_Ema	CAGAGGCTTT GGGCTCCAGA GTGTTGGGAC	GGGGTCTCTG GACACCCTGG CACATT	GCCAGATGGA GCTGATTTAC	CCAGTCTCTT AGCCGCCTGG	TTTAAGTCCA CCATAAAGGG
FOR_DS1535	CAGAGGCTTT GGGCTCCAGA	GGGGTCTCTG GACGCCCTGG	GCCAGACGGA GCTGATTTAC	CCAGTCTCTT AGCTGCCCGG	TTTAAGTCCA CCATAAAGGG

MAM1_SP134	GTGTTGGGAC CAGAGGCTTT GGGCTCCAGA GTGTTGGGAC	CACATT GGGGTCTGG GACGCCCTGG CACATT	GCCAGATGGA GCTGATTTAC	CCAGTCTCTT AGCCGCCCGG	TTTAAGTCCA CCATAAAGGG
MAST_A258_	GTGTTGGGAC CAGAGGCTTT GGGTTCCAGA GTGTTGGGAC	GGGGTCTGG GACGCCCTGG CACATT	GCCAGATGGA GCTGATTTAC	CCAGTCTCTT AGCCGCCCGG	TTTAAGTCTA CCATAAAGGG
SAV1_SE210	GTGTTGGGAC CAGAGGCTTT GGGCTCCAGA GTGTTGGGAC	GGGGTCTGG GACGCCCTGG CACATT	GCCAGACGGA GCTGATTTAC	CCAGTCTCTT AGCTGCCCGG	TTTAAGTCCA CCATAAAGGG

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ASIAN2_Ema	TTGAATATTT CCCTGTCTGT TGCCACTGGG	GAGAATTTTT GTCTGATCCC	-CAGAAATAT AGCGGTACCA	TTCATGGTCC CACCTATCTT	TGTATTGTGG AAAA-TGGAT
FOR_DS1535	TTGAATATTT CCCTGTCTGT TGCCACTGGG	GAGAATTTTT GTCTGATCCC	-CAGAAATAT AGCGGTACCA	TTCATGGTCC CACCTATCTT	TGTATTCTGG AAAA-TGGAT
MAM1_SP134	TTGAATATTT CCCTGTCTGT TGCCACTGGG	GAGAATTTTT GTCTGATCCC	-CAGAAATAT AGCGGTACCA	TTCATGGTCC CACCTATCTT	TGTATTCTGG AAAA-TGGAT
MAST_A259_	TTGAATATTT CCCTGTCTGT TGCCACTGGG	GAGAATTTTT GTCTGATCCC	TCAGAAATAT AGCGGTACCA	TTCATGGTCC CACTTATCTT	TGTATTCTGG AAAAATGGAT
SAV1_SE210	TTGAATATTT CCCTGTCTGT TGCCACTGGG	GAGAATTTTT GTCTGATCCC	-CAGAAATAT AGCGGTACCA	TTCATGGTCC TACCTATCTT	TGTATTCTGG AAAA-TGGAT

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ASIAN2_Ema	CATCATTA AACTGGTCTT A-GCA-CG	TTAG-AAACA GACCTGGGAT	AA-TGATGTA GACATCTCAT	TTTGCAGAAA ATCCGGAATG	TTGGTTTCTT TTTTCACCCA
FOR_DS1535	CATCATTA AACTGGTCTT A-GCA-CG	TTAG-AAACA GACCTGGGAT	AA-TGATGTA GACATCTCAT	TTTGCAGAAA ATCCAGAATG	TTGGTTTCTT TTTTCACCCA
MAM1_SP134	CATCATTA AACTGGTCTT A-GCA-CG	TTAG-AAACA GACCTGGGAT	AA-TGATGTA GACATCTCAT	TTTGCAGAAA ATCCGGAATG	TTGGTTTCTT TTTTCACCCA
MAST_A334_	CATCATTA AACTGGTCTT AAGCAACG	TTAAGAAACA GACCTGGGAT	AAATGATGTA GACATCTCAT	TTTGCAGAAA ATCCGGAATG	TTGGTTTCTT TTTTCACCCA
SAV1_SE210	CATCATTA AACTGGTCTT A-GCA-CG	TTAG-AAACA GACCTGGGAT	AA-TGATGTA GACATCTCAT	TTTGCAGAAA ATCCAGAATG	TTGGTTTCTT TTTTCACCCA

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ASIAN2_Ema	CAGAAAATCA GCTTTGGAGG AATTTT-CAT	CTAAACAATA GATTCCAGCA GGGTG	TTATTGATGC GCTGGAAAAT	CATTTTTCTT CAGTGTCTGTT	TCTAAGATCA CCCACAAAAA
FOR_DS1535	CAGAAAATCA GCTTTGGAGG AATTTT-CAT	CTAAACAATA GATTCCAGCA GGGTG	TTATTGATGC GCTGGAAAAT	CATTTTTCTT CAGTGTCTGTT	TCTAAGATCA CCCACAAAAA
MAM1_SP134	CAGAAAATCA GCTTTGGAGG AATTTT-CAT	CTAAACAATA GATTCCAGCA GGGTG	TTATTGATGC GCTGGAAAAT	CATTTTTCTT CAGTGTCTGTT	TCTAAGATCA CCCACAAAAA
MAST_A262_	TAGAAAATCA GCTTTGGAGG AATTTTACAC	CTAAACAATA GATTCCAGCA GGGTG	TTATTGATGC GCTGGAAAAT	CATTTTTCTT CAGTGTCTGTT	TCTAAGATCA CCCACAAAAA
SAV1_SE210	CAGAAAATCA GCTTTGGAGG A-TTTT-CAT	TTAAACAATA GATTCCAGCA GGGTG	TTATTGATGC GCTGGAAAAT	CATTTTTCTT CAGTGTCTGTT	TCTAAGATCA CCCACAAAAA

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ASIAN2_Ema	TCGATCACAG	ATGAACTTAG	CACCCACGGA	ATGGTTGATG	CCAGTAACTC
FOR_DS1535	TGTGTGTCTC	ATTCCCAGCA	GTCTAGTGGC	TGCCTGAAAG	TT
MAM1_SP134	TCGATCACAG	ATGAACTTAG	CACCCACGGA	ATGGTTGATG	CCAGTAACTC
MAST_A335_	TGTGTGTCTC	ATTCCCAGCA	GTCTAGTGGC	TGCCTGAAAG	TT
SAV1_SE210	TCGATCACAG	ATGAACTTAG	CACCCACGGA	ATGGTTGATG	CCAGTAACTC
	TGTGTGTCTC	ATTCCCAGCA	GTCTAGTGGC	TGCCTGAAAG	TT

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ASIAN2_Ema	AGAGAGAGAA	ATTGGAAGCTG	GGGCCACAGGA	ATTAGAATTT	GGGATTTAAC
FOR_DS1535	ATATAAAATG	TGCCTTAATA	CGTTTGCATC	CTGTAGACCA	AACCAG
MAM1_SP134	AGAGAGAGAA	ATTGGAAGCTG	GGGCCACAGGA	ATTAGAATTT	GGGATTTAAC
MAST_A264_	ATATAAAATG	TGCCTTAATA	CGTTTGCATC	CTGTAGACCA	AACCAG
SAV1_SE210	AGAGAGAGAA	ATTGGAAGCTG	GGGCCACAGGA	ATTAGAATTT	GGGATTTAAC
	ATATAAAATG	TGCCTTAATA	CGTTTGCATC	CTGTAGACCA	AACCAG

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ASIAN2_Ema	TTTTAAATCA	GGAAAGATGT	GTGTCACGGT	TGTATTCTTT	CACTATACTT
FOR_DS1535	ATTCAATCTG	TATGCTGAAC	AAATAATCCA	AGAATTGGCA	TCAGGAT
MAM1_SP134	TTTTAAATCA	GGAAAGATGT	GTGTCACGGT	TGTATTCTTT	CACTATACTT
MAST_A431_	ATTCAATCTG	TATGCTGAAC	AAATAATCCA	AGAATTGGCA	TCAGGAT
SAV1_SE210	TTTTAAATCA	GGAAAGATGT	GTGTCACGGT	TGTATTCTTT	CACTATACTT
	ATTCAATCTG	TATGCTGAAC	AAATAATCCA	AGAATTGGCA	TCAGGAT

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ASIAN2_Ema	ACCTGATGGA	GAGGTCTTGC	TTCATCCACC	TCCAGGGACC	TCCCTCACCA
FOR_DS1535	TCAATCCTGG	TGGCCTCTGG	CCAGGGTGAG	ACAAACAGGG	TCCCTCACCA
MAM1_SP134	ACCTGATGGA	GAGGTCTTGC	TTCATCCACC	TCCAGGGACC	TCCCTCACCA
MAST_A432_	TCAATCCTGG	TGGCCTCTGG	CCAGGGTGAG	ACAAACAGGG	TCCCTCACCA
SAV1_SE210	ACCTGATGGA	GAGGTCTTGC	TTCATCCACC	TCCAGGGACC	TCCCTCACCA
	TCAATCCTGG	TGGCCTCTGG	CCAGGGTGAG	ACAAACAGGG	TCCCTCACCA

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ASIAN2_Ema	CTTTTATAAG	TCACAGGACT	AGGGTCAGGG	AGGAGCAAGT	TTCCAGAAGC
FOR_DS1535	CATGGCAGTG	GAGCCATAAA	TCAGCCAGGC	TCTCCCCAGC	GGCA
MAM1_SP134	CTTTTATAAG	TCACAGGACT	AGGGTCAGGG	AGGAGCAAGT	TTCCAGAAGC
MAST_A337_	CATGGCAGTG	GAGCCATAAA	TCAGCCAGGC	TCTCCCCAGC	GGCA
SAV1_SE210	CTTTTATAAG	TCACAGGACT	AGGGTCAGGG	AGGAGCAAGT	TTCCAGAAGC
	CATGGCAGTG	GAGCCATAAA	TCAGCCAGGC	TCTCCCCAGC	GGCA

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ASIAN2_Ema	CACAGTCTCC	TCGTGGCTGG	AAAAGAGTGA	GATCACCACG	GTTGGGCTTC
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	TTGCCTTTCC	CCTATTGGCT	AAGCAGGATT	CTTTTACATT	CCAAAATAAG
FOR_DS1535	AAT CACAGTCTCC	TCGTGGCTGG	AAAAGAGTGA	GATCACCACG	GTTGGGCTTC
	TTGCCTTTCC	CCTATTGGCT	AAGCAGGATT	CTTTTACATT	CCAAAATAAG
MAM1_SP134	AAT CACAGTCTCC	TCGTGGCTGG	AAAAGAGTGA	GATCACCACG	GTTGGGCTTC
	TTGCCTTTCC	CCTATTGGCT	AAGCAGGATT	CTTTTACATT	CCAAAATAAG
MAST_A338_	AAT TACAGTCTCC	TCGTGGCTGG	AAAAGAGTGA	GATCACCAGA	GTTGGGCTTC
	TTGCCTTTCC	CCTATTGGCT	AAGCAGGATT	CTTTTACGTT	CCAAAATAAG
SAV1_SE210	AAT CACAGTCTCC	TCGTGGCTGG	AAAAGAGTGA	GATCACCACG	GTTGGGCTTC
	TTGCCTTTCC	CCTATTGGCT	AAGCAGGATT	CTTTTACATT	CCAAAATAAG
	AAT				

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ASIAN2_Ema	CCTGTGGCAA	CTTGGAGGAA	CCTCAGGTTA	GCTGCATTCC	TCAAGTATAG
	AAGTCTTGAG	ATAGCCCAGA	GCATCAGACT	ATTAAAGCTC	TTTCAATAGG
FOR_DS1535	G CCTGTGGCAA	CTTGGAGGAA	CCTCAGGTTA	GCTGCATTCC	TCAAGTATAG
	AAGTCTTGAG	ATAGCCCAGA	GCATCAGACT	ATTAAAGCTC	TTTCAATAGG
MAM1_SP134	G CCTGTGGCAA	CTTGGAGGAA	CATCAGGTTA	GCTGCATTCC	TCAAGTATAG
	AAGTCTTGAG	ACAGCCCAGA	GCATCAGACT	ATTAAAGCTC	TTTCAATAGG
MAST_A339_	G CCTGTGGCAA	CTTGGAGGAA	CCTCAGGTTA	GCTGCATTCC	TCAAGTATAG
	AAGTCTTGAG	ATAGCCCAGA	GCATCAGACT	ATTAAAGCTC	TTTCAATAAA
SAV1_SE210	A CCTGTGGCAA	CTTGGAGGAA	CCTCAGGTTA	GCTGCATTCC	TCAAGTATAG
	AAGTCTTGAG	ATAGCCCAGA	GCATCAGACT	ATTAAAGCTC	TTTCAATAGG
	G				

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ASIAN2_Ema	GTTCCAGCAT	GCCCCCA-TA	CTGCTGCTGT	ACTTTTCTGC	TTCTCTCATG
	GACTAATAAT	CTTGAGAGAG	GGATTAGATG	GCTAGTCAGT	GGAGA
FOR_DS1535	GTTCCAGCAT	GCCCCCA-TA	CTGCTGCTCT	ACTTTTCTGC	TTCTCTCATG
	GACTAATAAT	CTTGAGAGAG	GGATTAGATG	GCTAGTCAGT	GGAGA
MAM1_SP134	GTTCCAGCAT	GCCCCCA-TA	CTGCTGCTGT	ACTTTTCTGC	TTCTCTCATG
	GACTAATAAT	CTTGAGAGAG	GGATTAGATG	GCTAGTCAGT	GGAGA
MAST_A266_	GTTCCAGCAT	GCCCCCACTA	CTGCTGCTCT	ACTTTTCTGC	TTCTCTCATG
	GATTAATAAT	CTTGAGAGAG	GGATTAGATG	TCTAGTCAGT	GGAGG
SAV1_SE210	GTTCCAGCAT	GCCCCCA-TA	CTGCTGCTCT	ACTTTTCTGC	TTCTCTCATG
	GACTAATAAT	CTTGAGAGAG	GGATTAGATG	GCTAGTCAGT	GGAGA

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ASIAN2_Ema	CTGCAGACAC	TCAATGTGTT	ACTTTTCTATG	GCGAGGACAG	CCTAGCCCAG
	TTTATGTTCA	ACCACACCTG	TCATAATTGC	ATAATCACGG	CAT
FOR_DS1535	CTGCAGACAC	TCAATGTGTT	ACTTTTCTATG	GCGAGGACAG	CCTAGCCCAG
	TTTATGTTCA	ACCACACCTG	TCATAATTGC	ATAATCACGG	CAT
MAM1_SP134	CTGCAGACAC	TCAATGTGTT	ACTTTTCTATG	GCGAGGACAG	CCTAGCCCAG
	TTTATGTTCA	ACCACACCTG	TCATAATTGC	ATAATCACGG	CAT
MAST_A267_	CTGCAGACAC	TCAATGTGTT	ACTTTTCTATG	GCGAGGACAG	CCTAGCCCAG
	TTTATGTTCA	ACCACGCCTG	TCATAATTGC	ATAATCACGG	GCA
SAV1_SE210	CTGCAGACAC	TCAACGTGTT	ACTTTTCTATG	GCGAGGACAG	CCTGGCCCAG
	TTTATGTTCA	ACCACACCTG	TCATAATTGC	ATAATCACGG	CAT

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ASIAN2_Ema	TTGATGTTCT	CATCAAAGGG	GAAATGCCTG	AGAACCAAAA	TCAGACTCAC
	TTCTTCTATT	CTGTATGCC	AGGCTCTTAT	TCTGAGTCAG	TGGCC
FOR_DS1535	TTGAKGTTCT	CATCAAAGGG	GAAATRCCTG	AGAACCAAAA	TCAGACTCAC
	TTCTTCTATT	CTGTATGCC	AGGCTCTTAT	TCKGAGTCAG	TGGCC
MAM1_SP134	TTGATGTTCT	CATCAAAGGG	GAAATGCCTG	AGAACCAAAA	TCAGACTCAC
	TTCTTCTGTT	CTGTATGCC	AGGCTCTTAT	TCTGAGTCAG	TGGCC

MAST_A268_	TTGATGTTCT	CATCAAAGGG	GAAATGCCTG	AGAACCAAAA	TCAGACTCAC
SAV1_SE210	TTCTTCTATT	CTGTATGCC	AGGCTCTTAT	TCTGAGTCAG	TGGCC
	TTGAGGTTCT	CATCAAAGGG	GAAATGCCTG	AGAACCAAAA	TCAGACTCAC
	TTCTTCTGTT	CTGTATGCC	AGGCTCTTAT	TCGGAGTCAG	TGGCC

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ASIAN2_Ema	GCAAAATTGA	TTTTT-CTAA	GTGCAGAGGC	CAGTCTTATG	ACAATGCTGC
FOR_DS1535	CAATATGTCA	GGGTGTTATA	AGGGCGTGCA	ACAGAAAATT	TT
	GCAAAATTGA	TTTTT-CTAA	GTGCAGAGGC	CAGTCTTATG	ACAATGCTGC
	CAATATGTCA	GGGTGTTATA	RAGGCACGCA	ACAGAAAATT	TT
MAM1_SP134	GCAAAATTGA	TTTTT-CTAA	GTGCAGAGGC	CAGTCTTATG	ACAATGCTGC
	CAATATGTCA	GGGTGTTATA	AGGGCGTGCA	ACAGAAAATT	TT
MAST_A435_	GAAAAATTGA	TTTTTTCTAA	-TGCAGAGGC	CAGTCCTATG	ACAATGCTGT
	CAATATGTCA	GAGTGTAATA	AAAGCATGCA	ACAGAAAATT	TT
SAV1_SE210	GCAAAATTGA	TTTTT-CTAA	GTGCAGAGGC	CAGTCTTATG	ACAATGCTGC
	CAATATGTCA	GGGTGTTATA	AAGGCATGCA	ACAGAAAATT	TT

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ASIAN2_Ema	CTTGAAACT	CTATAGAGCC	ATTCTAGTCT	GCCCTGTAGG	GTTGTTATGA
	GTCAGAATTG	ACTCGATGGC	AGTGGGTTT-	GGTTTTTT--	GTTTTTTTTT
	--AGG				
FOR_DS1535	CTTGAAACC	CTATAGAGCC	ATTCTAGTCT	GCCCTGTAGG	GTTGTTATGA
	GTCAGAATTG	ACTCGATGGC	AGTGGGTTT-	GGTTTTTT--	GTTTTTTTTT
	--AGG				
MAM1_SP134	CTTGAAACT	CTATAGAGCC	ATTCTAGTCT	GCCCTGTAGG	GTTGTTATGA
	GTCAGAATTG	ACTCGATGGC	AGTGGGTTT-	GGTTTTTTT-	GTTTTTTTTT-
	--AGG				
MAST_A342_	CTTGAAACT	CTATAGAGCC	ATTCTAGTCT	GCCCTGTAGG	GTTGTTATGA
	GTCGGAATTG	ACTCGATGGC	AGTGGGTTTT	GGTTTTTTTT	ATTTTTTTTT
	TTAGG				
SAV1_SE210	CTTGAAACT	CTATAGAGCC	ATTCTAGTCT	GCCCTGTAGG	GTTGTTATGA
	GTCAGAATTG	ACTCGATGGC	AGTGGGTTT-	GGTTTTTTTT-	GTTTTTTTTT
	--AGG				

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ASIAN2_Ema	GAGCAATGGT	TCTTCTCTTG	AGCACCTCAG	TGTCTGGGGG	AAGTCAATGG
	CCGGGAGGGG	GGTGTAACTC	AATGAGATGA	GAATAGTTGG	GGGGCGTGAG
	AGATCA				
FOR_DS1535	GAGCAATGGT	TCTTCTCTTG	AGCACCTCAG	TGTCTGGGGG	AAGTCAATGG
	CCGGGAGGGG	GGTGTAACTC	AATGAGATGA	GAATAGTTGG	GGGGCGTGAG
	AGATCA				
MAM1_SP134	GAGCAATGGT	TCTTCTCTTG	AGCACCTCAG	TGTCTGGGGG	AAGTCAATGG
	CCGGGAGGGG	GGTGTAACTC	AATGAGATGA	GAATAGTTGG	GGGGCGTGAG
	AGATCA				
MAST_A343_	GAGCAATGGT	TCTTCTTTTG	AGCGCCTCAG	TGTCTGGGGG	AAGTCAATGG
	CCGGGAGGGG	GGTGTAACTC	AATGAGATGA	GAATAGTTGG	GGGCGGTGAG
	AGATCA				
SAV1_SE210	GAGCAATGGT	TCTTCTCTTG	AGCACCTCAG	TGTCTGGGGG	AAGTCAATGG
	CCGGGAGGGG	GGTGTAACTC	AATGAGATGA	GAATAGTTGG	GGGGCGTGAG
	AGATCA				

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ASIAN2_Ema	TGCAAAAGAG	GCTTTGTAGG	GAATACAAGA	AAATTGGAGA	CCCCTGGGAG
	GGCAGATCTC	GACTTAATAG	GAGCCTGTAA	TTACGTGGCA	AAG
FOR_DS1535	TGCAAAAGAG	GCTTTGTAGG	GAATACAAGA	AAATTGGAGA	CCCCTGGGAG
	GGCAGATCTC	GACTTAATAG	GAGCCTGTAA	TTACGTGGCA	AAG
MAM1_SP134	TGCAAAAGAG	GCTTTGTAGG	GAATACAAGA	AAATTGGAGA	CCCCTGGGAG
	GGCAGATCTC	GACTTAATAG	GAGCCTGTAA	TTACGTGGCA	AAG
MAST_A380_	TGCAAAAGAG	GCTTTGTAGG	GAATACAAGA	AAATTGGAGA	CCCCTGGGAG
	GGCAGATCTC	GACTTAATAG	GAGCCTGTAA	TTACATGGCA	AAG
SAV1_SE210	TGCAAAAGAG	GCTTTGTAGG	GAATACAAGA	AAATTGGAGA	CCCCTGGGAG
	GGCAGATCTC	GACTTAATAG	GAGCCTGTAA	TTACGTGGCA	AAG

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ASIAN2_Ema	GGAAGAGGAC	CTGGAGGATG	AGAGAGGAGC	CATTGAGGCC	AGGCTGGGGT
	GGGCAAGAGT	CAGGGAGACC	TCGCCAGTGT	CCAGCACAGG	TT
FOR_DS1535	GGAAGAGGAC	CTGGAGGATG	AGAGAGGAGC	CATTGAGGCC	AGGCTGGGGT
	GGGCAAGAGT	CAGGGAGACC	TCGCCAGTGT	CCAGCACAGG	TT
MAM1_SP134	GGAAGAGGAC	CTGGAGGATG	AGAGAGGAGC	CATTGAGGCC	AGGCTGGGGT
	GGGCAAGAGT	CAGGGAGACC	TCGCCAGTGT	CCAGCACAGG	TT
MAST_A344_	GGAAGAGGAC	CTGGAGGATG	AGAGAGGAGC	CACTGAGGCC	AGGCTGGGGT
	GGGCAAGAGT	CAGGGAGACC	TCGCCAGTGT	CCAGCACAGG	TT
SAV1_SE210	GGAAGAGGAC	CTGGAGGATG	AGAGAGGAGC	CATTGAGGCC	AGGCTGGGGT
	GGGCAAGAGT	CAGGGAGACC	TCGCCAGTGT	CCAGCACAGG	TT

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ASIAN2_Ema	AGGTTTAACT	ACATAGGGAC	CATCTTATTG	AGGAACGTCA	TCACCCTTTG
	TCTCTTCTTC	CTCCCAGAGT	CAAGCTTTCC	CCTTCCCCCT	TACAGTTGTA
	AT				
FOR_DS1535	AGGTTTAACT	ACATAGGGAC	CATCTTATTG	AGGAACGTCA	TCACYCTTTG
	TCTCTTCTTC	CTCCCAGAGT	CAAGCTTTCC	CCTTCCCCCT	TACAGTTGTA
	AT				
MAM1_SP134	AGGTTTAACT	ACATAGGGAC	CATCTTATTG	AGGAACGTCA	TCACCCTTTG
	TCTCTTCTTC	CTCCCAGAGT	CAAGCTTTCC	CCTTCCCCCT	TACAGTTGTA
	AT				
MAST_A438_	AGGTTTTACT	ATATAGGGAT	CATCTTATTG	AGGAATGTCA	CCACCCTTTG
	TCTCTTCTTC	CTCCCAGAGT	CAAGCTTTCC	CCTTCCCCCT	TACAGTTGTA
	AT				
SAV1_SE210	AGGTTTAACT	ACATAGGGAC	CATCTTATTG	AGGAACGTCA	TCACCCTTTG
	TCTCTTCTTC	CTCCCAGAGT	CAAGCTTTCC	CCTTCCCCCT	TACAGTTGTA
	AT				

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ASIAN2_Ema	CAATCCATAG	CTAAGTGGGA	CGAGGAAGGA	GCAGTGGACA	GTGCCATGGA
	TTCCCTTGGAC	TTTATTATCT	TGTTTACCTA	GTCTTTTTGA	TGTAG
FOR_DS1535	CAATCCATAG	CTAAGTGGGA	CGAGGAAGGA	GCAGTGGACA	GTGCCATGGA
	TTCCCTTGGAC	TTTATTATCT	TGTTTACCTA	GTCTTTTTGA	TGTAG
MAM1_SP134	CAATCCATAG	CTAAGTGGGA	CGAGGAAGGA	GCAGTGGACA	GTGCCATGGA
	TTCCCTTGGAC	TTTATTATCT	TGTTTACCTA	GTCTTTTTGA	TGTAG
MAST_A269_	CAATCCATAG	CTAAGTGGGA	CGAGGAAGGA	GCAGTGGACA	GTGCCATGGA
	TTCCCTTGGAC	TTTATTATCT	TGTTTACCTA	GTCTTTTTGA	TGTAG
SAV1_SE210	CAATCCATAG	CTAAGTGGGA	CGAGGAAGGA	GCAGTGGACA	GTGCCATGGA
	TTCCCTTGGAC	TTTATTATCT	TGTTTACCTA	GTCTTTTTGA	TGTAG

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ASIAN2_Ema	CCAATCCCTG	GAAAAGGACA	TCGTGCTTGG	TAAAGCAGAA	GGTCAGCGAC
	ACAATGGCTG	CAACAA-TGG	GCTCAAACAC	AGGGACAATT	GTGAAGATGG
	CA				
FOR_DS1535	CCAATCCCTG	GAAAAGGACA	TCGTGCTTGG	TAAAGCAGAA	GGTCAGCGAC
	ACAATGGCTG	CAACAA-TGG	GCTCAAACAC	AGGGACAATT	GTGAAGATGG
	CA				
MAM1_SP134	CCAATCCCTG	GAAAAGGACA	TCGTGCTTGG	TAAAGCAGAA	GGTCAGCGAC
	ACAATGGCTG	CAACAA-TGG	GCTCAAACAC	AGGGACAATT	GTGAAGATGG
	CA				
MAST_A381_	CCAATTTCTG	GAAAAGGACA	TCGTGCTTGG	TAAAGCAGAA	GGTCAGCGAC
	ACAATGGCTG	CAACAAACGG	GCTCAAACAC	AGGGACAATT	GTGAAGACGG
	CA				
SAV1_A381_	CCAATCCCTG	GAAAAGGACA	TCGTGCTTGG	TAAAGCAGAA	GGTCAGCGAC
	ACAATGGCTG	CAACAA-TGG	GCTCAAACAC	AGGGACAATT	GTGAAGATGG
	CA				

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ASIAN2_Ema	ATCTTTTTGC	TCTAACTTTC	ATACAATGTA	AGTGAGATTC	CAAGTATGCA
	AATGGTGGGA	GGAAAGAAAT	GCATTTTTCAC	TACCCCAATT	A

FOR_DS1535	ATCTTTTTGC	TCTAACTTTC	ATACAATGTA	AGTGAGATTC	CAAGTATGCA
	AATGGTGGGA	GGAAAGAAAT	GCATTTTCAC	TACCCCAATT	A
MAM1_SP134	ATCTTTTTGC	TCTAACTTTC	ATACAATGTA	AGTGAGATTC	CAAGTATGCA
	AATGGTGGGA	GGAAAGAAAT	GCATTTTCAC	TACCCCAATT	A
MAST_A439_	TTTTTTTTGC	TCTAACTTTC	ATACAATGTA	AGTGAGATTC	CAAGTATGCA
	AATGGTGGGA	GGAAAGAAAT	GCATTTTCAC	TACCCCAATT	A
SAV1_SE210	ATCTTTTTGC	TCTAACTTTC	ATACAATGTA	AGTGAGATTC	CAAGTATGCA
	AATGGTGGGA	GGAAAGAAAT	GCATTTTCAC	TACCCCAATT	A

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ASIAN2_Ema	ACAGGGTGGC	AGTCTGGGTC	ATCAGAGCCC	TCGTCACTCC	CGGAAGAGCT
	AGCCTTGCCC	CTTCTGGCCC	AGCCTCGCTC	CCTGACTCCT	ACAA
FOR_DS1535	ACAGGGTGGC	AGTCTGGGTC	ATCAGAGCCC	TCGTCACTCC	CGGAAGAGCT
	AGCCTTGCCC	CTTCTGGCCC	AGCCTCGCTC	CCTGACTCCT	ACAA
MAM1_SP134	ACAGGGTGGC	AGTCTGGGTC	ATCAGAGCCC	TCGTCACTCC	CGGAAGAGCT
	AGTCTTGCCC	CTTCTGGCCC	AGCCTCGCTC	CCTGACTCCT	ACAA
MAST_A270_	-CAGGGTGGC	AGTCTGGGTC	ATCAGAGCCC	TCGTCACTCC	CGGAAGAGCT
	AGCCTTGCCC	CTTCTGGCCC	AGCCTCACTC	CCTGACTCCT	ACAA
SAV1_SE210	ACAGGGTGGC	AGTCTGGGTC	ATCAGAGCCC	TCGTCACTCC	CGGAAGAGCT
	AGTCTTGCCC	CTTCTGGCCC	AGCCTCGCTC	CCTGACTCCT	ACAA

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ASIAN2_Ema	TGCTCCAG--	-CTTCTTGAT	GGTAGTGAGG	TCCCCCTCAG	CCTCTGTAGG
	ACTGGCCCTT	ATATTCAATT	TCAAGGCTTG	GCCCTCC-AG	CCAGAC
FOR_DS1535	TGCTCCAG--	-CTTCTTGAT	GGTAGTGAGG	TCCCCCTCAG	CCTCTGTAGG
	ACTGGCCCTT	ATATTCAATT	TCAAGGCATG	GCCCTCC-AG	CCAGAC
MAM1_SP134	TGCTCCAG--	-CTTCTTGAT	GGTAGTGAGG	TCCCCCTCAG	CCTCTGTAGG
	ACTGGCCCTT	ATATTCAATT	TCAAGGCTTG	GCCCTCC-AG	CCAGAC
MAST_A271_	CATTCCAGGC	TCTTCTTGAT	GGTGGTGAGG	TCCCCCTCAG	CCTCTGTAGG
	ATTGGCCCTT	ATATTCAATT	TCATGGCATG	GCCCTCCCAG	CCAGAC
SAV1_SE210	TGCTCCAG--	-CTTCTTGAT	GGTAGTGAGG	TCCCCCTCAG	CCTCTGTAGG
	ACTGGCCCTT	ATATTCAATT	TCAAGGCATG	GCCCTCC-AG	CCAGAC

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ASIAN2_Ema	TGATACGGCC	ACAGCTCTGC	CGAGAATGGA	GTCCTGGAT	GGTGCAAATG
	GCTAAGACGC	TGGGCTCCTA	ACCAAAAAGGT	TAGAGGTTCA	TCTC
FOR_DS1535	TGATATGGCC	ACAGCTCTGC	CGAGAATGGA	GTCCTGGAT	GGTGCAAATG
	GCTAAGACGC	TGGGCTCCTA	ACCAAAAAGGT	TAGAGGTTCA	TCTC
MAM1_SP134	TGATACGGCC	ACAGCTCTGC	CGAGAATGGA	GTCCTGGAT	GGTGCAAATG
	GCTAAGACGC	TGGGCTCCTA	ACCAAAAAGGT	TAGAGGTTCA	TCTC
MAST_A272_	TGATACAGCC	ACAGCTCTGC	CGAGAATGGA	GTCCTGGAT	GGTGCAAATG
	GCTAAGACGC	TGGGCTCCTA	ACCAAAAAGGT	TAGAGGTTCA	TATC
SAV1_SE210	TGATACGGCC	ACAGCTCTGC	CGAGAATGGA	GTCCTGGAT	GGTGCAAATG
	GCTAAGACGC	TGGGCTCCTA	ACCAAAAAGGT	TAGAGGTTCA	TGTC

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ASIAN2_Ema	ATCTGTTGAT	GTCAATTTCT	CCTTTCCTGC	AGCCTGGGCT	GCATCTGTGT
	CCTCCCTGGC	ATCGGTGTGC	ATGCCAGTAG	CTTCTTTTTC	T
FOR_DS1535	ATCTGTTGAT	GTCAATTTCT	CCTTTCCTGC	AGCCTGGGCT	GCATCTATGT
	CCTCCCTGGC	ATCGGTGTGC	ATGCCAGTAG	CTTCTTTTTC	T
MAM1_SP134	ATCTGTTGAT	GTCAATTTCT	CCTTTCCTGC	AGCCTGGGCT	GCATCTGTGT
	CCTCCCTGGC	ATCGGTGTGC	ATGCCAGTAG	CTTCTTTTTC	T
MAST_A382_	ATCTGTTGAT	GTCAATTTCT	CCTTTCCTGC	AGCCTGGGCT	GCGTCTATGT
	CCTCCCTGGC	TTCGGTGTGC	ATGCCAGTAA	CTTCTTTTTC	T
SAV1_SE210	ATCTGTTGAT	GTCAATTTCT	CCTTTCCTGC	AGCCTGGGCT	GCATCTGTGT
	CCTCCCTGGC	ATTGGTGTGC	RTGCCAGTAG	CTTCTTTTTC	T

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ASIAN2_Ema	GGAGACTGGC	CAAAAAGTGC	TACGGTGGGC	TTACCAGCCC	ATGGAGACAG
	GCAGCTGAAG	CGGGCTTGGC	AGCCACGGA	GCAAGAGAGC	TGAGTGCCTT
	TGGG				

FOR_DS1535	GGAGACTGGC GCAGCTGAAG TGGG	CAAAAACCTGC CGGGCTTGGC	TACGGTGGGC AGCCACCGGA	TTACCAGCCC GCAAGAGAGC	ATGGAGACAG TGAGTGCCTT
MAM1_SP134	GGAGACTGGC GCAGCTGAAG TGGG	CAAAAACCTGC CGGGCTTGGC	TACGGTGGGC AGCCACCGGA	TTACCAGCCC GCAAGAGAGC	ATGGAGACAG TGAGTGCCTT
MAST_A273_	GGAGACTGGC GCGGTTGAAG TGGG	CAAAAACCTGC CGGGCTTGGC	TACGGTGGGC AGCCACCGGA	TTACCAGCCC GCAAGAGAGC	ATGGAGACAG TGAGTGCCTT
SAV1_SE210	GGAGACTGGC GCAGCTGAAG TGGG	CAAAAACCTGC CGGGCTTGGC	TACGGTGGGC AGCCACCGGA	TTACCAGCCC GCAAGAGAGC	ATGGAGACAG TGAGTGCCTT

