

1110.000	GACGAGAAGCTGTATCCCTTTTGTGAGG...TTGTGCGCCCTTGAATTTGAGGCGCTGCAGACATGGAATT GACGAGAAGCTGTATCCCTTTTGTGAGG...GGCTGCGCCCTTGAATTTGAGGCGCTGCAGACATGGAATT GATGAGAAGCTGTATCCCTTTTGTGAGG...GGCTGCGCCCTTGAATTTGAGGCGCTGCAGACATGGAATT	Hsap NM_005072 123 Mmus NM_009195 123 Rnor NM_019229 123	01 1 0 OK 11 2 0 OK 11 3 0 OK
1110.001	GCCATTTCATATCCTTTCATGACC...CATATCGCCTTAAATGGATCGGCCAATTTTCAGCAT CAGTCCATTATATCCTTTCATGACC...AACATATCGCCTTAAATGGATCGGCCAATTTTCAGCAT CTGTCCATTATATCCTTTCATGACC...AGTGCCTGCGCCTTAAATGGATCGGCCAATTTTCAGCAT CTGTCCATTATATCCTTTCATGACC...GCGGGTCTGCGCCTTAAATGGATCGGCCAATTTTCAGCAT	Hsap NM_014139 i02 Hsap NM_014139 i02_fixed Mmus NM_011887 i03 Rnor NM_019265 i03	01 1 2 OK? 11 1 2 OK 11 1 2 OK 11 1 1 OK
1110.002	AGGACTCAAGGTATCCTTGAAGTGT...AAGTAACTTCTCTCTTACTCTCTACAGCTGACACAT AGGACTCAAGGTATCCTTGAAGTGT...CAGGTGTTTCTTCTCTTACTCTCTACAGCTGATACAT AGGACTCAAGGTATCCTTGAAGTGT...TGAAGATTTATTTCTTACTCTCTACAGCTGATACAT	Hsap NM_022048 i06 Mmus NM_173185 i07 Rnor NM_022288 i08	10 0 0 OK 11 2 2 OK 01 2 2 OK
1110.004	TATATAACGATATCCTTCTTCAAGT...CTGTGCGCCTTGAATTTGAGGCGCTGCAGACATGGAATT TGTATAAATGATATCCTTCTTCAAGT...GTTTGGCTCTTGAATTTGAGGCGCTGCAGACATGGAATT TGTATAACGATATCCTTCTTCAAGT...GTTTGGCTCTTGAATTTGAGGCGCTGCAGACATGGAATT	Hsap NM_001618 i22 Mmus NM_007415 i22 Rnor NM_013063 i22	11 1 0 OK 11 1 0 OK 11 1 0 OK
1110.005	GAGTTTATCTATCCTTCTCCACAG...ACCTATATGTCCTTACCTGGATACCTACAGCAAG GAGTTTATCTATCCTTCTCCACAG...TTTGGCTCTTGAATTTGAGGCGCTGCAGACATGGAATT GCTTTTCTCTATCCTTCTCCACAG...CCTTACCTGGATACCTACAGCAAG	Hsap NM_002108 i03 Mmus NM_010401 i02 Rnor NM_017159 i02	11 1 1 OK 11 1 1 OK 11 2 1 OK
1110.007	TCAAGAGCTGTATCCTTTCCTGCTG...ATTAATGTTTTCCTTAAACAGTGTCTTGAATTAAGATG TACAAGAGCTGTATCCTTTCCTGCTG...GTAGTTGCTCTCTTGAATTTGAGGCGCTGCAGACATGGAATT TACAAGAGCTGTATCCTTTCCTGCTG...GTAGTTGCTCTCTTGAATTTGAGGCGCTGCAGACATGGAATT	Hsap NM_002689 i03 Mmus NM_008893 i03 Rnor NM_053480 i03	11 1 1 OK 11 3 0 OK 11 2 0 OK
1110.008	GGAAAGATGTATCCTTCTGCGAA...AGCAAGGCTAAAGCCTTAACTGCAACAAGACCTGGACCA GCAAAGACTGTATCCTTCTGCGAA...AGCAAGGCTAAAGCCTTAACTGCGCAACAAGACCTGGACCA GCTAAGGACTGTATCCTTCTGCGAA...AGCAAGGCTAAAGCCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_002754 i08 Mmus NM_011950 i08 Rnor NM_019231 i08	11 1 1 OK 11 1 1 OK 11 1 1 OK