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ASIAN2_Ema	GCAGCCAGGA GGAAGGGG-C AGG	CTCAGACATG AGTTTTGAGA	CCCAGAAGGG GAGGGATAAG	GATGTGGATA TTGGGCAGGG	GGGAGACCTG GGG-CAGGAG
FOR_DS1535	GCAGCCAGGA GGAAGGGG-C AGG	CTCAGACATG AGTTTTGAGA	CCCAGAAGGG GAGGGATAAG	GATGTGGATA GTGGGCAGGG	GGGAGACCTG GGG-CAGGAG
MAM1_SP134	GCAGCCAGGA GGAAGGGG-C AGG	CTCAGACATG AGTTTTGAGA	CCCAGAAGGG GAGGGATAAR	GATGTGGATA GTGGGCAGGG	GGGAGACCTG GGG-CAGGAG
MAST_A277_	GCAGCCAGGA GGAAGGGGGC AGA	CTCAGACATG AGTTTTGAAA	CCCAGAAGGG GAGGGATAAG	GATGTGGATA GTGGGCAGGG	GGGAGATCTG GGGGCAGGAG
SAV1_SE210	GCAGCCAGGA GGAAGGGG-C AGG	CTCAGACATG AGTTTTGAGA	CCCAGAAGGG GAGGGATAAG	GATGTGGATA GTGGGCAGGG	GGGAGACCTG GGG-CAGGAG

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ASIAN2_Ema	CTGCCAAGCT TCTCTAAAAT TCCC	CCTGGTTCTG TGCCCTGCTT	GTCATGAATG ATGAATGCCA	TTATTTGTTT GAGTCCCAGC	TTCTAATTCC AAGCCTTATC
FOR_DS1535	CTGCCAAGCT TCTCTAAAAT TCCC	CCTGGTTCTG TGCCCTGCTT	GTCATGAATG ATGAATGCCA	TTATTTGTTT GAGTCCCAGC	TTCTAATTCC AAGMCTTATC
MAM1_SP134	CTGCCAAGCT TCTCTAAAAT TCCC	CCTGGTTCTG TGCCCTGCTT	GTCATGAATG ATGAATGCCA	TTATTTGTTT GAGTCCCAGC	TTCTAATTCC AAGCCTTATC
MAST_A442_	TTGTCAAGCT TCTTTAAAAT TCCC	TCTGGTTTTG TTCTCTGCTT	GTCATGAATG ATGAATGCCA	TTATTTGTTT GAGTCCCAGC	TTCTAATTCT AAGCCTTATC
SAV1_SE210	CTGCCAAGCT TCTCTAAAAT TCCC	CCTGGTTCTG TGCCCTGCTT	GTCATGAATG ATGAATGCCA	TTATTTGTTT GAGTCCCAGC	TTCTAATTCC AAGCCTTATC

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ASIAN2_Ema	TTGTTTTATT TAAGAACGTG TTTTTAA	TTATATTTAC TTTGAATGAC	CTTCAAAACA GGGTGTATAA	CATTGGCAAG AAGCAGTAGC	TGTTTTCCCA TTGAAATTTT
FOR_DS1535	TTGTTTTATT TAAGAACGTG TTTTTAA	TTATATTTAC TTTGAATGAC	CTTCAAAACA GGGTGTATAA	CATTGGCAAG WAGCAGTAGC	TGTTTTCCCA TTGAAATTTT
MAM1_SP134	TTGTTTTATT TAAGAACGTG TTTTTAA	TTATATTTAC TTTGAATGAC	CTTCAAAACA GGGTGTATAA	CATTGGCAAG AAGCAGTAGC	TGTTTTCCCA TTGAAATTTT
MAST_A278_	TTGTTTTATT TACGAACATG TTTTTAA	TTATATTTAC TTTGAATGAC	CTTCAAA-CA GGGTGTATAA	TTTTGGCAAG AAGCAGTAGC	TGTTTTCCCA TTGAAATTTT
SAV1_SE210	TTGTTTTATT TAAGAACGTG TTTTTAA	TTATATTTAC TTTGAATGAC	CTTCAAAACA GGGTGTATAA	CATTGGCAAG TAGCAGTAGC	TGTTTTCCCA TTGAAATTTT

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ASIAN2_Ema	CTGTGGCTTC	AGTTTAAAGAT	GGGAAGGTGT	GGCCTGCACA	GTCATACCAG
	TGAGTGGATG	CCTGTGGGAG	GAGGCAGCAG	TTGGAAAGGA	C
FOR_DS1535	CTGTGGCTTC	AGTTTAAAGAT	GGGAAGGTGT	GGCCTGCACA	GTCATACCAG
	TGAGTGGATG	CCTGTGGGAG	GAGGCAGCAG	TTGGAAAGGA	C
MAM1_SP134	CTGTGGCTTC	AGTTTAAAGAT	GGGAAGGTGT	GGCCTGCACA	GTCATACCAG
	TGAGTGGACG	CCTGTGGGAG	GAGGCAGCAG	TTGGAAAGGA	C
MAST_A385_	CTGTGGCTTC	AGTTTAAAGAT	GGGAAGGTGT	AGACTGCACA	GTCATACCAG
	TGAGTGGATG	CCTGTGGGAG	GAGACAGCAT	TTGGAAAGGA	C
SAV1_SE210	CTGTGGCTTC	AGTTTAAAGAT	GGGAAGGTGT	GGCCTGCACA	GTCATACCAG
	TGAGTGGATG	CCTGTGGGAG	GAGGCAGCAG	TTGGAAAGGA	C

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ASIAN2_Ema	CCTGGAATTC	AGTGTCTTTT	TCAGCTGTTT	TGGCCTGACC	TCCCAGCTGG
	CTGGGGTCAG	CGCCCCCCGC	TGCTTCAGGG	ACCCCATCCT	GGAGCCTCT
FOR_DS1535	CCTGGAATTC	AGTGTCTTTT	TCAGCTGTTT	TGGCCTGACC	TCCCAGCTGG
	CTGGGGTCAG	CGCCCCCCGC	TGCTTCAGGG	ACCCCATCCT	GGAGCCTCT
MAM1_SP134	CCTGGAATTC	AGTGTCTTTT	TCAGCTGTTT	TGGCCTGACC	TCCCAGCTGG
	CTGGGGTCAG	CGCCCCCCGC	TGCTTCAGGG	ACCCCATCCT	GGAGCCTCT
MAST_A279_	TCTGGAATTC	AGTGTCTTTT	TCAGCTGTTT	TGGCCTGACT	TCCCAGCTGG
	CTGGGGTCAG	CGCCCCCCGC	TGCTTCAGGG	ATCCCATCCT	GGAGCCTCT
SAV1_SE210	CCTGGAATTC	AGTGTCTTTT	TCAGCTGTTT	TGGCCTGACC	TCCCAGCTGG
	CTGGGGTCAG	CGCCCCCCGC	TGCTTCAGGG	ACCCCATCCT	GGAGCCTCT

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ASIAN2_Ema	CTTACTTCTG	GGTTCTTTCC	AAAAGAGACT	GTTGAGATAA	AACACCACTG
	AAATTCACAG	CAGCCAGAAC	GTCAACTGTT	TTCTTTGAGC	TTTAGGAGCT
	TTCCATTCTC	CA			
FOR_DS1535	CTTACTTCTG	GGTTCTTTCC	AAAAGAGACT	GTTGAGATAA	AACACTATTG
	AAATTCACAG	CAGCCAGAAC	GTCAACTGTT	TTCTTTGAGC	TTTAGGAGCT
	TTCCATTCTC	CA			
MAM1_SP134	CTTACTTCTG	GGTTCTTTCC	AAAAGAGACT	GTTGAGATAA	AACACCATTG
	AAATTCACAG	CAGCCAGAAC	GTCAACTGTT	TTCTTTGAGC	TTTAGGAGCT
	TTCCATTCTC	CA			
MAST_A386_	TTTACTTCTG	GGTTCTTTCC	AAAAGAGACT	GTTGAGATAA	AACACCATTG
	AAATTCACAG	CAGCCAGAAC	GTCAACTGTT	TTCTTTGAGC	TTTAGGAGCT
	TTCCATTCTC	CA			
SAV1_SE210	CTTACTTCTG	GGTTCTTTCC	AAAAGAGACT	GTTGAGATAA	AACACCATTG
	AAATTCACAG	CAGCCAGAAC	GTCAACTGTT	TTCTTTGAGC	TTTAGGAGCT
	TTCCATTCTC	CA			

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ASIAN2_Ema	AAGACATGAG	TCAATATGGA	AT-AGGACTG	AGGTCAGGTT	GAAAAAAAAA
	--GTGAGAGA	GTTCTGGATT	TCTTTATGGA	TGGGGCACAA	GTGTCCGTA
FOR_DS1535	AAGACATGAG	TCAATATGGA	ATTAGGACTG	AGGTCAGGTT	GAAAAAAAAA-
	--GTGAGAGA	GTTCTGGATT	TCTTTATGGA	TGGGGCACAA	GTGTCCGTA
MAM1_SP134	AAGACATGAG	TCAATATGGA	ATTAGGACTG	AGGTCAGGTT	GAAAAAAAAA
	--GTGAGAGA	GTTCTGGATT	TCTTTATGGA	TGGGGCACAA	GTGTCCGTA
MAST_A387_	AAGACATGAG	TCAATATGGA	ATTAGGACTG	AGGTCAAGTT	GAAAAAAAAA
	AAGTGAGAGA	GTTCTGGATT	TCTTTATGGA	TGGGGCACAA	GTGTCCCTA
SAV1_SE210	AAGACATGAG	TCAATATGGA	ATTAGGACTG	AGGTCAGGTT	GAAAAAAAAA
	-----	GTTCTGGATT	TCTTTATGGA	TGGGGCACAA	GTGTCCGTA

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ASIAN2_Ema	TGGAGACTGA	ATGCCATTTG	AGGTCAAGAC	CCAAATTAGA	AACTCTACCC
	AGGAATATTA	AGCTAGAGCT	GGGGTATGGG	GATAAGGGCA	T
FOR_DS1535	TGGAGACTGA	ATGCCATTTG	AGGTCAAGAC	CCAAATTAGA	AACTCTACCC
	AGGAATATTA	AGCTAGAGCT	GGGGTATGGR	GATAAGGGCA	T
MAM1_SP134	TGGAGACTGA	ATGCCATTTG	AGGTCAAGAC	CCAAATTAGA	AACTCTACCC
	AGGAATATTA	AGCTAGAGCT	GGGGTATGGG	GATAAGGGCA	T
MAST_A388_	TGGAGACTGA	ATGCCATTTG	AGGTCAAGAC	CCAAATTAGA	AACTCTACCC
	AAGAATATTA	AGCTAGAGCT	GGGGTATGAA	GATAAGGGCA	C

SAV1_SE210 TGGAGACTGA ATGCCATTTG AGGTCAAGAC CCAAATTAGA AACTCTACCC
AGGAATATTA AGCTAGAGCT GGGGTATGGG GATAAGGGCA T

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ASIAN2_Ema TGCATGTCGT ATGATTTTTT GAGAGCCCAT AAGCCCCAAA GAAAGGGTCA
GAGATGCCAG TGAATGTTAG AGCTGGTGAC CTGGAGCAGG TGCTTACA
FOR_DS1535 TGCATGTCGT ATGATTTTTT GAGAGCCCAT AAGCCCCAAA GAAAGGGTCA
GAGATGCCAG TGAATGTTAG AGCTGGTGAC CTGGAGCAGG TGCTTACT
MAM1_SP134 TGCATGTCGT ATGATTTTTT GAGAGCCCAT AAGCCCCAAA GAAAGGGTCA
GAGATGCCAG TGAATGTTAG AGCTGGKGAC CTGGAGCAGG TGCTTACA
MAST_A443_ TGCATGTTGT ATGATTTTTT GAGAGCCCAT AAGCCCCAAA GAAAGGGTCA
GAGATGCCAG CGAACGTTAG AGCTGGTGAC CTGGAGCAGG AGCTTACA
SAV1_SE210 TGCATGTCGT ATGATTTTTT GAGAGCCCAT AAGCCCCAAA GAAAGGGTCA
GAGATGCCAG TGAATGTTAG AGCTGGTGAC CTGGAGCAGG TGCTTACA

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ASIAN2_Ema CCAAACGCAT T-GCC-GTTG AGTCAATT-C CGACTCAGTG ACCCTATAAA
AACCGAGGGG AACTGCCCCA TAGGGTTTCT GAGGAAC-AG CTGTTGGATT
CCAACG
FOR_DS1535 CCAAACGCAT T-GCC-GTTG AGTCAATT-C CGACTCAGTG ACCCTATAAA
AACAGAGGGG AACTGCCCCA TAGGGTTTCT GAGGAAC-AG CTGTTGGATT
CCAACG
MAM1_SP134 CCAAACGCAT T-GCC-GTTG AGTCAATT-C CGACTCAGTG ACCCTATAAA
AACAGAGGGG AACTGCCCCA TAGGGTTTCT GAGGAAC-AG CTGTTGGATT
CCAACG
MAST_A347_ CCAAACGCAT TTGTCCGTTG AGTCAATTTT CGACTCAGTG ACCCTATAAA
AACAGAGGGG AACTGCCCGA TAGGGTTTCT GAGGAACTAG CTGTTGGATT
CCAACG
SAV1_SE210 CCAAACGCAT T-GTC-GTTG AGTCAATT-C CGACTCAGTG ACCCTATAAA
AACAGAGGGG AACTGCCCCA TAGGGTTTCT GAGGAAC-AG CTGTTGGATT
CCAACG

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ASIAN2_Ema CGCAAGGGCG CACCCAGCAT GGAGCAGCTC ACCAGGAAGA TGGCTTCGAT
GTGGCCGATA CCCCAGCGCA GGGAGGAACC CAGGCGGTCC CCGACCCCAG
CCAACAG
FOR_DS1535 CGCAAGGGCG CACCCAGCAT GGAGCAGCTC ACCAGGAAGA TGGCTTCGAT
GTGGCCGATA CCCCAGCGCA GGGAGGAACC CAGGCGGTCC CCGACCCCAG
CCAACAG
MAM1_SP134 CGCAAGGGCG CACCCAGCAT GGAGCAGCTC ACCAGGAAGA TGGCTTCGAT
GTGGCCGATA CCCCAGCGCA GGGAGGAACC CAGGCGGTCC CCGACCCCAG
CCAACAG
MAST_A390_ CGCAAGGGCG CACCCAGCAT GGAGCAACTC ACCAGGAAGA TGGCTTCGAT
GTGGCCGATA CCCCAGCGCA GGGAGGAACC CAGGCGGTCC CCGACCCCAG
CCAACAG
SAV1_SE210 CGCAAGGGCG CACCCAGCAT GGAGCAGCTC ACCAGGAAGA TGGCTTCGAT
GTGGCCGATA CCCCAGCGCA GGGAGGAACC CAGGCGGTCC CCGACCCCAG
CCAACAG

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ASIAN2_Ema CTCAAATAA AATGAAATAA TGTTCT-GGA AACATCAGAA CTCATGTTCC
CATGAGTCCC CATAAAAATC ACCACACCCG CTGAAATCGT AACCATGTGC
TGTTTGCA
FOR_DS1535 CTCAAATAA AATGAAATAA TGTTCT-GGA AACATCAGAA CTCATGTTCC
CATGAGTCTC CATAAAAATC ACCACACCCG CTGAAATCGT AACCGTGTGC
TGTTTGCA
MAM1_SP134 CTCAAATAA AATGAAATAA TGTTCT-GGA AACATCAGAA CTCATGTTCC
CATGAGTCCC CATAAAAATC ACCACACCCG CTGAAATCGT AACCGTGTGC
TGTTTGCA
MAST_A282_ -TCAAATAA AATGAAATAA TGTTTTTGGG AACATCAGAA CTCGTGTTCC
CATGAGTCCC CATAAAAATC ACCACACCCG CTGAAATCGT AACCGTGTGC
TGTTTACA
SAV1_SE210 CTCAAATAA AATGAAATAA TGTTCT-GGA AACATCAGAA CTCATGTTCC

CATGAGTCCC CATAAAAATC ACCACACCCG CTGAAATCGT AACCGTGTGC
TGTTTGCA

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ASIAN2_Ema	AACTTAAAAC	GTCCTTCTAA	CAGCTTCTTC	TTTTGAAATG	GAGATGTTGT
FOR_DS1535	TGCTAGGTTT	CTCTGAGTCA	GTTCCCACTC	ATAGTGACCA	TGA
MAM1_SP134	AAYTTAARAC	GTCCTTCTAA	CAGCTTCTTC	TTTTGAAATG	GAGATGTTGT
MAST_A393_	TGCTAGGTTT	CTCTGAGTCA	GTTCCCACTC	ATAGTGACCA	TGA
SAV1_SE210	AACTTAAAAC	GTCCTTCTAA	CAGCTTCTTC	TTTTGAAATG	GAGATGTTGT
	TGCTAGGTTT	CTCTGAGTCA	GTTCCCACTC	ATAGTGACCA	TGA

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ASIAN2_Ema	CTGGGAACTC	TGGGAGTCTT	TCCTCAGAGG	TGGTGGCAGT	GAAAACAGAG
FOR_DS1535	CAGGAGGGCG	GAGTCACCTG	CTCCCCACAT	TCAGCTCACA	GGG
MAM1_SP134	CTGGGAACTC	TGGGAGTCTT	TCCTCAGAGG	TGGTGGCAGT	GAAAACAGAG
MAST_A283_	CAGGAGGGCG	GAGTCACCTG	CTCCYCACAT	TCAGCTCACA	GGG
SAV1_SE210	CTGGGAACTC	TGGGAGTCTT	TCCTCAGAGG	TGGTGGCAGT	GAAAACAGAG
	CAGGAGGGCG	GAGTCACCTG	CTCCCCACAT	TCAGCTCACA	GGG

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ASIAN2_Ema	ATGAAATTTT	TGATGCATAT	GGATTTTTCT	ATTTGCATCC	TTGGG-TGAT
FOR_DS1535	GATATAACTT	CTGCTAACCA	ACTACCTGAG	ACAGCTCTGG	ACACAGG
MAM1_SP134	ATGAAATTTT	TGATGCATAT	GGATTTTTCT	ATTTGCATCC	TTGGG-TGAT
MAST_A285_	GATATAACTT	CTGCTAACCA	ACTACCTGAG	ACAGCTCTGG	ACACAGG
SAV1_SE210	ATGAAATTTT	TGATGCATAT	GGATTTTTCT	ATTTGCATCC	TTGGG-TGAT
	GATATAACTT	CTGCTAACCA	ACTACCTGAG	ACAGCTCTGG	ACACAGG

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ASIAN2_Ema	CTAGAGTCTG	TAGTCTTTAT	AAATAAAATC	CAAATAACAC	CTTAGCTGAA
FOR_DS1535	TATAATTTTC	CAGCTTATTG	CTGTTTTGAC	ACAAATGAAA	CCGAGATATA
MAM1_SP134	CTAGAGTCTG	TAGTCTTTAT	AAATAAAATC	CAAATAACAC	CTTAGCTGAA
MAST_A445_	TATAATTTTC	CAGCTTATTG	CTGTTTTGAC	ACAAATGAAA	CCGAGATATA
SAV1_SE210	CTAGAGTCTG	TAGTCTTTAT	AAATAAAATC	CAAATAACAC	CTTAGCTGAA
	TATAATTTTC	CAGCTTATTG	CTGTTTTGAC	ACAAATGAAA	CCGAGATATA

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ASIAN2_Ema	ACTTT-GTGA	AAATTCTTCC	TCTCTCTGCC	CACAGCCACC	GAGTTCACTC
FOR_DS1535	CGCAGCAGGG	TTAATGGCTG	TTTCCATATC	CCTCCAGAGA	CAC
MAM1_SP134	ACTTT-GTGA	AAATTCTTCC	TCTCTCTGCC	CACAGCCACC	GAGTTCACTC
MAST_A396_	CGCAGCAGGG	TTAATGGCTG	TTTCCATATC	CCTCCAGAGA	CAC
SAV1_SE210	ACTTT-GTGA	AAATTCTTCC	TCTCTCTGCC	CACAGCCACC	GAGTTCACTC
	CGCAGCAGGG	TAAATGGCTG	TTTCCATATC	CCTCCAGAGA	CAC

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ASIAN2_Ema	CCCACAGTCA GGAAGTGGGA CTCTCCCCC	CGCGTGGGGA AGTCGCCCCG CGCCCAGAAG	GAAATAAGTC CAGCGTGGGC CA	GAGAAGGCGG CGTTCTCTGA CA	CGGTGTCAGG AAGCCCAGCA CA
FOR_DS1535	CCCACAGTCA GGAAGTGGGA CTCTCCCCC	CGCGTGGGGA AGTCGCCCCG CGCCCAGAAG	GAAATAAGTC CAGCGTGGGC CA	GAGAAGGCGG CGTTCTCTGA CA	CGGTGTCAGG AAGCCCAGCA CA
MAM1_SP134	CCCACAGTCA GGAAGTGGGA CTCTCCCCC	CGCGTGGGGA AGTCGCCCCG -GCCCAGAAG	GAAATAAGTC CAGCGTGGGC CA	GAGAAGGCGG CGTTCTCTGA CA	CGGTGTCAGG AAGCCCAGCA CA
MAST_A398_	CCCACAGTCA GGAAGT---- CTCTCCCCC	CGCGTGGGGA ---CGCCCCG CGCCCAGAAG	GAAAGAAGTC CAGCGTGGGC CA	GAGAAGGCGG CGTTCTCTGA CA	CGGTGTCAGG AAGCCCAGCA CA
SAV1_SE210	CCCACAGTCA GGAAGTGGGA CTCTCCCCC	CGCGTGGGGA AGTCGCCCCG CGCCCAGAAG	GAAATAAGTC CAGCGTGGGC CA	GAGAAGGCGG CGTTCTCTGA CA	CGGTGTCAGG AAGCCCAGCA CA

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ASIAN2_Ema	GGGCAAGGAC CCGAGGTCAA	GAGAAGGCAG AAA-GGGGAA	TCAGGGACAG AGTGTTAACA	GAAAGCTGGA ATCAGAACAT	AATGGGAAAC GGAATGTGT
FOR_DS1535	GGGCAAGGAC CCGAGGTCAA	GAGAAGGCAG AAA-GGGGAA	TCAGGGACAG AGTGTTAACA	GAAAGCTGGA ATCAGAACAT	AATGGGAAAC GGAATGTGT
MAM1_SP134	GGGCAAGGAC CCAAGGTCAA	GAGAAGGCAG AAA-GGGGAA	TCAGGGACAG AGTGTTAACA	GAAAGCTGGA ATCAGAACAT	AATGGGAAAC GGAATGTGT
MAST_A399_	GGGCAAGGAC CCGAGGTCAA	GAGAAGGCAG AAAAGGGGAA	TCAGGGGCAG AGTGTTAACA	GAAAGCTGGA ATCAGAACAT	AATGCGGAAC GGAATGTGT
SAV1_SE210	GGGCAAGGAC CCGAGGTCAA	GAGAAGGCAG AAA-GGGGAA	TCAGGGACAG AGTGTTAACA	GAAAGCTGGA ATCAGAACAT	AATGGGAAAC GGAATGTGT

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ASIAN2_Ema	ACAGATTAGC AGGAAGACTG ACACC	AGGAGTGCTG TGTTCCCCCA	GACCTCATTC -GGCGTGTTG	AGAGATTGCC TCGGTTTGGG	RTGTGGTAAG GC-TGGGGTC
FOR_DS1535	ACAGATTAGC AGGAAGACTG ACACC	AGGAGTGCTG TGTTCCCCCA	GACCTCATTC -GGCGTGTTG	AGAGATTGCC TCGGTTTGGG	GTGTGGTAAG GC-TGGGGTC
MAM1_SP134	ACAGATTAGC AGGAAGACTG ACACC	AGGAGTGCTG TGTTCCCCCA	AACCTCATTC -GGCGTGTTG	AGAGATTGCC TCGGTTTGGG	GTGTGGTAAG GC-TGGGGTC
MAST_A401_	ACAGATTAGC AGGAAGACTG ACACC	AGAAGTGCTG TGTTCCCCCA	GACCTCATTC CGGCGTGTTG	AGAGATTGCC TCGGTTTGGG	ATGTGGTAAG GCGTGGGGTC
SAV1_SE210	ACAGATTAGC AGGAAGACTC ACACC	AGGAGTGCTG TGTTCCCCCA	GACCTCATTC -GGCGTGTTG	AGAGATTGCC TCGGTTTGGG	GTGTGGTAAG GC-TGGGGTC

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ASIAN2_Ema	GCTGAAATGC TGTTGAAGTG TGTTCTTTT	AGCAAAGGAA ATGGTATTGA	TAAATTCCTA GGCGGTATAT	CTTGTGGGAA CATT--TTCT	GAAATTTGTT TGTGGGA-AT
FOR_DS1535	GCTGAAATGC TGTTGAAGTG TGTTCTTTT	AGCAAAGGAA ATGGTATTGA	TAAATTCCTA GGCGGTATAT	CTTGTGGGAA CATT--TTCT	GAAATTTGTT TGTGGGA-AT
MAM1_SP134	GCTGAAATGC TGTTGAAGTG TGTTCTTTT	AGCAAAGGAA ATGGTATTGA	TAAATTYTTA GGCGGTATAT	CTTGTGGGAA CATT--TTCT	GAAATTTGTT TGTGGGA-AT
MAST_A286_	GTTGAAATGC TGTTGAAGTG TTTCCCGTT	AGCAAAGGAA ATGGTATTGA	TAAATTCCTA GGCGGTATAT	CTTGTGGGAA CATT-CATATT	GAAATTTGTT TAAACGACAT
SAV1_SE210	GCTGAAATGC TGTTGAAGTG TGTTCTTTT	AGCAAAGGAA ATGGTATTGA	TAAATTCCTA GGCGGTATAT	CTTGTGGGAA CATT--TTCT	GAAATTTGTT TGTGGGA-AT

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ASIAN2_Ema	CTTCGCATGG	GCATGACTGT	GCACATGGAA	TGTGCTGAAT	CTGGTTTGAA
	CTACCAAGAC	CTGTACAAGT	AACCTCAGCT	TCTGGAGTGT	
FOR_DS1535	CTTCGCATGG	GCATGACTGT	GCACATGGAA	TGTGCTGAAT	CTGGTTTGAA
	CTACCAAGAC	CTGTACAAGT	AACCTCAGCT	TCTGGAGTGT	
MAM1_SP134	CTTCACATGG	GCATGACTGT	GCACATGGAA	TGTGCTGAAT	CTGGTTTGAA
	CTACCAAGAC	CTGTACAAGT	AACCTCAGCT	TCTGGAGTGT	
MAST_A450_	CTTCGCATGG	GCATGACTGT	GCACATGGAA	TGTGCTGAAT	CTGGTTTGAA
	CTACCAAGAC	CTGTGCAAGT	AACCTCAGCT	TCTGGAGTGT	
SAV1_SE210	CTTCGCATGG	GCATGACTGT	GCACATGGAA	TGTGCTGAAT	CTGGTTTGAA
	CTACCAAGAC	CTGTACAAGT	AACCTCAGCT	TCTGGAGTGT	

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ASIAN2_Ema	ACCAAAAAGAC	CTTTCCCAGA	AGGCCAGAGG	GGAGCCACCT	ATGGGGGCAG
	GGCAGATGGA	ACCCTGCCCT	GTGCAGTTGG	AACAGTTTTT	-GGATTTCCC
	CA				
FOR_DS1535	ACCAAAAAGAC	TTTTCC-AGA	AGGCCAGAGG	GGAGCCACCT	ATGGGGGCAG
	GGCAGATGGA	ACCCTGCCCT	GTGCAGTTGG	AACAGTTTTT	-GGATTTCCC
	CA				
MAM1_SP134	ACCAAAAAGAC	CTTTCCCAGA	AGGCCAGAGG	GGAGCCACCT	ATGGGGGCAG
	GGCAGATGGA	ACCCTGCCCT	GTGCAGTTGG	AACAGTTTTT	-GTATTTCCC
	CA				
MAST_A404_	ACCAAAAAGAC	TTTTCCCAGA	AGGCCAGAGG	GGAGCCACCT	ATGGGGGCAG
	GGCAGATGGA	ACCCTGCCCT	GTGCAGTTGG	AACAGTTTTT	-GGATTTCCC
	CA				
SAV1_SE210	ACCAAAAAGAC	CTTTCCCAGA	AGGCCAGAGG	GGAGCCACCT	ATGGGGGCAG
	GGCAGATGGA	ACCCTGCCCT	GTGCAGTTGG	AACAGTTTTT	TGGATTTCCC
	CA				

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ASIAN2_Ema	CTTTCCCTTT	-GCATTCACA	ACTTGGCTAA	CTGTTGGACG	CAAGAGGCCT
	AGTTTTTGGC	CTGTCTTGGC	TTTCGACATG	CCTTCCTCAC	TAAGCTTAAT
	CATTTCTAG				
FOR_DS1535	CTTTCCCTTT	-GCATTCACA	ACTTGGCTAA	CTGTTGGACG	CAAGAGGCCT
	AGTTTTTGGC	CTGTCTTGGC	TTTCAACATG	CCTTCCTCAC	TAAGCTTAAT
	CATTTCTAG				
MAM1_SP134	CTTTCCCTTT	-GCATTCACA	ACTTGGCTAA	CTGTTGGACG	CAAGAGGCCT
	AGTTTTTGGC	CTGTCTTGGC	TTTCGACATG	CCTTCCTCAC	TAAGCTTAAT
	CATTTCTAG				
MAST_A451_	CTTTTCTTTT	TGCGTTTATA	ACTTGGCTAA	CTGTTGGGTG	CAAGAGGCCT
	AGTTTTTGGC	CTGTCTTGGC	TTTCAACTTG	CCTCCCTCAC	TAAGCTTAAT
	CATTTCTAG				
SAV1_SE210	CTTTCCCTTT	-GCATTCACA	ACTTGGCTAA	CTGTTGGACG	CAAGAGGCCT
	AGTTTTTGGC	CTGTCTTGGC	TTTCAACATG	CCTTCCTCAC	TAAGCTTAAT
	CATTTCTAG				

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ASIAN2_Ema	TTTCTCCTGA	AGCCGATGCC	CTGAATTTGG	ATTTGCAACC	TACTAGACTG
	TGAGATAAAA	A-TTTCTCTT	TGTTAAAGCC	ATCCAATTGT	GGTATTTCTG
	TTATGG				
FOR_DS1535	TTTCTCCTGA	AGSCGATGCC	CTGAATTTGG	ATTTGCAACC	TACTAGACTG
	TGAGATAAAA	AATTTCTCTT	TGTTAAAGCC	ATCCAATTGT	GGTATTTCTG
	TTATGG				
MAM1_SP134	TTTCTCCTGA	AGCCGATGCC	CTGAATTTGG	ATTTGCAACC	TACTAGACTG
	TGAGATAAAA	AATTTCTCTT	TGTTAAAGCC	ATCCAATTGT	GGTATTTCTG
	TTATGG				
MAST_A405_	TTTCTCCTGA	AGCCGATGCC	CTGAATTTGG	ATTTGCAACC	TACTAGACTG
	TGAGATAAAA	AATTTCTCTA	TGTTAAAGCC	ATCCAATTGT	GGTATTTCTG
	TTATGG				
SAV1_SE210	TTTCTCCTGA	AGGCGATGCC	CTGAATTTGG	ATTTGCAACC	TACTAGACTG
	TGAGATAAAA	AATTTCTCTT	TGTTAAAGCC	ATCCAATTGT	GGTATTTCTG
	TTATGG				

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ASIAN2_Ema	AATAAGGGCT TGGGCGCTTC CTGGCACAT	TGAAGCCACA TCAAATTGCA GGCCTCTCCT	TTATTGAATA GGCCTCTCCT	TCCCAACCCA CTTGCAAGTC	CCATAAAGGT GCAAAATAAA
FOR_DS1535	AATAAGGGCT TGGGCGCTTC CTGGCACAT	TGAAGCCACA TCAAATTGCA GGCCTCTCCT	TTATTGAATA GGCCTCTCCT	TCCCAACCCA CTTGCAAGTC	CCATAAAGGT GCAAAATAAA
MAM1_SP134	AATAAGGGCT TGGGCGCTTC CTGGCACAT	TGAAGCCACA TCAAATTGCA GGCCTCTCCT	TTATTGAATA GGCCTCTCCT	TCCCAACCCA CTTGCAAGTC	CCATAAAGGT GCAAAATAAA
MAST_A454_	AATAAGGGCT TGGGCGCTTC CTGCGACAA	TGAAGCCACA TCAAATTGCA GGCCTCTCCT	TTATTGAATA GGCCTCTCCT	TCCCAACCCA CTTGTAAGTC	CCATAAAGTT ACAAAATAAA
SAV1_SE210	AATAAGGGCT TGGGCGCTTC CTGGCACAT	TGAAGCCACA TCAAATTGCA GGCCTCTCCT	TTATTGAATA GGCCTCTCCT	TCCCAACCCA CTTGCAAGTC	CCATAAAGGT ACAAAATAAA

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ASIAN2_Ema	CCATGCCCT GACCTCTGCT	GGGCCCCTTG GCTGCCTCCC	CAGCTACTAC GGGGCTGCAG	ATCTGCTGCG CTGCCCGATG	GAAGTTTACA CAC
FOR_DS1535	CCATGCCCT GACCTCTGCT	GGGCCCCTTG GCTGCCTCCC	CAGCTACTAC GGGGCTGCAG	ATCTGCTGCG CTGCCCGATG	GAAGTTTACA CAC
MAM1_SP134	CCATGCCCT GACCTCTGCT	GGGCCCCTTG GCTGCCTCCC	CAGCTACTAC GGGGCTGCAG	ATCTGCTGCG CTGCCCGATG	GAAGTTTACA CAT
MAST_A407_	CCAAATCCCA GACCTCTGCT	GGCCCC-TTA GCTGCCTCCC	CAGCCACTAC GGGGCTGCAG	ATCTGCTGCA CTGCCCGACG	GAAGTTTACA CGC
SAV1_SE210	CCATGCCCT GACCTCTGCT	GGGCCCCTTG GCTGCCTCCC	CAGCTACTAC GGGGCTGCAG	ATCTGCTGCG CTGCCCGATG	GAAGTTTACA CGC

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ASIAN2_Ema	CCTTCAGGAG CTCCAGGCCC	TGAAACCTCA CCGCGTCTCT	GAGTTGTTTT GAGTCCTGGT	TGACCCCTCG TGTGCTGCAT	CTGCCCCAGA CTT
FOR_DS1535	CCTTCAGGAG CTCCAGGCCC	TGAAACCTCA CCGCGTCTCT	GAGTTGTTTT GAGTCCTGGT	TGACCCCTCG TGTGCTGCAT	CTGCCCCAGA CTT
MAM1_SP134	CCTTCAGGAG CTCCAGGCCC	TGAAACCTCA CCGCGTCTCT	GAGTTGTTTT GAGTCCTGCT	TGACCCCTCG TGTGCTGCAT	CTGCCCCAGA CTT
MAST_A409_	CCTTCAGGAG CTCCAGGCCC	TGAAACCTCA CCGCGTCTCT	GAGTTGTTTT GAGTCCTGAT	TGACCCCTCG TGTGCTGCCT	CTGCCCCAGA CTT
SAV1_SE210	CCTTCAGGAG CTCCAGGCCC	TGAAACCTCA CCGCGTCTCT	GAGTTGTTTT GAGTCCTGGT	TGACCCCTCG TGTGCTGCAT	CTGCCCCAGA CTT

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ASIAN2_Ema	GCTAGTCAGT TGGCTATGTG	TGATTGGCTA AGCATGTCTT	TGTGAATGTT CAAGTGCAGA	GGGGCAGCTG TTGAGAAAAT	GTCAGTAAGG A
FOR_DS1535	GCTAGTCAGT TGGCTATGTG	TGATTGGCTA AGCATGTCTT	TGTGAATGTT CAAGTGCAGA	GGGGCAGCTG TTGAGAAAAT	GTCAGTAAGG A
MAM1_SP134	GCTAGTCAGT TGGCTATGTG	TGATTGGCTA AGCATGTCTT	TGTGAATGTT CAAGTGCAGA	GGGGCAGCTG TTGAGAAAAT	GTCAGTAAGG A
MAST_A456_	GCTAGTTAGT TGGCTGTGTG	TGATTGGCTA AGCATGTCTT	TGTGAATGTT CAAGTGCAGA	GGGGCAGCTG TTGAGAAAAT	GTCAGTAAGG A
SAV1_SE210	GCTAGTCAGT TGGCTATGTG	TGATTGGCTA AGTATGTCTT	TGTGAATGTG CAAGTGCAGA	GGGGCAGCTG TTGAGAAAAT	GTCAGTAAGG A

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ASIAN2_Ema	CTGAATCTAC CAATCTGCAG	ATGCCTCTTG ATACTGTGAG	TTTTATTTCT GTACAGATTA	CTTTAAACTT TACTGTCGGC	GAAGAACAGT TACTG
FOR_DS1535	CTGAATCTAC CAATCTGCAG	ATGCCTCTTG ATACTGTGAG	TTTTATTTCT GTACAGATTA	CTTTAAACTT TACTGTCGGC	GAAGAACAGT TACTG
MAM1_SP134	CTGAATCTAC CAATCTGCAG	ATGCCTCTTG ATACTGTGAG	TTTTATTTCT GTACAGATTA	CTTTAAACTT TACTGTCGGC	GAAGAACAGT TACTG

MAST_A289_	TTGAATCTAC	ATGCCTCTTG	TTTTATTTCT	CTTTAAACTT	GAAGAACAGT
SAV1_SE210	CAATCTGCAG	ATACTGTGAG	GTACAGATTA	TACTGTCCGG	TACTG
	CTGAATCTAC	ATGCCTCTTG	TTTTATTTCT	CTTTAAACTT	GAAGAACAGT
	CAATCTGCAG	ATACTGTGAG	GTACAGATTA	TACTGTCCGG	TACTG

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ASIAN2_Ema	GAGGTTTCTT	CCTGCTGCCT	CAGTGTGTGG	AATGGGGCTA	GAGGCTGTAG
FOR_DS1535	CTAGGCCACC	CACCCACAAT	GCTCTGACCA	CGTTGCCTTC	TT
MAM1_SP134	GAGGTTTCTT	CCTGCTGCCT	CAGTGTGTGG	AACGGGGCTA	GAGGCTGTAG
MAST_A410_	CTAGGCCACC	CACCCACAAT	GCTCTGACCA	CGTTGCCTTC	TT
SAV1_SE210	GAGGTTTCTT	CCTGCTGCCT	CAGTGTGTGG	AATGGGGCTA	GAGGCTGTAG
	CTAGGCCACC	CACCCACAAT	GCTCTGACCA	CGTTGCCTTC	TT

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ASIAN2_Ema	AGCTTTGTGG	AAGGAAGACC	AGTCAGAAGT	AGGCCTACCC	TGGCAGAGAG
FOR_DS1535	GAACCTGGAG	GGGAGTGGGG	ACTAGGTGAA	CACCAAAAAA	GGTTCAGCTC
MAM1_SP134	TCAGTCA				
MAST_A412_	AGCTTTGTGG	AAGGAAGACC	AGTCAGAAGT	AGGCCTACCC	TGGCAGAGAG
SAV1_SE210	GAACCTGGAG	GGGAGTGGGG	ACTAGGTGAA	CACCAAAAAA	GGTTCAGCTC
	TCAGTCA				

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ASIAN2_Ema	AATTTTATTT	GCCAGATAAT	AGTAACACGG	GTCTTAAAAC	TTAAACAGTT
FOR_DS1535	TTGAGCGACG	ATGTCTTAGC	CACATCACCA	CTCCAATATT	TAGCTGTTTT
MAM1_SP134	T				
MAST_A414_	AATTTTATTT	GCCAGATAAT	AGTAACACGG	GTCTTAAAAC	TTAAACAGTT
SAV1_SE210	TTGAGCGACG	ATGTCTTAGC	CACATCACCA	CTCCAATATT	TAGCTGTTTT
	T				

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ASIAN2_Ema	AAAAGAGGTG	TGGGCTACCC	TTCCAGAAAA	-GAGTGAACA	GAAATGCAAA
FOR_DS1535	CAATTTCCAG	AGTGTCTGGG	CATGTGGCCA	TGCTTGGCAC	TCCACAGTTT
MAM1_SP134	ACAGTTAGTT	CCCT			
MAST_A291_	AAAAGAGGTG	TGGGCTACCC	TTCCAGAAAA	-GAGTGAACA	GAAATGCAAA
	CAATTTCCAG	AGTGTCTGGG	CATGTGGCCA	TGCTTGGCAC	TCCACAGTTT
	ACAGTTAGTT	CCCT			

SAV1_SE210	ACAGTTAGTT AAAAGAGGTG CAATTTCCAG ACAGTTAGTT	CCCC TGGGCTACCC AGTGTCTGGG CCCT	TTCCAGAAAA CATGTGGCCA	-GAGTGAACA TGCTTGGCAC	GAAATGCAAA TCCACAGTTT
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ASIAN2_Ema	GGGAA-GTCT CACATTCTCA CACGTTGCTG CCCCAGGCAC	GGTGGGAGAA GGCCTAACAA- TCAAGTCAGC TA	AAGTGGGGCA CACATAACA- CCT-CAA----	GGGGTGGGCA CAAATCCAAA -----C	GGAGGAACAC AA--TC-AAA TTATGGC-GA
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FOR_DS1535	GGGAA-GTCT CACATTCTCA CACGTTGCTG CCCCAGGCAC	GGTGGGAGAA GGCCTAACAA- TCAAGTCAGC TA	AAGTGGGGCA CACATAACA- CCT-CAA----	GGGGTGGGCA CAAATCCAAA -----C	GGAGGAACAC AA--TC-AAA TTATGGC-GA
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MAM1_SP134	GGGGA-GTCT CACATTCTCA CACGTTGCTG CCCCAGGCAC	GGTGGGAGAA GGCCTAACAA- TCAAGTCAGC TA	AAGTGGGGCA CACATAACA- CCT-CAA----	GGGGTGGGCA CAAATCCAAA -----C	GGAGGAACAC AA--TC-AAA TTATGGC-GA
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MAST_B003_	GGGAAGGTCT CACATTCTCA CACATTGCTG CTCTCTACCT	GGTGGGAGAA GGCCTAACAC TCAAGTCA-C TA	AAGTGGGGCA CACATAACAC CTTAGAAGAG	GGGGTGGGCA CAGATCCAAA TGTTCTCTGTC	GGAGGAACAC AAACTCAAAA TTTTCACTGA
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SAV1_SE210	GGGAA-GTCT CACATTCTCA CACGTTGCTG CCCCAGGCAC	GGTGGGAGAA GGCCTAACAA- TCAAGTCAGC TA	AAGTGGGGCA CACATAACA- CCT-CAA----	GGGGTGGGCA CAAATCCAAA -----C	GGAGGAACAT AA--TC-AAA TTATGGC-GA
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ASIAN2_Ema	AGGCCCATTT CTCGTCCTCT AGGGCAGCTG	GCCTCCTTAC AGCAGGAGAC CTACCCGCTT	TGAGGAYGGC CCAGGTTGTA GTCAGTGGTA	AGTGGTCCAG TTCCTGGCTA GCTTGCGTGT	TGGCAGAATT ACGCACCTCC TGCTATGA
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FOR_DS1535	AGGCCCATTT CTCGTCCTCT AGGGCAGCTG	GCCTCCTTAC AGCAGGAGAC CTACCCGCTT	TGAGGACGGC CCAGGTTGTA GTCAGTGGAA	AGTGGTCCAG TTCCTGGCTA GCTTGCGTGT	TGGCAGAATT ACGCACCTCC TGCTATGA
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MAM1_SP134	AGGCCCATTT CTCGTCCTCT AGGGCAGCTG	GCCTCCTTAC AGCAGGAGAC CTACCCGCTT	TGAGGACGGC CCAGGTTGTA GTCAGTGGAA	AGTGGTCCAG TTCCTGGCTA GCTTGCGTGT	TGGCAGAATT ACGCACCTCC TGCTATGA
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MAST_B008_	AGGCCCATTT CTTGTCCTCT AGTGCAGCTG	GCCTCCTTAC AGCAGGAGAC CTACCCGCTT	TGAGGACGGC CCAGGTTGTA GTCAGTGGAA	AGTGGTCCAG TTCCTGGCTA GCTTGCGTGT	TGGCAGAATT ACGCACCTCC TGCTATGA
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SAV1_SE210	AGGCCCATTT CTCGTCCTCT AGGGCAGCTG	GCCTCCTTAC AGCAGGAGAC CTACCCGCTT	TGAGGACGGC CCAGGTTGTA GTCAGTGGAA	AGTGGTCCAG TTCCTGGCTA GCTTGCGTGT	TGGCAGAATT ACGCACCTCC TGCTATGA
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ASIAN2_Ema	ACTGGGGACA TGCCTCTAGG GAATTTCAAT	TTTATGTTTG AAGGAAGTCT AGG-TCTCTC	CTGGTTACTA AGTGGAGGGG TTCCTCCTCA	CGGAAATTAC GCTTAGGGAG TATCTCTTTT	TATGGATTAC GAGGTTTACC TGCT
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FOR_DS1535	ACTGGGGACA TGCCTCTAGG GAATTTCAAT	TTTATGTTTG AAGGAAGTCT AGG-TCTCTC	CTGGTTACTA AGTGGAGGGG TTCCTCCTCA	CGGAAATTAC GCTTAGGGAG TATCTCTTTT	TATGGATTAC GAGGTTTACC TGCT
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MAM1_SP134	ACTGGGGACA TGCCTCTAGG GRATTTCAAT	TTTATGTTTG AAGGAAGTCT AGG-TCTCTC	CTGGTTACTA AGTGGAGGGG TTCCTCCTCA	CGGAAATTAC GCTTAGGGAG TATCTCTTTT	TATGGATTAC GAGGTTTACC TGCT
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MAST_B011_	ATTGGGGATA TGCCTCTAGG GAATTTCAAT	TTTATGTTTG AAGGAAGTCT AGGGTCTCTC	CTGGTTACTA AGTGGAGGGG TTCCTCCTCA	TGGAAATTAC GCTTGGGGAG TATCTCTTTT	TATGGATTAC GAGGTT-ACC TGCT
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SAV1_SE210	ACTGGGGACA TGCCTCTAGG GAATTTCAAT	TTTATGTTTG AAGGAAGTCT AGG-TCTCTC	CTGGTTACTA AGTGGAGGGG TTCCTCCTCA	CGGAAATTAC GCTTAGGGAG TATCTCTTTT	TATGGATTAC GAGGTTTACC TGCT
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ASIAN2_Ema	CGTTTCTCCG	GGTGCACATC	CAAGTCAAAT	AAGGTGGAAT	GCCTCAGCAT
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	CCACTGGCCA	CACCCTTCCC	ACTTGCCCCA	GGTGGGTGCC	AAGGGAGGCA
FOR_DS1535	ACCCCAGAGA	GCACACACAG	GACTATCCAC	GCCAGCACCG	CTG
	CGTTTCTCCG	GGTGCACATC	CAAGTCAAAT	AAGGTGGAAT	GCCTCAGCAC
	CCACTGACCA	CACCCTTCCC	ACTTGCCCCA	GGTGGGTGCC	AAGGGAGGCA
MAM1_SP134	ACCCCAGAGA	GCACACACAG	GACTATCCAC	GCCAGCACCG	CTG
	CGTTTCTCCG	GGTGCACATC	CAAGTCAAAT	AAGGTGGAAT	GCCTCAGCAC
	CCACTGGCCA	CACCCTTCCC	ACTTGCCCCA	GGTGGGTGCC	AAGGGAGGCA
MAST_B014_	ACCCCAGAGA	GCACACACAG	GACTATCCAC	GCCAGCACCG	CTG
	TGTTTCTTTCG	GGTGCACATC	CAAGTCAAAT	AAGGTGGAAT	GCCTCAGCAC
	CCACTGGCCA	CACCCTTCCC	ACTTGCCCCA	AGTGGGTGCC	AAGGGAGGCA
SAV1_SE210	ACCCCAGAGA	GCACACACAG	GACTATCCAC	GCCAGCACCG	CTG
	CGTTTCTCCG	GGTGCACATC	CAAGTCAAAT	AAGGTGGAAT	GCCTCAGCAC
	CCACTGGCCA	CACCCTTCCC	ACTTGCCCCA	GGTGGGTGCC	AAGGGAGGCA
	ACCCCAGAGA	GCACACACAG	GACTATCCAC	GCCAGCACCG	CTG

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ASIAN2_Ema	GGTACCATGA	CCTCTGAGGG	TCCTCCAGCC	TCAATCAGAC	CATTAAGTCT
	GGTCTTTTTA	C-CAGAATTT	GAGGTCTACC	ACCCACTGTT	CTCCTGCTCC
FOR_DS1535	ATCAAGGATT	CTCTGTAGTG	TTCCCAGTCA	TTGGTGGTAG	CTGG
	GGTACCATGA	CCTCTGAGGG	TCCTCCAGCC	TCAATCAGAC	CATTAAGTCT
	GGTCTTTTTA	CCTAGAATTT	GAGGTCTACC	ACCCACTGTT	CTCCTGCTCC
MAM1_SP134	ATCAAGGATT	CTCTGTAGAG	TTCCCAGTCA	TTGGTGGTAG	CTGG
	GGTACCATGA	CCTCTGAGGG	TCCTCCAGCC	TCAATCAGAC	CATTAAGTCT
	GGTCTTTTTA	C-CAGAATTT	GAGGTCTACC	ACCCACTGTT	CTCCTGCTCC
MAST_B017_	ATCAAGGATT	CTCTGTAGTG	TTCCCAGTCA	TTGGTGGTAG	CTGG
	GGTACCATGA	ACTCTGAGGG	TCCTCCAGCC	TCAATCAGAC	CATTAAGTCT
	GGTCTTTTT-A	C-TAGAATTT	GAGGTTTACC	ACCCACTGTT	CTCCTGCTTC
SAV1_SE210	ATCAAGGATT	CTCTGTAGTG	TTCCCAGTCA	TTGGTGGTAA	CTGA
	GGTACCATGA	CCTCTGAGGG	TCCTCCAGCC	TCAATCAGAC	CATTAAGTCT
	GGTCTTTTTA	C-TAGAATTT	GAGGTCTACC	ACCCACTGTT	CTCCTGCTCC
	ATCAAGGATT	CTCTGTAGTG	TTCCCAGTCA	TTGGTGGTAG	CTGG

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ASIAN2_Ema	TCCTGTTGTG	CAGTTAAGAA	A-CGGATTTT	-CATGAAAAA	AA-TAATTCC
	TCTTATGTTG	GGTTGG-AAA	-TGGTTGACA	GTGGACTCCA	TCTCAGTGCA
FOR_DS1535	TCCACGGAGC	-AGCACCTAG	TAGGAATGTT	GGAGAACAC	
	TCCTGTTGTG	AAGTTAAGAA	A-CGGATTTT	-CATGAAAAA	AA-TAATTCC
	TCTTATGTTG	GGTTGG-AAA	-TGGTTGACA	GTGGACTCCA	TCTCAGTGCA
	TCCAYGGAGC	-AGCACCTAG	TAGGAATGTT	GGAGAACAC	
MAM1_SP134	TCCTGTTGTG	CAGTTAAGAA	A-CGGATTTT	-CATGAAAAA	AA-TAATTCC
	TCTTATGTTG	GGTTGG-AAA	-TGGTTGACA	GTGGACTCCA	TCTCAGTGCA
	TCCACGGAGC	-AGCACCTAG	TAGGAATGTT	GGAGAACAC	
MAST_B022_	TCCTGTTGTG	AAGTTAAGAA	AATGGATTTT	TCATGAAAAA	AAATAATTCC
	TCTTATGTTG	GGTTGGGAAA	ATGGTTGACA	GTGGACTCCA	TCTCAGTGCA
	TCCACAGAGC	GAGCACCTAG	TAGGAATGTT	GGAGAACAC	
SAV1_SE210	TCCTGTTGTG	AAGTTAAGAA	A-CGGATTTT	-CATGAAAAA	AA-TAATTCC
	TCTTATGTTG	GGTTGG-AAA	-TGGTTGACA	GTGGACTCCA	TCTCAGTGCA
	TCCACGGAGC	-AGCACCTAG	TAGGAATGTT	GGAGAACAC	

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ASIAN2_Ema	TCCTGTTGGG	TTATT-CTGC	TGACAGCTAC	CTTTTGGTRT	GGGGACCCAG
	CCCATTTAGG	GCTCTGGAGA	TTGTGTTGCA	GAAGGGGTAT	AAACTTTTCT
FOR_DS1535	GGACCCTGC-	ACCC-ACC-T	G-TGTTTGTG	GTGGCCAGT	
	TCCTGTTGGG	TTATT-CTGC	TGACAGCTAC	CTTTTGGTGT	GGGGACCCAG
	CCCATTTAGG	GCTCTGGAGA	TTGTGTTGCA	GAAGGRGTAT	AAACTTTTCT
	GGACCCTGC-	ACCC-ACC-T	G-TGTTTGTG	GTGGCCAGT	
MAM1_SP134	TCCTGTTGGG	TTATT-CTGC	TGACAGCTAC	CTTTTGGTGT	GGGGACCCAG
	CCCATTTAGG	GCTCTGGAGA	TTGTGTTGCA	GAAGGGGTAT	AAACTTTTCT
	GGACCCTGC-	ACCC-ACC-T	G-TGTTTGTG	GTGGCCAGT	
MAST_B023_	TTTTGTTGGG	TTATTTCTGC	TAACAACCTAC	CTTTTAGTGT	GGGGACCCAG
	CCCATTTAGG	GCTCTANAAA	TTGTGTTGCA	GAAGGTGTAT	AAACTNCCCT
	GGACCCTGCC	ACCCACCCT	GGTGTGTTGTG	GTGGCCAGT	
SAV1_SE210	TCCTGTTGGG	TTATT-CTGC	TGACAGCTAC	CTTTTGGTGT	GGGGACCCAG
	CCCATTTAGG	GCTCTGGAGA	TTGTGTTGCA	GAAGGGGTAT	AAACTTTTCT
	GGACCCTGC-	ACCC-ACC-T	G-TGTTTGTG	GTGGCCAGT	

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ASIAN2_Ema	CCTGCGCTGG AGTGTTTAAAC ACTGATAACT	CGTCCAGGCT CTCTCTGTGC GTGTCATTGT	CTCCCGTTTA CTCGGTTTCC GAGCATTGG	TCAGCTTCTA TCACTGA-TA AACTGT	AAGCCTGGGA AACA-TGGGA
FOR_DS1535	CCTGCGCTGG AGYGCTTAAAC ACTGATAACT	CATCCAGGCT CTCTCTGTGC GTGTCATTGT	CTCCCATTTA CTCGGTTTCC GAGCAYTTGG	TCAGCTTCTA TCACTGA-TA AACCGT	AAGCCTGGGA AACA-TGGGA
MAM1_SP134	CCTGCGCTGG AGTGCTTAAAC ACTGATAACT	CGTCCAGGCT CTCTCTGTGC GTGTCATTGT	CTCCCATTTA CTCGGTTTCC GAGCATTGG	TCAGCTTCTA TCACTGA-TA AACCGT	AAGCCTGGGA AACA-TGGGA
MAST_B025_	CCTGCCCTGG AGTGCTTAAAC ACTGATAACT	CGTCCAGGCT CTCTCTGTGC GTGTCATTGT	CTCCCATTTA CTCGGTTTCC GAGCATTGG	TCAGCTTCTA TCACTGAATA AACAAT	AAGCCTGGGA AACAGTGGGA
SAV1_SE210	CCTGTGCTGG AGTGCTTAAAC ACTGATAACT	CGTCCAGGCT CTCTCTGTGC GTGTCATTGT	CTCCCATTTA CTCGGTTTCC GAGCATTGG	TCAGCTTCTA TCACTGA-TA AACCGT	AAGCCTGGGA AACA-TGGGA

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ASIAN2_Ema	TCCCTGCAGG CCGGCTCCCT CGGTCTCGGC	GGCAGGAGAG CTAGTCACCA TTTAGCTTCT	TGGCAGAGTT GAGACTAATA GTGATGTTGC	TGGCTCACCT GGAACCATGC CTGTG	CCCTCCTGGC CAGCCCCAGC
FOR_DS1535	TCCCTGCAGG CCGGCTCCCT CGGTCTCGGC	GGCAGGAGAG CTAGTCACCA TTTAGCTTCT	TGGCAGAGTT GAGACTAATA GTGATGTTGC	TGGCTCACCT GGAACCATGC CTGTG	CCCTCCTGGC CAGCCCCAGC
MAM1_SP134	TCCCTGCAGG CCGGCTCCCT CAGTCTCAGC	GGCAGGAGAG CTAGTCACCA TTTAGCTTCT	TGGCAGAGTT GCGACTAATA GTGATGTTGC	TGGCTCACCT GGAACCATGC CTGTG	CCCTCCTGGC CAGCCCCAGC
MAST_B029_	TCCCTGCAGG TCGGCTCCCT CGGTCTCAGC	GGCAGGAGAG CTAGTCACCA TTTAGCTTCT	TGGCAGAATT GAGATTAATA GTGATGTTGC	TGGTTACCT GGAACCATGT CTGTA	CCCTCCTGGC CAGCCCCAGC
SAV1_SE210	TCCCTGCAGG CCGGCTCCCT CGGTCTCAGC	GGCAGGAGAG CTAGTCACCA TTTAGCTTCT	TGGCAGAGTT GAGACTAATA GTGATGTTGC	TGGCTCACCT GGAACCATGC CTGTG	CCCTCCTGGC CAGCCCCAGC

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ASIAN2_Ema	CTTAATCTTC TTTGAGCTGG CCCATTTTGG	TTTAGGCCTG GGCTGGAGTT GGTCCCC-TT	GGCACAACAC CAGACTGAGG CAAGGGCCCT	AGTCAGTGCG TGGGGAGTTG CAGGAC	CAGGGAGGGA TGGAACTTGC
FOR_DS1535	CTTAATCTTC TTTGAGCTGG CCCATTTTGG	TTTAGGCCTG GGCTGGAGTT GGTCCCCCTT	GGCACAACAC CAGACTGAGG CAAGGGCCCT	AGTCAGTGCG TGGGGAGTTG CAGGAC	CAGGGAGGGA TGGAACTTGC
MAM1_SP134	CTTAATCTTC TTTGAGCTGG CCCATTTTGG	TTTAGGCCTG GGCTGGAGTT GGTCCCC-TT	GGCACAACAC CAGACTGAGG CAAGGGCCCT	AGTCAGTGCG TGGGGAGTTG CAGGAC	CAGGGAGGGA TGGAACTTGC
MAST_B082_	CTTAATCTTC TTTGAGCTGG CCCATTTTGG	TTTAGGCCTG GGCTGGAGTT G-TCCCC-TT	GGCACAACAC CAGACTGAGG CAAGGGTCTT	AGTCAGTGCG TGGGGAGTTG CAG-AT	CAGGGAGGGA TGGAACTTGC
SAV1_SE210	CTTAATCTTC TTTGAGCTGG CCCATTTTGG	TTTAGGCCTG GGCTGGAGTT GGTCCCCCTT	GGCACAACAC CAGACTGAGG CAAGGGCCCT	AGTCAGTGCG TGGGGAGTTG CAGGAC	CAGGGAGGGA TGGAACTTGC

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ASIAN2_Ema	CCCATGAGCC GAAAA-CCAG TGACCCAGAG	CCCAGCCATC TCTGAATTCA ACTACAAATG	TCTTGAGATG GCATTTATGA TTTTTCTTAA	CTTCCTCCCA GAACAAAAGA GC	GACCATTGGG GAAGCAGTTG
FOR_DS1535	CCCATGAGCC GAAAAGCCAG TGACCCAGAG	CCCAGCCATC TCTGAATTCA ACTACAAATG	TCTTGAGATG GCATTTATGA TTTTTCTTAA	CTTCCTCCCA GAACAAAAGA GC	GACCATTGGG GAAGCAGTTG
MAM1_SP134	CCCATGAGCC GAAAAGCCAG TGACCCAGAG	CCCAGCCATC TCTGAATTCA ACTACAAATG	TCTTGAGATG GCATTTATGA TTTT-CTTAA	CTTCCTCCCA GAACAAAAGA GC	GACCATTGGG GAAGCAGTTG
MAST_B033_	CCCATGAGCC GAAAA-CCAG TGACCCAGAG	CCCAGCCATC TCTGAATTCA ACTACAAATG	TCTTGAGATG GCATTTATGA TTTT-CTTAA	CTTCCTCCCA GAACAAAAGA GC	GACCATTGGG GAAGCAGTTG

SAV1_SE210	GAAAAGCCAG TGACCCAAAG CCCATGAGCC GAAAAGCCAG TGACCCAGAG	TCTGAATTCA ACTACAAATG CCCAGCCATC TCTGAATTCA ACTACAAATG	GCATTTATGA TTTTTCTTAA TCTTGAGATG GCATTTATGA TTTTTCTTAA	GAACAAAAGA AC CTTCCTCCCA GAACAAAAGA GC	GAAGCAGTTG GACCATTGGG GAAGCAGTTG
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ASIAN2_Ema	TTGA--CCTG GAACTTGCAT CTCTGGGGGT	CCTGGGGGAT CACCTATGTC GCCTTTTACA	CTGCCCCAC- AATGTGCCAG AGTGTAGGAG	ACCCTTCCCC ACAGCCAGGA C	TGAGTCTTTG GGTCCAAGGC
FOR_DS1535	TTGA--CCTG GAACTTGCAT CTCTGGGGGT	CCTGGGGGAT CACCTATGTC GCCTTTTACA	CTGCCCCAC- AATGTGCCAG AGTGTAGGAG	ACCCTTCCCC ACAGCCAGGA C	TGAGTCTTTG GGTCCAAGGC
MAM1_SP134	TTGA--CCTG GAACTTGCAT CTCTGGGGGT	CCTGGGGGAT CACCTATGTC GCCTTTTACA	CTGCCCCAC- AATGTGCCAG AGTGTAGGAG	ACCCTTCCCC ACAGCCAGGA C	TGAGTCTTTG GGTCCAAGGC
MAST_B035_	TTCAAACTG GAACTTGCAT CTCTAGGAAT	CCTGGGGGAT CACCTATGTC GCCTTTTACG	CTGCCCCACC AATGTGCCAG AGTGTAGGAG	ACCCTTCACC ACAGCCAGGA C	TGGGTCTTTG GGTCCAAGGC
SAV1_SE210	TTGA--CCTG GAACTTGCAT CTCTGGGGGT	CCTGGGGGAT CACCTATGTC GCCTTTTACA	CTGCCCCAC- AATGTGCCAG AGTGTAGGAG	ACCCTTCCCC ACAGCCAGGA C	TGAGTCTTTG GGTCCAAGGC

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ASIAN2_Ema	TGGTTAAGTG CAAAGGCCAG ACACCGTTTA	GCTTGTCTGA GGCTATGTGA GCCCCAGCCA	GGATACTCAG GTCCACGCCC AGCTTTCTCT	CTAGGTGAAG AACCCCAACA CT	CCAAGAAGGT TCACCCCAAA
FOR_DS1535	TGGTTAAGTG CAAAGGCCAG ACACCGTTTA	GCTTGTCTGA GGCTATGTGA GCCCCAGCCA	GGATACTCAG GTCCACGCCC AGCTTTCTCT	CTAGGTGAAG AACCCCAACA CT	CCAAGAAGGT TCACCCCAAA
MAM1_SP134	TGGTTAAGTG CAAAGGCCAG ACACCGTTTA	GCTTGTCTGA GGCTATGTGA GCCCCAGCCA	GGATACTCAG GTCCACGCCC AGCTTTCTCT	CTAGGTGAAG AACCCCAACA CT	CCAAGAAGGT TCACCCCAAA
MAST_B036_	TGGTTAAGTG CAAAGGCCAG ACACCGTTTA	GCTTGTCTGA GGCTATGTGA GCCCCAGCCA	GGATACTCAG GTCCATGTCC AGCTTTCTCT	CTAGGTGAAG AACTCCAACA CT	CCAAGAAGGT TCACCC-AA
SAV1_SE210	TGGTTAAGTG CAAAGGCCAG ACACCGTTTA	GCTTGTCTGA GGCTATGTGA GCCCCAGCCA	GGATACTCAG GTCCACGCCC AGCTTTCTCT	CTAGGTGAAG AACCCCAACA CT	CCAAGAAGGT TCAGCCCAAA

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ASIAN2_Ema	TTGGAAAGAG GGCAGAGACA AAAGGAGGGA	TATCTTAAGC GAGAGAAAGA GGGAGTGGAA	ACAAAGGGTT GAGAGGGAGA AAGGGAAAAA	CTTGATAAAC GAAGAAAGAA GG	ATTGAATAAT AGGAAGGAGG
FOR_DS1535	TTGGAAAGAG GGCAGAGACA AAAGGAGGGA	TATCTTAAGC GAGAGAAAGA GGGAGTGGAA	ACAAAGGGTT GAGAGGGAGA AAGGGAAAAA	CTTGATAAAC GAAGAAAGAA GG	ATTGAATAAT AGGAAGGAGG
MAM1_SP134	TTGGAAAGAG GGCAGAGACA AAAGGAGGGA	TATCTTAAGC GAGAGAAAGA GGGAGTGGAA	ACAAAGGGTT GAGAGGGAGA AAGGGAAAAA	CTTGATAAAC GAAGAAAGAA GG	ATTGAATAAT AGGAAGGAGG
MAST_B083_	TTGGAAAGAG GGCAGAGACA AAAAGAGGGA	TATCTTAAGC NAGAGAAAGA GGGAGTGGAA	ACAAAGGGTT GAGAGGGAGA AAGGGAAAAA	-TTGATAAAC GAAGAAAGAA GG	ATTGAATAAT AGGAAGGAGG
SAV1_SE210	TTGGAAAGAG GGCAGAGACA AAAGGAGGGA	TATCTTAAGC GAGAGAAAGA GGGAGTGGAA	ACAAAGGGTT GAGAGGGAGA AAGGGAAAAA	CTTGATAAAC GAAGAAAGAA GG	ATTGAATAAT AGGAAGGAGG

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ASIAN2_Ema	GAGCCGCTG GCCGTGGGAA G-C-AGCTGG	CTCGAGGAGA GACCTCTGCC AGGAGGA-GA	A-GGAA-TCT -ACCC-AGAG GC-AAGGTGG	-C-TGATT-A CCTAGAGGAG	GCCAGC-TGA CTAC-GG-AG
FOR_DS1535	GAGCCGCTG GCCGTGGGAA	CTCGAGGAGA GACCTCTGCC	A-GGAA-TCT -ACCC-AGAG	-C-TGATT-A CCTAGAGGAG	GCCAGC-TGA CTAC-GG-AG

MAM1_SP134	G-C-AGCTGG GAGCCGCTG GCCGTGGGAA	AGGAGGA-GA CTCGAGGAGA GACCTCTGCC	GC-AAGGTGG A-GGAA-TCT -ACCC-AGAG	-C-TGATT-A CCTAGAGGAG	GCCAGC-TGA CTAC-GG-AG
MAST_B084_	G-C-AGCTGG GAGCCGCTG GCCATGGGAA	AGGAGGA-GA CTCGAGGAGA GACCTCTGCC	GC-AAGGTGG AAGGAACTCT CACCCCAGAG	TCCTGATTTA CCTAGAGGAG	GCCAGCCTGA CTACCGGGAG
SAV1_SE210	GGCGAGCTGG GAGCCGCTG GCCGTGGGAA	AGGAGGAAGA CTCGAGGAGA GACCTCTGCC	GCCAAGGTGA A-GGAA-TCT -ACCC-AGAG	-C-TGATT-A CCTAGAGGAG	GCCAGC-TGA CTAC-GG-AG
	G-C-AGCTGG	AGGAGGA-GA	GC-AAGGTGG		

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ASIAN2_Ema	GAGTGTGGG GCAGATGGGA GCCATTTTCAG	GAAAGGGATT CTAGGTTGTT GCTCTTCTCC	ACCAGGGAGC GCCTGGGCAA GAAGATGGCA	ATCGGCATGC TACCACACAG AT	TCACTGGGAG CAGCCTGCAT
FOR_DS1535	GAGTGTGGG GCAGATGGGA GCCATTTTCAG	GAAAGGGATT CTAGGTTGTT GCTCTTCTCC	ACCAGGGAGC GCCTGGGCAA GAAGATGGCA	ATCGGCATGC TACCACACAG AC	TCACTGGGAG CAGCCTGCAT
MAM1_SP134	GAGTGTGGRG GCAGATGGGA GCCATTTTCAG	GAAAGGGATT CTAGGTTGTT GCTCTTCTCC	ACCAGGGAGC GCCTGGGCAA GAAGATGGCA	ATCGGCATGC TACCACACAG AT	TCACTGGGAG CAGCCTGCAT
MAST_B037_	GAGTGTGGG GCAGATGGGA GCCATTTTCAG	-AAAGGGATT CTAGGTTGTT GCTCTTCTCC	ACCAGG-AGC GCCTGGGCAA GAAGATGGCA	ATCGGCATGC TACCACACAG AC	TCACTGGGAG CAGCCTGCAT
SAV1_SE210	GAGTGTGGG GCAGATGGGA GCCATTTTCAG	GAAAGGGATT CTAGGTTGTT GCTCTTCTCC	ACCAGGGAGC GCCTGGGCAA GAAGATGGCA	ATCGGCATGC TACCACACAG AC	TCACTGGGAG CAGCCTGCAT