1110.009	GACCTGTTCCCTATCCTTCTGCGCT...CATCCCGACTGCTCTTAACTGCGCAACAAGACCTGGACCA GACCTGTTCCCTATCCTTCTGCGCT...GCTAGTACTGCTCTTAACTGCGCAACAAGACCTGGACCA GACCTGTTCCCTATCCTTCTGCGCT...GCTAGTACTGCTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_002861 i07 Mmus NM_024229 i08 Rnor NM_053568 i08	11 2 1 OK 11 1 2 OK 01 1 2 OK
1110.011	ATCGAGGAATATCCTTCTGCTAGG...TCCTCAGTGGCTCTTAACTGCGCAACAAGACCTGGACCA ATCGAGGAATATCCTTCTGCTAGG...AACCTCAGTGGCTCTTAACTGCGCAACAAGACCTGGACCA ATCGAGGAATATCCTTCTGCTAGG...AACCTCAGTGGCTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_003195 i06 Mmus NM_009326 i06 Rnor NM_057098 i06	11 1 1 OK 11 1 1 OK 11 1 1 OK
1110.012	GAACATCATTGTATCCTTCTAGAA...CTGTGATCTCTCTTAACTGCGCAACAAGACCTGGACCA GAACATCATTGTATCCTTCTAGAA...CCCAAGGCTAAAGCCTTAACTGCGCAACAAGACCTGGACCA GAACATCATTGTATCCTTCTAGAA...CCCAAGGCTAAAGCCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_003951 i09 Mmus NM_011398 i10 Rnor NM_053501 i10	11 1 0 OK 11 1 1 OK 11 1 1 OK
1110.013	ATCTAGTTCTATCCTTCTGACAA...AGCTGCTTAACTCTTAACTGCGCAACAAGACCTGGACCA ACGTGTTCTATCCTTCTGACAA...AGCAATATGCTTAACTCTTAACTGCGCAACAAGACCTGGACCA ACGTGTTCTATCCTTCTGACAA...GACCTTAGCTTAACTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_003968 i06 Mmus NM_011666 i05 Rnor NM_057205 i06	11 3 1 OK 11 1 1 OK 11 2 1 OK
1110.014	TCGAAACACCTATCCTTCTGCTAG...GTCAGCTTCTCTTAACTGCGCAACAAGACCTGGACCA TCGAAACACCTATCCTTCTGCTAG...TTTGGCTCTTGAATTTGAGGCGCTGCAGACATGGAATT TCGAAACACCTATCCTTCTGCTAG...GTCAGCTTCTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_004581 i15 Mmus NM_019519 i15 Rnor NM_031654 i15	11 2 0 OK 11 1 0 OK 11 1 0 OK
1110.015	ACTTTGGCCAATATCCTTCTGAA...AAATATGACCTTAACTGCGCAACAAGACCTGGACCA ACTCTGGCCAATATCCTTCTGAA...AGGATGCTTAACTGCGCAACAAGACCTGGACCA ACTCTGGCCAATATCCTTCTGAA...AAGTGTGCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_004871 i08 Mmus NM_016810 i08 Rnor NM_053584 i08	11 1 2 OK 11 1 1 OK 11 2 1 OK