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ASIAN2_Ema	CCCGCCAGAG GCCTGGCAGG AGGCCCAGGC	TCCAGCTCTG GCACTTGGCG TGGGGGAGGG	CAGAGCTCCC AACCTGCTGC GACTCTGGAG	TAGTAACACC ATCTCCACCG	TGGGCTCCCA TGAATACCAC
FOR_DS1535	CCCGCCAGAG GCCTGGCAGG AGGCCCAGGC	TCCAGCTCTG GCACTTGGCG TGGGGGAGGG	CAGAGCTCCC AACCTGCTGC GACTCTGGAG	TAGTAACACC GTCTCCACCG	TGGGCTCCCA TGAATACCAC
MAM1_SP134	CCCGCCAGAG GCCTGGCAGG AGGCCCAGGC	TCCAGCTCTG GCACTTGGCG TGGGGGAGGG	CAGAGCTCCC AACCTGCTGC GACTCTGGAG	TAGTAACACC ATCTCCACCG	TGGGCTCCCA TGAATACCAC
MAST_B038_	TCCGCCAGAG GCCTGGCAGG AGGCCCAGGC	TCCAGCTCTG GCACTTGGCG TGGGGGAGGG	TAGAGCTCCC AACCTGCTGC GACTCTGAAA	TAGTAACACT GTCTCCACCG	TGGGCTCCCA TGAATACCAC
SAV1_SE210	CCCGCCAGAG GCCTGGCAGG AGGCCCAGGC	TCCAGCTCTG GCACTTGGCG TGGGGGAGGG	CAGAGCTCCC AACCTGCTGC GACTCTGGAG	TAGTAACACC GTCTCCACCG	TGGGCTCCCA TGAATACCAC

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ASIAN2_Ema	CCAAAGTCAG GGCTAGTCTT TGTTGCCTGA	AACTCAAAAA TCAGTGCCG GGCCGTCAAT	GGGCAGCCCA CCACCTTCCA GAATTCTTA	CCGCTCACAG ACCATCTCCA	CAGCCTGCCA GCCATTGCCC
FOR_DS1535	CCAAAGTCAG GGCTAGTCTT TGTTGCCTGA	AACTCAAAAA TCAGTGCTG GGCCGTCAAT	GGGCAGCCCA CCACCTTCCA GAATTTTTA	CCGCTCACAG ACCATCTCCA	CAGCCTGCCA GCCATTGCCC
MAM1_SP134	CCAAAGTCAG GGCTAGTCTT TGTTGCCTGA	AACTCAAAAA TCAGTGCCG GGCCGTCAAT	GGGCAGCCCA CCACCTTCCA GAATTCTTA	CCGCTCACAG ACCATCTCCA	CAGCCTGCCA GCCATTGCCC
MAST_B040_	TCAAAGTCAG GGCTAGTCTT TGTTGCCTGA	AACTCAAAAA TCAGTGCTG GGCCGTCAAT	GGGCAGCCCA CCACCTTCCA GAATTCTTA	CTGCTCACAG ACCATCTCCA	CAGCCTGCCA GCCATTGCCC
SAV1_SE210	CCAAAGTCAG GGCTAGTCTT TGTTGCCTGA	AACTCAAAAA TCAGTGCTG GGCCGTCAAT	GGGCAGCCCA CCACCTTCCA GAATTTTTA	CCGCTCACAG ACCATCTCCA	CAGCCTGCCA GCCATTGCCC

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ASIAN2_Ema	TCTCCCGAAC AATGAGCACT CTGGAGACTT	GCCTTGGTTC ACAAAAGAAT CCTCTAGATT	CAGGAACCAA CAGAGCTGCT AGACAACCTG	GGAAATCCTG TGCAGGATGA	TCACGAAGTG GCTCTGCCTC
FOR_DS1535	TCTCCCGAAC AATGAGCACT CTGGAGACTT	GCCTTGGTTC ACAAAAGAAT CCTCCAGATT	CAGGAACCAA CAGAGCTGCT AGACAACCTG	GGAAATCCTG TGCAGGATGA	TCACGAAGTG GCTCTGCCTC
MAM1_SP134	TCTCCCGAAC AATGAGCACT CTGGAGACTT	GCCTTGGTTC ACAAAAGAAT CCTCCAGATT	CAGGAACCAA CAGAGCTGCT AGACAACCTG	GGAAATCCTG TGCAGGATGA	TCACGAAGTG GCTCTGCCTC
MAST_B041_	TCTCCGGAAC AATGAGCACT CTGGAGACTT	ACCTTGGTTC ACAAA-GAAT CCTCCAGATT	CAGGAACCAA CAGAGCTGCT AGACAACCTG	GGAAATCCTG TGCAGGATGA	TCACGAAGTG GCTCTGCCTC
SAV1_SE210	TCTCCCGAAC AATGAGCACT CTGGAGACTT	GCCTTGGTTC ACGAAAGAAT CCTCCAGATT	CAGGAACCAA CAGAGCTGCT AGACAACCTG	GGAAATCCTG TGCAGGATGA	TCACGAAGTG GCTCTGCCTC

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ASIAN2_Ema	CCATGAAGTT ATCAATGTCA GCTTCCTGGC	AC-CTGCAGA TCCTCTTAAA CTTGCTCTTT	GCTTTGGCTG CAACAACAAA ACTTCCGC	TCCAGAGATT AAAGCAGTGG	TCAGTCTTCC CCCCAATGAG
FOR_DS1535	CCATGAAGTT ATCAATGTCA GCTTCCTGGC	AC-CTGCAGA TCCTCTTAAA CTTGCTCTTT	GCTTTGGCTG CAACAACAAA ACTTCCGC	TCCAGAGATT AAAGCAGTGR	TCAGTCTTCC CCCCAATGAG
MAM1_SP134	CCATGAAGTT ATCAATGTCA GCTTCCTGGC	AC-CTGCAGA TCCTCTTAAA CTTGCTCTTT	GCTTTGGCTG CAACAACAAA ACTTCCGC	TCCAGAGATT AAAGCAGTGG	TCAGTCTTCC CCCCAATGAG
MAST_B086_	TCATGAAGTT ATCAATGTCA GCTTCCTGGC	ATTCTGCAGA TCCTCTTAAA CTTGCTCTTT	GCTTTGGCTA CAACAACAAA ACTTCTGC	TCCAGAGATT AAAGCAGTGG	TCAGTCTTCC CCC-AATGAG
SAV1_SE210	CCATGAAGTT ATCAATGTCA GCTTCCTGGC	AC-CTGCAGA TCCTCTCAA CTTGCTCTTT	GCTTTGGCTG CAACAACAAA ACTTCCGC	TCCAGAGATT AAAGCAGTGG	TCAGTCTTCC CCCCAATGAG

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ASIAN2_Ema	ATTTAGTCTG GGCAATTAAC ATAATA-TAA	CCTGTTAC-A AACAATGGTT AATTTAACCC	CAGAAGATTG TACTTAAAAA AATTATT	TTATGAGTCG AATATAGCAA	GAGATTCGAT ATTCTCAGTC
FOR_DS1535	ATTTAGTCTG GGCAATTAAC ATAATA-TAA	CCTGTTAC-A AACAAYGGTT AATTTAACCC	CAGAAGATTG TACTTAAAAA AATTATT	TTATGAGTCG AATATAGCAA	GAGATTCGAT ATTCTCAGTC
MAM1_SP134	ATTTAGTCTG GGCAATTAAC ATAATA-TAA	CCTGTTAC-A AACAATGGTT AATTTAACCC	CAGAAGATTG TACTTAAAAA AATTATT	TTATGAGTCG AATATAGCAA	GAGATTCGAT ATTCTCAGTC
MAST_B048_	ATTTAGTCTG GGCAATTAAC ATAATAATAA	CCTGTTACCA AACAATGGTT AATTTAACCC	CAGAAGATTG TACTTAAAAA AATTATT	TTATGAGTCG A-TATAGCAA	GAGATTCGAT ATTCTCAGTC
SAV1_SE210	ATTTAGTCTG GGCAATTAAC ATAATA-TAA	CCTGTTAC-A AACAACGGTT AATTTAACCC	CAGAAGATTG TACTTAAAAA AATTATT	TTATGAGTCG AATATAGCAA	GAGATTCGAT ATTCTCAGTC

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ASIAN2_Ema	CATTAGATTC CACTGTAATG CTCTCCCAT	ATTCTTTAGC TGGAGTGAGA CTTTGTGTTG	AAAAATCATC GCTTATCCTA TTGGAA	AAGGGAATCA ATTTGTTTGG	GACCAGCCTT CACCTCTTAA
FOR_DS1535	CATTAGATTC CACTGTAATG CTCTCCCAT	ATTCTTTAGC TGGAGAGAGA CTTTGTGTTG	AAAAATCATC GCTTATCCTA TTGGAA	AAGGGAATCA ATTTGTTTGG	GACCAGCCTT CACCTCTTAA
MAM1_SP134	CATTAGATTC CACTGTAATG CTCTCCCAT	ATTCTTTAGC TGGAGAGAGA CTTTGTGTTG	AAAAATCATC GCTTATCCTA TTGGAA	AAGGGAATCA ATTTGTTTGG	GACCAGCCTT CACCTCTTAA
MAST_B088_	TATTAGATTC CACTGTAATG CTCTCCCAT	ATTTTTTAGC TGGAGAGAGA ATTTGTGTTG	AAAAATCATC GCTTATCCTA TTGGAA	AAGGGAATCA ATTTGTTTGG	GACCAGCCTT CACCTCTTAA
SAV1_SE210	CATTAGATTC CACTGTAATG	ATTCTTTAGC TGGAGAGAGA	AAAAATCATC GCTTATCCTA	AAGGGAATCA ATTTGTTTGG	GACCAGCCTT TACCTCTTAA

CTCTCCATT CTTTGTGTTG TTGGAA

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ASIAN2_Ema	AGCGCTGTGT GTTTAAAGAC GACAGGCGAG	TCTCAACAGC TGCCCATCTG GCCTGGGAGC	TCATAAATCA TTGGCTGGCG CTTGC	CGCATCTCCT CCCTCCTCTC CCCTCCTCTC	TCAGAGGGGA CCTTCCGGCG CCTTCCGGCG
FOR_DS1535	AGCGCTGTGT GTTTAAAGAC GACAGGCGAG	TCTCAACAGC TGCCCATCTG GCCTGGGAGC	TCATAAATCA TTGGCTGGCG CTTGC	CGCATCTCCT CCCTCCTCTC CCCTCCTCTC	TCAGACGGGA CCTTCCGGCG CCTTCCGGCG
MAM1_SP134	AGCGCTGTGT GTTTAAAGAC GACAGGCGAG	TCTCAACAGC TGCCCATCTG GCCTGGGAGC	TCATAAATCA TTGGCTGGCG CTTGC	CGCATCTCCT CCCTCCTCTC CCCTCCTCTC	TCAGAGGGGA CCTTCCGGCG CCTTCCGGCG
MAST_B050_	AGTGTGTGT GTTTAAAGAC GACAGGCGAG	TTTCAACAGC TGCCCGTCTG GCCTGGGAGC	TCATAAATCA CTGGCTGGCA CTTTA	CGCATTTCTC CCCTCCTCTC CCCTCCTCTC	TCAGAGGGGA CCTTCCGGCG CCTTCCGGCG
SAV1_SE210	AGCGCTGTGT GTTTAAAGAC GACAGGCGAG	TCTCAACAGC TGCCCATCTG GCCTGGGAGC	TCATAAATCA TTGGCTGGCG CTTGC	CGCATCTCCT CCCTCCTCTC CCCTCCTCTC	TCAGAGGGGA CCTTCCGGCG CCTTCCGGCG

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ASIAN2_Ema	GCTAATGAGC GGTGCCTTGG CAGAAGTGGG	TTGAAGTAAA CCAAGTGCCT TCTCCGAATG	AA-GAAA-TT GCAGCCATGC GTGC	TA-TCTCTGC CAGGCAGAAG CAGGCAGAAG	ATCTGCCACT CCAGTTCTA CCAGTTCTA
FOR_DS1535	GCTAATGAGC GGTGCCTTGG CAGAAGTGGG	TTGAAGTAAA CCAAGTGCCT TCTCCGAATG	AA-GACA-TT GCAGCCATGC GTGC	TA-TCTCTGC CAGGCAGAAG CAGGCAGAAG	AGCTGCCACT CCAGTTCTA CCAGTTCTA
MAM1_SP134	GCTAATGAGC GGTGCCTTGG CAGAAGTGGG	TTGAAGTAAA CCAAGTGCCT TCTCCGAATG	AA-GAAA-TT GCAGCCATGC GTGC	TA-TCTCTGC CAGGCAGAAG CAGGCAGAAG	ATCTGCCACT CCAGTTCTA CCAGTTCTA
MAST_B054_	TTAAATGAGC GGTGCCTTGG CAGAAGTGGG	TTGAAGTAAA CCAAGTGCCT TCTCCGAATA	AAAGAAAATT GCAGCCATGC ATGC	TAATCTCTGC CAGGCAGAAG CAGGCAGAAG	AACTGCCACT CCAGTTCTA CCAGTTCTA
SAV1_SE210	GCTAATGAGC GGTGCCTTGG CAGAAGTGGG	TTGAAGTAAA CCAAGTGCCT TCTCCAAATG	AA-GACA-TT ACAGTCATGC GTGC	TA-TCTCTGC CAGGCAGAAG CAGGCAGAAG	AGCTGCCACT CCAGTTCTA CCAGTTCTA

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ASIAN2_Ema	TTACCCTTAC CCGAATCAAA CGAAGAGCCA	AAGTCTGTGA GAGGTAAAAT GGATTCAATC	ATTAGACATG GCCATCCTCA CTAA	TTTATTCCGT AGGTCACACA AGGTCACACA	TTTACAGAGG TCTATTAAGT TCTATTAAGT
FOR_DS1535	TTACCCTTAC CCGAATCAAA CGAAGAGCCA	AAGTCTGTGA GAGGTAAAAT GGATTCAATC	ATTAGACATG GCCATCCTCA CTAA	TTTATTCCCT AGGTCACACA AGGTCACACA	TTTACAGAGG TCTATTAAGT TCTATTAAGT
MAM1_SP134	TTACCCTTAC CCGGATCAAA CGAAGAGCCA	AAGTCTGTGA GAGGTAAAAT GGATTCAATC	ATTAGACATG GCCATCCTCA CTAA	TTTATTCCCT AGGTCACACA AGGTCACACA	TTTACAGAGG TCTATTAAGT TCTATTAAGT
MAST_B056_	TTACCGTTAC CCAAATCAAA CAAAGAGCCA	AAGTCTGTGA GAGGTAAAAT GGATTCAATC	ATTAGACATT GCCATCCTCA CTAA	TTTATTCCCT AGGTTACACA AGGTTACACA	TTTACAGAGG TCTATTAAGT TCTATTAAGT
SAV1_SE210	TTACCCTTAC CCGAATCAAA CGAAGAGCCA	AAGTCTGTGA GAGGTAAAAT GGATTCAATC	ATTAGACATG GCCATCCTCA CTAA	TTTATTCCCT AGGTCACACA AGGTCACACA	TTTACAGAGG TCTATTAAGT TCTATTAAGT

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ASIAN2_Ema	TGAAGACACC TAAAGATTAC AGGATTGCTA	AGTGGCCCT AGTCTAGGAA A-GAGTCAGA	CGACAGAAAA ACTCTATGGG ATCA	GACCAGGTTA GCAGTTCTAC GCAGTTCTAC	TCTGCTCCGG TCTGTCCTAT TCTGTCCTAT
FOR_DS1535	TGAAGACACC TAAAGATTAC AGAATTGCTA	AGTGGCCCT AGTCTAGGAA A-GAGTCAGA	CGACAGAAAA ACTCTATGGG ATCA	GACCAGGTTA GCAGTTCTAC GCAGTTCTAC	TCTGCTCCGG TCTGTCCTAT TCTGTCCTAT
MAM1_SP134	TGAAGACACC TAAAGATTAC AGGATTGCTA	AGTGGCCCT AGTCTAGGAA A-GAGTCAGA	CGACAGAAAA ACTCTATGGG ATCA	GACCAGGTTA GCAGTTCTAC GCAGTTCTAC	TCTGCTCCGG TCTGTCCTAT TCTGTCCTAT

MAST_B057_	TGAAGACACC TAAAGATTAT TGGGTT-CTA	AGTGGCCCCT AGTCTAGGAA ATGAGTCAGA	CGACAGAAAA ACCCTATGGG ATTG	GACCAGGTGA GCAGTTCTAC	TCCGCTCCGG TCCATCATAT
SAV1_SE210	TGAAGACACC TAAAGATTAC AGGATTGCTA	AGTGGCCCCT AGTCTAGGAA A-GAGTCAGA	CGACAGAAAA ACTCTATGGG ATCA	GACCAGGTGA GCAGTTCTAC	TCTGCTCCGG TCTGTCCTAT

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ASIAN2_Ema	CAGAGCTAAA TCAGACTGCT AGCCACCCAC	AGAGAGAGAA AGCCTCCTAA TTGTGGTATT	TG-TTTCCCC ACTGTGAGAA TCTGT	TAGAGGTGGC AATAAATTTT	ACTCTGAA-T TGCTTGTTAA
FOR_DS1535	CAGAGCTAAA TCAGACTTCT AGCCACCCAC	AGAGASAGAA AGCCTCCTAA TTGTGGTATT	YR-TTTCCCC ACTGTGAGAA TCTGT	TAGAGGTGGC AATAAATTTT	ACTCTGAA-T TGCTTGTTAA
MAM1_SP134	CAGAGCTAAA TCAGACTTCT AGCCACCCAC	AGAGAGAGAA AGCCTCCTAA TTGTGGTATT	TG-TTTCCCC ACTGTGAGAA TCTGT	TAGAGGTGGC AATAAACTTC	ACTCTGAA-T TGCTTGTTAA
MAST_B060_	TAGAGCTGAC TCAGACTTTT AGCCACCCAT	AGAGAG--AA AGCCTCCTAA TTGTGGTATT	GGCTTTCCCC TCTGTGAGAA TCTAT	TAGAGTTGGC AATAAATTTT	AC-CTGAAAT TGCTTGTTAA
SAV1_SE210	CAGAGCTAAA TCAGACTTCT AGCCACCCAC	AGAGAGAGAA AGCCTCCTAA TTGTGGTATT	TG-TTTCCCC ACTGTGAGAA TCTGT	TAGAGGTGGC AATAAATTTT	ACTCTGAA-T TGCTTGTTAA

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ASIAN2_Ema	AGGAATATTT ACACTGTGCC TTCCCAACCT	TCTAGCCCAA ATTCAGGATA CCTCGAAAGG	ACTACCAGGA TCACGCAGCT AACATTTTTT	GTTTTCCAAG CCGTTCCAA CCA	CAAATTTT GGGAATAAAA
FOR_DS1535	AGGAATATTT ACACTGTGCC TTCCCAACCT	TCTAGCCCAA ATTCAGGATA CCTCGAAAGG	ACTACCAGGA TCACGCAGCT AACATTTTTT	GTTTTCCAAG CCGTTCCAA CCA	CAAATTTT GGGAATAAAA
MAM1_SP134	AGGAATATTT ACACTGTGCC TTCCCAACCT	TCTAGCCCAA ATTCAGGATA CCTCGAAAGG	ACTACCAGGA TCATGCAGCT AACATTTTTT	GTTTTCCAAG CCGTTCCAA CCA	CAAATTTT GGGAATAAAA
MAST_B094_	AGGAATATTT ATATTGTGCT TTACGA----	TCTAGCGCAA ATTTAGGATA --TGTAAG-	ACTACCAGGA TCAGGCAGCT ---ATTTTTT	GTTTTCCAAG CTGTTCCAA GCT	CAATTTT GGGAATA--
SAV1_SE210	AGGAATATTT ACACTGTGCC TTCCCAACCT	TCTAGCCCAA ATTCAGGATA CCTCGAAAGG	ACTACCAGRA TCACGCAGCT AACATTTTTT	GTTTTCCAAG CCGTTCCAA CCA	CAAATTTT GGGAATAAAA

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ASIAN2_Ema	TATCCACCTA ACCGTCACTT ATAGGGCACA	GGGGAGCCTG GCTAATTCAG AAA-GTGAG	TCTCATAACC TCCATATAACC	GATGAACCCC ACCATCTTCA	GATACACCTT GCAAACCCCT
FOR_DS1535	TATCCACCTA ACCGTCACTT ATAGGGCACA	GGGGAGCCTG GCTAATTCAG AAA-GTGAG	TCTCGTAACC TCCATATAACC	GATGAACCCC ACCATCTTCA	GATACACCTT GCAAACCCCT
MAM1_SP134	TATCCACCTA ACCGTCACTT ATAGGGCACA	GGGGAGCCTG GCTAATTCAG AAA-GTGAG	TCTCGTAACC TCCATATAACC	GATGAACCCC ACCATCTTCA	GATACACCTT GCAAACCCCT
MAST_B099_	TATCCACCTA ACCGTCACTT NTAGGGCACA	GGGGAGCCTG GCTAATTCAG AAAAGTAAA	TCTCGTAACC TCCATATAACC	GATGAACCCC ACCATTTTCA	GGTATACCTT GTAAACCCCT
SAV1_SE210	TATCCACCTA ACCGTCACTT ATAGGGCACA	GGGGAGCCTG GCTAATTCAG AAA-GTGAG	TCTCGTAACC TCCATATAACC	GATGAACCCC ACCATCTTCA	GATACACCTT GCAAACCCCT

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ASIAN2_Ema	TGGTGATTAG GCAGATTCTT AAGCAGCCAA	AGCCCCTGCA GGGCCTCCAA GTGTTCTT	TCGGAATCTC GGGTGGGGCC	TGGGAATATC TGGGATTCTG	TGTTAATACT CATTCTCAAC
FOR_DS1535	TGGTGATTAG	AGCYCCTGCA	TCGGAATCTC	TGGGAATATC	TGTTAATACT

	GCAGATTCT	GGGCCTCCAA	GGGTGGGGCC	TGGGATTCTG	CATTCTCAAC
MAM1_SP134	AAGCAGCCAA	GTGTTCT			
	TGGTGATTAG	AGCCCCTGCA	TCGGAATCTC	TGGGAATATC	TGTTAATACT
	GCAGATTCT	GGGCCTCCAA	GGGTGGGGCC	TGGGATTCTG	CATTCTCAAC
	AAGCAGCCAA	GTGTTCT			
MAST_B100_	TGGTGATTAG	AGCCCCTGCA	TCGGAATCTC	TGGGAATATC	TGTTAATACT
	GCAGATTCT	GGGCCTCCAA	GGGTGGGGCC	TGGGATTCTG	CATTCTCAAC
	AAGCAGCCAA	ATATTCT			
SAV1_SE210	TGGTGATTAG	AGCCCCTGCA	TCGGAATCTC	TGGGAATATC	TGTTAATACT
	GCAGATTCT	GGGCCTCCAA	GGGTGGGGCC	TGGGATTCTG	CATTCTCAAC
	AAGCAGCCAA	GTGTTCT			

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ASIAN2_Ema	CTGGAAGCAC	TTACTCTTAA	CAGTAGGTTA	AAGTCACCGC	ATTTCTGATT
	GCTTCATCTG	GCAAAGGCAG	CTTCACTCAA	GGCCATATCA	CAGAATTCCA
	GGTGTAGCAG	TTCAAT			
FOR_DS1535	CTGGAAGCAC	TTACTCTTAA	CAGTAGGTTA	AAGTCACCGC	ATTTCTGATT
	GCTTCATCTG	GCAAAGGCAG	CTTYGCTCAA	GGCCATATCA	CAGAATTCCA
	GGTGTAGCAG	TTCAAT			
MAM1_SP134	CTGGAAGCAC	TTACTCTTAA	CAGTAGGTTA	AAGTCACCGC	ATTTCTGATT
	GCTTCATCTG	GCAAAGGCAG	CTTCACTCAA	GGCCATATCA	CAGAATTCCA
	GGTGTAGCAG	TTCAAT			
MAST_B101_	CTGGAAGTAC	TTACTCTTAA	CAGTAGGTTA	AAGTCACCGC	ACTTCTGATT
	GCTTCATCTG	GCAAAGGCAG	CTTCGCTCAA	GGCCATATCA	CAGAATTCCA
	GGTGTAGCAG	TTCAAT			
SAV1_SE210	CTGGAAGCAC	TTACTCTTAA	CAGTAGGTTA	AAGTCACCGC	ATTTCTGATT
	GCTTCATCTG	GCAGAGGCAG	CTTTGCTCAA	GGCCATATCA	CAGAATTCCA
	GGTGTAGCAG	TTCAAT			

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ASIAN2_Ema	AGATGAAATG	AAATGGGGCT	AATAGGCATT	TTTAAAGAGA	AGGCAAAGTA
	ATTCAGAGCA	GGAGGTATGA	AGCTCAGGAC	CATGGAGATT	T-CTTGCTTT
	-GGTTTTAGA	ATCTTA			
FOR_DS1535	AGATGAAATG	AAATGGGTGCT	AATAGGCATT	TTTAAAGAGA	AGGCAAAGTA
	ATTCGGAGCA	GGAGGTATGA	AGCTCAGGAC	CGTGGAGATT	T-CTTGCTTT
	-GGTTTTAGA	ATCTTA			
MAM1_SP134	AGATGAAATG	AAATGGGTGCT	AATAGGCATT	TTTAAAGAGA	AGGCAAAGTA
	ATTCGGAGCA	GGAGGTATGA	AGCTCAGGAC	CGTGGAGATT	T-CTTGCTTT
	-GGTTTTAGA	ATCTTA			
MAST_B102_	AGATGAAATG	AAATGGGTGCT	AATAGGCATT	TTTAAAGAGA	AGGCAAAGTA
	ATTCGGAGCG	GGAGATATGA	AGCTCAGGAC	CGTGGAGATT	TTCTTGCTTT
	TGGTTTTGGA	ATCTTA			
SAV1_SE210	AGATGAAATG	AAATGGGTGCT	AATAGGCATT	TTTAAAGAGA	AGGCAAAGTA
	ATTCGGAGCA	GGAGGTATGA	AGCTCAGGAC	CGTGGAGATT	T-CTTGCTTT
	-GGTTTTAGA	ATCTTA			

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ASIAN2_Ema	AGCCCTACCC	CTATTTTCCC	AAGAAGGATC	CAATTCCTTC	CGAGCTGTGT
	GCTTTCTCAT	GCTGACCTGA	TATCTGAAAC	TTTGCTGAAA	A-GTTCTTGT
	CTTTCTAACT	AAACC			
FOR_DS1535	AGCCCTACCC	CTATTTTCCC	AAGAAGGATC	CAATTCCTTC	CGAGCTGTGT
	GCTTTCTCAT	GCTGACCTGA	TATCTGAAAC	TTTGCTGAAA	A-GTTCTTGT
	CTTTCTAACT	AAACC			
MAM1_SP134	AGCCCTACCC	CTATTTTCCC	AAGAAGGATC	CAATTCCTTC	CGAGCTGTGT
	GCTTTCTCAT	GCTGACCTGA	TATCTGAAAC	TTTGCTGAAA	A-GTTCTTGT
	CTTTCTAACT	AAACC			
MAST_B152_	AGTTCTACCC	CTATTTTCCC	AAGAAGGATC	CAATTCCTTC	TGAGCTGTGT
	GCTTTCTTAT	GCTGACCTGA	TATCTGAAAC	TTTGCTGAAA	AAATTCTTAT
	CTTTCTAACT	AAACC			
SAV1_SE210	AGCCCTACCC	CTATTTTCCC	AAGAAGGATC	CAATTCCTTC	CGAGCTGTGT
	GCTTTCTCAT	GCTGACCTGA	TATCTGAAAC	TTTGCTGAAA	A-GTTCTTGT
	CTTTCTAACT	AAACC			

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ASIAN2_Ema	CTTCCGTAAA GCTATGAGTT GTTTTTTT-G	GATTATAGCC GGAACCAACT GTATCT	TGTGGAAACC CAATGGCAAT	CTACCCTGTT AGGTTTC-AG	TTATAGGGCT GGTTTTTTT-
FOR_DS1535	CTTCCGTAAA GCTATGAGTT GTTTTTTT-G	GATTATAGCC GGAACCAACT GTATCT	TGTGGAAACC CAATGGCAAT	CTACCCTGTT AGGTTTC-AG	TTATAGGGCT GGTTTTTTT-
MAM1_SP134	CTTCCGTAAA GCTATGAGTT GTTTTTTT-G	GATTATAGCC GGAACCAACT GTATCT	TGTGGAAACC CAATGGCAAT	CTACCCTGTT AGGTTTC-AG	TTATAGGGCT GGTTTTTTT-
MAST_B105_	TTTTCGTAAA GCTATGAGTT ATTTTTTT-G	GATTATAGCC GGAACCAACT GTATCT	TGTGGAAACC CAATGGCAAT	CTACCCTGTT AGGTTTCTAG	TTATAGGGCT GGTTTTTTTTT
SAV1_SE210	CTTCCGTAAA GCTATGAGTT GTTTTTTT-G	GATTATAGCC GGAACCAACT GTATCT	TGTGGAAACC CAATGGCAAT	CTACCCTGTT AGGTTTC-AG	TTATAGGGCT GGTTTTTTT-

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ASIAN2_Ema	TCTGCTGTGA GTAGAGCTCA GCCAGAAGAT	TTTGTGAGTG CCCTT----C GTTCA	TGGCTGAGAG AGGAGGCGGG	CTGGGACCTG TTCAAGGCCA	TTCTCCCTCC TGAGAGCCAA
FOR_DS1535	TCTGCTGTGA GTAGAGCTCA GCCAGAAGAT	TTTGTGAGTG CCCTTACTYC GTTCA	TGGCTGAGAG AGGAGGCGGG	CTGGGACCTG TTCAAGGCCA	TTCTCCCTCC TGAGAGCCAA
MAM1_SP134	TCTGCTGTGA GTAGAGCTCA GCCAGAAGAT	TTTGTGAGTG CCCTTACTTC GTTCA	TGGCTGAGAG AGGAGGCGGG	CTGGGACCTG TTCAAGGCCA	TTCTCCCTCC TGAGAGCCAA
MAST_B106_	TCTGCTGTGA GTAGAGCTCA GCCAGAAAAT	TTTGTGAGTG CCCTTACTTC ATTCA	TGGCTGAGAG AGGAGACAAA	CTGGGACCTG TTCAAGGCCA	TTCTCCCTCC TGAAAGCCAA
SAV1_SE210	TCTGCTGTGA GTAGAGCTCA GCCAGAAGAT	TTTGTGAGTG CCCTTACTTC GTTCA	TGGCTGAGAG AGGAGGCGGG	CTGGGACCTG TTCAAGGCCA	TTCTCCCTCC TGAGAGCCAA

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ASIAN2_Ema	GAAGCCGACT TACTCTTGGC AATT--ATCA	GCTGAGCCC- TCCAATTCTC -AGAA	TGCAGCGTGG TGTGAAGGGC	TCACTCATCA TTGCACTCTC	ACGATGACCA TGT-----G
FOR_DS1535	GAAGCCGACT TACTCTTGGC AATT--MTCA	GCTGAGCCC- TCCAATTCTC -AGAA	TGCAGCGTGG TGTGAAGGGC	TCACTCATCA TTGCACTCTC	ACRATGACCA TGT-----G
MAM1_SP134	GAAGCCGACT TACTCTTGGC AATT--ATCA	GCTGAGCCC- TCCAATTCTC -AGAA	TGCAGCGTGG TGTGAAGGGC	TCACTCATCA TTGCACTCTC	ACGATGACCA TGT-----G
MAST_B107_	GAAGTTGATT TACTCTTGGC TATGCTATCC	GCTGAACCCC TTTAATTCTC TACAA	TGCAGCGTGG TGTGAAGGGC	TCACTCATCA TTGCACTCTC	ACGATGACCA TGTTGAGGCG
SAV1_SE210	GAAGCCGACT TACTCTTGGC AATT--ATCA	GCTGAGCCC- TCCAATTCTC -AGAA	TGCAGCGTGG TGTGAAGGGC	TCACTCATCA TTGCACTCTC	ACGATGACCA TGT-----G

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ASIAN2_Ema	TCAGTGATTC AGTTTGCTGT CGAGGAGGAG	TAAATATGAA TCATAGCATC GCATATCG	ACCWTCTCCC GGCAACACCT	AGCTCTGCTC ACCACATCCA	TGGAGCTGTC CGAATGTGCG
FOR_DS1535	TCAGTGATTC AGTTTGCTGT CGAGGAGGAG	TAAATATGAA TCATAGCATC GCATATCG	ACCATCTCCC GGCAACACCT	AGCTCTGCTC ACCACATCCA	TGGAGCTGTC CGAATGTGCG
MAM1_SP134	TCAGTGATTC AGTTTGCTGT CGAGGAGGAG	TAAATATGAA TCATAGCATC GCATATCG	ACCATCTCCC GGCAACACCT	AGCTCTGCTC ACCACATCCA	TGGAGCTGTC CGAATGTGCG
MAST_B154_	TTAGTGATTC AGTTTGCTGT -GAAGAGGAG	TAAATATGAA TCATAGCATC GCATATCA	ACCATCTCCC GGCAACACCT	AGCTCTGCTC AC-ACATC-A	TGGAGCTGTC CGAATGTGCG
SAV1_SE210	TCAGTGATTC	TAAATATGAA	ACCATCTCCC	AGCTCTGCTC	TGGAGCTGTC

AGTTTGCTGT TCATAGCATC GGCAACACCT ACCACATCCA CGAATGTCGC
CGAGGAGGAG GCATATCG

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ASIAN2_Ema	CCTTCGTCTC GAGTGCCACC CTTTTCAAAG	ATGCATTATG TGCCACAGT GGTG	AGGAGTTCTG ACACCCCGAG	GCCACCTTGG GCKKAGATCT	CTGCCATGCT GCTGCCTTTG
FOR_DS1535	CCTTCGTCTC GAGTGCCACC CTTTTCAAAG	ATGCATTATG TGCCACAGT GGTG	AGGAGTTCTG ACACCCCGAG	GCCACCTTGG GCCRAGATCT	CTGCCATGCT GCTGCCTTTG
MAM1_SP134	CCTTCGTCTC GAGTGCCACC CTTTTCAAAG	ATGCATTATG TGCCACAGT GGTG	AGGAGTTCTG ACACCCCGAG	GCCACCTTGG GCCGAGATCT	CTGCCATGCT GCTGCCTTTG
MAST_B156_	CCTTCGTCTC GGGTGCCACC CTTTTCAAAG	ATGCATTATA TGCCACAGT GGTA	AGGAGTTCTG ACACCCCGAG	GCCACCTTGG GCCGAGATCT	CTGCCATGCT GCTGCCTTTG
SAV1_SE210	CCTTCGTCTC GAGTGCCACC CTTTTCAAAG	ATGCATTATG TGCCACAGT GGTG	AGGAGTTCTG ACACCCCGAG	GCCACCTTGG GCCGAGATCT	CTGCCATGCT GCTGCCTTTG

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ASIAN2_Ema	TAAAGTGGCC AAGCAGTGAA -----AAA	TTGGTGCAAT GTTCTGGAG TACATC	GGCAAAAATA ATCACATGGC	TGAAGCCGAC AGGAGCCGTC	AACGATTCTG -CTG-----
FOR_DS1535	TAAAGTGGCC AAGCAGTGAA -----AAA	TTGGTGCAAT GTTCTGGGG TACATC	GGCAAAAATA ATCACATGGC	TGAAGCCGAC AGGAGCCGTC	AACGATTCTG -CTG-----
MAM1_SP134	TAAAGTGGCC AAGCAGTGAA -----AAA	TTGGTGCAAT GTTCTGGGG TACATC	GGCAAAAATA ATCACATGGC	TGAAGCCGAC AGGAGCCGTC	AACGATTCTG -CTG-----
MAST_B109_	TAAAGTGGCC AAGCAGTGAA GGGCAAAAAA	TTGGTGCAAT GTTCTGGGG TACCTT	GGCAAAAATA GTGG-AGGG-	TGAAGCCGAC ATGTTTCTTC	AACGATTCTG TCTGCAGAAA
SAV1_SE210	TAAAGTGGCC AAGCAGTGAA -----AAA	TTGGTGCAAT GTTCTGGGG TACATC	GGCAAAAATA ATCACATGGC	TGAAGCCGAC AGGAGCCGTC	AACGATTCTG -CTG-----

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ASIAN2_Ema	TTTATTAGGT GGCCAACCTG TGGAGTCCAC	GAGTGGCTTG TGCTTCCAGA TCTC	CCGACCCCAG CGCCTCACAC	AGCTGACATG AAGATGCTGG	GCTGCTCAAT TCAGGGAAAC
FOR_DS1535	TTTATTAGGT GGCCAACCTG TGGAGTCCAC	GAGTGGCTTG TGCTTCCAGA TCTC	CCGACCCCAG CGCCTCACAC	AGCTGACATG AAGATGCTGG	GCTGCTCAAT TCAGGGAAAC
MAM1_SP134	TTTATTAGGT GGCCAACCTG TGGAGTCCAC	GAGTGGCTTG TGCTTCCAGA TCTC	CCGACCCCAG CGCCTCACAC	AGCTGACATG AAGATGCTGG	GCTGCTCAAT TCAGGGAAAC
MAST_B110_	TTTATTAGGT GGCCAACCTG TGGAGTCCAC	GAGTGGCTTG TGCTTCCAGA TCTC	CCGACCCCAG CGCCTCACAC	AGCTGACATG AAGATGCTGG	GCTGCTCAAT TCAGGGAAAC
SAV1_SE210	TTTATTAGGT GGCCAACCTG TGGAGTCCAC	GAGTGGCTTG TGCTTCCAGA TCTC	CCGACCCCAG CGCCTCACAC	AGCTGACATG AAGATGCTGG	GCTGCTCAAT TCAGGGAAAC

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ASIAN2_Ema	TTTSTATTTT CCCAYTTGAC TTCCAGTTTG	ATTGCAAGAT CACAGCRAAA TCTT	TCTGCCTTTC GGACAAACCT	ATACATATGA CATCACAGCC	CCCACAATTT ATTAGGGTAC
FOR_DS1535	TTTCTATTTT CCCATTTGAC TTCCAGTTTG	ATTGCAAGAT CACAGCGAAA TCTT	TCTGCCTTTC GGACAAACCT	ATACATATGA CATCACAGCC	CCCACAATTT ATTAGGGTAC
MAM1_SP134	TTTGTGTTTC CCCATTTGAC	ATTGCAAGAT CACAGCAAAA	TCTGCCTTTC GGACAAACCT	ATACATATGA CATCACAGCC	CCCACAATTT ATTAGGGTAC

MAST_B111_	TTCCAGTTTG TTTGTATTTT CCCATTTGAC TTCCAGTTTG	TCTT ATTGCAAGAT CACAGCAAAA TCTT	TCTGCCTTTC GGACAAACCT	ATACATATGA CATCACAGCC	CCCACAATTT ATTAGGGTAC
SAV1_SE210	TTTGTATTTT CCCATTTGAC TTCCGGTTTG	ATTGCAAGAT CACAGCGAAA TCTT	TCTGCCTTTC RGACAAACCT	ATACATATGA CATCACAGCC	CCCACAATTT ATTAGGGTAC

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ASIAN2_Ema	CTGCAGACAG CTGTCAGGAA GAGAGCAAAT	GCCTAGAACG ACAGGACAGG AGGA	AAGGCTGCAT GGGCCGGCGT	GTCCCTGCCT CCTCCAAGGA	GGGCTGCTTG CTGTCACGTG
FOR_DS1535	CTGCAGACAG CTGTCAGGAA GAGAGCAAAT	GCCTAGAATG ACCGGACAGG AGGA	AAGGCTGCAT GGGCCGGCGT	GTCCCTGCCT CCTCCAAGGA	GGGCTGCTTG CTGTCATGTG
MAM1_SP134	CTGCAGACAG CTGTCAGGAA GAGAGCAAAT	GCCTAGAACG ACAGGACAGG AGGA	AAGGCTGCAT GGGCCGGCGT	GTCCCTGCCT CCTCCAAGGA	GGGCTGCTTG CTGTCACGTG
MAST_B112_	CTGCAGACAG CTGTCAGGAA GAAAACAAAT	GCCTAGAATG ACTGGACAGG AGAA	AAGGCTGCAT GAGCCGGCGT	GTCCCAGCCT CCTCCAAGGA	GGGCTGCTTG CTGTCACGTA
SAV1_SE210	CTGCAGACAG CTGTCGGGAA GAGAGCAAAT	GCCTAGAACG ACCGGACAGG AGGA	AAGGCTGCAT GGGCCGGCGT	GTCCCTGCCT CCTCCAAGGA	GGGCTGCTTG CTGTCATGTG

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ASIAN2_Ema	GTGCAACCAT TGCTGTTTTA CCTTGACAAC	TACCGTGTTT CAACCTGCAA AATG	CCAGCCTGTG TTCCATTAAT	AAGGAGAGCT ACTGAAAAAG	GGATAGCCAA AAGGTAAGTGA
FOR_DS1535	GTGCAACCAT TGCCGTTTTA CCTTGACAAC	TACCGTGTTT CAACCTGCAA AATG	CCAGCCTGTG TTCCATTAAT	AAGGAGAGCT ACTGAAAAAG	GGATAGCCAA AAGGTAAGTGA
MAM1_SP134	GTGCAACCAT TGCCGTTTTA CCTTGACAAC	TACCGTGTTT CAACCTGCAA AATG	CCAGCCTGTG TTCCATTAAT	AAGGAGAGCT ACTGAAAAAG	GGATAGCCAA AAGGTAAGTGA
MAST_B157_	GTGCAACCAT TGCCGTTTTA CCTTGACAAC	TACCGTGTTT CAACCTGCAA AATG	CCGGCTTGTG TTCCATTAAT	AAGGAGAGCT ACTGAAAAAG	GGATAGCCAA AAGGTAAGTGA
SAV1_SE210	GTGCAACCAT TGCCGTTTTA CCTTGACAAC	TACCGTGTTT CAACCTGCAA AATG	CCAGCCTGTG TTCCATTAAT	AAGGAGAGCT ACTGAAAAAG	GGATAGCCAA AAGGTAAGTGA

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ASIAN2_Ema	TTTCCATGTA GGGGAGCCCA -CAGCTGCTC	CTGAAGGCTT TGGCACGTTA ATCC	G-CTCTCAGA GTTGTCTGGA	AGCTGGGGAG AAAGCCCATG	CTGGGAGAAC AGGCAGCCAA
FOR_DS1535	CTTCCATGTA GGGGAGCCCA -CGGCTGCTC	CTGAAGGCTT TGGCACGTTA ATCC	G-CTCTCAGA GTTGTCTGGA	AGCTGGGGAG AAAGCCCATG	CTGGGAGAAC AGGCAGCCAA
MAM1_SP134	TTTCCATGTA AGGGAGCCCA -CAGCTGCTC	CTGAAGGCTT TGGCACGTTA ATCC	G-CTCTCAGA GTTGTCTGGA	AGCTGGGGAG AAAGCCCATG	CTGGGAGAAC AGGCAGCCAA
MAST_B158_	TTTTTCATGTA GGGGAGCCCA ACAGCTGCTC	CTGAAGGCTT TGGCACATTA ATCC	GTCTCTCAGA GTTGTCTGGA	AGCTGGGG-G AAAGCCCATG	CTGGGAGAAC AGGCAGCTAA
SAV1_SE210	CTTCCATGTA GGGGAGCCCA -CGGCTGCTC	CTGAAGGCTT TGGCACGTTA ATCC	G-CTCTCAGA GTTGTCTGGA	AGCTGGGGAG AAAGCCCATG	CTGGGAGAAC AGGCAGCCAA

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ASIAN2_Ema	CACCACGTAT ACCCACGGTT AAGCTGAAAC	AAGAATTTT CTGCTGAGAC ACCAAT	CACCTAGAAC TGTGAGGATT	CATAAAACTT GAGAAAGTGA	AGGATACAGA TGTGGCTTTT
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FOR_DS1535	CACCACGTAT ACCCACGGTT AAGCTGAAAC	AAGAATTTTA CTGCTGAGAC ACCAAT	CACCTAGAAC TGTGAGGATT	CATAAAACTT GAGAAAGTGA	AGGATACAGA TGTGGCTTTT
MAM1_SP134	CACCACGTAT ACCCACGGTT AAGCTGAAAC	AAGAATTTTA CTGCTGAGAC ACCAAT	CACCTAGAAC TGTGAGGATT	CATAAAACTT GAGAAAGTGA	AGGATACAGA TGTGGCTTTT
MAST_B159_	CACCAGGTAT ACCTACGGTT AAGCTGAAAC	AAGAATTTTA CTGCTGAGAC ACCAAT	CACCTAGAAC TGTGAGGATT	-ATGAA-CTT GAGAAAGTGA	AG-ATACAGA TGTGGCTTTT
SAV1_SE210	CACCACGTAT ACCCACGGTT AAGCTGAAAC	AAGAATTTTA CTGCTGAGAC ACCAAT	CACCTAGAAC TGTGAGGATT	CATAAAACTT GAGAAAGTGA	AGGATACAGA TGTGGCTTTT

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ASIAN2_Ema	TCGATTCTGA AGAGTTTCCA GCAGCCGTAG	CTCATAGCGA AGGAGCACCT CAC	CCCTATAGGA GGCAGATTTG	CAGAGTAGAA AAGTGCCGAC	CTGCCCCAC- CCTTTGATTA
FOR_DS1535	TCGATTCTGA AGAGTTTCCA GCAGCYGTAG	CTCATAGCGA AGGAGCACCT CAC	CCCTATAGGA GGCAGATTTG	CAGAGTAGAA AACTGCCGAC	CTGCCCCAC- CCTTTGATTA
MAM1_SP134	TCGATTCTGA AGAGTTTCCA GCAGCCGTAG	CTCATAGCGA AGGAGCACCT CAC	CCCTATAGGA GGCAGATTTG	CAGAGTAGAA AAGTGCCGAC	CTGCCCCAC- CCTTTGATTA
MAST_B114_	TCGATTCTGA AGAGTTTCTA GCATCTGTAG	CACGTAGCGA AGGAGCTCTT CAC	CCCTACAGGA GACAGATTTG	CAGAGCAGAA AACTGCCGAC	CTGCCCCACC CCTTTAATTA
SAV1_SE210	TCGATTCTGA AGAGTTTCCA GCAGCTGTAG	CTCATAGCGA AGGAGCACCT CAC	CCCTATAGGA GGCAGATTTG	CAGAGTAGAA AACTGCCGAC	CTGCCCCAC- CCTTTGATTA

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ASIAN2_Ema	CCTGCCATGC AAAAAAAAAAW GCACTCAGTA	TCAGCATTTG CCAAGAGCCT AATGTCAGTT	TGAACACGTA ACTGTGGACA GTTTAGTTGC	CCAAGAGCCG GAGTATTAGC TTTGTTGTTG	GCACTAGAAA CACCCAGTAA CCA
FOR_DS1535	CCTGCCATGC -----T GCACTCAGTA	TCAGCATTTG -----T AATGTCAGTT	TGAACACGTA ACTGTGGACA GTTTAGTTGC	CCAAGAGCC- GAGTATTAGC TTTGTTGTTG	----- CACCCRGTAA CCA
MAM1_SP134	CCTGCCATGC -----T GCACTCAGTA	TCAGCATTTG -----T AATGTCAGTT	TGAACACGTA ACTGTGGACA GTTTAGTTGC	CCAAGAGCC- GAGTATTAGC TTTGTTGTTG	----- CACCCAGTAA CCA
MAST_B116_	TTTGTTATGC -----T GCACTCAGTA	TCAGCATTTG -----T AATGTCAGTT	TGAACACGTA ACTGTGGACA GTTTAGTTGC	CCAAGAGCC- GAGTATTAGC ATTGTTGTTG	----- CACCCAGTAA CCA
SAV1_SE210	CCTGCCATGC -----T GCACTCAGTA	TCAGCATTTG -----T AATGTCAGTT	TGAACACGTA ACTGTGGACA GTTTAGTTGC	CCAAGAGCC- GAGTATTAGC TTTGTTGTTG	----- CACCCAGTAA CCA

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ASIAN2_Ema	GATCTGGAGG GTGAGCCCCT ATGTTTTGAG	GATTTCT-CT TTTTGGGTGG ATG	T-ACTTT-TT CGATGAGGGA	-CAGCGAGGA GATGGGTCTT	AAGACACTGG CATCAGATGG
FOR_DS1535	GATCTGGAGG GTGAGCCCCT ATGTTTTGAG	GATTTCT-CT TTTTGGGTGG ATG	T-ACTTT-CT CGATGAGGGA	-CAGYGAGGA GATGGGTCTT	AAGACACTGG CATCAGATGG
MAM1_SP134	GATCTGGAGG GTGAGCCCCT ATGTTTTGAG	GATTTCT-CT TTTTGGGTGG ATG	T-ACTTT-CT CGATGAGGGA	-CAGCGAGGA GATGGGTCTT	AAGACACTGG CATCAGATGG
MAST_B163_	ATTTTGGAGG GTGAGCCCCT ATGTTTTGAG	GATTTCTTCT TTTTGGGTGG ATG	TACTTTTCT CGATGAGG-A	TCAGCGAGGA GATGGGTCTT	AAGACACTGG CATCAGATGG
SAV1_SE210	GATCTGGAGG GTGAGCCCCT ATGTTTTGAG	GATTTCT-CT TTTTGGGTGG ATG	T-ACTTT-CT CGATGAGGGA	-CAGCGAGGA GATGGGTCTT	AAGACACTGG CATCAGATGG

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ASIAN2_Ema	GAGTC-TGAT ATAGGCCTCA CCCAGCCGGC	AAGATTAGGA CCACCTCAGG CAAAGTTCTT	CAGAAAAAGC AGAAACGGCT TGGGCTGGGA	CACCTTT-GT GCTCCGCATA ATT	TTGAAGGTAC GGTGGTCACG
FOR_DS1535	GAGTC-TGAT ATAGGCCTCA CCCAGCCGGC	AAGATTAGGA CCACCTCAGG CAAAGTTCTT	CAGAAAAAGC AGAAACGGCT TGAGCTGGGA	CACCTTT-GT GCTCCGCATA ATT	TTGAAGGTAC GGTGGTCACG
MAM1_SP134	GAGTC-TGAT ATAGGCCTCA CCCAGCCGGC	AAGATTAGGA CCACCTCAGG CAAAGTTCTT	CAGAAAAAGC AGAAACGGCT TGAGCTGGGA	CACCTTT-GT GCTCCGCATA ATT	TTGAAGGTAC GGTGGTCACG
MAST_B120_	GAGTCCTGAT ATAGGCCTCA CCCAGCCAGC	AAGATTAGGA CCACCTCA-- CAA--TTCTT	CAGAAAAAGG ----- TGAGCTAGGA	CACCTTTTGT -----TA ATT	TTGAAGGTAC GGTGGTCACG
SAV1_SE210	GAGTC-TGAT ATAGGCCTCA CCCAGCCGGC	AAGATTAGGA CCACCTCAGG CAAAGTTCTT	CAGAAAAAGC AGAAACGGCT TGAGCTGGGA	CACCTTT-GT GCTCCGCATA ATT	TTGAAGGTAC GGTGGTCACG

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ASIAN2_Ema	AAACTCCTGG CATCCCAGGC ACTCACAGAC	ACTGGGGCCT TCCTGGCTCT AC	GGCTGGAGCT ATTCCAGGGG	TTTGGGAACC TTGGATGAGG	ACTCCCTGCC CTGCTCGCCT
FOR_DS1535	AAACTCCTGG CATCCCAGGC ACTCACAGAC	ACTGGGGCCT TCCTGGCTCT AC	GGCTGGAGCT ATTCCAGGGG	TTTGGGAACC TTGGATGAGG	ACTCCCTGCC CTGCTCGCCT
MAM1_SP134	AAACTCCTGG CATCCCAGGC ACTCACAGAC	ACTGGGGCCT TCCTGGCTCT AC	GGCTGGAGCT ATTCCAGGGG	TTTGGGAACC TTGGATGAGG	ACTCCCTGCC CTGCTCGCCT
MAST_B166_	AAACTCCTGG CATCCCAGGC ACTCACAGAC	ACTGGGGCCT TCCTGGCTCT AC	GGCTGGAGCT ATTCCAGGGG	TTTGGAAACC TTGGATGAGG	ACTCCCTGCC CTGCTCGCCT
SAV1_SE210	AAACTCCTGG CATCCCAGGC ACTCACAGAC	ACTGGGGCCT TCCTGGCTCT AC	GGCTGGAGCT ATTCCAGGGG	TTTGGGAACC TTGGATGAGG	ACTCCCTGCC CTGCTCGCCT

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ASIAN2_Ema	TGGAGAAGGT ATGCCCTGTA AAAAAATACT	GGGGACAGGG GATTTTGAGA TCTC	T-GACCACAG ATCAAGTGAG	AACCTACGAG GCAGATCTAC	CAAACCTGAA GAAAAATAAG
FOR_DS1535	TGGAGAAGGT ATGCCCTGTA AAAAAATACT	GGGGACAGGG GATTTTGAGA TCTC	T-GACCACAG ATCAAGTGAG	AACCTACGAG GCAGATCTAC	CAAACCTGAA GAAAAATAAG
MAM1_SP134	TGGAGAAGGT ATGCCCTGTA AAAAAATACT	GGGGACAGGG GATTTTGAGA TCTC	T-GACCACAG ATCAAGTGAG	AACCTACGAG GCAGATCTAC	CAAACCTGAA GAAAAATAAG
MAST_B167_	TGGAGAAGGT ATGCATAGTA AAAAA-TACT	GGGGACAGGG GATTTTGAGA TCTC	T-GACCACAG ATCAAGTGAG	AACCTACGAG GCAGATCTAC	CAAACCTGAA GAAAAATAAG
SAV1_SE210	TGGAGAAGGT ATGCCCTGTA AAAAAATACT	GGGGACAGGG GATTTTGAGA TCTC	T-GACCACAG ATCAAGTGAG	AACCTACGAG GCAGATCTAC	CAAACCTGAA GAAAAATAAG

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ASIAN2_Ema	CACTCACCTC CTGAAGAGAA CTGGCCCATG	CTCCTAACCT AGCTGAGGAC G	CATAGCTGGA TSCTGGGAGC	GTCCTGGAT CACAGATTAG	GCCTCTGAAC CCCAGAGCTG
FOR_DS1535	CACTCACCTC CTGAGGAGAA CTGGCCCATG	CTCCTAACCT AGCTGAGGAC G	CATAGCTGGA TGCTGGGAGC	GTCCTGGAT CACAGATTAG	GCCTCTGAAC CCCAGAGCTG
MAM1_SP134	CACTCACCTC CTGAGGAGAA CTGGCCCATG	CTCCTAACCT AGCTGAGGAC G	CATAGCTGGA TGCTGGGAGC	GTCCTGGAT CACAGATTAG	GCCTCTGAAC CCCAGAGCTG
MAST_B121_	CACTCACGTC CTGAGGAGAA CTGGCCCATG	CTCCTAACCT AGCTGAGGAC A	CATAGCTGGA TGCTGGGAGC	GTCCTAGAT CACAGATTAG	GCCTCTGAAC CCCAGAGCTG

SAV1_SE210	CACTCACCTC CTGAGGAGAA CTGGCCCATG	CTCCTAACCT AGCTGAGGAC G	CATAGCTGGA TGCTGGGAGC	GTCCTGGAT CACAGATTAG	GCCTCTGAAC CCCAGAGCTG
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ASIAN2_Ema	CCCCAGGAGG CTCTGCCCTC CTAGATACCA	AAGGGGA-CA TGTAGTAGTT ACCT	CACTCCTCTT TCCAAGCCCA	TGGGCCCTGT GGACCGAGTC	-CTCTCCCAG AGGGTGTGTT
FOR_DS1535	CCCCAGGAGG CTCTGCCCTC CTAGATACCA	AAGGGGA-CA TGTAGTAGTT ACCT	CACTCCTCTT TCCAAGCCCA	TGGGCCCTGT GGACCGAGTC	-CTCTCCCAG AGGGTGTGTT
MAM1_SP134	CCCCAGGAGG CTCTGCCCTC CTAGATACCA	AAGGGGA-CA TGTAGTAGTT ACCT	CACTCCTCTT TCCAAGCCCA	TGGGCCCTGT GGACCGAGTC	-CTCTCCCAG AGGGTGTGTT
MAST_B122_	TCCCAGGAGG CTCTG-CCTC -TAGATACCA	AAGGGGACCA TGTAGTAGTT ACCT	CACTCCTCCT TCCAAGCCCA	TTGGCCCTGT GGACCGAGTC	CCTCT-CCAG AGGGTGTGTT
SAV1_SE210	CCCCAGGAGG CTCTGCCCTC CYAGATACCA	AAGGGGA-CA TGTAGTAGTT ACCT	CACTCCTCTT TCCAAGCCCA	TGGGCCCTGT GGACCGAGTC	-CTCTCCCAG AGGGTGTGTT

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ASIAN2_Ema	CAAGCTTCTG GAAGGTCAGT AAAGGAAGGC	AGAAAGGTGC GTGGCTACTC T	TCTGGGCTCA ACCTTAACCA	TTTTACAGGT AGTAGTGAGG	GTCAGA-GCC GATGAGGCC
FOR_DS1535	CAAGCTTCTG GAAGGTCAGT AAAGGAAGGC	AGAAAGGTGC GTGGCTACTC T	TCTGGGCTCA ACCTTAACCA	TTTTACAGGT AGTAGTGAGG	GTCAGA-GCC GATGAGGCC
MAM1_SP134	CAAGCTTCTG GAAGGTCAGT AAAGGAAGGC	AGAAAGGTGC GTGGCTACTC T	TCTGGGCTCA ACCTTAACCA	TTTTACAGGT AGTAGTGAGG	GTCAGA-GCC GATGAGGCC
MAST_B123_	TAAGCTTCTG GAAGATCAAT AAAGGAAGGC	AGAAAGGTGC ATAGCTACTC T	TCTGGGCTCA ACCTTAACCA	TTTTACAAAT AGTAGTGAGG	ATCAAAAGCC AATGAGGCC
SAV1_SE210	CAAGCTTCTG GAAGGTCAGT AAAGGAAGGC	AGAAAGGTGC GTGGCTACTC T	TCTGGGCTCA ACCTTAACCA	TTTTACAGGT AGTAGTGAGG	GTCAGA-GCC GATGAGGCC

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ASIAN2_Ema	AGACCTGAGC GAGGCCTCAG CAGGTCTAGT	TCACATCCTG TTTCCACATC T	GTTCTGCTAG TGTA AAAATGC	CTCTAAGACA AGGCAGTGAC	TAGGCAGCCT CCCATCTTCA
FOR_DS1535	AGACCTGAGC GAGGCCTCAG CAGGTCTAGT	TCACATCCTG TTTCCACATC T	GTTCTGCTAG TGTA AAAATGC	CTCTAAGACA AGGCAGTGAC	TAGGCAGCCT CYCATCTTCA
MAM1_SP134	AGACCTGAGC GAGGCCTCAG CAGGTCTAGT	TCACATCCTG TTTCCACATC T	GTTCTGCTAG TGTA AAAATGC	CTCTAAGACA AGGCAGTGAC	TAGGCAGCCT CCCATCTTCA
MAST_B169_	AGATCTGAGC GAGGCCTCAG CAAGTCTAGT	TCACATCCTG TTTCCACATC T	GTTCTGCTAG TGTA AAAATGC	CTCTAAGACA AGGCAGTGAC	TAGGCAGCAT CCCATCTTCA
SAV1_SE210	AGACCTGAGC GAGGCCTCAG CAGGTCTAGT	TCACATCCTG TTTCCACATC T	GTTCTGCTAG TGTA AAAATGC	CTCTAAGACA AGGCAGTGAC	TAGGCAGCCT CCCATCTTCA

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ASIAN2_Ema	GCAA-GAGTC GG-AGAAA-C CCTATTCTTA	ATAGTCCTTG AAA-GAAC-A A	TAAGAGGAGA AAA-TTGTCC	AACAGGTAAT ATTGGGATGG	ATGACTTGTC AATAGAAGAT
FOR_DS1535	GCAA-GAGTC GG-AGAAA-C CCTATTCTTA	ATAGTCCTTG AAA-GAAC-A A	TAAGAGGAGA AAA-TTGTCC	AACAGGTAAT ATTGRGATGG	ATTACTTGTT AATAGAAGAT
MAM1_SP134	GCAA-GAGTC GG-AGAAA-C CCTATTCTTA	ATAGTCCTTG AAA-GAAC-A A	TAAGAGGAGA AAA-TTGTCC	AACAGGTAAT ATTGRGATGG	ATTACTTGTT AATAGAAGAT

	GG-AGAAA-C CCTATTCCTA	AAA-GAAC-A A	AAA-TTGTCC	ATTGGGATGG	AATAGAAGAT
MAST_B170_	GCAAAGAGTC GGGAGAAAAC CCTATTCCTA	ATAGTCCTTG AAAAGAACCA A	TAAGAGGAGA	AACAGGTAAT ATTGGGATGG	ATTACTTGTC AGTAGAAAAT
SAV1_SE210	GCAA-GAGTC GG-AGAAA-C SCTATTCCTA	ATAGTCCTTG AAA-GAAC-A A	TAAGAGGAGA AAA-TTGTCC	AACAGGTAAT ATTGGAATGG	ATGACTTGTC AATAGAAGAT

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ASIAN2_Ema	TGTTCTAAG CTGCCTYCCT GGTCTTCTCA	CTAT-GCTTC AGATTTTTTC- G	TGGGGTCCCT ACTCTGGATG	CAAACCTCTG GAGGCAGAAT	TG-CATGATT GTGAGGTGGG
FOR_DS1535	TGTTCTAAG CTGCCTCCCT GGTCTTCTCA	CTAT-GCTTC AGATTTTTTC- G	TGGGGTCCCT ACTCTGGATG	CAAACCTCTG GAGGCAGAAT	TG-CATGATT GTGAGGTGGG
MAM1_SP134	TGTTCTAAG CTGCCTCCCT GGTCTTCTCA	CTAT-GCTTC AGATTTTTTC- G	KGGGGTCCCT ACTCTGGATG	CAAACCTCTG GAGGCAGAAT	TG-CATGATT GTGAGGTGGG
MAST_B171_	TGTTCTAAG CTGCTTCCCT GGTCTTCTCA	CTATCGCTTC AGATTTTTTC G	TGGGGTCCCT ACTCTGGATG	CAAACCTCTG GAGGCAGAAT	TGTCATGATT GTGAGGTGGA
SAV1_SE210	TGTTCTAAG CTGCCTCCCT GGTCTTCTCA	CTAT-GCTTC AGATTTTTTC- G	TGGGGTCCCT ACTCTGGATG	CAAACCTCTG GAGGCAGAAT	TG-CATGATT GTGAGGTGGG

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ASIAN2_Ema	TGTCTTAGAT AAGTGAACCA TTTAGACAGA	AACACTTCTG AGGAGGGGCA T	TTTCTGAGAA GCTTGCCTGC	AGTGACCCAT AGGGAAAACA	GACTGTTAGC CTTAGTATAT
FOR_DS1535	TGTCTTAGAT AAGTGAACCA TTTAGACAGA	AACACTTCTG AGGAGGGGCA T	TTTCTGAGAA GCTTGCCTGC	AGTGACCCAT AGGGAAAACA	GACTGTTAAC CTTASTATAT
MAM1_SP134	TGTCTTAGAT AAGTGAACCA TTTAGACAGA	AACACTTCTG AGGAGGGGCA T	TTTCTGAGAA GCTTGCCTGC	AGTGACCCAT AGGGAAAACA	GACTGTTAAC CTTAGTATAT
MAST_B172_	TGTCTTAGAT AAGTGAACCA TTTAGACAGA	AACACTTCTG AGGAGGGGCA T	TTTCTAAGAA GCTTGCCTGC	AGTGACCCAT AGAGAAAACA	GACTGTTAAC CTTAATATAT
SAV1_SE210	TGTCTTAGAT AAGTGAACCA TTTAGACAGA	AACACTTCTG AGGAGGGGCA T	TTTCTGAGAA GCTTGCCTGC	AGTGACCCAT AGGGAAAACA	GACTGTTAAC CTTACTATAT

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ASIAN2_Ema	CCAAAGACGC CTGGAGGAAA AAAA-GCCCA	CTGTTCCAGC CACTTGGCCA G	TGCAAGGAGG CTCAAAGGTA	TCAGCATTCC GACCAGGATG	AAGGGGAGAG AAGGA-GAAA
FOR_DS1535	CCAAAGACGC CTGGAGGAAA AAAA-GCCCA	CTGTTCCAGC CACTTGGCCA G	TGCAAGGAGG CTCAAAGGTA	TCAGCATTCC GACCGGGATG	AAGGGGAGAG AAGGA-GAAA
MAM1_SP134	CCAAAGACGC CTGGAGGAAA AAAA-GCCCA	CTGTTCCAGC CACTTGGCCA G	TGCAAGGAGG CTCAAAGGTA	TCAGCATTCC GACCAGGATG	AAGGGGAGAG AAGGA-GAAA
MAST_B126_	CTAAAGATGC CTGGAGAAAA AAAAAGCCCA	CTGTTCCAGC CACTTGGCCA A	TGCAAGGAGG CTCAAAGGTA	TCAGCATTCC GACCAGGATG	AAGGGGAGAG AAGGAAGAAA
SAV1_SE210	CCAAAGACGC CTGGAGGAAA AAAA-GCCCA	CTGTTCCAGC CACTTGGCCA G	TGCAAGGAGG CTCAAAGGTA	TCAGCATTCC GACTGGGATG	AAGGGGAGAG AAGGA-GAAA

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ASIAN2_Ema	GTCCTTGAGC TCACAAGGAC	ATAGAGAATG ACATCAACTG	TGATTCAGCT GGCCCTGAGA	GGAGATGGGC TATAAAGACA	TCACAAGGAC ATACCTAGGA
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FOR_DS1535	CAACCTTGGA GTCCTTGAGC TCACAAGGAC CAACCTTGGA	ATAGAGAATG ACATCAACTG	TGATCCAGCT GGCCCTGAGA	GGAGATGGGC TATAAAGACA	TCACAAGGAC ATACCTAGGA
MAM1_SP134	GTCCTTGAGC TCACAAGGAC CAACCTTGGA	ATAGAGAATG ACATCAACTG	TGATTCAGCT GGCCCTGAGA	GGAGATGGGC TATAAAGACA	TCACAAGGAC ATACCTAGGA
MAST_B174_	GTCCTTGAGC TCACAAGGAC CAACCTTGGA	ATAGAGAATG ACATCAACTG	TGATCCAGCT GGCCCTGAGA	GGAGATGGGC TATAAAGACA	TCACAAGGAC ATACCTAGGA
SAV1_SE210	GTCCTTGAGC TCACAAGGAC CAACCTTGGA	ATAGAGAATG ACATCAACTG	TGATCCAGCT GGCCCTGAGA	GGAGATGGGC TATAAAGACA	TCACAAGGAC ATACCTAGGA

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ASIAN2_Ema	TTCATYCTCT ATACAGACAA CAAGGCAGGC	TCTTATTAAC ACACTTCTAA	CCCTTCCTCC TAGGAAGATA	TTCCATGCCT CATGTCCTAC	TC-ATAGARG TCATTATAAA
FOR_DS1535	TTCATCCTCT ATACAGACAA CAAGGCAGGC	TCTTATTAAC ACACTTCTAA	CCCTTCCTCC TAGTAAGATA	TTCCATGCCT CATGTCCTAC	TC-ATAGAGG TCATTATAAA
MAM1_SP134	TTCATTCTCT ATACAGACAA CAAGGCAGGC	TCTTATTAAC ACACTTCTAA	CCCTTCCTCC TAGGAAGATA	TTCCATGCCT CATGTCCTAC	TC-ATAGAGG TCATTATAAA
MAST_B175_	TTCATCCTCT ATACAGACAA CAAGGCAGGC	TCTTATTAAC ACACTTCTAA	CCCTTCCTCC TAGGAAGATA	TTCCATGCCT CATGTCCTAC	TCCATAGAGG TCATTATAAA
SAV1_SE210	TTCATCCTCT ATACAGACAA CAAGGCAGGC	TCTTATTAAC ACACTTCTAA	CCCTTCCTCC TAGTAAGATA	TTCCATGCCT CATGTCCTAC	TC-ATAGAGG TCATTATAAA

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ASIAN2_Ema	TGCTTTGCAT GTTAGCTAAG TGTCTTGGGG	ACAGAGTATA CTCCTGCCTC	TTTCCCAATA TCCCCTTTAT	GTTGAAGAGA GGTCTCACAC	AAAGGCAGCA AGAAGTTACC
FOR_DS1535	TGCTTTGCAT GTTAGCTAAG TGTCTTRGGG	ACAGAGTATA CTCCTGCCTC	TTTCCCAATA TCCCCTTTAT	GTTGAAGAGA GGTCTCACAC	AAAGGCAGCA AGAAGTTACC
MAM1_SP134	TGCTTTGCAT GTTAGCTAAG TGTMTTGGGG	ACAGAGTATA CTCCTGCCTC	TTTCCCAATA TCCCCTTTAT	GTTGAAGAGA GATCTCACAC	AAAGGCAGCA AGAAGTTACC
MAST_B176_	TGTTTTTCAT GTTAGCTAAG TGTCTTGGGA	ACAGAGTATA CCCCTGCCTC	TTTCCCAATA TCCCCTTTAT	GTTGAAGAGA GGTCTCACAC	AAAGGCAGCA AGAAGTTACC
SAV1_SE210	TGCTTTGCAT GTTAGCTAAG TGTCTTGGGG	ACAGAGTATA CTCCTGCCTC	TTTCCCAATA TCCCCTTTAT	GTTGAAGAGA GGTCTCACAC	AAAGGCAGCA AGAAGTTACC