1110.016	GGATCTTCCGATATCCTTCTGCTAG...TTCCAAAGTAACTCTTAACTGCGCAACAAGACCTGGACCA GGATCTTCCGATATCCTTCTGCTAG...CCCAAGGCTAAAGCCTTAACTGCGCAACAAGACCTGGACCA GGATCTTCCGATATCCTTCTGCTAG...CCCAAGGCTAAAGCCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_004935 i09 Mmus NM_007668 i09 Rnor NM_080885 i09	11 1 0 OK 11 1 1 OK 11 1 1 OK
1110.017	TGCTGCTGTATCCTTCTCCAGGC...GAGGCGAGTTTCTCTTAACTGCGCAACAAGACCTGGACCA TGCTGCTGTATCCTTCTCCAGGC...CAGGCTGCTTCTCTTAACTGCGCAACAAGACCTGGACCA TGCTGCTGTATCCTTCTCCAGGC...GGAATCTCTAGCTCTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_005072 i10 Mmus NM_009195 i10 Rnor NM_019229 i10	11 1 0 OK 11 1 0 OK 11 1 1 OK
1110.018	TTATCACCCTATATCCTTCTACATAG...GTTCTCCATTCCCTTAACTGCGCAACAAGACCTGGACCA TTGAATCTATATCCTTCTACATAG...CTTCCATTTCCTTAACTGCGCAACAAGACCTGGACCA TTCTTCTATATATCCTTCTACATAG...AGCTTGGATTTCTCTTAACTGCGCAACAAGACCTGGACCA TTCAAGATCTATATCCTTCTACATAG...AGCTTGGATTTCTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_005739 i03 Mmus NM_011246 i03 Mmus NM_011246 i03_fixed Rnor NM_019211 i03 Rnor NM_019211 i03_fixed	11 2 1 OK 01 2 2 OK? 11 2 2 OK 01 1 0 OK? 11 1 0 OK?
1110.019	TTGTGACCAATATCCTTCTCAGTCC...GATGTTGGGTTCCCTTAACTGCGCAACAAGACCTGGACCA TTGTGACCAATATCCTTCTCAGTCC...TTGTTGGGTTCCCTTAACTGCGCAACAAGACCTGGACCA TTGTGACCAATATCCTTCTCAGTCC...CATGTTGGGTTCCCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_006105 i13 Mmus NM_144850 i13 Rnor NM_021690 i12	11 2 1 OK 11 2 1 OK 11 2 1 OK
1110.020	CGGGCTGTCTATCCTTCTGCGCT...TTACTTATTTCTCTTAACTGCGCAACAAGACCTGGACCA CCAAAGATTGTATCCTTCTGCGCT...CTTCTCTTCTCTTAACTGCGCAACAAGACCTGGACCA CTTCAAGATTGTATCCTTCTGCGCT...TTCTACTCTTCTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_006214 i01 Mmus NM_010726 i01 Rnor NM_053674 i01	11 1 2 OK 11 1 1 OK 11 1 1 OK
1110.022	TTACATGGCTGTATCCTTCTCATGTA...ATATGTTATTTTCTTAACTGCGCAACAAGACCTGGACCA TTGCATGGCTGTATCCTTCTCATGTA...CTATGTTATTTTCTTAACTGCGCAACAAGACCTGGACCA TTGCATGGCTGTATCCTTCTCATGTA...TCTATGTTATTTTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_014016 i07 Mmus NM_030692 i07 Rnor NM_053798 i07	11 1 2 OK 11 1 1 OK 11 1 2 OK
1110.026	CAACAGAGACTATCCTTCTCAGTCC...TTGGTGTCTGCTTAACTGCGCAACAAGACCTGGACCA CAACAGAGACTATCCTTCTCAGTCC...GTGGCAGTAACTGCGCAACAAGACCTGGACCA CAACAGAGACTATCCTTCTCAGTCC...GTGGCAGTAACTGCGCAACAAGACCTGGACCA	Hsap NM_021213 i03 Mmus NM_08796 i03 Rnor NM_017225 i03	11 1 1 OK 11 1 1 OK 11 2 1 OK