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ASIAN2_Ema	TT----- ACCTGCTGGA CTCTAAAAGA	--CAT-GTTT AAACAGTTTG ATGGG	GCAGCATTTT ATTCCATCTT	TTCTCATCTT TACTATCTTC	TC-ATCCCCT CTGAGTCCAT
FOR_DS1535	TT----- ACCTGCTGGA CTCTAAAAGA	--CAT-GTTT AAACAGTTTG ATGGG	GCAGCATTTT ATTCCATCTT	TTCTCATCTT TACTATCTTC	TC-ATCCCCT CTGAGTCCAT
MAM1_SP134	TT----- ACCTGCTGGA CTCTAAAAGA	--CAT-GTTT AAACAGTTTG ATGGG	GCAGCATTTT ATTCCATCTT	TTCTCATCTT TACTATCTTC	TC-ATCCCCT CTGAGTCCAT
MAST_B130_	TTAGAAAAAG ACCTGCTGGA CTCTAAAAGA	AGTATACTTT AAACAGTTTG ATGGT	GCAGCA-TTC ATT-CA-CCT	TTCTCATCTT TACTAT-TTC	TCTATCCCCT CTGAGT-CAT
SAV1_SE210	TT----- ACCTGCTGGA CTCTAAAAGA	--CAT-GTTT AAACAGTTTG ATGGG	GCAGCATTTT ATTCCATCTT	TTCTCATCTT TACTATCTTC	TC-ATCCCCT CTGAGTCCAT

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ASIAN2_Ema	TGTGCACACT TT-CACTTGT AAGACCAAGT	GGGGACAAAG CACGCACTTT	CCAGTGATCT GGTTTACGTA	TCCCCCAGAG CATCGGGAGC	CACTTTTT-G GAGGACAGAA
FOR_DS1535	TGTGCACACT TT-CACTTGG AAGACCAAGT	GGGGACAAAG CACGCACTTT	CCAGTGATCT GGTTTACGTA	TCCCCCAGAG CATCGGGAGC	CACTTTTT-G GAGGACAGAA
MAM1_SP134	TGTGCACACT TT-CACTTGT AAGACCAAGT	GGGGACAAAG CACGCACTTT	CCAGTGATCT GGTTTACGTA	TCCCCCAGAG CATCGGGAGC	CACTTTTT-G GAGGACAGAA
MAST_B178_	GTGCACACTG TTTCACTTAT AAGACCAAGT	GGGACAAAAG CACGCACTTT	CCAGTGATCT GGTTTACGTA	TCCCCCAGAG CATCGGGAGC	CACTTTTTTG GAGGACAGAA
SAV1_SE210	TGTGCACACT TT-CACTTGG AAGACCAAGT	GGGGACAAAG CACGCACTTT	CCAGTGATCT GGTTTACGTA	TCCCCCAGAG CATCGGGAGC	CACTTTTT-G GAGGACAGAA

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ASIAN2_Ema	TGTAGGCTCT GGAGCTCGGT GACTCACCTG	ATGAAGGGAG GTTGGGGTGC	CGAGGAGGCT CAATTAGGCC	GGGCACGGTG ATCGGCACCC	AGCTGTTGGG ACTTCCGATG
FOR_DS1535	TGTAGGCTCT GGAGCTYGGT GACTCACCTG	ATGAAGGGAG GTTGGGGTGC	CGAGGAGGCT CAATTAGGCC	GGGCACGGTG ATCGGCACCC	AGCTGTTGGG ACTTCCGATG
MAM1_SP134	TGTAGGCTCT GGAGCTCGGT GACTCACCTG	ATGAAGGGAG GTTGGGGTGC	CGAGGAGGCT CAATTAGGCC	GGGCACGGTG ATCGGCACCC	AGCTGTTGGG ACTTCCGATG
MAST_B179_	TGTAGGCTCT GGAGCTCGGT GACTCACCTG	ATGAAGGGAG GTTGGGGTGC	GGAGGAGGCT CAATTAGGCC	GGGCACGGTG ATCGGCACCC	AGCTGTTGGG ACTTCTGATG
SAV1_SE210	TGTAGGCTCT GGAGCTCGGT GACTCACCTG	ATGAAGGGAG GTTGGGGTGC	CGAGGAGGCT CAATTAGGCC	GGGCACGGTG ATCGGCACCC	AGCTGTTGGG ACTTCCGATG

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ASIAN2_Ema	AAAGTGAAA- TTTGCTGAGC AACAGAACGG	TGAATGTGTG ACCCCTTACG	AGGCTATTCC CAGTAGACCT	TACTCATT GTGTGGGGTG	CACCAAA-TG CTGGAGACAC
FOR_DS1535	AAAGTGAAA- TTTGCTGAGC AACAGAACGG	TGAATGTGTG GCCCTTACG	AGGCTATTCC CAGTAGACCT	TACTCATT GTGTGGGGTG	CACCAAA-TG CTGGAGACAC
MAM1_SP134	AAAGTGAAA- TTTGCTGAGC AACAGAACGG	TGAATGTGTG GCCCTTACG	AGGCTATTCC CAGTAGACCT	TACTCATT GTGTGGGGTG	CACCAAA-TG CTGGAGACAC
MAST_B180_	AAAGTGAAA TTTGCTGAGC AACAGAACGA	TGAATGTGTG GCCCTTACG	AGGCTATTCC CAGTAGACCT	TACTCATT GTGTGGGGTG	CACCAAAATG CTGGAGACAC
SAV1_SE210	AAAGTGAAA- TTTGCTGAGC AACAGAACGG	TGAATGTGTG GCCCTTACG	AGGCTATTCC CAGTAGACCT	TACTCCTT GTGTGGGGTG	CACCAAA-TG CTGGAGACAC

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ASIAN2_Ema	GGAAAATGCA GAGCTGGGCT GTCCAGAAA	AATGYTTCCC CATCCAAGAA	TGAAACAGAG CCCAAATACA	GTGCTTAGGG GAGGCAAGGT	GGAAGGAGAG GGACAGAAAA
FOR_DS1535	GGAAAATGCA GAGCTGGGCT GTCCAGAAA	AATGTTTCCC CATCCAAGAA	TGAAACAGAG CCCAAATACA	GTGCTTAGGG GAGGCAAGGT	GGAAGGAGAG GGACAGAAAA
MAM1_SP134	GGAAAATGCA GAGCTGGGCT GTCCAGAAA	AATGTTTCCC CATCCAAGAA	TGAAACAGAG CCCAAATACA	GTGCTTAGGG GAGGCAAGGT	GGAAGGAGAG GGACAGAAAA
MAST_B135_	GGAAAATGCA AAGCTGGGCT	AATGTTTCTT CATCCAAGAA	TGAAATAGAG CCCAAATACA	GTGCTTAGGG GAGGCAAGGT	GGAAGGAGAG GGACAGAAAA

SAV1_SE210	ATCCAAAAA GGAAAATGCA GAGCTGGGCT GTCCAGAAA	AATGTTTTCC CATCCAAGAA	TGAAACAGAG CCCAAATACA	GTGCTTAGGG GAGGCAAGGT	GGAAGGAGAG GGACAGAAAA
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ASIAN2_Ema	GAGAAACCAA TATCAACCCT ACCTGGTAG	AA-CC--AAA ATCGGACAGA	CCC-GTTGCC TTMGAAGTGT	CTCAAGTCAA CCGTAGGGTT	TTCTGACTCA TCCAAGGAGC
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FOR_DS1535	GAGAAACCAA TATCAACCCT ACCTGGTAG	AA-CC--AAA ATCGGACAGA	CCC-GTTGCC TTAGAAGTGT	CTCAAGTCAA CCRTAGGGTT	TTCTGACTCA TCCAAGGAGC
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MAM1_SP134	GAGAAACCAA TATCAACCCT ACCTGGTAG	AA-CC--AAA ATCGGACAGA	CCC-GTTGCC TTAGAAGTGT	CTCAAGTCAA CCGTAGGGTT	TTCTGACTCA TCCAAGGAGC
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MAST_B181_	AGAAAACCAA TATCGACCTT ACCTGATAA	AAACCCGAAA ATCGGACAGA	CCCCTTTGCC TTAGAAGTGT	CTCAAGTCGA CCGTAGGGTT	TTCTGACTCA TCCAAGGAGC
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SAV1_SE210	GAGAAACCAA TATCAACCCT ACCTGGTAG	AA-CC--AAA ATCGGACAGA	CCC-GTTGCC TTAGAAGTGT	CTCAAGTCAA CCATAGGGTT	TTCTGACTCA TCCAAGGAGC
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ASIAN2_Ema	CAAAAAAGGA TGGGCATGTA TGGCTGCAGT	CCTGTGGGTT GAAAAGTATG C	TCCAGGTGGA AACACACAAG	GGTATGGCAG AGGGTGGTGG	AAAGGCTTTC TTTTGGGGAA
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FOR_DS1535	CAAAAAAGGA TGGGCATGTA TGGCTGCAGT	CCTGTGGGTT GAAAAGTATG C	TCCAGGTGGA AACACACAAG	GGTATGGCAG AGGGTGGTGG	AAAGGCTTTC TTTTGGGGAA
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MAM1_SP134	CAAAAAAGGA TGGGCATGTA TGGCTGCAGT	CCTGTGGGTT GAAAAGTATG C	TCCAGGTGGA AACACACAAG	GGTATGGCAG AGGGTGGTGG	AAAGGCTTTC TTTTGGGGAA
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MAST_B184_	CAAAAAATGA TGGGCATGTA TGGTT-CAGT	TTTGTGGGTT GAAAAGTATG C	TTTAGGTGGA AACACACAAG	GGTATGGCAG AGGGTGGTGG	AAAGGCTTTC TTTTGGG-AA
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SAV1_SE210	CAAAAAAGGA TGGGCATGTA TGGCTGCAGT	CCTGTGGGTT GAAAAGTATG C	TCCAGGTGGA AACACRCAAG	GGTATGGCAG AGGGTGGTGG	AAAGGCTTTC TTTTGGGGAA
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ASIAN2_Ema	-TTTTTTTTT GCTCTAGACC TTCCAGATC	TTTAGCATAG TAAAGAATCA GTA	TTACCAGGAA ATTCCCCCAT	CATCGGTGGT TCCCCTCCT	GACTION-CA GCCCCACTGTC
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FOR_DS1535	--TTTTTTTT GCTCTAGACC TTCCAGATC	TTTAGCATAG TAAAGAATCA GTA	TTACCAGGAA ATTCCCCCAT	CATCGGTGGT TCCCCTCCT	GACTION-CA RCCCCACTGTC
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MAM1_SP134	TTTTTTTTTT GCTCTAGACC TTCCAGATC	TTTAGCATAG TAAAGAATCA ATA	TTACCAGGAA ATTCCCCCAT	CATCGGTGGT TCCCCTCCT	GACTION-CA GCCCCACTGTC
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MAST_B137_	TTTTTTTTTT GCTCTAGACC TTCCAAATC	TTTAGCATAG TAAAGAATCA GTA	TTACCAGGAA ATTCCCCCAT	CATCGGTGGT TCCCCTCCT	GACTION-CA GCCCCACTGTC
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SAV1_SE210	-TTTTTTTTT GCTCTAGACC TTCCAGATC	TTTAGCATAG TAAAGAATCA GTA	TTACCAGGAA ATTCCCCCAT	CATCGGTGGT TCCCCTCCT	GACTION-CA GCCCCACTGTC
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ASIAN2_Ema	GGGAGATACC GCTTGGGGCT GCTTTCCAGA	TCACCACTTG TTAGCACAGA	GGGGCTGGTG TGTGGGGCCC	AAGAGAGGGT TCTAGGTCGG	CTGAGAAGAG GGACCACTTA
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FOR_DS1535	GGGAGATACC GCTTGGGGCT GCTTTCCAGA	TCACCACTTG TTAGCACAGA	GGGGCTGGTG TGTGGGGCCC	AAGAGAGGGT TCTAGGTCGG	CTGAGAAGAG GGACCACTTA
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MAM1_SP134	GGGAGATACC GCTTGGGGCT GCTTTCCAGA	TCACCACTTG TTAGCACAGA	GGGGCTGGTG TGTGGGGCCC	AAGAGAGGGT TCTAGGTCGG	CTGAGAAGAG GGACCACTTA
MAST_B139_	GGGAGATACC GCTTGGGGCT GCTTTCCAGA	TCACCACTTG TTAGCACAGA	GGG-CTGGTG TGTGGGGCCC	AAGAGAGGGT TCTAGGTCGG	CTGAGAAGAG GGACCACTTA
SAV1_SE210	GGGAGATACC GCTTGGGGCT GCTTTCCAGA	TCACCACTTG TTAGCACAGA	GGGGCTGGTG TGTGGGGCCC	AAGAGAGGGT TCTAGGTCGG	CTGAGAAGAG GGACCACTTA

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ASIAN2_Ema	GTTTCAACCT AGCTCYGTGG GGCCTAAT	TTAGTTAGAA GATGGAGACC	AAGATGTGCT TGGAGTCTTG	AGCTTAGAAG CCTGATGTCA	AAAACATTCC AACCCCTTGA
FOR_DS1535	GTTTCAACCT AGCTCCGTGG GGCCTAAT	TTAGTTAGAA GATGGAGACC	AAGATGTGCT TGGAGTCTTG	AGCTTAGAAG CCTGATGTCA	AAAACATTCC AACCCCTTGA
MAM1_SP134	GTTTCAACCT AGCTCCGTGG GGCCTAAT	TTAGTTAGAA GATGGAGACC	AAGATGTGCT TGGAGTCTTG	AGCTTAGAAG CCTGATGTCA	AAAACATTCC AACCCCTTGA
MAST_B140_	GTTTCAACCT AGCTCCGTGG GGCCTAAT	TTAGTCAGAA GATGGAGACC	AAGATGTGCT TGGAGTCTTG	AGCTTAGAAG CCTGATGTCA	AAAACATTCC AACCCCTTGA
SAV1_SE210	GTTTCAACCT AGCTCCGTGG GGCCTAAT	TTAGTTAGAA GATGGAGACC	AAGATGTGCT TGGAGTCTTG	AGCTTAGAAG CCTGATGTCA	AAAACATTCC AACCCCTTGA

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ASIAN2_Ema	ACATGAAAGA TATGCAATTA TACCTTAA	AGATTTACAA ATGA-TC-TT	CCCAGATTTA CCCTATATGA	AATGCAGGA- TACTTCA-TT	TTCTGTA-TA TTGGCTTCTT
FOR_DS1535	ACATGAAAGA TATGCAATTA TACCTTAA	AGATTTACAA ATGA-TC-TT	CCCAGATTTA CCCTATATGA	AATGCAGGA- TACTTCA-TT	TTCTGTA-TA TTGGCTTCTT
MAM1_SP134	ACATGAAAGA TATGCAATTA TACCTTAA	AGATTTACAA ATGA-TC-TT	CCCAGATTTA CCCTATATGA	AATGCAGGA- TACTTCA-TT	TTCTGTA-TA TTGGCTTCTT
MAST_B188_	ACAAGAAAGA TATGCAATTA TACCTTAA	AGATTTACAA ATGAATCGTT	CCCAGATTTA CCCTATATGA	AATGCAGGAG TACTTCAGTT	TTCTGTACTA TTGGCTTCTT
SAV1_SE210	ACATGAAAGA TATGCAATTA TACCTTAA	AGATTTACAA ATGA-TC-TT	CCCAGATTTA CCCTATATGA	AATGCAGGA- TACTTCA-TT	TTCTGTA-TA TTGGCTTCTT

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ASIAN2_Ema	TGCCCTGTTT CCAGTTTATC GTCCTGTC	GGGCCCTGGT CTTTCCTGGA	CATCCATTAT GTCTCACCTT	GGGTCTCCCT GCCTCTAGCC	GTGTTGGAGG CTGGAAC-TG
FOR_DS1535	TGCCCTGTTT CCASTTTATC GTCCTGTC	GGGCCCTGGT CTTTCCTGGA	CATCCATTAT GTCTCACCTT	GGGTCTCCCT GCCTCTAGCC	GTGTTGGAGG CTGGAAC-TG
MAM1_SP134	TGCCCTGTTT CCAGTTTATC GTCCTGTC	GGGCCCTGGT CTTTCCTGGA	CATCCATTAT GTCTCACCTT	GGGTCTCCCT GCCTCTAGCC	GTGTTGGAGG CTGGAAC-TG
MAST_B141_	TGCCCTGTTT CCACTTTATC GTCCTATC	GGGCCCTGGT CTTTTCTGGA	CAACCACTAT GTCTCACCTT	GGGTCTCCCT GCCTCTAGCC	GTGTTGGAGG CTGGAACGTG
SAV1_SE210	TGCCCTGTTT CCASTTTATC GTCCTGTC	GGGCCCTGGT CTTTCCTGGA	CATCCATTAT GTCTCACCTT	GGGTCTCCCT GCCTCTAGCC	GTGTTGGAGG CTGGAAC-TG

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ASIAN2_Ema	TGCAAAATTC	TATCATTTGA	TCTCTGGCAT	TGTTTTCTATC	ACCAAGGCCA
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	TATTTTCCAA	CTACCCATCC	TTCTTCTTTG	TTTCCAACCT	TTGCATTCCA
	ATCACCAG				
FOR_DS1535	TGCAAAATTC	TATCATTGGA	TCTCTGGCAT	TGTTTCTATC	ACCAAGGCCA
	TATTTTCCAA	CTACCCATCC	TTCTTCTTTG	TTTCCAACCT	TTGCATTCCA
	ATCACCAG				
MAM1_SP134	TGCAAAATTC	TATCATTGGA	TCTCTGGCAT	TGTTTCTATC	ACCAAGGCCA
	TATTTTCCAA	CTACCCATCC	TTCTTCTTTG	TTTCCAACCT	TTGCATTCCA
	ATCACCAG				
MAST_B143_	TGCAAAATTC	TATCCTGTGA	TCTCTGGCAT	TGTTTCTATC	ACCAAGGCCA
	TATTTTCCAG	CTACCAATCC	TTCTTCTTTG	TTTCCAACCT	TTGCATTCCA
	ATCACCAA				
SAV1_SE210	TGCAAAATTC	TATCATTGGA	TCTCTGGCAT	TGTTTCTATC	ACCAAGGCCA
	TATTTTCCAA	CTACCCATCC	TTCTTCTTTG	TTTCCAACCT	TTGCATTCCA
	ATCACCAG				

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ASIAN2_Ema	CAAGATAAAG	AATTACCCGT	TAAACAGTA-	TTTGAGGAAT	GTT-GGTCAT
	TGTGACACTG	GGGTCGTTTT	TAAAATCACT	CACAAGGCGT	CAGTCTTCAT
	AATAATTGGC	TC			
FOR_DS1535	CAAGATAAAG	AATTACCCGT	TAAACAGTA-	TTTGAGGAAT	GTT-GGTCAT
	TGTGACACTG	GGGTCGTTTT	TAAAATCACT	CACAAGGCGT	CAGTCTTCAT
	AATAATTGGC	TC			
MAM1_SP134	CAAAATAAAG	AATTACCCAT	TAAACAGTA-	TTTGAGGAAT	GTT-GGTCAT
	TGTGACACTG	GGGTAGTTTT	TAAAATCACT	CACAAGGCGT	CAGTCTTCAT
	AATAATTGGC	TC			
MAST_B189_	TAAGATAAAG	AATTACCCGT	TAAACAGTAC	TTTGAGGAAT	GTTTGGTCAT
	TGTGACACTG	GGGTCGTTTT	TAAAATCAC-	---AAGGCGT	CAGTCTTCAT
	AATAATTGGC	TC			
SAV1_SE210	CAAGATAAAG	AATTACCCGT	TAAACAGTA-	TTTGAGGAAT	GTT-GGTCAT
	TGTGACACTG	GGGTCGTTTT	TAAAATCACT	CACAAGGCGT	CAGTCTTCAT
	AATAATTGGC	TC			

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ASIAN2_Ema	CAGCAGTAGG	TTCAGCCTTA	GTGSTCTTTA	ACTTGTGGGT	CCYGAGCACA
	GCTGGGCCTT	TTGGGGTACT	CCCAGATACG	GTCACATGTG	GAGACTTTCT
	GGCTGGAG				
FOR_DS1535	CAGCAGTAGG	TTCAGCCTTA	GTGGTCTTTA	ACTTGTGGGT	CCCGAGCACA
	GCTGGGCCTT	TTGGGGTACT	CCCAGAAACG	GTCACATGTG	GAGACTTTCT
	GGCTGGAG				
MAM1_SP134	CAGCAGTAGG	TTCAGCCTTA	GTGGTCTTTA	ACTTGTGGGT	CCCGAGCACA
	GCTGGGCCTT	TTGGGGTACT	CCCAGATACG	GTCACATGTG	GAGACTTTCT
	GGCTGGAG				
MAST_B191_	TAGCAGCAGG	TTCAGCCTTA	GTGGTCTTTA	ACTTGTGGGT	CCCGAGCACA
	GCTGGGCCTT	TTGGGGTACT	CCCAGATACG	GTCACATGTG	GAGACTTTCT
	GGCTGGAA				
SAV1_SE210	CAGCAGTAGG	TTCAGCCTTA	GTGGTCTTTA	ACTTGTGGGT	CCCGAGCACA
	GCTGGGCCTT	TTGGGGTACT	CCCAGAAACG	GTCACATGTG	GAGACTTTCT
	GGCTGGAG				

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ASIAN2_Ema	ATAATCATTG	TTGAGTTGTT	GGAGSCCACT	GTGAAGACTA	TTTTCGACAT
	GACRACTTAG	AGCCATTTAT	CCCTTCATTC	TCTAGCTTCT	CCCTCCAGC-
	AGAGAAC				
FOR_DS1535	ATAATCATTG	TTGAGTTGTT	GGAGCCCACT	GTGAAGACTA	TTTTCGACAT
	GACGACTTAG	AGCCATTTAT	CCCTTCATTC	TCTAGCTTCT	CCCTCCAGC-
	AGAGAAC				
MAM1_SP134	ATAATCATTG	TTGAGTTGTT	GGAGCCCACT	GTGAAGACTA	TTTTCGACAT
	GATGACTTAG	AGCCATTTAT	CCCTTCATTC	TCTAGCTTCT	CCCTCCAGC-
	AGAGAAC				
MAST_B192_	ATAATCATTG	TTGAGTTGTT	GGAGCCCACT	GTGAAGACTA	TTTTCGACAT
	GACGACTTAG	AGCCATTTAT	CCCTTCATTC	TCTAGCTTCT	CCCTCCAGCG
	AGAGAAC				
SAV1_SE210	ATAATCATTG	TTGAGTTGTT	GGAGCCCACT	GTGAAGACTA	TTTTCGACAT
	GACGACTTAG	AGCCATTTAT	CCCTTCATTC	TCTAGCTTCT	CCCTCCAGC-
	AGAGAAC				

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ASIAN2_Ema	GTACAGGAAC AGGGTATGTT TAAAAAA	AGATGTGTGG CTACAATCTT	GACAACAAGA ATTAAAAAGC	TCATTTGT-A AAACCAAAAC	CCTAGTTCAG AAAACCTCAAT
FOR_DS1535	GTACAGGAAC AGGGTATGTT TAAAAAA	AGATGTGTGG CTACAATCTT	GACAACAAGA ATTAAAAAGC	TCATTTGT-A AAACCAAAAC	CCTAGTTCAG AAAACCTCAAT
MAM1_SP134	GTACAGGAAC AGGGTATGTT TAAAAAA	AGATGTGTGG CTACAATCTT	GACAACAAGA ATTAAAAAGC	TCATTTGT-A AAACCAAAAC	CCTAGTTCAG AAAACCTCAAT
MAST_B193_	GTGTAGGAAC AGGGTATGTT TAAAAAA	AGATATGTGG CCACAATCTT	GACAACAAGA ATTAAAAAGC	TCATTTGT-A AAACCAAAAC	CTTAGTTGAG AAAACCTCAAT
SAV1_SE210	GTACAGGAAC AGGGTATGTT TAAAAAA	AGATGTGTGG CTACAATCTT	GACAACAAGA ATTAAAAAGC	TCATTTGT-A AAACCAAAAC	CCTAGTTCAG AAAACCTCAAT

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ASIAN2_Ema	GATAACGAGC TGCCAGAAAG CCCTTTC	TGAACGCAGG TCCACATATA	ATCCAGAGCA TTGGATGCAG	GAGCAAAAGC GCCACACCCC	CAGCGAGCTT CAAGGAAACT
FOR_DS1535	GATAACGAGC TGCCAGAAAG CCCTTTC	TGAATGCAGG TCCACATATA	ATCCAGAGCA YTGGATGCAG	GAGCAAAAGC GCCACACCCC	CAGCGAGCTT CAAGGAAACT
MAM1_SP134	GATAACGAGC TGCCAGAAAG CCCTTTC	TGAATGCAGG TCCACATATA	ATCCAGAGCA TTGGATGCAG	GAGCAAAAGC GCCACACCCC	CAGCGAGCTT CAAGGAAACT
MAST_B194_	GTCAATGAGC TGCCAGAAAG CCGTTTC	TGAATGCAAG TCCACATATA	ATCCAGAGCA TTGGATGCAG	AAGCAGAAGC GCCACACACC	CTGCGAGCTT CGAGGAAACT
SAV1_SE210	GATAACGAGC TGCCAGAAAG CCCTTTC	TGAATGCAGG TCCACATATA	ATCCAGAGCA TTGGATGCAG	GAGCAAAAGC GCCACACCCC	CAGCGAGCTT CAAGGAAACT

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ASIAN2_Ema	TCTTTACAAG TACCAAATC AGCAGCA	ATCAGATATT AAGGCAGACA	TTACAATCAG AGAGATAAAG	GAACATTCTT CCTCAGCTGC	AGAGAACCAA ACCAGCCAAG
FOR_DS1535	TCTTTACAAG TACCAAATC AGMAGCA	ATCAGATATT AAGGCAGACA	TTACAATCAG AGMRATAAAG	GAACATTCTT CCTCAGCTGC	AGAGAACCAA ACCAGCCAAG
MAM1_SP134	TCTTTACAAG TACCAAATC AGCAGCA	ATCAGATATT AAGGCAGACA	TTACAATCAG AGAGATAAAG	GAACATTCTT CCTCAGCTGC	AGAGAACCAA ACCAGCCAAG
MAST_B217_	TCTTTACAAG TACCAAATC AGCAGCA	ATCAGATATT AAGGCAGACA	TTACAATCAG AGAGATAAAG	GAACATTCTT CCTCAGCTGC	AGAGAACCAA ACCAGCCAAG
SAV1_SE210	TCTTTACAAG TACCAAATC AGCAGCA	ATCAGATATT AAGGCAGACA	TTACAATCAG AGAGATAAAG	GAACATTCTT CCTCAGCTGC	AGAGAACCAA ACCAGCCAAG

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ASIAN2_Ema	TGAGCATTGG CTGGCCCTCG TCCCAAAC	GACTGGCTCC GCTGGTTCCT	TGTGTAGGCG CATCCTCCCC	TCTGGGGAGA TCATCTCCAG	CTGCGGCCCT ATCTGGACAC
FOR_DS1535	TGAGCATTGG CTGGCCCTCG TCCCAAAC	GACTGGCTCC GCTGGTTCCT	TGTGTAGGCG CATCCTCCCC	TCTGGGGAGA TCATCTCCAG	CTGCGGCCCT ATCTGGACAC
MAM1_SP134	TGAGCATTGG CTGGCCCTCG TCCCAAAC	GACTGGCTCC GCTGGTTCCT	TGTGTAGGCG CATCCTCCCC	TCTGGGGAGA TCATCTCCAG	CTGCGGCCCT ATCTGGACAC
MAST_B219_	TGAGCATTGG	GACTGGCTCC	TGTGTAGGCG	TCTGGGGAGA	CTGCGGCC-T

	CTGGCCCTCG TCCCAAAC	GCTGGTTCCT	CATCCTCCCC	TCATCTCCAG	ATCTGGACAC
SAV1_SE210	TGAGCATTGG CTGGCCCTCG TCCCAAAC	GACTGGCTCC GCTGGTTCCT	TGTGTAGGCG CATCCTCCCC	TCTGGGGAGA TCATCTCCAG	CTGCGGGCCT ATCTGGACAC

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ASIAN2_Ema	TAGATGACTG CTGGATTTGG GTGAAAG	GGTGGG-TCC TTTCAGGTGT	ACCAAGTTTA TGGAGATCAT	TGAAAGAAGA GGTTGAAATT	TAGGAATAT- TAGGGACAGA
FOR_DS1535	TAGATGACTG CTGGATTTGG GTGAAAG	GGTGGG-TCC TTTCAGGTGT	ACCAAGTTTA TGGAGATCAT	TGAAAGAAGA GGTTGAAWTT	TAGGAATAT- TAGGGACAGA
MAM1_SP134	TAGATGACTG CTGGATTTGG GTGAAAG	GGTGGG-TCC TTTCAGGTGT	ACCAAGTTTA TGGAGATCAT	TGAAAGAAGA GGTTGAAATT	TAGGAATAT- TAGGGACAGA
MAST_B220_	TAGGGAAAAA CTGGATTTGG GTAAAAG	AATAAAGAAT TTTCAGGTGT	ACCAAGTTTA TGGAGATCAT	TGAGAGAAGA GGTTGAAATT	TGGGAATATT TAGGGACAGA
SAV1_SE210	TAGATGACTG CTGGATTTGG GTGAAAG	GGTGGG-TCC TTTCAGGTGT	ACCAAGTTTA TGGAGATCCT	TGAAAGAAGA GGTTGAAATT	TAGGAATAT- TAGGGACAGA

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ASIAN2_Ema	CCTCAGGGCC GAGAAGGATC TCGTGAG	CCACCACGAT AACCGCACTG	GCACGTGCAG TGATTGGGAT	CTGATCATGG GAGCCGACAG	AGCGGCTGCT TCTCCCCACA
FOR_DS1535	CCTCAGGGCC GAGAAGGATC TCGTGAG	CCACCACGAT AACCGCACTG	GCACGTGCAG TGATTGGGAT	CTGATCATGG GAGCCGACAG	AGCGGCTGCT TCTCCCCACA
MAM1_SP134	CCTCAGGGCC GAGAAGGATC TCGTGAG	CCACCACGAT AACCGCACTG	GCACGTGCAG TGATTGGGAT	CTGATCATGG GAGCCGACAG	AGCGGCTGCT TCTCCCCACA
MAST_B221_	TCTCAGGGCC GAGAAGGATC TCGTAAA	CCACCACGAT AACCGCACTG	GCACGTGCAG TGATTGAGAT	CTGATCATGG GAGCCGACAG	AGCGGTTGTT TCTCCCCACA
SAV1_SE210	CCTCAGGGCC GAGAAGGATC TCGTGAG	CCACCACGAT AACCGCACTG	GCACGTGCAG TGATTGGGAT	CTGATCATGG GAGCCGACAG	AGCGGCTGCT TCTCCCCACA

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ASIAN2_Ema	TTGGACACAT CAATGTGTTA TTCAGGC	CTGCCAAACG GTAAGGAGGG	GACCCGTGTG TCCCCGAAG	AGTGAGGCAA GGATGAAGAG	GGCCAGGTCT CTGAGCGAGC
FOR_DS1535	TTGGACACAT CAATGCGTTA TTCAGGC	CTGCCAAACG GTAAGGAGGG	GACCCGTGTG TCCYCCGAAG	AGTGAGGCAA GGATGAAGAG	GGCCAGGTCT CTGAGCGAGC
MAM1_SP134	TTGGACACAT CAATGTGTTA TTCAGGC	CTGCCAAACG GTAAGGAGGG	GACCCGTGTG TCCCCGAAG	AGTGAGGCAA GGATGAAGAG	GGCCAGGTCT CTGAGCGAGC
MAST_B222_	TTGGACATAT CAATGCGTTA TTCAGGC	TTGCCAAACG GCAAGGAGGG	GACCCGTGTG TCCCCAAAG	AGTGAGGCAA GGATGAAGAG	GGCCAGGTCT CTGAGCAAGC
SAV1_SE210	TTGGACACAT CAATGCGTTA TTCAGGC	CTGCCAAACG GTAAGGAGGG	GACCCGTGTG TCCCCGAAG	AGTGAGGCAA GGATGAAGAG	GGCCAGGTCT CTGAGCGAGC

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ASIAN2_Ema	CCCTCCTGGC CCTCCACTTG ATTATAC	TCTGAGGAAC GGCTGTACAT	ACATGACCCT CCARTGAACT	CCTCTAGTTA CCAGTTCATT	ATAACCAATC CAGGAGCCTT
FOR_DS1535	CCCTCCTGGC CCTCCACTTG	TCTGAGGAAC GGCTGTACAT	ACATGACCCT CCAGTGAECT	CCTCTAGTTA CCAGTTCATT	ATAACCAATC CAGGAGCCTT

MAM1_SP134	ATTATAC CCCTCCYGGC CCTCCACTTG ATTATAC	TCTGAGGAAC GGCTGTACAT	ACATGACCCT CCAGTGAAC	CCTCTAGTTA CCAGTTCATT	ATAACCAATC CAGGAGCCTT
MAST_B195_	CCCTCCTGGC CCTCCACTTG ATTATAC	TCTGAGGAAC GGCTGTACAT	ACATGACCCT CCAGTGAAC	CCTCTAGTTA CCAGTTCATT	ATAACCAATC CAGGAGCCTT
SAV1_SE210	CCCTCCTGGC CCTCCACTTG ATTATAC	TCTGAGGAAC GGCTGTACAT	ACATGACCCT CCAGTGAAC	CCTCTAGTTA CCAGTTCATT	ATAACCAATC CAGGAGCCTT

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ASIAN2_Ema	CCCACCTTGA GGGCAAGGTC GTGAAACTGG	GGTCACTTGG CAGACAGAGA	GGCTGGGGTT GAGCAAAGGC	GCATAAGGAA AGGTAAGTGA	CTCAAAGTGA GGAAGGAGAA
FOR_DS1535	CCCACCTTGA GGGCAAGGTC GTGAAACTGG	GGTCACTTGA CAGACAGAGA	GGCTGGGGTT GAGCAAAGGC	GCATAAGGAA AGGTAAGTGA	CTCAAAGTGA GGAAGGAGAA
MAM1_SP134	CCCACCTTGA GGGCAAGGTC GTGAAACTGG	GGTCACTTGG CAGACAGAGA	GGCTGGGGTT GAGCAAAGGC	GCATAAGGAA AGGTAAGTGA	CTCAAAGTGA GGAAGGAGAA
MAST_B196_	TTTATCTTGA GGGCAAGGTC GTGAAACTGG	GGTCACTTGG CAGACAGAGA	G-CTGGG-TT GAGCAAAGGC	GCATAAGGAA AGGTAAGTGA	CTCAAAGTGA G-AAGGAGAA
SAV1_SE210	CCCACCTTGA GGGCAAGATC GTGAAACTGG	GGTCACTTGG CAGACAGAGA	GGCTGGGGTT GAGCAAAGGC	GCATAAGGAA AGGTAAGTGA	CTCAAAGTGA GGAAGGAGAA

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ASIAN2_Ema	TAAAATTATA TGGGAAGTGG GCTAGTGA	CGTTATTTTC AGAGAAGAAC	TTCTTTGCTG AGCTATCAGC	GTGCGAGGGG TCAGGAAGAT	AGGAAGGTGA TGAGGCATGA
FOR_DS1535	TAAAATTATA TGGGAAGTGG GCTAGTGA	CGTTATTTTC AGAGAAGAAC	TTCTTTGCTG AGCTATCAGC	GTGCGAGGGG TCAGGAAGAT	AGGAAGGTGA TGAGGCATGA
MAM1_SP134	TAAAATTATA TGGGAAGTGG GCTAGTGA	CGTTATTTTC AGAGAAGAAC	TTCTTTGCTG AGCTATCAGC	GTGCGAGGGG TCAGGAAGAT	AGGAAGGTGA TGAGGCATGA
MAST_B223_	TAAAATTATA -GGGAAGTGG GCTAGTGA	CGTTATTTTC AGAGAAGAAC	TTCTTTGCTG AGCTATGAGC	GTGCGAGGGG TCAGGAAGAT	AGGAAGGTGA TGAGGCATGA
SAV1_SE210	TAAAATTATA TGGGAAGTGG GCTAGTGA	CGTTATTTTC AGAGAAGAAC	TTCTTTGCTG AGCTATCAGC	GTGCGAGGGG TCAGGAAGAT	AGGAAGGTGA TGAGGCATGA

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ASIAN2_Ema	CAAGAAATTT GTTTGTGCCC GAACAA	TAAAGACAGT ATTCCAAAGA	TACCTGGCCA AAGGTGGTCC	ACTGACTGGA AACAGAATGC	ATAGATTCAT AGAAATTATT
FOR_DS1535	CAAGAAATTT GTTTGTGCCC GAACAA	TAAAGACAGT ATTCCAAAGA	TACCTGGCCA AAGGTGGTCC	ACTGACTGGA AACAGAATGC	ATAGATCCAT AGAAATTATT
MAM1_SP134	CAAGAAATTT GTTTGTGCCC GAACAA	TAAAGACAGT ATTCCAAAGA	TACCTGGCCA AAGGTGGTCC	ACTGACTGGA AACAGAATGC	ATAGATCCAT AGAAATTATT
MAST_B226_	TAAGAAATTT GTTTGTGCCC GAACAA	TAAAGACAGT ATTCCAAAGA	TACCTGGCCA AAGGTGGTCC	ACTGACTGGA AACAGAATGC	ATAGATCCAT AGAAATTATT
SAV1_SE210	CAAGAAATTT GTTTGTGCCC GAACAA	TAAAGACAGT ATTCCAAAGA	TACCTGGCCA AAGGTGGTCC	ACTGACTGGA AACAGAATGC	ATAGATCCAT AGAAATTATT

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ASIAN2_Ema	TTGCCAGGAA AGGGTACATC GGGGGG	TTTCTGGACC TGTGCACCCA	TCCTTGGGAC GAGTTCCTCC	CAAGGGCTGA CCTTGGGGGG	TCTGGGTGCT AGTCAAGCAA
FOR_DS1535	TTGCCAGGAA AGGGTACATC GGGGGG	TTTCTGGACC TGTGCACCCA	TCCTTGGGAC GAGTTCCTCC	CAAGGGCTGA CCTTGGGGGY	TCTGGGTGCT AGTCAAGCAA
MAM1_SP134	TTGCCAGGAA AGGGTACATC GGGGGG	TTTCTGGACC TGTGCACCCA	TCCTTGGGAC GAGTTCCTCC	CAAGGGCTGA CCTTGGGGGG	TCTGGGTGCT AGTCAAGCAA
MAST_B197_	TTGCCAGGAA AAAGTACATC GGAGGA	TTTCTGGACC TGTGCACCCA	TCTTTGGGAC GAGTTCCTCC	CAAGGGCTGA CCTTGGGGGG	TCTGGGTGCT AGTCAAGCAA
SAV1_SE210	TTGCCAGGAA AGGGTACATC GGGGGG	TTTCTGGACC TGTGCACCCA	TCCTTGGGAC GAGTTCCTCC	CAAGGGCTGA CCTTGGGGGG	TCTGGGTGCT AGTCAAGCAA

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ASIAN2_Ema	GAAACATCAG CTACCTTACC CTCTTTT-CT	GCCTAAGCAT TAGAGTCACA	CCAAAGAAAT GACAGATCAT	GGAGACCC-A C-AAG-TCCT	GAGAGGTTAG TT-CTCTTCA
FOR_DS1535	GAAACATCAG CTACCTTACC CTCTTTT-CT	GTCTAMGCAT TAGAGTCACA	CCAAAGAAAT GACAGATCAT	GGAGACCC-A C-AAG-TCCT	GAGAGGTTAG TT-CTCTTCA
MAM1_SP134	GAAACATCAG CTACCTTACC CTCTTTT-CT	GCCTAAGCAT TAGAGTCACA	CCAAAGAAAT GACAGATCAT	GGAGACCCCA C-AAG-TCCT	GAGAGGTTAG TT-CTCTTCA
MAST_B198_	GAA-CATCAG CTACCTTACC CTCTTTTTCT	GTCTAAGCAT TAGAGTCACA	CCAA-GAA-T GACAGATCAT	GGAGACCC-A CGAAGGTCT	GAGAGGTTAG TTTCTCTTCA
SAV1_SE210	GAARCATCAG CTACCTTACC CTCTTTT-CT	GTCTAAGCAT TAGAGTCACA	CCAAAGAAAT GACAGATCAT	GGAGACCC-A C-AAG-TCCT	GAGAGGTTAG TT-CTCTTCA

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ASIAN2_Ema	CAAAGAGGCA CCCTATCTGC AGTGGA	AAAG----- TCGAATCCAA	--TAGGACAT GGAGTATCAC	GGACAAGCAT AGAATAGGCA	GCTGCCTGAG AAAGTCAGAA
FOR_DS1535	CAAAGAGGCA CCCTATCTGC AGTGGA	AAAG----- TCGAATCCAA	--TAGGACAT GGAGTATCAC	GGACAAGCAT AGAATAGGCA	GCTGTCTGAG AAAGTCAGAA
MAM1_SP134	CAAAGAGGCA CCCTATCTGC AGTGGA	AAAG----- TCGAATCCAA	--TAGGACAT GGAGTATCAC	GGACAAGCAT AGAATAGGCA	GCTGCCTGAG AAAGTCAGAA
MAST_B229_	CAAAAAAGAG CCCTATCTGC AGTGGA	AAAGTCCCTT TCGAATCCAA	GATAGGACAC GGAGTATCAC	AGACAAGCAT AGAATAGGCA	GCTGCCCGAG AAAGTCAGAA
SAV1_SE210	CAAAGAGGCA CCCTATCTGC AGTGGA	AAAG----- TCGAATCCAA	--TAGGACAT GGAGTATCAC	GGACAAGCAT AGAATAGGCA	GCTGCCTGAG AAAGTCAGAA

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ASIAN2_Ema	AGAACAGACG -----	AGTGTGTGCA ---G-CTGTG	GTGTCA---- CC-AGGGCTC	----- TG-TGGAAAA	----- GCTGCTGGGA
FOR_DS1535	GAACAGA AGAACAGACG GCTCCCTGGG	AGTGTGTGCA ACAG-CTGTG	GTGTCAGAAG CC-AGGGCTC	GTGCCCCCG- TG-TGGAAAA	CCTCACACGC GCTGCTGGGA
MAM1_SP134	GAACAGA AGAACAGACG GCTCCCTGGG	AGTGTGTGCA ACAG-CTGTG	GTGTCAGAGG CC-AGGGCTC	GTGTCCCCG- TG-TGGAAAA	CCTCACACGC GCTGCTGGGA
MAST_B230_	GAACAGA AGAACAGACG GCTCCCTGGG	AGTGTATGCA ACAGGCTGTG	GCGTCAGA-G CCGAGGGCTC	GTGCCCCCGG TGGTGGAAAA	CCTCACACGT GCTGCTGGGA
SAV1_SE210	GAACAGA AGAACAGACG ACTCCCTGGG	AGTGTGTGCA ACAG-CTGTG	GTGTCAGAAG CC-AGGGCTC	GTGCCCCCG- TG-TGGAAAA	CCTCACACGC GCTGCTGGGA

GAACAGA

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ASIAN2_Ema	TCTAAGTGAA GAGGGGCTTC AGCCCA	GATGAGACGT AGGAAATGAG	CTCAAGGAAT TGAAGAAGGC	CAAGGCACTG ACAGCCTCAG	CAGTGGGCAG CCTCCTGGTG
FOR_DS1535	TCTAAGTGAA GAGGGGCTTC AGCCCA	GATGAGACGT AGGAAATGAG	CTCAAGGAAT TRAAGAAGGC	CAAGGCACTG ACAGCCTCAG	CAGTGGGCAG CCTCCTGGTG
MAM1_SP134	TCTAAGTGAA GAGGGGCTTC AGCCCT	GATGAGACGT AGGAAATGAG	CTCAAGGAAT TGAAGAAGGC	CAAGGCACTG ACAGCCTCAG	CAGTGGGCAG CCTCCTGGTG
MAST_B233_	TCTAAGTGAA GAGGGGCTTC AGCCCA	GATGAGCCGT AGGAAATGAG	CTCAAGGAAT TGAAGAAGGC	CAAGGCACTG ACAACCTCAG	CAGTGGGCAG CCTCCTGGTG
SAV1_SE210	TCTAAGTGAA GAGGGGCTTC AGCCCA	GATGAGCCGT AGGAAATGAG	CTCAAGGAAT TGAAGAAGGC	CAAGGCACTG ACAGCCTCAG	CAGTGGGCAG CCTCCTGGTG

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ASIAN2_Ema	TCTCAGGCCT GA	C-AGTCTTCA	CATCCGCCC-	AC-AGGGGCT	TGTCTGTTTT
FOR_DS1535	TCTCAGGCCT GA	C-AGTCTTCA	CATCCGCCC-	AC-AGGGGCT	TGTCTGTTTT
MAM1_SP134	TCTCAGGCCT GA	C-AGTCTTCA	CATCCGCCC-	AC-AGGGGCT	TGTCTGTTTT
MAST_B234_	CTTCAG-CCT AA	CGAGTCTCCA	CATCCGCCCT	ACGAGGGGCT	TGTCTGTTTT
SAV1_SE210	TCTCAGGCCT GA	C-AGTCTTCA	CATCCGCCC-	AC-AGGGGCT	TGTCTGTTTT

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ASIAN2_Ema	GGGCCTCTCA TCAGCCC CTGCCC	GTCTCTCCAG TGCTCTGTGT	AGTCTTTGGC CTCCAGGTAA	CAGAGATAAC GAGTCTACCA	TGGGCTCCAC CATGCCCAGC
FOR_DS1535	GGGCCTCTCA TCAGCCC CTGCCC	GTCTCTCCAG TGCTCTGTGT	AGTCTTTGGC CTCCAGGTAA	CAGAGATAAC GAGTCTACCA	TGGGCTCCAC CATGCCCAGC
MAM1_SP134	GGGCCTCTCA TCAGCCC CTGCCC	GTCTCTCCAG YGCTCTGTGT	AGTCTTTGGC CTCCAGGTAA	CAGAGATAAC GAGTCTACCA	TGGGCTCCAC CATGCCCAGC
MAST_B200_	GGGCCTCTCA TCAGCCC CTGCCC	GTCTCTCCAG TGCTATATGT	AGTCTTTGGC CTCCAGGTAA	CAGAGATAAC GAGTCTACCA	TGGGCTGCAC CATGCCCAGC
SAV1_SE210	GGGCCTCTCA TCAGCCC CTGCCC	GTCTCTCCAG TGCTCTGTGT	AGTCTTTGGC CTCCAGGTAA	CAGAGATAAC GAGTCTACCA	TGGGCTCCAC CATGCCCAGC

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ASIAN2_Ema	CGATAAGAGA TAGGAATCCA ATTCTA	TTGAAA-TC- TGTAGCAATT	TGAGTGCAAG TCA-TAAACA	AACGTC-TGA AATGCTGTGG	AACATTTTTTC -AAAGGA-GC
FOR_DS1535	CGATAAGAGA TAGGAATCCA ATTCTA	TTGAAA-TC- TGTAGCAATT	TGAGTGCAAG TCA-TAAACA	AACGTC-TGA AATGCTGTGG	AACATTTTTTC -AAAGGA-GC
MAM1_SP134	CGATAAGAGA TAGGAATCCA ATTCTA	TTGAAA-TC- TGTAGCAATT	TGAGTGCAAG TCA-TAAACA	AACGTC-TGA AATGCTGTGG	AACATTTTTTC -AAAGGA-GC
MAST_B236_	TGATAAGAGA TAGGAATCCA ATTCTA	TTGAAAATCC TGTAGCAATT	TGAGTGCAAG TCAGTAAGCA	AATGTCCTGA AATGCTGTGG	AACATTTTTTT TAAAGGACGC
SAV1_SE210	CGATAAGAGA TAGGAATCCA	TTGAAA-TC- TGTAGCAATT	TGAGTGCAAG TCA-TAAACA	AACGTC-TGA AATGCTGTGG	AACATTTTTTC -AAAGGA-GC

ATTCTA

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ASIAN2_Ema	AGTCCACAAA AGCTGCGGTA TCTTGG	-GTTAGCCAT GGCTCCTGAG	GTGAGCATGA GATAAAGGACG	ACCCTCAAGG CATACTCTGG	GAGAAGGGCA TTTTAAACTC
FOR_DS1535	AGTCCACAAA AGCTGCGGTA TCTTGG	-GTTAGCCAT GGCTCCTGAG	GTGAGCATGA GATAAAGGACG	ACCCTCAAGG CATACTCTGG	GAGAAGGGCA TTTTAAACTC
MAM1_SP134	AGTCCACAAA AGCTGCGGTA TCTTGG	-GTTAGCCAT GGCTCCTGAG	GTGAGCATGA GATAAAGGACG	ACCCTCAAGG CATACTCTGG	GAGAAGGGCA TTTTAAACTC
MAST_B237_	AGTTCACAAA AGCTGTGGTA TCTTAA	AGTTAGCCAT GGCTCCTGAG	GTGAGCATGA GATAAAGGATG	ACCCTCAAGG CCTACTCTGG	GAGAAGGGCA TTTTAAACTC
SAV1_SE210	AGTCCACAAA AGCTGCGGTA TCTTGG	-GTTAGCCAT GGCTCCTGAG	GTGAGCATGA GATAAAGGACG	ACCCTCAAGG CATACTCTGG	GAGAAGGGCA TTTTAAACTC

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ASIAN2_Ema	GCATTATTAA ATCCCTCAGC GAGAG	TTTCTCTTAC ATCTG-CAAA	CTGTCTCCTA TGCCAGTAAC	GTTGTAATCT GAGTTTC-TC	CAGATACTAC ATACTAAATA
FOR_DS1535	GCATTATTAA ATCCCTCAGC GAGAG	TTTCTCTTAC ATCTG-CAAA	CTGTCTCCTA TGCCAGTAAC	GTTGTAATCT GAGTTTC-TC	CAGATACTAC ATACTAAATA
MAM1_SP134	GCATTATTAA ATCCCTCAGC GAGAG	TTTCTCTTAC ATCTG-CAAA	CTGTCTCCTA TGCCAGTAAC	GTTGTAATCT GAGTTTC-TC	CAGATACTAC ATACTAAATA
MAST_B240_	GCATTATTAA ATCCCTCAGC GAGAT	TTTCTCTTAC ATCTGGCAAA	CTGTCTCCTA TGCCAGTAAC	GTTGTAATCT GAGTTTCGTC	CAGATACTAC ATACTAAATG
SAV1_SE210	GCATTATTAA ATCCCTCAGC GAGAG	TTTCTCTTAC ATCTG-CAAA	CTGTCTCCTA TGCCAGTAAC	GTTGTAATCT GAGTTTC-TC	CAGATACTAC ATACTAAATA

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ASIAN2_Ema	TGGCCTACCC C-AGGCCCC- GTCCT	CAGCCCCTGT TCC-TGCCTG	CATTTGAGGA CACAAGTGAA	TGACCCAAAG GGGCAGCTCT	CGTTCACCCC CAGGGGTACA
FOR_DS1535	TGGCCTACCC C-AGGCCCC- GTCCT	CAGCCCCTGT TCC-TGCCTG	CATTTGAGGA CACAAGTGAA	TGACCCAAAG GGGCAGCTCT	SGTTCACCCC CAGGGGTACA
MAM1_SP134	TGGCCTACCC C-AGGCCCC- GTCCT	CAGCCCCTGT TCC-TGCCTG	CATTTGAGGA CACAAGTGAA	TGACCCAAAG GGGCAGCTCT	CGTTCACCCC CAGGGGTACC
MAST_B241_	GTTTTATTTT CCAGGCCCCC GTCCT	TAGTTCCTGT TCCCTGCCTG	NATTTGAGGA CACAAGTGAA	TGACCCAAAG GGGCAGCTCT	GGTTCACCCC CAGGGGTACA
SAV1_SE210	TGGCCTACCC C-AGGCCCC- GTCCT	CAGCCCCTGT TCC-TGCCTG	CATTTGAGGA CACAAGTGAA	TGACCCAAAG GGGCAGCTCT	GGTTCACCCC CAGGGGTACA

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ASIAN2_Ema	TAACCCACCC GGACAGAGTA CAAAC	AGTGCTGTCG GAACTGCCTC	AGTTGATTAC ATAGAGTTTC	TGACTCATAG CAAGGAGTGC	CGACCCTAAA CTGGCGGATT
FOR_DS1535	TAACCCACCC GGACAGAGTA CAAAC	AGTGCTGTCG GAACTGCCTC	AGTTGATTAC ATAGAGTTTC	TGACTCATAG CAAGGAGTGC	CGACCCTAAA CTGGCGGATT
MAM1_SP134	TAACCCACCC GGACAGAGTA CAAAC	AGTGCTGTCG GAACTGCCTC	AGTTGATTAC ATAGAGTTTC	TGACTCATAG CAAGGAGTGC	CGACCCTAAA CTGGCGGATT

MAST_B242_	TAACCCACCC GGACAGAGTA CAAAC	AGTGCTGTCG GAATTGCCTT	AGTTGATTAC ATAGAGTTTC	TGACTCATAG CAAGGAGCGT	CGACCCTGTA CTGGCAGATT
SAV1_SE210	TAACCCACCC GGACAGAGTA CAAAC	AGTGCTGTCG GAACTGCCTC	AGTTGATTAC ATAGAGTTTC	TGACTCATAG CAAGGAGTGC	CGACCCTAAA CTGGCGGATT

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ASIAN2_Ema	GTGCCCCGACC GTCTGTATAC AGAAG	TCAGTCAACT ATCTGACCAC	GCTGAGAGTG ACGTCCTCC	TTCTTAAGTC TTTCTCTCTC	CTGTGTGTAT TTCTTAGTAC
FOR_DS1535	GTGCCCCGACC GTCCGTATAC AGAAG	TCAGTCAACT ATCTGACCAC	GCTGAGAGTG ACGTCCTCC	TTCTTAAGTC TTTCTCTCTC	CTGTGTGTAT TTCTTAGTAC
MAM1_SP134	GTGCCCCGACC GTCCATATAC AGAAG	TCAGTCAACT ATCTGACCAC	GCTGAGAGTG ACGTCCTCC	TTCTTAAGTC TTTCTCTCTC	CTGTGTGTAT TTCTTAGTAC
MAST_B243_	GTGCCCCGACC GTCTGTATAC AAAAA	TCAGTCAATT ATCTGACCAC	GCTGAGAGTG ACGTCCTCC	TTCTTAAGTC TTTCTCTCTC	CTGTGTGTAT TTCTTAGTAC
SAV1_SE210	GTGCCCCGACC GTCCGTATAC AGAAG	TCAGTCAACT ATCTGACCAC	GCTGAGAGTG ACGTCCTCC	TTCTTAAGTC TTTCTCTCTC	CTGTGTGTAT TTCTTAGTAC

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ASIAN2_Ema	TTCTTAACTG AAACAGTAGC ATGGGG	CAGCCTGGAG AGAGAATCAA	AAAAGTGGTG TAGACATATC	TCAGAAAACA ACACCGACAG	AATATTTGGG AGTGATGTCC
FOR_DS1535	TTCTTAACTG AAAGAGTAGC ATGGGG	CAGCCTGGAG AGAGAATCAA	AAAAGTGGTG TAGACATATC	TCAGAAAAGA ACAGCAACAG	AATATTTGGG AGTGATGTCC
MAM1_SP134	TTCTTAACTG AAAGAGTAGC ATGGGG	CAGCCTGGAG AGAGAATCAA	AAAAGTGGTG TAGACATATC	TCAGAAAAGA ACAGCGACAG	AATATTTGGG AGTGATGTCC
MAST_B244_	TTCTTAACTG AAAGAGGAGC ATGGAA	CAGCCTGGAG AGAGAATCAC	AAAAGTGGTG TAGACATATC	TCAGAAAAGA ACAGCGACAG	AATATTTGG- AGTGATGTCC
SAV1_SE210	TTCTTAACTG AAAGAGTAGC ATGGGG	CAGCCTGGAG AGAGAATCAA	AAAAGTGGTG TAGACATATC	TCAGAAAAGA ACAGCGACAG	AATATTTGGG AGTGATGTCC

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ASIAN2_Ema	AGGTGACAGC CCGTGCGGAA AGCTTC	TGGGTCTGCA GGTAGCCTGG	AGTCTGTCCT TCTCCCTGTG	TTCTGATGGC GGAATTACCT	CACCAGCGCA GGCGTCTGCC
FOR_DS1535	AGGTGACAGC CCGTGCGGAA AGCTTC	TGGGTCTGCA GGTAGCCTGG	AGTCTGTCCT TCTCCCTGTG	TTCTGATGGC GGAATTACCT	CACCAGCGCA GGCGTCTGCC
MAM1_SP134	AGGTGACAGC CCGTGCGGAA AGCTTC	TGGGTCTGCA GGTAGCCTGG	AGTCTGTCCT TCTCCCTGTG	TTCTGATGGC GGAATTACCT	CACCAGCGCA GGCGTCTGCC
MAST_B245_	AGGTGAGAGC CTGTGCGGAA AGCTTC	TGGGTCTGCA GGTAACCTGG	AGTCTGTCCT TCTCCCTATG	TTCTGATGGC G-AATTACCT	CACCAGCGCA GGCGTCTGCC
SAV1_SE210	AGGTGACAGC CCGTGCGGAA AGCTTC	TGGGTCTGCA GGTAGCCTGG	AGTCTGTCCT TCTCCCTGTG	TTCTGATGGC GGAATTACCT	CACCAGCGCA GGCGTCTGCC

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ASIAN2_Ema	GCCCCGCC-T CTAGGCCTGT ATCTG	CCTGGCAGGT GCTCTGGAGG	CGATCACCTT GCCTCCAGGC	GACTGGTCGA TGGCCATCTC	GGCACCCGCA CCCCTCGAAC
FOR_DS1535	GCCCCGCC-T	CCTGGCAGGT	CGATCACCTT	GACTGGTCGA	GGCACCCGCA

	CTAGGCCTGT	GCTCTGGAGG	GCCTCCAGGC	TGGCCATCTC	CCCCTCGAAC
MAM1_SP134	ATCTG GCCCCGCC-T	CCTGGCAGGT	CGATCACCTT	GA CTGGT CGA	GGCACCCGCA
	CTAGGCCTGT	ACTCTGGAGG	GCCTCCAGGC	TGGCCATCTC	CCCCTCGAAC
MAST_B246_	ATCTG GCCCCGCCCT	CCTGGCAGGT	CGATCACCTT	GA CTGGT CGA	GGCACTCGCA
	CTAGGCCTGT	GCTCTGGAGG	GCCTCCAGGC	TGGCCATCTC	CCCCTCGAAC
SAV1_SE210	ATCTG GCCCCGCC-T	CCTGGCAGGT	CGATCACCTT	GA CTGGT CGA	GGCACCCGCA
	CTAGGCCTGT	GCTCTGGAGG	GCCTCCAGGC	TGGCCATCTC	CCCCTCGAAC
	ATCTG				

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ASIAN2_Ema	AACGAAGGTG	TTGTAATCAC	CTGTCAGACA	GGTGATTAGA	CCAGGCCATC
	TTCATCTCAC	CTCAGGGAAT	CTGTGACCTT	TGCCGTTGCA	CACGTGTCTG
	TCTGA				
FOR_DS1535	AACGAAGGTG	TTGTAATCAC	CTGTCAGACA	GGTGATTAGA	CCAGGCCATC
	TTCATCTCAC	CTCAGGGAAT	CTGTGACCTT	TGCCGTTGCA	CACGTGTCTG
	TCTGA				
MAM1_SP134	AACGAAGGTG	TTGTAATCAC	CTGTCAGACA	GGTGATTAGA	CCAGGCCATC
	TTCATCTCAC	CTCAGGGAAT	CTGTGACCTT	TGCCGTTGCA	CACGTGTCTG
	TCTGA				
MAST_B203_	AACAAAGGTG	TTGTAATCAC	CTGTCAGACA	GGTGATTAGA	CCAGGCCAGC
	TTCATCTCAC	CTCAGGGAAT	CTGTGACCTT	TGCCGTTGCA	CACGTGTCTG
	TCTGA				
SAV1_SE210	AACGAAGGTG	TTGTAATCAC	CTGTCAGACA	GGTGATTAGA	CCAGGCCATC
	TTCATCTCAC	CTCAGGGAAT	CTGTGACCTT	TGCCGTTGCA	CACGTGTCTG
	TCTGA				

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ASIAN2_Ema	GTTAGGAAAC	TTCCTCAGGG	AGAAGGTGGC	CAACAACGTG	GCTTTTACCA
	GAAGCACTTG	GAGCTTCTGG	TCTTCCTGAC	ACTTTATGTC	TTCAATCTCA
	TCTCTC				
FOR_DS1535	GTTAGGAAAC	TTCCTCAGGG	AGAAGGTGGC	CAACAACGTG	GCTTTTACCA
	GAAGCACTTG	GAGCTTCTGG	TCTTCCCGAC	ACTTTAKGTC	TTCAATCTCA
	TCTCTC				
MAM1_SP134	GTTAGGAAAC	TTCCTCAGGG	AGAAGGTGGC	CAACAACGTG	GCTTTTACCA
	GAAGCACTTG	GAGCTTCTGG	TCTTCCCGAC	ACTTTAKGTC	TTCAATCTCA
	TCTCTC				
MAST_B247_	GTTAGGAAAC	TTC-TCAGGG	AGAAGGTGGC	CAACAACGTG	GCTTTTACCA
	GAAGCACTTG	GAGCTTCTGG	TCTTCCCGAC	ACTTTATGTC	TTCAATCTCA
	TCTCTC				
SAV1_SE210	GTTAGGAAAC	TTCCTCAGGG	AGAAGGTGGC	CAACAACGTG	GCTTTTACCA
	GAAGCACTTG	GAGCTTCTGG	TCTTCCTGAC	ACTTTATGTC	TTCAATCTCA
	TCTCTC				

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ASIAN2_Ema	TCTGTCTTCC	TGAGTCCTAG	CATCCCTCAG	CTGCTAATGT	CTGAATTCTA
	ACTACCTTTC	ATGACCCATC	ATACAACATT	GTTCCATTTT	CTATGTAAGC
	ATCAT				
FOR_DS1535	TCTGTCTTCC	TGAGTCCTAG	CATCCTTCAG	CTGCTAATGT	CTAAATTCTA
	ACTACCTTTC	ATGACCCATC	AAACAACATT	GTTCCATTTT	CTATGTAAGC
	ATCTT				
MAM1_SP134	TCTGTCTTCC	TGAGTCCTAG	CATCCTTCAG	CTGCTAACGT	CTAAATTCTA
	ACTACCTTTC	ATGACCCATC	ATACAACATT	GTTCCATTTT	CTATGTAAGC
	ATCAT				
MAST_B248_	TTTGTCTTCC	TGAGTCCTAG	CATCCTTCAG	CTGCTAATGT	CTAAATTCTA
	ACTACCTTTC	ATGACCCATC	ATACAACATT	GTTCCATTTT	CTATGTAAGC
	ATCAT				
SAV1_SE210	TCTGTCTTCC	TGAGTCCTAG	CATCCTTCAG	CTGCTAATGT	CTAAATTCTA
	ACTACCTTTC	ATGACCCATC	ATACAACATT	GTTCCATTTT	CTATGTAAGC
	ATCAT				

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ASIAN2_Ema	TATGCCATCA CCCTGTCTTG AATAA	TAAGCCTTGG CACATCCATA	GGACCAAGTC TTATTTCTAA	AGTTATGCTG CATGATTTTG	AAAAATTCTG TATCTTTGCT
FOR_DS1535	TATGCCATCA CCCTGTCTTG ARTAA	TAAGCCTTGG CACATCCATA	GGACCAAGTC TTATTTCTAA	AGTTATGCTG CATGATTTTG	AAAAATTCTG TATCTTTGCT
MAM1_SP134	TATGCCATCA CCCTGTCTTG AATAA	TAAGCCTTGG CACATCCATA	GGACCAAGTC TTATTTCTAA	AGTTATGCTG CATGATTTTG	AAAAATTCTG TATCTTTGCT
MAST_B250_	TATGCCTTCA CCCTGTCTTG AATAA	TAAGCCTTGG CACATCCATA	GGACCAAGTC TTATTTCTAA	AGTTATGCTG CATGATTTTG	AAAAATTCTG TATCTTTGCT
SAV1_SE210	TATGCCATCA CCCTGTCTTG AATAA	TAAGCCTTGG CACATCCATA	GGACCAAGTC TTATTTCTAA	AGTTATGCTG CATGATTTTG	AAAAATTCTG TATATTTGCT

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ASIAN2_Ema	CCCATGGCAC CCTCCTTTTC CCAT	ATTTCAAAGT TGGTATAGTT	CTCAGCATT TTGGACCATT	GTGCTCACTG GAGAGCCAGG	GCTGATAGGA AGACAAAGRG
FOR_DS1535	CCCATGGCAC CCTCCTTTTC CCAT	ATTTCAAAGT TGGTATAGTT	CTCAGCATT TTGGACCATT	GTGCTCACTG GAGAGCCAGG	GCTGATAGGA AGACAAAGAG
MAM1_SP134	CCCATGGCAC CCTCCTTTTC CCAT	ATTTCAAAGT TGGTATAGTT	CTCAGCATT TTGGACCATT	GTGCTCACTG GAGAGCCAGG	GCTGATAGGR AGACAAAGAG
MAST_B251_	CCCATGGCAC CCTCCTTTTC CCAT	ATTTCAAAGT TGGTATAGTT	CTCAGCATT ATGGACCATT	GTGCTCACTG GAGAGCCAGG	GCTGATAGGA AGACAAAAG
SAV1_SE210	CCCATGGCAC CCTCCTTTTC CCAT	ATTTCAAAGT TGGTATAGTT	CTCAGCATT ATGGACCATT	GTGCTCACTG GAGAGCCAGG	GCTGATAGGA AGAAAAACAG

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ASIAN2_Ema	TCCCTTGGAG GACTTGGGAAG ACAC	GTGAAAAGTG AAAGGACTGG	CTGCTGACTC TGATCTACAT	AAAGCCTCCA CTGAAAATTC	GACTAAAAGA ACCAATGAAA
FOR_DS1535	TCCCTCGGAG GACTTGGGAAG ACAC	GTGAAAAGTG AAAGGCCTGG	CTGCTGACTC TGATCTACAT	AAAGCCTCCA CTGAAAATTC	GACTAAAAGA ACCAATGAAA
MAM1_SP134	TCCCTCGGAG GACTTGGGAAG ACAC	GTGAAAAGTG AAAGGCCTGG	CTGCTGACTC TGATCTACAT	AAAGCCTCCA CTGAAAATTC	GACTAAAAGA ACCAATGAAA
MAST_B205_	TCCCTCAGAG GACTTGGGAAG ACAC	GTGAAAAGTG AAAGGCCTGG	CTGCTGACTC TGATCTATAT	AAAGCCTCCA CTGAAAATTC	GACTAAAAGA ACCAATGAAA
SAV1_SE210	TCCCTCGGAG GACTTGGGAAG ACAC	GTGAAAAGTG AAAGGCCTGG	CTGCTGACTC TGATCTACAT	AAAGCCTCCA CTGAAAATTC	GACTAAAAGA ACCAATGAAA

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ASIAN2_Ema	CTCAACTTGT TTGGCCGATA AAGG	ACTGGCTTCA CTGTGAACAG	GAGACAACCA TGCTATCCAC	CATATATATT TGGTACTGCA	CGTATACTTC AAATTAGGCT
FOR_DS1535	CTCAACTTGT TTGGCCGATA AAGG	ACTGGCTTCA CTGTGAACAG	GAGACAACCA TGCTATCCAC	CATATATATT TGGTACTGCA	CGTATACTTC AAATTAGGCT
MAM1_SP134	CTCAACTTGT TTGGCCGATA AAGG	ACTGGCTTCA CTGTGAACAG	GAGACAACCA TGCTATCCAC	CATATATATT TGGTACTGCA	CGTATACTTC AAATTAGGCT
MAST_B253_	CTTAACTTGT TTGGCCAATA AAGA	ACTGGCTTCA CTGTGAACAG	GAGACAACCA TGCTATCCAC	CATATATATT TGGTACTGCA	CGTATACTTC AAATTAGGCT
SAV1_SE210	CTCAACTTGT	ACTGGCTTCA	GAGACAACCA	CATATRTATT	CGTATACTTC

TTGGCCGATA CTGTGAACAG TGCTATCCAC TGGTACTGCA AAATTAGGCT
AAGG

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ASIAN2_Ema	CCAGAGAAAC ACAGTTCAGG CCAT	TCACCTTTGA GTAGAGGTGT	GTGGCCAAAT GTGCACAGAC	GGGGATGAAC ATCAA-TAAG	AGGTGATAAG AGACTCCTTT
FOR_DS1535	CCAGAGAAAC ACAGTTCAGG CCAT	TCACCTTTGA GTAGAGGTGT	GTGGCCAAAT GTGCACAGAC	GGGGATGAAC ATCAA-TAAG	AGGTGATAAG AGACTCCTTT
MAM1_SP134	CCAGAGAAAC ACAGTTCAGG CCAT	TCACCTTTGA GTAGAGGTGT	GTGGCCAAAT GTGCACAGAC	GGGGATGAAC ATCAA-TAAG	AGGTGATAAG AGACTCCTTT
MAST_B256_	CCAGAAAAAC ACAGTTCAGG CCAT	TCACCTTTGA GTAGAGATGT	GTGGCCAAAT GTGCACAGAC	GGGGATGAAC ATCAAATAAA	AGGTGATAAG AGACTCCTTT
SAV1_SE210	CCAGAGAAAC ACAGTTCAGG CCAT	TCACCTTTGA GTAGAGGTGT	GTGGCCAAAT GTGCACAGAC	GGGGATGAAC ATCAA-TAAG	AGGTGATAAG AGACTCCTTT