1110.027	GAGTTGATATATCCTTCTCAGTCC...ATCTATTTTCTTAACTGCGCAACAAGACCTGGACCA GAGTTGATATATCCTTCTCAGTCC...ATCTATTTTCTTAACTGCGCAACAAGACCTGGACCA GAGTTGATATATCCTTCTCAGTCC...ATCTATTTTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_022488 i11 Mmus NM_026402 i11 Rnor NM_134394 i10	11 1 1 OK 11 1 1 OK 11 1 1 OK
1110.028	TGAAAGATGTATCCTTCTTAGGCA...TTGGTGTCTTAACTGCGCAACAAGACCTGGACCA TGAAAGATGTATCCTTCTTAGGCA...AGTGTGCTTAACTGCGCAACAAGACCTGGACCA TGAAAGATGTATCCTTCTTAGGCA...TGTAGAGTTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_138957 i02 Mmus NM_011949 i02 Rnor NM_053842 i02	11 1 1 OK 11 2 1 OK 11 1 1 OK
1110.029	GGTACAGACCCTATCCTTCTTAAACGT...CCAAACATTTCTTAACTGCGCAACAAGACCTGGACCA GGTACAGACCCTATCCTTCTTAAACGT...CCGACATTTCTTAACTGCGCAACAAGACCTGGACCA GGTACAGACCCTATCCTTCTTAAACGT...CCGACATTTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_139012 i08 Mmus NM_011951 i08 Rnor NM_031020 i08	11 1 2 OK 11 1 2 OK 11 1 2 OK
1111.003	ATCAAGGGCACTATCCTTCTCAGTCC...AAGCAGCCAGCCCTCTTAACTGCGCAACAAGACCTGGACCA ATCAAGGGCACTATCCTTCTCAGTCC...AGCAGTCTCTTAACTGCGCAACAAGACCTGGACCA ATCAAGGGCACTATCCTTCTCAGTCC...AAGCAGCCAGCCCTCTTAACTGCGCAACAAGACCTGGACCA	Hsap NM_001287 i05 Mmus NM_011930 i05 Rnor NM_031568 i05	11 1 1 OK 11 1 0 OK 11 1 0 OK

1111.006	GAGAGCTGTGTATCCTTGGGTGGT.....TTTACACTCCCTTAACGACAGATATTCAGATTTCGGCCT	Hsap	NM_002613	i04	11	1	0	OK
	GAAGAGCTGTGTATCCTTGGGTGGT.....TCCAATCTCCCTTAACGCAGAAAATTGAGATTTCGGCCT	Mmus	NM_011062	i04	11	1	0	OK
	GAAGAGCTGTGTATCCTTGGGTGGT.....TCCAGTCTCCCTTAACGCAGAAAATTGAGATTTCGGCCT	Rnor	NM_031081	i04	11	1	0	OK
1111.010	AAATCCAACAATATCCTTGGGTGGT.....TTGAAACCAGAGTCCTTAACAAGCATTCAGATATATTCT	Hsap	NM_002880	i13	11	1	0	OK
	AAATCCAACAATATCCTTGGGTGGT.....AAACTGTCAGTTCCTTAACAAGCATTCAGATATATTCT	Mmus	NM_029780	i13	11	1	0	OK
	AAATCCAACAATATCCTTGGGTGGT.....GAAGTGTGAGTTCCTTAACAAGCATTCAGATATATTCT	Rnor	NM_012639	i12	11	1	0	OK
1111.021	CTTCACTAATATCCTTGGGTGGT.....TTGCTCAGCTGGATTCCTTAACGCAGACCTGAAACCT	Hsap	NM_012305	i17	11	1	0	OK
	TCAAACATAATCCTTGGGTGGT.....GTCGCTGGAGTCCTTAATGCACTCACATCGAACTGCG	Mmus	NM_007459	i16	01	3	1	OK?
	CTTCACTAATATCCTTGGGTGGT.....TTGCTCAGCTGGATTCCTTAACGCAGACCTGAAACCT	Rnor	NM_031008	i17	11	2	1	OK
1111.023	TGATACATTATATCCTTGGGTGGT.....TTTTAATAATGCGCCTTGAATCTCTCTACAGATTTCAGC	Hsap	NM_014191	i03	11	1	1	OK
	TGATACATTATATCCTTGGGTGGT.....GACCTGGCTCGCCCTTAACCTCTCTACAGATTTCAGC	Mmus	NM_011323	i02	11	2	1	OK
	TGATACATTATATCCTTGGGTGGT.....GACCTGGCTCGCCCTTAACCTCTCTACAGATTTCAGC	Rnor	NM_019266	i02	11	1	1	OK
1111.024	TATGAGCTAATATCCTTGGGTGGT.....TTGCTCAGCTGGATTCCTTAACGCAGACCTGAAACCT	Hsap	NM_016652	i06	11	1	1	OK
	TATGAGCTAATATCCTTGGGTGGT.....CCGCTCTTTCCTTCACTGCTGCGCTAGTTGTGTGGT	Mmus	NM_028820	i05	11	2	1	OK
	TATGAGCTAATATCCTTGGGTGGT.....GGTGGCTCTTTCCTTCACTGCTGCGCTAGTTGTGTGGT	Rnor	NM_053797	i05	11	1	1	OK
1111.025	CCAGTTACAAATATCCTTGGGTGGT.....TTAAATGTTTCCTTAATCTTTCTTTAGTGAGTATCTT	Hsap	NM_018126	i03	11	2	1	OK
	CCAGTTACAAATATCCTTGGGTGGT.....TAACTGAGGCTTCCTTAATGGCTCTCCAGTGAGTATTTT	Mmus	NM_028975	i04	11	1	1	OK
	CCAGTTACAAATATCCTTGGGTGGT.....TTGAAGGCTTCCTTAATGGCTCTCCAGTGAGTATTTT	Rnor	NM_021671	i04	11	1	1	OK
1111.030	GGAGAAGACTGTATCCTTGGGTGGT.....CAGTTGTATTTCCTCAAGAACTTCCTTAGATATTGATCA	Hsap	NM_139069	i06	11	1	2	OK
	GGAGAAGACTGTATCCTTGGGTGGT.....CAGTTGTATTTCCTCAAGAACTTCCTTAGATATTGATCA	Hsap	NM_002752	i06	11	1	2	OK
	GGAGAAGACTGTATCCTTGGGTGGT.....TAGCTGTGTTTCCTCAAGAACTTCCTTAGATATTGATCA	Mmus	NM_016961	i07	11	2	2	OK
1111.031	AAAGCTCTACAATATCCTTGGGTGGT.....TGGTTGTCATTTCCTTGAACGTCGCCCAGAGTTCTCTCT	Hsap	NM_153273	i03	11	1	0	OK
	AAAGCTCTACAATATCCTTGGGTGGT.....TGGTTGTCATTTCCTTGAACGTCGCCCAGAGTTCTCTCT	Mmus	NM_013785	i04	11	1	1	OK
	AAAGCTCTACAATATCCTTGGGTGGT.....TGGTTGTCATTTCCTTGAACGTCGCCCAGAGTTCTCTCT	Rnor	NM_053316	i04	11	1	1	OK
1111.032	CTGGTCTCAATATCCTTGGGTGGT.....CTACTGAAGATTCCTTACCTCTCTTTAGCTGGAGTCTT	Hsap	NM_153342	i06	11	2	1	OK
	CTGGTCTCAATATCCTTGGGTGGT.....CTACTGAAGATTCCTTACCTCTCTTTAGCTGGAGTCTT	Mmus	NM_144916	i07	11	1	1	OK
	CTGGTCTCAATATCCTTGGGTGGT.....CTACTGAAGATTCCTTACCTCTCTTTAGCTGGAGTCTT	Rnor	NM_139107	i06	11	1	1	OK