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ASIAN2_Ema	TATAAGTCCC CAACCCTTGT AATG	ATCTAGCTGA GAGCACCTCC	CACACCCTCG CGTGTGCCGG	GTGGCCCAGC ACACCGTGCT	AGGGCTCCAA AAGAGCTAGG
FOR_DS1535	TATAAGTCCC CAACCCTTGT AATG	ATCTGGCTGA GAGCACATCC	CACACCCTCG -GTGTGCCGG	GTGGCCCAGC ACACCATGCT	AGGGCTCCAA AAGAGCTAGG
MAM1_SP134	TATAAGTCCC CAACCCTTGT AATG	ATCTGGCTGA GAGCACCTCC	CACACCCTCG CGTGTGCCGG	GTGGCCCAGC ACACCGTGCT	AGGGCTCCAA AAGAGCTAGG
MAST_B207_	TATAAGTCCC TAACCCTTGT AATA	ATCTGGCTGA GAGCACCTCC	CACACCCTCG CGTGTGCCGG	GTGGCCCAGC ATACCGTGTT	AGGGCTCCAG AAGAGCTAGG
SAV1_SE210	TATAAGTCCC CAACCCTTGT AATG	ATCTGGCTGA GAGCACATCC	CACACCCTCG -GTGTGCCGG	GTGGCCCAGC ACACCATGCT	AGGGCTCCAA AAGAGCTAGG

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ASIAN2_Ema	TTTCTGGAGC AAAGGTCCAC GCAG	CCTGGTGGTG AGTTCAAACC	C-AGTGGTTA CACCAGCCAT	AGAGCTATGG TCCTTGGA	CTGCTAACCA CTCTATAGGG
FOR_DS1535	TTTCTGGAGC AAAGGTCCAC GCAG	CCTGGTGGTG AGTTCAAACC	C-AGTGGTTA CACCAGCCAT	AGAGCTATGG TCCTTGGA	CTGCTAACCA CTCTATAGGG
MAM1_SP134	TTTCTGGAGC AAAGGTCCAC GCAG	CCTGGTGGTG AGTTCAAACC	C-AGTGGTTA CACCAGCCAT	AGAGCTATGG TCCTTGGA	CTGCTAACCA CTCTAYAGGG
MAST_B259_	TCTTTGGAGC AAAGGTCCAC TAAT	CCTGGTGGTG AGTTCAAATC	CCAGTGGTTA CACCAGCCAT	AGAGCTATGG TCCTTGGA	CTACAAACCA TCCGCGTGGG
SAV1_SE210	TTTCTGGAGC AAAGGTCCAC GCAG	CCTGGTGGTG AGTTCAAACC	C-AGTGGTTA CACCAACCAT	AGAGCTATGG TCCTTGGA	CTGCTAACCA CTCTATAGGG

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ASIAN2_Ema	TGGCTCCCTC TGCTGTGTCC AGAG	CGAAGAAAGG CCTTGGGGGT	GTGGAAGAAG GGGGAGGCTG	GGCGGGTCCA GAGGGCACAG	GCAACCACAC GAGGAGTTCC
FOR_DS1535	TGGCTCCCTC TGCTGGGTCC AGAG	CGAAGAAAGG CCTTGGGGGT	GTGGAAGAAG GGGGAGGCTG	GGCGGGTCCA GAGGGCACAG	GCAACCACAC GAGGAGTTCC
MAM1_SP134	TGGCTCCCTC TGCTGTGTCC	CGAAGAAAGG CCTTGGGGGT	GTGGAAGAAG GGGGAGGCTG	GGCGGGTCCA GAGGGCACAG	GCAACCACAC GAGGAGTTCC

MAST_B260_	AGAG TGGTTCCTC TGCTGTGTCC AAAA	CGAAGAAAGG CCTTGGGGGT	GTGGAAGAAG GGGAAGGCTG	GGCGGGTCCA AAAGACACAA	GCAACCACAC GAAAAATTCC
SAV1_SE210	TGGCTCCCTC TGCTGGGTCC AGAG	CAAAGAAAGG CCTTGGGGGT	GTGGAAGAAG GGGGAGGCTG	GGCGGGTCCA GAGGGCACAG	GCAAYCACAC GAGGAGTTCC

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ASIAN2_Ema	CAAATCCAGA CAGTGAGGAA ATAG	GGAAGGCTAG GAAC TTT-CC	AGGAAGTCAA AA-GAAGCCA	TTCTAGAAGC CCAAAAAACC	TGTCTCAGAA AAACTGGGTC
FOR_DS1535	CAAATCCAGA CAGTGAGGAA ATAG	GGAAGGCTAG GAAC TTT-CC	AGGAAGTCAA AA-GAAGCCA	TTCTAGAAGC CCAAAAAACC	TGTCTCAGAA AAACTGGGTC
MAM1_SP134	CAAATCCAGA CAGTGAGGAA ATAG	GGAAGGCTAG GAAC TTT-CC	AGGAAGTCAA AA-GAAGCCA	TTCTAGAAGC CCAAAAAACC	TGTCTCAGAA AAACTGGGTC
MAST_B261_	TAAATCCAGA CAGTGAGGAA ATAA	GGAAGGCTAG GAAC TTTTCC	AGGAAGTCAA AAAGAAGCCA	TTCTAGAAGC CCAAAAAACC	TGTCTCAGAA AAACTGGGTC
SAV1_SE210	CAAATCCAGA CAGTGAGGAA ATAG	GGAAGGCTAG GAAC TTT-CC	AGGAAGTCAA AA-GAAGCCA	TTCTAGAAGC CCAAAAAACC	TGTCTCAGAA AAACTGGGTC

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ASIAN2_Ema	CCYGGCCTGG ACTCACTGTC TATG	AGCAAGTAAG ACTTTGGGCT	GCTCTCAACT CAGATCCTTA	CACGAACTGC GACTTCGGGA	ACACTTTTAA GCCGGTTTCT
FOR_DS1535	CCCGGCCTGG ACTCACTGTC TATG	AGCAAGTAAG ACTTTGGGCT	GCTCTCAACT CAGATCCTTA	CACGAACTGC GACTTCGGGA	ACACTTTTAA GCCGGTTTCT
MAM1_SP134	CCCGGCCTGG ACTCACTGTC TATG	AGCAAGTAAG ACTTTGGGCT	GCTCTCAACT CAGATCCTTA	CACGAACTGC GACTTCGGGA	ACACTTTTAA GCCGGTTTCT
MAST_B262_	TCCGGCTTGG ACTCACTGTC TATA	AGCAAGTAAG ACTTTGGGCT	GCTCTCACCT CAGATCCTTA	CACGAACTGC GACTTCGGGA	ACACTTATAA GCCAGTTTCT
SAV1_SE210	CCCGGCCTGG ACTCACTGTC TATG	AGCAAGTAAG ACTTTGGGCT	GCTCTCAACT CAGATCCTTA	CAGGAACTGC GACTTCGGGA	ACACTTTTAA GCCGGTYTCT

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ASIAN2_Ema	TAAGGTGGGG	TGCCCCAGCG	CACACCTCTG	ATGAAAACAG	GCTACGCACG
FOR_DS1535	TAAGGTGGGG	TGCCCCAGCG	CACACCTCTG	ATGAAAACAG	GCTACGCACG
MAM1_SP134	TAAGGTGGGG	TGCCCCAGCG	CACACCTCTG	ATGAAAACAG	GCTACGCACG
MAST_B264_	TAAGGTGGGG	TGCCCCAGCG	CACACCTCTG	ATGAAAACAG	GCTACGCACG
SAV1_SE210	TAAGGTGGGG	TGCCCCAGCG	CACACCTCTG	ATGAAAACAG	GCTACGCACG

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ASIAN2_Ema	CAGAAAGCTC ATAGAAGACC CAGC	C-GGAAGCCT CCCAGAGAGA	TGCCAACAGC AAGGCTGCTG	CCTGGAGGCT ATGGCCAGGC	GAGTCCAGAA TGCCCTCTGC
FOR_DS1535	CAGAAAGCTC ATAGAAGACC CAGC	C-GGAAGCCT CCCAGAGAGA	TGCCAACAGC AAGGCTGCTG	CCTGGAGGCT ATGGCCAGGC	GAGTCCAGAA TGCCCTCTGC
MAM1_SP134	CAGAAAGCTC ATAGAAGACC CAGC	C-GGAAGCCT CCCAGAGAGA	TGCCAACAGC AAGGCTGCTG	CCTGGAGGCT ATGGCCAGGC	GAGTCCAGAA TGCCCTCTGC
MAST_B209_	CAGAAAGTTT ATAGAAGACC CAGC	TTAGAAGTTT CCCAGAGAGA	TGCCAACAGC AAGGCTGCTG	CCTGGAGGCT ATGGCCAGGC	GAGTCCAGAA TGCCCTCTGC
SAV1_SE210	CAGAAAGCTC	C-GGAAGCCT	TGCCAACAGC	CCTGGAGGCT	GAGTCCAGAA

ATAGAAGACC CCCAGAGAGA AAGGCTGCTG ATGGCCAGGC TGCCCTCTGC
CAGC

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ASIAN2_Ema	GCTTATTCTT GTGGGATAGC TGAT	CTTTCCTGTT CTCTTCTCTC	GAAAGAAAAA TCCTTCCTCA	-GCTTT-AAT TCTCCATTTT	TTCAAGCTCT AATCAATTAA
FOR_DS1535	GCTTATTCTT GTGGGATAGC TRAT	CTTTCCTGTT CTCTTCTCTC	GAAAGAAAAA TCCTTCCTCA	-GCTTT-AAT TCTCCATTTT	TTCAAGCTCT AATCAATTAA
MAM1_SP134	GCTTATTCTT GTGGGATAGC TGAT	CTTTCCTGTT CTCTTCTCTC	GAAAGAAAAA TCCTTCCTCA	-GCTTT-AAT TCTCCATTTT	TTCAAGCTCT AATCAATTAA
MAST_B210_	GCTTATTCTT GTGGGATAGC TGAT	CTTTCCTGTT CTCTTCTCTT	GAAAGAAAAA TCCTTCCTCA	AGCTTTTAAT TCTCCATTTT	TTCAAGCTCT AATCAATTAA
SAV1_SE210	GCTTATTCTT GTGGGATAGC TGAT	CTTTCCTGTT CTCTTCTCTC	GAAAGAAAAA TCCTTCCTCA	-GCTTT-AAT TCTCCATTTT	TTCAAGCTCT AATCAATTAA

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ASIAN2_Ema	CTCAGGGTCA GACCATTTTA TTAC	GGAGATGGAT AGTTCTTTAA	GTGAGTCTAA TCACCCTGAT	ACGTTGGCCT CTCAATTCT	TCGTAAGTGT TATCCTTATT
FOR_DS1535	CTCAGGGTCA GACCATTTTA TTAC	GGAGATGGAT ARTTCTTTAA	GTGAGTCTAA TCACCCTGAG	ACGTTGGCCT CTCAATTCT	TCGTAAGTGT TATCCTTATT
MAM1_SP134	CTCAGGGTCA GACCATTTTA TTAC	GGAGATGGAT AGTTCTTTAA	GTGAGTCTAA TCACCCTGAT	ACGTTGGCCT CTCAATTCT	TCGTAAGTGT TATCCTTATT
MAST_B265_	CTCAGGGTCA GACCATTTTA TTAC	GGAGATGGAT AGTTCTTTAA	CTGAGTCTAA TCACCCTGAG	ACGTTGGCCT CTCAATTCT	TCGTAAGTGT TATCCTTATT
SAV1_SE210	CTCAGGGTCA GACCATTTTA TTAC	GGAGATGGAT AGTTCTTTAA	GTGAGTCTAA TCACCCTGAG	ACGTTGGCCT CTCAATTCT	TCGTAAGTGT TATCCTTATG

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ASIAN2_Ema	TCAGGAGCTC TCTGCTAGAT CTC	TCTGGTCCTG ATCTGCAGAC	CAGCTCTGTC AAAGTTCCCG	CTCGGCCAAG TGACCTCCA	CACAGCCCAG ATGGCCTCAT
FOR_DS1535	TCAGGAGCTC TCTGCTAGAC CTC	TCTGCTCCTG ATCTGCAGAC	CAGCTCTGTC AAAGTTCCCG	CTCGGCCAAG TGACCTCCA	GACAGCCCAG ATGGCCTCAT
MAM1_SP134	TCAGGAGCTC TCTGCTAGAT CTC	TCTGGTCCTG ATCTGCAGAC	CAGCTCTGTC AAAGTTCCCG	CTCGGCCAAG TGACCTCCA	GACAGCCCAG ATGGCCTCAT
MAST_B267_	TCAGGAGCTC TCTGCTAGAC CTC	TCTGCTCCTG ATTTGCAGAC	CAGCTCTGTC AGACTTTCCG	CTCGGCCAAG TGACCTCCC	GACAGCCCAG ATGGCCTCAT
SAV1_SE210	TCAGGAGCTC TCTGCTAGAC CTC	TCTGCTCCTG ATCTGCAGAC	CAGCTCTGTC AAAGTTCCCG	CTCGGCCAAG TGACCTCCA	GACAGCCCAG ATGGCCTCAT

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ASIAN2_Ema	TGTGGTTATT AGGTCARGAC ACC	TAATAAATGT CATATCTGTG	CACTGTCCCC TTGGTCACCA	ACTAGACTGC GGGTATTCT	AAGCTGCATG AGTGCCTAGC
FOR_DS1535	TGTGGTTATT AGGTCAGGAC ACC	TAATAAATGT CATATCTGTG	CACTGTCCCC TTGGTCACCA	ACTAGACTGC GGGTATTCT	AAGCTGCATG AGTGCCTAGC
MAM1_SP134	TGTGGTTATT AGGTCAGGAC	TAATAAATGT CATATCTGTG	CACTGTCCCC TTGGTCACCA	ACTAGACTGC GGGTATTCT	AAGCTGCATG AGTGCCTAGC

MAST_B269_	ACC TGTGGTTATT AGGTCAGGAC	TAATAAATGT CTTATCTGTG	CACTGTCCCC TTGGTCACCA	ACTAGACTGC GGGTATTCCC	AAGCTGTATG AGTGCCTAGC
SAV1_SE210	ACC TGTGGTTATT AGGTCAGGAC	TAATAAATGT CATATCTGTG	CACTGTCCCC TTGGTCACCA	ACTAGACTGC GGGTATTCTT	AAGCTGCATG AGTGCCTAGC

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ASIAN2_Ema	AAGTGTTTAT ATACACACAC GTGGCT	CCATATAGTG TCATGCACAC	TGACTCACAG ACATTGCCCC	ATGTCCCCC TAGTCCCAGC	ACACACACAC TGAGCTCACA
FOR_DS1535	AAGTGTTTAT ATACACACAC GTGGCT	CCATATAGTG TCATGCACAC	TGACTCACAG ACATTGCCCC	ATGTCCCCC TAGTCCCAGC	ACACACACAC TGATCTCACA
MAM1_SP134	AAGTGTTTAT ATACACACAC GTGGCT	CCATATAGTG TCATGCACAC	TGACTCACAG ACATTGCCCC	ATGTCCCCC TAGTCCCAGC	ACACACACAC TGAGCTCACA
MAST_B211_	AAGTGTTTAT ATACACACAC GTGGCT	CCATATAGTG TCATGCACAC	TGACTCACAG ACATTGCCC-	ATGTCCCCC TAGTCC-AGC	C-ACACACAC TGATCTCACA
SAV1_SE210	AAGTGTTTAT ATACACACAC GTGGCT	CCATATAGTG TCATGCACAC	TGACTCACAG ACATTGCCCC	ATGTCCCCC TAGTCCCAGC	CCACACACAC TGAGCTCACA

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ASIAN2_Ema	AACATTTGAG CAGAAGGTCT TCA	CCAAGATCTC TGTTACATC	CCTGTCTAGT TGGGCAGCCG	TTGAAGCTGA CTCTTCTTTT	GACAGTTGAA TATCTTTATT
FOR_DS1535	AACATTTGAG CAGAAGGTCT TCA	CCAAGATCTC TGTTACATC	CCTGTCTAGT TGGGCAGCCG	TTGAAGCTGA CTCTTCTTTT	GACAGTTGAA TATCTTTATT
MAM1_SP134	AACATTTGAG CAGAAGGTCT TCA	CCAAGATCTC TGTTACATC	CCTGTCTAGT TGGGCAGCCG	TTGAAGCTGA CTCTTCTTTT	GACAGTTGAA TATCTTTATT
MAST_B212_	AACATTTGAG CAGAAGGTCT TCA	CCAAGATCTC TGTTACATC	TTTGTCTAGT TGGGCAGCTG	TTGAAGCTGA CTCTTCTTTT	GACAGTTGAA TATCTTTATT
SAV1_SE210	AACATTTGAG CAGAAGGTCT TCA	CCAAGATCTC TGTTACATC	CCTGTCTAGT TGGGCAGCCG	TTGAAGCTGA CTCTCCTTTT	GACAGTTGAA TATCTTTATT

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ASIAN2_Ema	TGACCCCTCC TAGACCTT-A AAAT	AGACA-TTTG TTGCAAGCTG	AGAGACACCA GTCAAGCAAG	AGCCTTTGAG GAGCTCAGAG	AAAGAGAAAG ACTAAGTCTC
FOR_DS1535	TGACCCCTCC TAGACCTT-A AAAT	AGACA-TTTG TTGCAAGCTG	AGAGACACCA GTCAAGCAAG	GGCCTTTGAG GAGCTCAGAG	AAAGAGAAAG ACTAAGTCTC
MAM1_SP134	TGACCCCTCC TAGACCTT-A AAAT	AGACA-TTTG TTGCAAGCTG	AGAGACACCA GTCAAGCAAG	AGCCTTTGAG GAGCTCAGAG	AAAGAGAAAG ACTAAGTCTC
MAST_B271_	TTCGCCCTCC T-GACCTTTA AAAC	AGTCAATTAG CCGTAAGCTG	AGAAACACTA GTCAAGCAAG	GGCCTTTGAG GAGCTCAGAG	GAGGAGAAAG ACTAAGTCTC
SAV1_SE210	TGACCCCTCC TAGACCTT-A AAAT	AGACA-TTTG TTGCAAGCTG	AGAGACACCA GTCAAGCAAG	GGCCTTTGAG GAGCTCAGAG	AAAGAGAAAG ACTAAGTCTC

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ASIAN2_Ema	TCCATTAAAR AGCAATAGAT CAG	CCATGATGTA CATCAAAGT	CAGGCCTTGA GCTGCACAGT	GTCAGAAAGA TTCAGCAAA-	GCTGGGGAAG GAAAGCCAGT
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FOR_DS1535	TCCATTAAAG AGCAATAGAT CAG	CCATGATGCA CATCAAACCTG	CAGGCCTTGA GCTGCACAGT	GTCAGAAAGA TTCAGCAAAA-	GCTGGGGAAG GAAAGCCAGT
MAM1_SP134	TCCATTAAAG AGCAATAGAT CAG	CCATGATGTA CATCAAACCTG	CAGGCCTTGA GCTGCACAGT	GTCAGAAAGA TTCAGCAAAA-	GCTGGGGAAG GAAAGCCAGT
MAST_B273_	TCCATTAAAG AGCAACAGAT CAA	CCATGATGCA CATCAAATTG	CAGGCCTTGA GCTACACAAT	GTCAGAAAGA TTCAGCAAAA	GCTGGGGAAG GAAAACCCAGT
SAV1_SE210	TCCATTAAAG AGCAATAGAT CAG	CCATGATGCA CATCAAACCTG	CAGGCCTTGA GCTGCACAGT	GTCAGAAAGA TTCAGCAAAA-	GCTGGGGAAG GAAAGCCAGT

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ASIAN2_Ema	CTCACTCCCC GGTCCCCAAG GGT	AGTCAGGGTG GTCCCTGGGC	CAGCCAGGTA CATGATGCCC	GAAATGGAAG CCCAGAACGA	TCACCGTCCA ACCTGTTGTT
FOR_DS1535	CTCACTCCCC GGTCCCCAAG GGT	AGTCAGGGTG GTCCCTGGGC	CAGCCAGGTA CATGATGCCC	GAAATGGAAG CCCAGAACGA	TCACCGTCCA ACCTGTTGTT
MAM1_SP134	CTCACTCCCC GGTCCCCAAG GGT	AGTCAGGGCG GTCCCTGGGC	CAGCCAGGTA CATGATGCCC	GAAATGGAAG CCCAGAACGA	TCACCGTCCA ACCTGTTGTT
MAST_B214_	TTCACCTCCCC GGTCCCCAAG GGT	AGTCAGGGTG GTCCCTGGGC	CAGCCAGGTA CATGATCGCC	GAAATGGAAG CCCAGAACGA	TCACCGTCCA ACCTGTTGTT
SAV1_SE210	CTCACTCCCC GGTCCCCAAG GGT	AGTCMGGGTG GTCCCTGGGC	CAGCCAGGTA CATGATGCCC	GAAATGGAAG CCCAGAACGA	TCACCGTCCA ACCTGTTGTT

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ASIAN2_Ema	AGGTCTCTTT AGGCTTTTCC AGC	CTTCATGTCG TAACTTCCCT	CCTTGGCCCA TCCCAGTGGG	AACATCTAGG ATTCTTAATT	CTTACCACTT AGGTAGGTTT
FOR_DS1535	AGGTCTCTTT AGGCTTTTCC AGC	CTTCATGTCG TAACTTCCCT	CCTTGGCCCA TCCCAGTGGG	AACATCTAGG ATTCTTAATT	CTTACCACTT AGGTAGGTTT
MAM1_SP134	AGGTCTCTTT AGGCTTTTCC AGC	CTTCATGTCG TAACTTCCCT	CCTTGGCCCA TCCCAGTGGG	AACATCTAGG ATTCTTAATT	CTTACCACTT AGGTAGGTTT
MAST_B277_	AGGTCTCTTT AGGCTTTTCC AAC	CTTTATGTCG TAACTTCCCT	CCTTGGCCCA TCCCAATGAA	AACATCTAGG ATTCTTAATT	CTTACCACTT AAATAAATTT
SAV1_SE210	AGGTCTCTTT AGGCTTTTCC AGC	CTTCATGTCG TAACTTCCCT	CCTTGGCCCA TCCCAGTGGG	AACATCTAGG ATTCTTAATT	CTTACCACTT AGGTAGGTTT

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ASIAN2_Ema	CTGCTAGGCA GTGGGARCTG AGC	GTTTTCAAAG CTCAGAGAAA	CATCTTTGAG TGATACTGTA	TATATTGGGG TGTGGAGGGG	CCCGCCAGG TGCCTAGCC
FOR_DS1535	CTGCTAGGCA GTGGGAGCTG AGC	GTTTTCAAAG CTCAGAGAAA	CATCTTTGAG TGATACTGTA	TATATTGGGG TGTGGAGGGG	CCCGCCAGG TGCCTAGCC
MAM1_SP134	CTGCTAGGCA GTGGGAGCTG AGC	GTTTTCAAAG CTCAGAGAAA	CATCTTTGAG TGATACTGTA	TATATTGGGG TGTGGAGGGG	CCCGCCAGG TGCCTAGCC
MAST_B278_	CTGCTAGGCA GTGGGAGCTG AGC	GTTTTCAAAG CTCAAAGAAA	CATTTTTGAC TGATACTGTA	TATATTGGGG TGTGGTGGGG	CCCGCCAGG TGCCTAGCC
SAV1_SE210	CTGCTAGGCA GTGGGAGCTG AGC	GTTTTCAAAG CTCAGAGAAA	CATCTTTGAG TGATACTGTA	TATATTGGGG TGTGGAGGGG	CCCGCCAGG TGCCTAGCC

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ASIAN2_Ema	GGGATGGAAG TGGTGGTTGT CACA	ATTCTCCAAG TAGCTGTTCT	GACYGGGGAA GGAGTCGCTC	GAGGACAAAC TGACTCAGGG	TGGAGAACAG CAACCCCATG
FOR_DS1535	GGGATGGAAG TGGTGGTTGT CACA	ATTCTCCAAG TAGCTGTTCT	GACTGGGGAA GGAGTCGCTC	GAGGACAAAC TGACTCAGGG	TGGAGAACAG CAACCCCATG
MAM1_SP134	GGGATGGAAG TGGTGGTTGT CACA	ATTCTCCAAG TAGCTGTTCT	GACTGGGGAA GGAGTCACTC	GAGGACAAAC TGACTCAGGG	TGGAGAACAG CAACCCCATG
MAST_B279_	GGGATGGAAG TGGCGGTTTT CACA	ATTCTCCAAG TAGCTGTTCT	GACTGGG-AA GGAGTCGCTC	GAGGACAAAC TGACTCAGGG	TGGAGAACAG CAACCCCATG
SAV1_SE210	GGGATGGAAG TGGTGGTTGT CACA	ATTCTCCAAG TAGCTGTTCT	GACTGGGGAA GGAGTCGCTC	GAGGACAAAC TGACTCAGGG	TGGAGAACAG CAACCCCATG

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ASIAN2_Ema	GTGAGGTGCC CTTGCCAGAG GCAC	TCTGGGCACT CAGGGCAGAG	CATCAGAAGA GCCACAGGCC	GCAAAAAGAG AGAGAGAGGC	CTTTGTAACA ATACTTGTGA
FOR_DS1535	GTGAGGTGCC CTTGCCAGAG GCAC	TCTGGGCACT CAGGGCAGAG	CATCAGAAGA GCCACAGGCC	GCAAAAAGAG AGAGAGAGGC	CTTTGTAACA ATACTTGTGA
MAM1_SP134	GTGAGGTGCC CTTGCCAGAG GCAC	TCTGGGCACT CAGGGCAGAG	CATCAGAAGA GCCACAGGCC	GCAAAAAGAG AGAGAGAGGC	CTTTGTAACA ATACTTGTGA
MAST_B281_	GTGAGGTGCC CTTGCTAGAG GCAC	TCTGGGCACT CAGG-CAGAG	CATCAGAAGA GCCACAGGCC	GCAAAA-GAG AGAGAGAGGC	CTTGTAACA ATACTTGTGA
SAV1_SE210	GTGAGGTGCC CTTGCCAGAG GCAC	TCTGGGCACT CAGGGCAGAG	CATCAGAAGA GCCACAGGCC	GCAAAAAGAG AGAGAGAGGC	CTTTGTAACA ATACTTGTGA

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ASIAN2_Ema	TGTATTATCT GCATTTACAG AAG	CATTTAATCC AGGCAACATT	TTT-CAGCAG TGTGATTTTG	CCCT-GCCAG ACTCTTTGAA	TTGGCCATA AACAACTCCA
FOR_DS1535	TGTATTATCT GCATTTACAG AAG	CATTTAATCC AGGCAACATT	TTT-CAGCAG TGTGATTTTG	CCCT-GCCAG ACTCTTTGAA	TTGGCCATA AACAACTCCA
MAM1_SP134	TGTATTATCT GCATTTACAG AAG	CATTTAATCC AGGCAACATT	TTT-CAGCAG TGTGATTTTG	CCCT-GCCAG ACTCTTTGAA	YTGGCCATA AACAACTCCA
MAST_B215_	TGTATTATCT GCATTTACAG AAA	CATTTAATTC AGACAACATT	TTTTCAGCAG TGTGATTTTG	CCCTCGCCAG ACTCTT-GAA	TTGGCCATA AACAACTCCA
SAV1_SE210	TGTATTATCT GCATTTACAG AAG	CATTTAATCC AGGCAACATT	TTT-CAGCAG TGTGATTTTG	CCCT-GCCAG ACTCTTTGAA	TTGGTCCATA AACAACTCCA

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ASIAN2_Ema	GGCCCAATTG CTGAGACATG GG	GTTCTCTGAG GGAAGAAATG	ATTCCGCAAG GCCTAGGGCC	CCACTGTTGC CATGCTATAC	TGCCTGGACC TCTTGTTGAG
FOR_DS1535	GGCCCAATTG CTGAGACATG GG	GTTCTCTGAG GGAAGAAATG	ATTCCGCAAG GCCTAGGGCC	CCACTGTTGC CATGCTATAC	TGCCTGGACC TCTTGTTGAG
MAM1_SP134	GGCCCAATTG CTGAGACATG GG	GTTCTCTGAG GGAAGAAATG	ATTCCGCAAG GCCTAGGGCC	CCACTGTTGC CATGCTATAC	TGCCTGGACC TCTTGTTGAG
MAST_B283_	GGCCCAATTG CTGAGATATG GA	GTTCTCTGAG GGAAGAAATG	ATTCTGTAAG GCCTAGGGCC	CCACTGTTGC CATGCTATAC	TGCCTGGACC TCTTGTTGAA

SAV1_SE210 GGCCAATTG GTTCTCTGAG ATTCCGCAAG CCACTGTTGC TGCCTGGACC
CTGAGACATG GGAAGAAATG GCCTAGGGCC CATGCTATAC TCTTGTTGAG
GG

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ASIAN2_Ema AAAGACGGAG ACACTGTGTT CCTGAGGCGA TTTACCTCTG ATCTCTGTCT
CTGTACCTC TGGACTGGTG CTCAGGGCCT TGCTGAGGAG CTGAGGGGG-
CA

FOR_DS1535 AAAGACGGAG ACACTGTGTT CCTGAGGCGA TTTACCTCTG ATCTCTGTCT
CTGTACCTC TGGACTGGTG CTCAGGGCCT TGCTGAGGAG CTGAGGGGG-
CA

MAM1_SP134 AAAGACGGAG ACACTGTGTT CCTGAGGCGA TTTACCTCTG ATCTCTGTCT
CTGTACCTC TGGACTGGTG CTCAGGGCCT TGCTGAGGAG CTGAGGGGG-
CA

MAST_B284_ AAAGACGGAG ACACTGTGTT CCTGAGGCGA TTTACCTCTG ATCTCTGTCT
CTGTACCTC TGGACTGGTG CTCAGGGCCT TGCTGAGGAG CTAAGAAAA
CA

SAV1_SE210 AAAGACGGAG ACACTGTGTT CCTGAGGCGA TTTACCTCTG ATCTCTGTCT
CTGTACCTC TGGACTGGTG CTCAGGGCCT TGCTGAGGAG CTGAGGGGG-
CA

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ASIAN2_Ema TTTTGATTGA TGTA AAAATCC AGTGACCCAA GGGAGGAAGC CCTAATGTTA
GACTTCTCAC CAACTGTGGG TGGGATTTGG GACCAGATTT AAA-TAAATT
TGGA

FOR_DS1535 TTTTGATTGA TGTA AAAATCC AGTGACCCAA GGGAGGAAGC CCTAATGTTA
GACTTCTCAC CAACTGTGGG TGGGATTTGG GACCAGATTT AAA-TAAATT
TGGA

MAM1_SP134 TTTTGATTGA TGTA AAAATCC AGTGACCCAA GGGAGGAAGC CCTAATGTTA
GACTTCTCAC CAACTGTGGG TGGGATTTGG GACCAGATTT AAA-TAAATT
TGGA

MAST_B285_ TTTTGATTGA TGTA AA-TCC AGTGACCCAA AGGAGGAAGC CCTAATGTTA
GACTTCTCAC CAACTGTGGG TGGGATT-GG GACCAAATTT AAAATAAAGT
TTAA

SAV1_SE210 TTTTGATTGA TGTA AAAATCC AGTGACCCAA GGGAGGAAGC CCTAATGTTA
GACTTCTCAC CAACTGTGGG TGGGATTTGG GACCAGATTT AAA-TAAATT
TGGA

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ASIAN2_Ema AATTATTAGA GCAAATTTGC TCATACATTT TGCTGAATAT TCAAAATAAT
TCATGTTTCC TCCCCTCTT TAACATAAGA GCTTTGGGTA GGCTTTCCCT
TG

FOR_DS1535 AATTATTAGA GCAAATTTGC TCATACATTT TCCTGAATAT TCAAAATAAT
TCATGTTTCC TCCCCTCTT TAACATAAGA GCTTTGGGTA GGCTTTCCCT
TG

MAM1_SP134 AATTATTAGA GCAAATTTGC TCATACATTT TGCTGAATAT TCAAAATAAT
TCATGTTTCC TCCCCTCTT TAACATAAGA GCTTTGGGTA GGCTTTCCCT
TG

MAST_B286_ AATTATTAGA GCAAATTTGC TTATACATTT TGCTGAATAT TCAAAATAAT
TCATGTTTCC TCCCCTCTT TAACATAAGA GCTTTGGGTA GGCTTTCCCT
TG

SAV1_SE210 AATTATTAGA GCAAATTTGC TCATACATTT TGCTGAATAT TCAAAATAAT
TCATGTTTCC TCCCCTCTT TAACATAAGA GCTTTGGGTA GGCTTTCCCT
TG

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ASIAN2_Ema ACCAAGACAG ATCCTGAGCC TTCGAAGAGG CTGCCACACT GCCCAGCGG
CCCCACACGC CAGGGGCTGG AAGTGGGCTC GCTTAGGGCA GGGACACCTC
TC

FOR_DS1535 ACCAAGACAG ATCCTGAGCC TTCGAAGAGG CTGCCACACT GCCCAGCGG
CCCCACACGC CAGGGGCTGG AAGTGGGCTC GCTTAGGGCA GGGRCACCTC
TC

MAM1_SP134 ACCAAGACAG ATCCTGAGCC TTCGAAGAGG CTGCCACACT GCCCAGCGG

	CCCCACACGC	CAGGGGYTGG	AAGTGGGCTC	GCTTAGGGCA	GGGACACCTC
MAST_B287_	TC	ATTAAGATAG	ATCCCGAGCC	TTCGAAGAGG	GTGCCACACT
	CCCCACACGC	CAGGGGCTGG	AAGTGGTCTC	GCTTAGGGCA	GGGACACCTC
SAV1_SE210	TC	ACCAAGACAG	ATCCTGAGCC	TTCGAAGAGG	CTGCCACACT
	CCCCACACGC	CAGGGRCTGG	AAGTGGGCTC	GCTTAGGGCA	GGGACACCTC
	TC				
1 1 1 1 1					
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ASIAN2_Ema	TCCTACACAG	CTCAGTTCGC	CTGACTGCAG	CTTTCTGAGT	TCACCTAGTG
	CTTCTCCCAG	ACAAAATCAT	GACTAAGCAG	AGGCAAAATT	CATGTTATGC
	TC				
FOR_DS1535	TCCTACACAG	CTCAGTTCGC	CTGACTGCAG	CTTTCTGAGT	TCACCTAGTG
	CTTCTCCCAG	ACAAAATCAT	GACTAAGCAA	AGGCAAAATT	CATGTTATGC
	TC				
MAM1_SP134	TCCTACACAG	CTCAGTTCGC	CTGACTGCAG	CTTTCTGAGT	TCACCTAGTG
	CTTCTCCCAG	ACAAAATCAT	GACTAAGCAA	AGGCAAAATT	CATGTTATGC
	TC				
MAST_B288_	TTTTATACAG	CTCAGGTCGC	CTGACTGCAG	CTTTCTGAGT	TGACCTAGTG
	CTTCTGCCAG	ACAAAATCAT	GACTAAGCAA	AGGCAAAATT	CATGTTATGC
	TC				
SAV1_SE210	TCCTACACAG	CTCAGTTCGC	CTGACTGCRG	CTTTCTGAGT	TCACCTAGTG
	CTTCTCCCAG	ACAAAATCAT	GACTAAGCAA	AGGCAAAATT	CATGTTATGC
	TC				